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# E v o l D i r

June 1, 2025

M o n t h i n R e v i e w

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## Foreword

This listing is intended to aid researchers in population genetics and evolution. To add your name to the directory listing, to change anything regarding this listing or to complain please send me mail at [Golding@McMaster.CA](mailto:Golding@McMaster.CA).

Listing in this directory is neither limited nor censored and is solely to help scientists reach other members in the same field and to serve as a means of communication. Please do not add to the junk e-mail unless necessary. The nature of the messages should be “bulletin board” in nature, if there is a “discussion” style topic that you would like to post please send it to the USENET discussion groups.

Instructions for the EvolDir are listed at the end of this message.

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### Ankara EcolEvolutionaryBiology Jul9-11

Dear colleagues,

We are pleased to inform you that the abstract submission deadline for the 11th Ecology and Evolutionary Biology Symposium (EEBST2025) has been extended to 31 May 2025. We encourage all researchers to take advantage of this extension and submit their abstracts via our website: <https://eebst.ekoevo.org>. The symposium will take place from 9-11 July 2025 at Hacettepe University, Ankara, Türkiye, and is co-organized by Hacettepe University and the Ecology and Evolutionary Biology Society of Türkiye (EkoEvo). Key dates related to registration and notifications have also been updated; please refer to the website for the latest information.

We are proud to host the following plenary speakers: Dr. Natália Martínková - \*Genome polarization: Tracing the threads of hybridization and evolutionary flux\* Dr. Jalil Noroozi - \*Plant biodiversity and biogeography of the high mountains of the Irano-Anatolian Biodiversity Hotspot\* Dr. Paraskevi Karachle - \*Non-indigenous species in the Mediterranean Sea: status, impacts and perspectives\*

Several associated events will complement the scientific program of EEBST2025. On 8 July 2025, a mini-symposium on \*the Philosophy of Biology\* (to be held in Turkish) will take place as a joint event. During the

main symposium, we will also host a panel on \*Integrating Biodiversity Knowledge into Conservation Practice\*, a short event on \*Paleobiology and Anthropology\*, and \*the General Assembly of the Ecology and Evolutionary Biology Society of Türkiye\* (EkoEvo). Further details will be announced soon.

We welcome contributions from all areas of ecology and evolutionary biology, including theoretical, empirical, and applied studies. Abstract guidelines and updated schedule details are available on the symposium website.

We look forward to your participation and to welcoming you in Ankara!

Best regards,

Âa>>atay TavÂoano>>lu On behalf of the EEBST2025 Organizing Committee

Mehmet Somel <[somel.mehmet@googlemail.com](mailto:somel.mehmet@googlemail.com)>

(to subscribe/unsubscribe the EvolDir send mail to [golding@mcmaster.ca](mailto:golding@mcmaster.ca))

### CapeTown Biobanking Sep29-Oct3

To all interested in biobanking,

we are excited to announce a joint meeting between 2 highly impactful networks, the GGBN (Global Genome Biodiversity Network) and the International Society for

Biological and Environmental Repositories (ISBER).

The meeting, 'Where Worlds Align: biodiversity and human biobanks. Same, but different' will explore the intersection of science, policy, and best practices in these fields.

When?: Sep 29 - Oct 03 2025 Where?: Cape Town, South Africa

Registration and abstract submission are open: <https://biobanksafrica2025.org/> Please forward this message to colleagues and collaborators you feel may be interested. We look forward to your participation - see you in Cape Town!

Best wishes the GGBN/ISBER 2025 organizing committee

Jonas Astrin Biobank Leibniz Institute for the Analysis of Biodiversity Change (LIB) Museum Koenig

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<https://leibniz-lib.de/en/biobank> <https://www.GGBN.org/> <https://fogs-portal.de> | <https://ggbc.eu> | <http://bolgermany.de> Leibniz-Institut zur Analyse des Biodiversitätswandels Stiftung des oeff. Rechts | Direktion: B. Misof, A. Grueter | Sitz: Bonn

Jonas Astrin <[J.Astrin.ZFMK@uni-bonn.de](mailto:J.Astrin.ZFMK@uni-bonn.de)>

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## Concepcion Chile InvertebrateEvolution Aug10-14

Hi Fellow Evolutionary and Invertebrate Biologists,

I wanted to bring your attention to the upcoming ICIM6 to be held in Concepcion, Chile, 10-14 August. All the information about attending and topics covered can be found on the conference website, <https://icim6.com/>. This is a really exciting meeting where you can see and hear about all the modern techniques used to dig into how animals are built, work, and have evolved.

Hope to see you there, Karen

– Karen Osborn Research Zoologist/Curator of Polychaetes, Peracarids and Plankton Department of Invertebrate Zoology w 202.633.3668 [osbornk@si.edu](mailto:osbornk@si.edu) <http://>

[/orcid.org/0000-0002-4226-9257](https://orcid.org/0000-0002-4226-9257) Mail: Department of Invertebrate Zoology, Smithsonian National Museum of Natural History, MRC-163 P.O. Box 37012, Washington, D.C. 20013-7012 USA

Courier Address: Smithsonian Institution, MR 0163, Natural History, West Loading Dock, 10th and Constitution Ave NW, Washington, D.C. 20560

\*\* Due to my schedule, you may get an email outside of your normal working hours. Please do not feel that you need to respond outside of your normal working hours. \*\*

“Osborn, Karen” <[OsbornK@si.edu](mailto:OsbornK@si.edu)>

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## Edinburgh BiometricsInPlantBreeding Sep15-19

Dear Friends and Colleagues,

We have now opened registration for the 2025 EUCARPIA Biometrics in Plant Breeding Conference. The conference will be in Edinburgh 17-19th September, preceded by an optional AlphaSimR & FieldSimR workshop 15-16th September.

Key dates: \* Abstract submission due: 15th June \* Abstract feedback (talk vs. poster): 30th June \* Early registration closes: 15th July \* Registration closes: 15th August \* AlphaSimR & FieldSimR workshop (limited to 40 spaces): 15-16th September \* Conference: 17-19th September

Please head to <https://highlanderlab.github.io/-EUCARPIA2025BiometricsPlantBreeding> for more information, registration link, and abstract submission.

Edinburgh is very busy with tourists in the month of August (due to the Fringe festival), which also affects accommodation prices in the period of July-August-September. We advise you to organise accommodation as soon as possible!

On behalf of the Edinburgh Organising Group and the International Scientific Board.

With regards!

University of Edinburgh Gregor Gorjanc, PhD The Roslin Institute Professor & Royal Society Indus-

try Fellow Easter Bush GregorGorjanc@Linkedin <  
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Gregor Gorjanc <Gregor.Gorjanc@roslin.ed.ac.uk>

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## Edinburgh Simultaneous Hermaphrodites May 7-8

Dear all,

We have decided to extend registration for the SHOW workshop until March 30th. Please find more information about the workshop below.

\*\*\*\*

Dear all,

We are delighted to announce this year's edition of the Simultaneous Hermaphroditic Organisms Workshop (SHOW) in Edinburgh on the 7th and 8th of May at the King's Buildings campus. This meeting is a forum for researchers studying hermaphroditism to share their findings and plan long-term collaborations. Its relaxed environment encourages early-career researchers to present topics relating to hermaphrodite evolution, including population genetics, gene expression, sexual conflict, mating systems, gamete evolution, and experimental evolution.

Please see our website - <https://show2025.github.io/> - where you can find all the information, including directions. If you'd like to attend, please complete the registration form: <https://docs.google.com/forms/d/e/1FAIpQLSeG6P8U2DV5BBCLxzmMI76FQoB9E6IKkSTIQITQZR4kKx6NJg/viewform>. The deadline for registration is 30th March, and we will let people know if they are accepted in April. It is also possible to attend online. Please note that there is no registration fee. We have space for 50 in-person attendees.

We have included time for discussion in the programme.

The topics have not yet been finalised, so if you have any suggestions then please do not hesitate to submit them on the registration form.

Thanks to sponsorship from the Genetics Society, we will be able to offer a Carer's Award to allow people to attend if they need costs to cover caring responsibilities. If you would like to take advantage of this, please see the registration form. In addition, we are happy to help you find cheaper accommodation if needed; please contact us if you need any advice on this.

We hope to see you soon in Edinburgh. With best wishes from your SHOW 2025 organising team, Elpida Skarlou, Roman Stetsenko, Freya Way, Matthew Hartfield, Chenxi Wang, Fanny Laugier.

Matthew Hartfield Room 1.19 Institute of Ecology and Evolution The University of Edinburgh Ashworth Laboratories Charlotte Auerbach Road Edinburgh EH9 3FL, UK

Tel: +44 (0)131 650 8632 Email: [m.hartfield@ed.ac.uk](mailto:m.hartfield@ed.ac.uk)  
 Web: [hartfieldlab.com](http://hartfieldlab.com) The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336. Is e buidheann carthannais a th' ann an Oilthigh Dh'Àine Àideann, clàraichte an Alba, àireamh clàraidh SC005336.

Matthew Hartfield <[m.hartfield@ed.ac.uk](mailto:m.hartfield@ed.ac.uk)>

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## GfBS Hamburg Systematics May 29-Jun 1

Dear colleagues,

we would like to draw your attention to the GfBS's Annual Meeting 2025 in Hamburg, Germany.

26th Conference of the Society of Biological Systematics (GfBS) 2025

For further information on the conference programme and abstract submission, please visit: <https://www.gfbs-home.de/en/conferences/gfbs-conference> Deadlines: abstract submission ends 25th May 2025 registration deadline is 28th May 2025 ï½

Kind regards

Alexandra Muellner-Riehl

GfBS Board

Alexandra Muellner <muellner.alexandra@yahoo.de>  
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golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

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## HacettepeU Turkey EcolEvolution Jul9-11

We would like to announce the Ecology and Evolutionary Biology Symposium in Turkey (EEBST), which will take place this year on 09-11 July 2025 at the Hacettepe University, Ankara.

EEBST2025 will be the eleventh in a series of international symposia organized annually by the Ecology and Evolutionary Biology Society of Turkey. This year's keynote speakers will be Natálie Martínková (Institute of Vertebrate Biology, Czech Academy of Sciences, Czechia), Paraskevi Karachle (Hellenic Center for Marine Research (HMCR), Greece) and Jalil Noroozi (University of Vienna, Austria). We are pleased to invite oral and poster presentations in all areas of Ecology and Evolutionary Biology. Registration and abstract submissions are now open and the deadline for abstract submission is May 25th, 2025. For further information please visit <https://eebst.ekoevo.org/>. We look forward to seeing you in Ankara. EEBST2025 Organizing Committee (Contact: [eebst@ekoevo.org](mailto:eebst@ekoevo.org))

Sibel Kucukyildirim, PhD Hacettepe University Department of Biology Beytepe Āankaya Ankara 06800 TURKEY

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## NHM London MathStatMolBiol Sep8-9

Dear evoldir community,

We are thrilled to open abstract submission for the \*Mathematical and Statistical Aspects of Molecular Biology (MASAMB) 2025\* meeting, to be held at the \*Natural History Museum, London\*, on \*8-9 September 2025\*. MASAMB 2025 is dedicated to advancing

research on the mathematical, statistical, and computational aspects of molecular biology. The primary focus of the conference is on methodological innovations and theoretical developments. However, we also strongly encourage submissions that feature empirical studies, especially those that highlight methodological challenges, address data complexity, or showcase the practical application and effectiveness of specific methods.

We invite contributions from diverse areas, including but not limited to:

- Evolutionary, Comparative, and Biodiversity Genomics
- Museomics and Ancient DNA Genomics - Phylogenomics and Population Genomics - AI and Machine Learning applications in Molecular Biology

\*Abstract Submission\* We welcome abstract submissions for oral and poster presentations. Please visit the official event page for full details on abstract submission: \*MASAMB Annual Meeting - Natural History Museum <<https://www.nhm.ac.uk/our-science/study/-events/masamb-annual-meeting.html>>\* \*The deadline for abstract submission is 20th of June.\* \*Registration\* will open on \*15th of June\*, and the conference program will be announced on the event webpage later in the summer. Please feel free to forward this announcement to colleagues or anyone who might be interested.

For any questions or further information, feel free to contact us at <[masamb2025@nhm.ac.uk](mailto:masamb2025@nhm.ac.uk)>.

We look forward to receiving your abstracts and seeing you at MASAMB 2025!

Best regards,

The MASAMB 2025 Organizing Committee Natural History Museum, London

Paschalia Kapli, PhD Research Leader and Genomics Theme Leader Natural History Museum Cromwell Road London SW7 5BD U.K.

Paschalia Kapli <[k.pashalia@gmail.com](mailto:k.pashalia@gmail.com)>

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## Online BrainEvolution May28

Join us for the 2nd seminar in The Integrative Biology of Brain Evolution (TIBBE) seminar series. This event brings together 2 outstanding evolutionary neuroscientists who will present their work, followed by an

interactive discussion with the audience.

\*Second TIBBE Seminar of the Series\* \*Topic:\* Linking brain & behavior \*Date:\* \*Wednesday, May 28, 2025\*  
\*Time:\* 7 AM Seattle | 10 AM Baltimore | 3 PM UK | 4 PM Paris/Barcelona/Prague

\*Seminar on Theory in Brain Evolution Research:\* \*How do we better connect behaviours and brain functions?\*

Come join us as \*Robert Barton\* will present on “Mosaic evolution of brains and sensory-motor systems” and \*Susan Healy\* will present on “Measuring cognition and the problem of brain size as a proxy” and lead a lively discussion, hosted by Katja Heuer and Ornella Bertrand.

Sign up here: <https://www.crowdcast.io/c/linking-brain-and-behaviour> Join the TIBBE ESEB special topic network here: [tibble-network.github.io](https://tibble-network.github.io)

Alexandra Allison de Sousa  
<alexandraallisonsousa@gmail.com>

(to subscribe/unsubscribe the EvolDir send mail to [gold-ing@mcmaster.ca](mailto:gold-ing@mcmaster.ca))

## Online SORTEE DeadlineJun2

2025 SORTEE Conference Reminder: Submit Your Content Proposal by June 2nd

Dear Colleague, This is just to remind you that content submissions are still open for the fifth annual SORTEE conference (The Society for Open, Reliable, and Transparent Ecology and Evolutionary Biology). The conference will be held online from

Dear Colleague,

This is just to remind you that content submissions are still open for the fifth annual SORTEE conference (The Society for Open, Reliable, and Transparent Ecology and Evolutionary Biology). The conference will be held online from 15 October 07:00 UTC to 16 October 10:00 UTC to cover all time zones.

To submit a content proposal, please go to: <https://www.sortee.org/upcoming> We accept the following types of proposals:

1) Unconferences: Facilitated discussions of ideas for how to make ecology, evolutionary biology, and related disciplines more open, reliable, and transparent. Facilitation involves moderating the conversation with ideas and examples, but there are no formal presentations.

2) Hackathons: Group projects with well-defined goals (papers, techniques, software, protocols, organizations, etc.).

3) Workshops: Teach tips and tools for producing open, reliable and transparent research practices.

Submissions will close on June 2nd.

The conference is a forum to discuss and develop ideas, while also exploring current practices for advancing research in fields related to ecology and evolutionary biology. If these topics interest you then please consider becoming a member: <https://www.sortee.org/join>. The conference will be FREE for SORTEE members.

You are also welcome to submit a proposal and facilitate your session in a language other than English. We will organise live translation during the conference to support this.

Conference registration will also soon open on the SORTEE webpage:

<https://www.sortee.org/upcoming>. We're also excited to announce that nominations are open for the SORTEE Commendation Awards! These awards celebrate projects that support open, reliable and transparent practices in eco-evo research. Nominations are open until August 15, 2025. Submit a nomination or learn more on the SORTEE Awards website.

For more information on the conference, do not hesitate to contact us at [conference@sortee.org](mailto:conference@sortee.org)

We hope to see you in October.

Sincerely, The SORTEE Conference Committee

SUBMIT CONTENT HERE

2355 State St Ste 101 Salem, OR 97301-4541, USA

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SORTEE Conference Committee  
<[conference@sortee.org](mailto:conference@sortee.org)>

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## Online SORTEE Oct15-16 ProposalsJun2

2025 SORTEE Conference Reminder: Submit Your Content Proposal by June 2nd

Dear Colleague,

This is just to remind you that content submissions are still open for the fifth annual SORTEE conference (The Society for Open, Reliable, and Transparent Ecology and Evolutionary Biology), which will be held virtually in October 2025. The conference will run continuously from 15 October 07:00 UTC to 16 October 10:00 UTC to cover all time zones.

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For more information on the conference, do not hesitate to contact us at [conference@sortee.org](mailto:conference@sortee.org)

We hope to see you in October.

Sincerely, The SORTEE Conference Committee

SORTEE Conference Committee  
<[conference@sortee.org](mailto:conference@sortee.org)>

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## Online ULausanne ReproductiveModes May27

Dear all,

We started a series of seminars on the “Evolution and mechanisms of atypical reproductive modes”. These monthly meetings (each fourth Tuesday) aim to promote the exchange of ideas and feedback on conceptually similar questions approached with different methods and applied to various systems. The format is about 1-hour meetings, with approximately 20-minute presentations followed by discussion.

Andre Pires da Silva (Warwick University) will present on the “Germline-specific genome sequences controlling sex ratios in the nematode *Auanema*” for our next meeting, Tuesday, May 27th at 1pm (UTC+0, check your time zone).

Link to calendar and Zoom : <https://tinyurl.com/y35rykj3> To subscribe to our mailing list : [https://sympa.unil.ch/sympa/subscribe/evo\\_repro\\_mailing\\_list](https://sympa.unil.ch/sympa/subscribe/evo_repro_mailing_list)  
Caroline S. Blanc, Luca Soldini & Morgane Massy  
Department of Ecology and Evolution, University of Lausanne

Luca Soldini <[luca.soldini@unil.ch](mailto:luca.soldini@unil.ch)>

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## QMUL London EvoDevo Jul11

Dear all,

We are pleased to announce the support of the Genetics Society for the upcoming UK EvoDevo 2025 symposium, which will happen on July 11th (Friday) at Queen Mary University of London.

This will be a day-long (10 am to 6:30 pm) meeting with two exciting keynote speakers (Edwige Moyroud from the University of Cambridge and Chris Lowe from Stanford University) and plenty of opportunities for oral and poster contributions. Registration is only £15 and will include coffee breaks, a light lunch and drinks for the poster session.

To register, please visit: < <https://eshop.qmul.ac.uk/-conferences-and-events/conferences-events/-conferences-events/uk-evodevo> >

To submit your abstract, go to: < <https://forms.gle/-FKyaFp2TZrCDNi699> >

As always, more information about sponsors, the venue, and the programme is at [londonevodevo.co.uk](http://londonevodevo.co.uk) < <http://londonevodevo.co.uk/> >

Please feel free to share this information with your contacts and within your institutions. We look forward to seeing you all in July!

Best wishes,

London EvoDevo committee

Jose M (Chema) Martin Duran Reader in Organismal Biology Queen Mary University of London School of Biological and Behavioural Sciences Mile End Road. Fogg Building E1 4NS London UK

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## Roscoff France Polyploidy Sep15-19 Reminder

Dear colleagues, We are pleased to announce the organization of a CNRS funded Jacques Monod Conference on “/Evolutionary and ecological genomics of polyploidy in plants:temporal dynamics across scales of biological organization from molecules to ecosystems/” to be held in Roscoff (France), September 15-19, 2025. \*Deadline for registration is 5 may 2025\_\*, and details on the Conference can be found at < <https://www.insb.cnrs.fr/fr/evolutionary-and-ecological-genomics-polyploidy-plants-temporal-dynamics-across-scales-biological> > (English version) < <https://www.insb.cnrs.fr/fr/genomique-et-ecologie-evolutive-des-plantes-polyploides-dynamique-temporelle-differentes-echelles> > (French version)

Best regards, Malika AINOUCHE (U. Rennes, France) & Jonathan WENDEL (Iowa State University, USA)

Malika Ainouche Professeur Emérite, Université de Rennes UMR CNRS 6553 Ecobio Bât 14 A Campus de Beaulieu 35 042 Rennes Cedex (France) <https://ecobio.univ-rennes.fr/evolution-des-genomes-traits-dhistoire-de-vie-et-adaptation> Malika Ainouche <[malika.ainouche@univ-rennes1.fr](mailto:malika.ainouche@univ-rennes1.fr)>

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## Roscoff Speciation Oct20-24 Reminder

Dear all,

A quick reminder: the registration deadline for the Jacques Monod Conference “A Multidimensional View of Speciation: Bridging Micro- and Macroevolution”, to be held in Roscoff from October 20 to 24, 2025, is June 6.

All practical and scientific information is available



here: <https://cjm.sb-roscoff.fr/en/conference/-multidimensional-view-speciation-bridging-micro-and-macro-evolution> Registration includes 1) accommodation, 2) on-site meals, and, of course, 3) access to all scientific sessions.

Invited speakers: Stuart BAIRD (Czech Academy of Sciences, Brno, Czech Republic) Nicolas BIERNE (Université de Montpellier, Montpellier, France) Roger BUTLIN (University of Sheffield, Sheffield, United Kingdom) Isobel EYRES (University of Sheffield, Sheffield, United Kingdom) Sophie KARRENBERG (University of Uppsala, Uppsala, Sweden) Jonna KULMUNI (University of Amsterdam, Amsterdam, Netherlands) Amaury LAMBERT (Collège de France, Paris, France) Violaine LLAURENS (Muséum national d'Histoire naturelle, Paris, France) Konrad LOHSE (University of Edinburgh, Edinburgh, United Kingdom) Daniel MATUTE (University of North Carolina, Chapel Hill, USA) Joana MEIER (Wellcome Sanger Institute, Hinxton, United Kingdom) Claire MÂROT (Université de Rennes, Rennes, France) Hélène MORLON (Ecole Normale Supérieure, Paris, France) Craig MORITZ (The Australian National University, Canberra, Australia) Leonie MOYLE (Indiana University, Bloomington, USA) Ludovic ORLANDO (University of Toulouse, Toulouse, France) Catherine PEICHEL (University of Bern, Bern, Switzerland) Daven PRESGRAVES (University of Rochester, Rochester, USA) Dan RABOSKY (University of Michigan, Ann Arbor, USA) Sonal SINGHAL (California State University, Carson, USA) Andrea SWEIGART (University of Georgia, Athens, USA) Maud TENAILLON (Université Paris-Saclay, Gif-sur-Yvette, France) John WELCH (University of Cambridge, Cambridge, United Kingdom)

Please feel free to share this information with colleagues, students, postdocs, and anyone who may be interested.

Best regards! The organizers

camille roux <camille.roux@univ-lille.fr>

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## SMBE Houston AntimicrobialPeptides Oct13-15

SMBE Satellite Meeting: Evolutionary Biochemistry of Insect Antimicrobial Peptides

The SMBE Satellite Meeting on Evolutionary Biochemistry of Insect Antimicrobial Peptides will be held at the University of Houston (Texas, USA) on Oct 13-15, 2025. Microbes that cause disease to humans, livestock, crops, and wild species are incredibly diverse and rapidly evolve resistance to existing antibiotic drugs. Naturally occurring insect antimicrobial peptides have tremendous promise to help address the challenge of antibiotic resistance, but realizing this potential requires transdisciplinary collaboration across disciplines including genomics, microbiology, biochemistry, data science, and engineering. The conference will promote growth in this area by bringing together researchers from a variety of disciplines and career stages to understand modes of action and potential applications of insect AMPs as novel antibiotic agents.

Research areas covered by this conference will include: - Phylogenetic and comparative genomics of arthropod antimicrobial peptides - Novel antimicrobials, biomimetics design, and peptide biochemistry - Microbiology, in vitro and in vivo experimentation - Machine learning and data science - Translational research

There will be multiple breakout sessions at the conference, which we intend to use to develop at least one white paper on Insect Antimicrobial Peptides and Antibiotic Drug Design.

The SMBE Satellite Meeting on Evolutionary Biochemistry of Insect Antimicrobial Peptides is FREE to attend, but attendance requires admission following review of your application. Application review begins on July 1, 2025, and will continue on a rolling basis until the deadline of July 14, 2025. Applications from Early Career Researchers and scholars from diverse research areas are highly encouraged. Travel awards are available to support attendance for early career scholars.

Are you interested in the meeting but cannot attend in person? Please consider attending online (also free). Online attendees will be eligible to give talks and will be invited to participate in discussions.

Please visit the meeting website for more information, including application and registration

links: <https://uh.edu/nsm/biology-biochemistry/news-events/smbe-meeting/> Richard Meisel [rpmeisel@uh.edu](mailto:rpmeisel@uh.edu)

“Meisel, Richard P” <[rpmeisel@Central.UH.EDU](mailto:rpmeisel@Central.UH.EDU)>

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## SouthAfrica Palaeontology Nov30-Dec3

Hello, I would like to share information about the next IPC7.

Dear Colleagues,

We are delighted to be hosting the 7th International Palaeontological Congress (IPC7) in South Africa in 2026. This is the second time that this meeting will be held in the global South and the first time in Africa. The meeting will be held during the height of our very pleasant summer season at the Baxter Theatre Complex and the University of Cape Town between the 30 November - 3 December. The venues have the capacity to host hundreds of delegates, both in large rooms and smaller breakaway rooms.

The fossil heritage of South Africa is renown globally for its importance in understanding the history of life on Earth and extends from the very beginnings of life on Earth to the world-famous hominin relatives that have been recovered here. We already have several symposium topics. We are also organising a series of fieldtrips to give delegates a feel for the rich fossiliferous rocks in South Africa that span significant periods of time. Furthermore, delegates attending the IPC7 will have the opportunity to visit important museum collections in South Africa.

We look forward to hosting palaeoscientists from around the world, and we hope to see you in 2026 in Cape Town.

See our web page (<https://ipc7.site/>) and social media for more info (X: @IPC7\_ ; Instagram: @ipc7\_2026 ; Facebook: IPC7 ; Bluesky: @ipc7.bsky.social).

Yours sincerely,

Organizing Committee

“Maria.Eugenia

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Pereyra”

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## Tuscany EcolEvolGenomics Jul13-18

The Gordon Research Conference on Ecological & Evolutionary Genomics will be happening in Tuscany, Italy, this July 13-18th 2025. This year’s meeting includes a fantastic lineup of invited speakers and you could be one of them! See website for details: <https://www.grc.org/ecological-and-evolutionary-genomics-conference/2025/> . Details: The Ecological and Evolutionary Genomics GRC is a premier, international scientific conference focused on advancing the frontiers of science through the presentation of cutting-edge and unpublished research, prioritizing time for discussion after each talk and fostering informal interactions among scientists of all career stages. The conference program includes a diverse range of speakers and discussion leaders from institutions and organizations worldwide, concentrating on the latest developments in the field. The conference is five days long and held in a remote location to increase the sense of camaraderie and create scientific communities, with lasting collaborations and friendships. In addition to premier talks, the conference has designated time for poster sessions from individuals of all career stages, and afternoon free time and communal meals allow for informal networking opportunities with leaders in the field.

As genomic information becomes increasingly accessible across model and non-model organisms, evolutionary and ecological genomics have become essential frameworks to understand how mutation processes, selection and drift shape biodiversity and phenotypes. The 2025 Gordon Research Conference on Ecological and Evolutionary Genomics will highlight recent advances in our understanding of interactions between genomes and their environment, covering a variety of scales over space and time from population studies to comparative genomics, deep evolution, and theoretical models. This conference aims to shed light on how genomic diversity and structure are influenced by ecological interactions and evolutionary processes. Through a series of keynote presentations, panel discussions, and interactive workshops, participants will delve into cutting-edge research on genomic evolution, the role of natural selection in shaping genetic landscapes, and how environmental pressures drive genetic innovation. Attendees will have the unique opportunity to engage with pioneering studies on gene flow, adaptation, and the genetic mechanisms underpinning species resilience and biodiversity. The conference

seeks to foster cross-disciplinary collaborations, pushing the boundaries of our understanding of genomes in the natural world. The conference will include talks that focus on prokaryotic and eukaryotic systems, with comparisons between them providing insights about how evolution is constrained or shaped by each. Co-chairs, Sam Yeaman (University of Calgary) and Irene Newton (Indiana University) invite you to Renaissance Tuscany Il Ciocco, where we are assembling a diverse group of established and early career investigators to discuss their latest work across a wide variety of organisms. A subset of the submitted abstracts will be selected for short talk presentations and a limited number of travel grants will be available. Whether you're a geneticist, ecologist, evolutionary biologist, or a student aspiring to contribute to this vibrant field, the 2025 GRC on Ecological and Evolutionary Genomics promises to be an enlightening experience that will inspire new perspectives and approaches in the study of life's genetic foundations. Join us to participate in creative discussions in an inclusive social and scientific atmosphere, to empower the future research in the field.

Samuel Yeaman <samuel.yeaman@ucalgary.ca>

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## UStAndrews UK SpeciationGenomicsAI Jun24-27

\*\*\* Call for Participation and Abstracts \*\*\*

We are happy to announce the workshop "Short and long timescales in speciation genomics: Machine Learning approaches" (ML Speciation Genomics) to be held on 24th-27th June 2025 at University of St Andrews/Scotland. Please see the program for the lectures and hands-on sessions here

<https://github.com/ckosiol/MLSpeciationGenomics/blob/main/program.md> There is only a few slots left for contributed talks but we will keep the submission for poster abstracts open till the deadline on 2nd June 2025.

\*\*\*About the Workshop \*\*\*

How new species emerge is one of the big questions in evolutionary biology. Speciation genomics investigates the genetic basis of this process. Until recently researchers were only able to sequence a few individuals

at a single time-point. Yet, with the growing affordability of genome sequencing, it is now possible to consider multiple individuals at multiple points in time.

These multiple time-points could include samples from Natural History Museums, they could be multiple generations of a population housed in controlled laboratory environments or diverse samples collected from the wild. This workshop will bring researchers together to make the best use of the new data. We will have introductory lectures, contributed talks as well as hands-on sessions on museum genomics, phylogenomics and machine learning methods.

\*\*\* Important dates \*\*\*

We have conference rates for students of  $\pounds \frac{1}{2}30$  and  $\pounds \frac{1}{2}70$  for all academics and industry participants. Reduced rate conference accommodation can be booked at Agnes Blackadder Hall.

Reduced rate accommodation: 1st June 2025 Registration closes: 2nd June 2025 Conference: 24th- 27th June 2025

For registration use the following link at

<https://www.eventsforce.net/standrews/264/home> For abstract submission, please send an email to: [MLSpeciationGenomics@gmail.com](mailto:MLSpeciationGenomics@gmail.com)

Looking forward to seeing you in St Andrews!

Dr Carolin Kosiol Reader in Bioinformatics Centre for Biological Diversity School of Biology University of St Andrews St Andrews, Fife KY16 9TF, UK

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<https://biology.st-andrews.ac.uk/kosiol-lab/> Carolin Kosiol <[ck202@st-andrews.ac.uk](mailto:ck202@st-andrews.ac.uk)>

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## WoodsHole MobileDNA Aug28-30

To Evolutionary Biologists Interested in Mobile DNA:

The eighth edition of the Mobile Genetic Elements meeting in Woods Hole, MA, USA will take place from Thursday, August 28 to Saturday, August 30, 2025, at the Marine Biological Laboratory (MBL). Registration and abstract submission are available at: <https://www.eventsquid.com/event.cfm?id=3D28372> This meeting brings together experimental and computational

scientists seeking to narrow the gap between the fast-paced discovery of transposable elements in silico and the limited number of experimental models amenable to functional studies of structural, mechanistic, and regulatory properties of transposable elements and their impact on prokaryotic and eukaryotic hosts. The deadline for talk abstract submission is Friday, July 25, 2025. Abstracts submitted after this date will be accepted only as posters. Online registration ends August 7, 2025 at 6 pm EDT. Late registrants can register after this date

by emailing [conferences@mbl.edu](mailto:conferences@mbl.edu), however accommodations are limited. We hope that you'll join us and/or invite your associates to participate. Looking forward to seeing you in Woods Hole in August!

Your 2025 organizers: Blair Paul, Vladimir Kapitonov, Irina Arkhipova, Phoebe Rice, Cedric Feschotte

[iarkhipova@mbl.edu](mailto:iarkhipova@mbl.edu)

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### Angers France BeetleAdaptation

Dear all,

We are pleased to announce a fully funded 3-year PhD position on the topic: "The role of olfaction and feeding plasticity in resource exploitation by carabid beetles in relation to crop pest regulation."

The position is based at the IGEPP research unit (INRAE / Institut Agro / University of Rennes) in Angers, France , and will be supervised by Bruno Jaloux, Anne-Marie Cortesero , and Benjamin Carbonne .

This PhD is funded by the PARSADA ARDECO project and Institut Agro Rennes-Angers , with a gross annual salary of approximately €26,600 .

The expected start date is October 2025 , and the application deadline is June 16th, 2025 . Please find the full position description and application details bellow.

Feel free to circulate this announcement to interested candidates.

Ph D CONTEXT, MISSIONS AND ACTIVITIES: To reduce the use of chemical inputs, biological control is a key ecosystem service that limits pest damage and reduces reliance on pesticides. This service can be enhanced by conserving naturally occurring beneficial insects such as carabids (Carabidae). These diverse and

abundant predators contribute to the regulation of crop pests and weeds by consuming seeds. While the effects of agricultural practices and landscape on carabid communities and their effectiveness are well documented, the role of the biotic context (prey diversity, intraguild interactions, competition) is still underexplored. In particular, studying the foraging behavior and dietary choices of carabids is essential to better understand their role in biological control within agricultural systems.

Many adult carabid species are generalist predators capable of consuming various prey types, including crop pests (insect pests, mollusks) and weed seeds. Their diets range from granivorous to omnivorous to strictly carnivorous, making them widely recognized as beneficial biological control agents. However, carabids also consume neutral prey and other beneficial organisms (e.g., other predators, earthworms, detritivorous arthropods), which serve as alternative food sources. Their food preferences are likely driven by the availability or profitability of exploitable resources and their physiological needs. The choices made when multiple prey types coexist may indirectly influence their pest control effectiveness. Our limited understanding of the trophic strategies of carabids—especially their ability to locate and select resources—accurate prediction of their biological control potential. Advances in molecular tools now allow more precise identification of prey consumed in the field, offering new perspectives to understand their dietary flexibility, whether involving pests, competitors, or other service providers.

The ability of carabids to perceive various food resources in their environment and their capacity to adjust their foraging behavior (adaptive foraging) remain poorly documented. Olfaction appears to play a key role in detecting seeds and animal prey. However, it is still unclear whether olfaction influences choices between multiple simultaneously available resources (pests, weed seeds, springtails, etc.). Moreover, no electrophysiological studies have yet identified which volatile organic compounds (VOCs) are actually detected by carabids at the antenna level. The presence or the perception of an alternative prey via its odors trigger significant behavioral changes, influencing food choices by carabids. For example, detecting an alternative prey might reduce consumption of a less profitable, less abundant, or less accessible pest.

This PhD project aims to deepen our understanding of the resource exploitation strategies of carabids. Specifically, we will assess potential indirect competition between different resources: pests (e.g., aphids), weed seeds, and alternative prey (e.g., springtails, spiders), which are simultaneously present in the field and consumed by carabids. Based on the hypothesis that the

resource exploitation by carabids is odor-mediated but varies with species, dietary type (strict carnivore to granivore), and individual status (sex, size, age, satiation, experience), the PhD will address three main questions:

- Work Package 1 (2025-2026): How do spatial and temporal variations in food resources affect dietary choices and predation in the field across different carabid species? This part will evaluate carabid dietary flexibility at both species and community levels, using data from 60 cereal fields across Europe (BioAware project). It will rely on multiplex PCR molecular data revealing field prey consumption and corresponding prey availability data.
- Work Package 2 (2026-2027): What role does olfaction play in selecting different types of food resources, and which volatile compounds are involved? This part will investigate the role of olfaction in perceiving, locating, and selecting resources. We will (i) characterize

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## BiologyCentre Czech EvolGenomicsAmphizoicProtists

PhD/MSc Position in Evolutionary Genomics of Amphizoic Microbial Eukaryotes

Join our research team to explore the genomic and metabolic underpinnings of a rare and fascinating evolutionary phenomenon amphizoic lifestyle in microbial eukaryotes. We study *Hexamita inflata*, a unique unicellular flagellate (Diplomonada) that thrives both freely in aquatic sediments and inside animal hosts. This project combines fieldwork, single cell transcriptomics, comparative genomics, and experimental evolution to uncover how organisms switch between host-associated and free-living lifestyles an event exceptionally rare in nature.

You will participate in: - Generating and analyzing genomic/transcriptomic data from natural populations and lab cultures - Investigating gene flow, expression patterns, and evolutionary pressures across habitats - Developing and applying cutting-edge methods in single cell biology and experimental evolution



Start date: Flexible (2025). Duration: 4 years.

Ideal candidates will have a background in evolutionary biology, parasitology, bioinformatics, molecular biology, or microbiology. Previous experience with omics data is a plus but not required. A PhD candidate has to hold a Master's degree, be at minimum conversational in English and have good communication and organisational skills.

The position is fully funded. The minimum starting student net income will be ca 1,100 EUR/month sufficient to comfortably cover life expenses in Āeské BudĀ. Additional salary will be negotiated based on skills and results. We expect several articles to be published in the course of the study in high quality journals. Active participation at international scientific conferences will be encouraged and supported.

Our lab is based at the Institute of Parasitology, Biology Centre of the Czech Academy of Sciences, Āeské BudĀ. The PhD/MSc studies will be performed at the Faculty of Science, University of South Bohemia (<https://www.prf.jcu.cz/en/study-at-the-faculty/information-for-phd-students>). The Laboratory of Genomics and Diversity of Protists is a friendly and supportive environment of an international team. Āeské BudĀ is a pleasant and safe mid-sized city of 100,000 people with relatively low living costs, situated in the South Bohemia region, less than 2 hour train ride from Prague. The BC CAS' campus is directly adjacent to the University of South Bohemia with an international student community.

All questions and applications (CV + half-page motivation letter + contact details of 1-2 references) should be sent directly to Jan Brabec.

Jan Brabec, PhD. ([brabcak@paru.cas.cz](mailto:brabcak@paru.cas.cz))

Laboratory of Genomics and Diversity of Protists  
Biology Centre of the Czech Academy of Sciences  
BraniĀovská 31, Āeské BudĀ, 37005 Czech Republic

Brabec Jan <[brabcak@paru.cas.cz](mailto:brabcak@paru.cas.cz)>

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## Bolzano Italy ApplePestModelling

A PhD position is offered at the Free University of Bozen-Bolzano (Italy) in the lab of Hannes Schuler and aims to investigate factors influencing the current out-

break of wooly apple aphids. The position is funded for three years and will start in November 2025.

The wooly apple aphid (*Eriosoma lanigerum*) is a significant pest on apple. These insects feed on the plant's phloem, leading to growths on roots and shoots and weakening of the infested trees. The infestation by the wooly apple aphid and the limited defense strategies pose significant challenges, especially for organic apple growers in South Tyrol. Large differences in wooly apple aphid infestation suggest that there are numerous unknown factors influencing the spread and infestation of this insect. This project aims to identify factors that play a role in the dissemination and infestation of the wooly apple aphid through systematic surveys in practical orchards. The collected data will be analyzed through modeling to identify influencing factors which range from traditional cultivation measures to soil parameters and plant protection measures. We are looking for an enthusiastic candidate with a background in Agricultural or Biological Sciences, Agricultural Biotechnology, Ecology and Evolution. Competences with multifactorial analyses as well as experience with ecological studies and field work are desired. The candidate should have excellent skills in statistics and should have a driver's license to perform field work independently.

The following activities are planned: - Survey in apple orchards - Analysis of phenological, physiological as well as soil composition data - Multifactorial analysis of different parameters

The Free University of Bozen-Bolzano is located in one of the most fascinating European regions, at the crossroads between the German-speaking and Italian cultures. Its trilingualism in teaching and research, its high level of internationalisation as well as an ideal study environment guaranteed by its excellent facilities are some of the reasons why unibz regularly reaches top positions in national and international rankings.

The Schuler lab is member of the newly funded Competence Centre for Plant Health, a joint institution which consists of several research groups in the field of Biology, Agricultural Sciences and Engineering <https://www.unibz.it/en/home/research-competence-centre-plant-health> We are a young and dynamic research group studying various aspects of insect-microbe interactions in a collaborative atmosphere <http://hshchuler.people.unibz.it> General requirements for the position: Master's degree (or close to completion) in Agricultural or Biological Science or related field. Moreover, a B2 level (or higher) certificate of English is required. Deadline for applications is 11.06.2025 (noon).

All documents for the application procedure can be



found here: <https://www.unibz.it/en/faculties/-agricultural-environmental-food-sciences/phd-mountain-environment-agriculture/> For informal inquiries, and for questions about the hiring process, please contact Hannes Schuler [hannes.schuler@unibz.it](mailto:hannes.schuler@unibz.it)

Prof. Hannes Schuler Competence Centre for Plant Health Faculty of Agricultural, Environmental and Food Sciences Free University of Bozen-Bolzano Universitätsplatz 5 I-39100 Bozen-Bolzano Tel: +39 0471 017648 <tel:+390471017648> <http://hschuler.people.unibz.it> Schuler Hannes <Hannes.Schuler@unibz.it>

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## Bolzano Italy Parasitoids Stinkbugs

A PhD position is offered at the Free University of Bozen-Bolzano (Italy) in the lab of Hannes Schuler. The position is in close collaboration with the entomology group at the Research Centre Laimburg and aims to investigate the impact and adaptation of non-native stinkbugs parasitoids. The position is funded for three years and will start in November 2025.

The research project is part of the long-term monitoring of the effects of the release of the parasitoid *Trissolcus japonicus* on the Asian Stinkbug (*Halyomorpha halys*) and native stink bug species in South Tyrol. The main objective is to determine the parasitisation efficacy of *T. japonicus*, evaluating both its impact on the target population and potential effects on non-target species through host-parasitoid interactions. The invasion of *H. halys* has caused severe damage to Italian agricultural important plants since 2004, and is present in South Tyrol since 2019. Traditional control methods have proved insufficient results, leading to the start of a national release programme of its natural antagonist *T. japonicus* in 2020. Field monitoring of stink bug eggs revealed the presence of closed eggs, raising questions about the presence of parasitoid species unable to complete their development. Although, these parasitoids may still contribute to biological control, their identification is important for accurately assessing the effectiveness of the programme and specificity of the biological control agent.

This project aims to identify the factors influencing the adaptation of parasitoids to invasive stink bugs. We

will apply molecular methods to characterize parasitoid species within unhatched eggs. Furthermore, the analysis of interactions between hosts and parasitoids, both autochthonous and allochthonous, will contribute to the understanding of their ecological dynamics.

We are looking for an enthusiastic candidate with a background in Agricultural or Biological Sciences, Agricultural Biotechnology, Ecology and Evolution. Competences with molecular genetic methods, next generation sequencing and bioinformatics as well as experience with ecological studies and field work are desired. The candidate should have excellent communication skills and should be fluent in English.

The following activities are planned: - Sampling of stink bug egg masses in the field - Rearing of insects in the lab - Genetic characterization of unhatched eggs - Analysis of molecular data

The Free University of Bozen-Bolzano is located in one of the most fascinating European regions, at the crossroads between the German-speaking and Italian cultures. Its trilingualism in teaching and research, its high level of internationalisation as well as an ideal study environment guaranteed by its excellent facilities are some of the reasons why unibz regularly reaches top positions in national and international rankings. The Schuler lab is member of the newly funded Competence Centre for Plant Health, a joint institution which consists of several research groups in the field of Biology, Agricultural Sciences and Engineering <https://www.unibz.it/en/home/research/competence-centre-plant-health> We are a young and dynamic research group studying various aspects of insect-microbe interactions in a collaborative atmosphere <http://hschuler.people.unibz.it> The Laimburg Research Centre is the leading research institution for South Tyrolean agriculture and food processing. Our research activities place great emphasis on practical relevance and pursue the goal of increasing the competitiveness and sustainability through a decisive knowledge advantage. We work on concrete solutions for the agricultural practice in our trial fields and in our excellently equipped laboratories, but we also deal with basic research on key topics. Our newly acquired knowledge is passed on directly and via extension services to our stakeholders in order to ensure the fastest possible implementation in practice.

General requirements for the position: Master's degree (or close to completion) in Agricultural or Biological Science, Biotechnology or related field. Moreover, a B2 level (or higher) certificate of English is required.

Deadline for applications is 11.06.2025 (noon).

All documents for the application procedure can be

found here: <https://www.unibz.it/en/faculties/-agricultural-environmental-food-sciences/phd-mountain-environment-agriculture/> For informal inquiries, and for questions about the hiring process, please contact Hannes Schuler [hannes.schuler@unibz.it](mailto:hannes.schuler@unibz.it)  
 Prof. Hannes Schuler Competence Centre for Plant Health Faculty of Agricultural, Environmental and Food Sciences Free University of Bozen-Bolzano Universitàsplatz 5

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## CEFE-Montpellier Evolutionary Genomics And Theory

Hello,

I have \*two\* fully funded PhD opportunities in my lab (to start Oct 2025), with genomics and population genetics theory. This is part of the ERC RegEvol project dedicated to better understand the multifaceted evolutionary consequences of cis and trans regulatory variation.

One is to work on sex-asex transitions with Christoph Haag; see project description, and application instructions here: [bit.ly/4hp1q1A](http://bit.ly/4hp1q1A)

One is to work on allele-specific expression with Sylvain Gli;  $\frac{1}{2}$  min; see project description, and application instructions here: [bit.ly/4iuKLuQ](http://bit.ly/4iuKLuQ)

The PhDs will be based in the GEE < <https://www.cefe.cnrs.fr/en/research/evolutionary-ecology/-genetique-et-ecologie-evolutive-3> > team in CEFE lab in Montpellier, a large and international group of evolutionary geneticists and will interact with several close collaborators

Interested candidates can contact me informally for extra details if needed.

Thanks to spread the word to interested master students!

Thomas Lenormand

Thomas Lenormand CNRS research director PI ERC RegEvol < <https://www.cefe.cnrs.fr/fr/recherche/ee/-gee/800-c/193-thomas-lenormand> > Lab website <

<https://www.cefe.cnrs.fr/en/> > CEFE Lab, Montpellier France

Thomas

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## ILIM AUSTRIA EcoEvoDyn

PhD position at the Research Institute for Limnology (ILIM) in Mondsee, University of Innsbruck, Austria

We are offering a PhD position within a running FWF START project on eco-evolutionary dynamics and admixture at ILIM in Mondsee (<https://www.uibk.ac.at/-limno/index.html.en>) which is part of the University of Innsbruck.

We investigate secondary contact in the context of global change in important aquatic grazers (*Daphnia* spp.) and study the consequences of admixture on eco-evolutionary dynamics on the species, communities and ecosystem level.

The position is planned for 42 months with a possible extension up to a total of 48 months.

Your Project The goal of this PhD project is to characterize phenotypic differences among parental species and their hybrids in the *Daphnia longispina* species complex and to experimentally test the ecological consequences of phenotypic admixture variation in mesocosms. The lab maintains a large collection of unadmixed and admixed isofemale *Daphnia* lines for which whole-genome data is available and which can be used for experimental work to investigate eco-evolutionary dynamics and potential feedback loops. The lab and the University's Research Institute for Limnology (ILIM) in Mondsee are well-equipped to support life history, aquaria and mesocosm experiments.

Your Skills We are seeking a candidate with a pronounced interest in research and evolutionary ecology. Good problem-solving skills, a high degree of self-motivation, independence and the ability to work in a team are essential. Prior experience in any of the following areas will be of advantage but is not strictly required: (i) phenotyping, life-history and/or mesocosm experiments (design, experimentation), (ii) statistical analysis and coding (e.g., R, Python, bash), (iii) genetic data analysis. The work within our international team

and with international collaborators requires proficiency in English.

**Position and Place** The annual gross salary is ~49.320,00 EURO. The contract includes health insurance and 5 weeks of holidays per year. Furthermore, the university has additional attractive offers: <https://www.uibk.ac.at/universitaet/zusatzleistungen/index.html.en> We aim to ensure an excellent working environment in which everyone can contribute their experience, ideas and ways of thinking and we offer and support professional training. Moreover, we strive for cultural and gender equity, diversity, and inclusion for anyone to be involved in this project. Candidates with a broad range of backgrounds, perspectives, and ideas will be welcomed and are encouraged to apply.

The institute (ILIM) has a focus on research on evolutionary ecology in freshwater systems and is located directly at the lake in the market town Mondsee (<https://www.uibk.ac.at/limno/index.html.en>). Mondsee is part of the Salzkammergut region offering beautiful sceneries and many opportunities for outdoor recreation including swimming, hiking, climbing and biking. Mondsee is also close to the city of Salzburg which is renowned for its cultural highlights and offers various opportunities for leisure activities. Lab members preferring this more urban environment commute to work by bus, car or bike.

For more information on the position, the project, the group, the place or the University, please do not hesitate to contact [Markus.Moest@uibk.ac.at](mailto:Markus.Moest@uibk.ac.at).

**How to apply** We are looking forward to receiving your application and we are reviewing on a rolling basis. Please send a single pdf file including a letter of motivation, curriculum vitae, a list of publications (if any) and contact details of two references to [Markus.Moest@uibk.ac.at](mailto:Markus.Moest@uibk.ac.at). Applications should be written in English.

**MÄST Markus**, PhD Research Institute for Limnology, Mondsee, University of Innsbruck Mondseestraße 9 A-5310 Mondsee Austria Tel: +43 512 507-51771 Web: <https://www.uibk.ac.at/limno/personnel/moest/index.html.en> E-mail: [Markus.Moest@uibk.ac.at](mailto:Markus.Moest@uibk.ac.at)

“Möst, Markus Hartmann” <[Markus.Moest@uibk.ac.at](mailto:Markus.Moest@uibk.ac.at)> (to subscribe/unsubscribe the EvolDir send mail to [golding@mcmaster.ca](mailto:golding@mcmaster.ca))

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## LMU Munich Speciation Genomics EyeSizeHeliconius

### PhD: Speciation Genomics of Butterfly Eye Size

We invite applications for a DFG funded PhD position to study the Speciation Genomics of Eye Size Variation in Butterflies. The student will join the Behaviour and Speciation Group < <https://www.evol.bio.lmu.de/-research/merrill/index.html> > led by Prof Richard Merrill at LMU Munich, and is also expected to join the International Max Planck Research School - Biological Intelligence (IMPRS-BI) < <https://imprs-bi.mpg.de/> > .

**APPLICATION DEADLINE:** 31st May 2025 (see below for details of how to apply) Informal enquiries to: [merrill@bio.lmu.de](mailto:merrill@bio.lmu.de)

The project. The major objective of this project is to understand the molecular basis and evolution of eye size variation in tropical *Heliconius* butterflies, and how it may contribute to a barrier to gene flow between species. *Heliconius* butterflies are a classic study organism in evolutionary biology, and rely heavily on vision for foraging and mate choice. We have previously shown that corneal area and ommatidia number vary both within and between species, that this variation relates to visual acuity (the ability to resolve spatial detail), and that it is likely an adaptation to different visual environments (see references below).

Taking advantage of extensive collections of wild-caught butterflies and established genetic crosses, the student will characterize eye size variation within and between species, focusing on *Heliconius melpomene* and its close relatives. The student will use GWAS and QTL mapping techniques to address our overall aim of identifying genetic loci associated with this variation, and then test whether these loci overlap with known reproductive barrier loci (i.e., whether they contribute to speciation). As such, the student will gain experience in both morphological and genomic analysis. They will be encouraged to attend the Workshop on Population and Speciation Genomics < <https://evomics.org/workshops/workshop-on-population-and-speciation-genomics/2025-workshop-on-population-and-speciation-genomics-cesky-krumlov/> >, or a similar training opportunity, as well as present their findings locally and at international conferences. Depending on

interests and progress, the project could be extended to include field experiments in the tropics and/or functional work (e.g., CRISPR-based approaches) etc.

Suggested background reading:

1. Wright, D.S., Rodriguez, J., Ammer, L., Dargatzis K., Kuo C-Y, McMillan W.O., Jiggins, C.D., Montgomery, S.H. & Merrill, R.M. (2024) Selection drives divergence of outer eye morphology in sympatric—*Heliconius*—butterflies < <https://academic.oup.com/evolut/article-abstract/78/7/1338/7670775?redirectedFrom=fulltext> >. *Evolution* 78: 1338-1346
2. Merrill, R.M., Dasmahapatra, K., Davey, J., Dell'Aglio, D., Hanly J.J., Huber B., Jiggins C.D., Joron, M., Kozak K., Llaurens V., Martin S.H., Montgomery S.H., Morris, J., Pinharanda A.L., Rosser N., Thompson M.J., Vanjari, S., Wallbank R.W., Yu, Q. (2015) The diversification of—*Heliconius*—butterflies. What have we learned in 150 years? < <https://onlinelibrary.wiley.com/doi/10.1111/jeb.12672> > *J. Evolutionary Biology* 28: 1417-38.
3. Kittelmann, M. & McGregor, A. P. (2024) Looking across the gap: Understanding the evolution of eyes and vision among insects < <https://onlinelibrary.wiley.com/doi/full/10.1002/bies.202300240> >. *BioEssays* 2300240.
4. Rossi, M., Hausmann, A.E., Alcamí, P., Möst, M., Roussou, R., Van Belleghem, S., Wright, D.S., Kuo, C-Y, Lozano, D., Maulana, A., Melo-Flórez, L., Rueda, G., McMahon, S., Linares, M., Osman, C., McMillan, W.O., Pardo-Diez, C., Salazar, C. & Merrill, R.M. (2024) Adaptive introgression of a visual preference gene < <https://www.science.org/doi/10.1126/science.adj9201> >. *Science* 383: 1368-1373. \*Show-casing the kinds of approaches we take\*.

You. Primarily, we are seeking a self-motivated candidate with strong interest in evolutionary biology/genetics. The student will be expected to work independently, but also part of a team both within LMU and the broader international *Heliconius* community. As such, strong written and oral communication skills, and a proficiency in English are required. Prior experience in (i) morphological analyses, (ii) statistical analysis and coding (e.g., R, Python, bash), (iii) genetic

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

## NatHistMuseum Berlin AvianMuseomics

Fully funded 3-year PhD position at the Museum für Naturkunde Berlin, Germany

The Evolutionary Genomics & Biodiversity research group, led by Dr. Mozes Blom, invites applications for a 3-year fully funded PhD position. We are seeking a creative, collaborative and motivated colleague to join our team. The successful candidate will participate in a large-scale Leibniz funded research project that aims to push the boundaries of museomics and further integrate Natural History Collections in population genomics research. We are therefore looking for an enthusiastic researcher that is keen to undertake an interdisciplinary project that spans the fields of computational biology, genomics and evolutionary biology.

Background: New Guinea is the largest tropical island in the world and well-known for its unique tropical biodiversity. However, with a large mountain range that includes peaks over 4,500 meters, the corresponding elevational gradient has played an important role in the diversification of New Guinean flora and fauna. Previously (e.g. <https://www.nature.com/articles/s41467-021-27858-5>), we have generated whole-genome resequence data and denovo reference genomes for 13 New Guinean bird species to study population connectivity across mountain ranges and many of these samples were sourced from Natural History Collections due to the difficulty of conducting fieldwork in this remote region. In this PhD project, we will expand on this dataset, use long-read sequencing to assemble new genomes and employ a comparative approach to investigate whether species adapted to distinct climatic environments consistently differ in demographic history due to past climate change. Moreover, we will focus on a few key species groups (e.g. Birds-of-Paradise) and characterize hybridization dynamics along altitudinal gradients. This research is embedded within the BirdMORE project and funded by the Leibniz Junior Research Group program.

### Key Information

Start date: Fall 2025 Location: Museum für Naturkunde, Berlin, Germany Duration: 3 years Minimum Qualifications (see link to advertisement for further details):

\* MSc in biological sciences, computer science or related



field \* Background and deep interest in evolutionary biology \* Experience with (population) genomic data \* Familiar with R, Python or other coding languages \* Experience working with HPC clusters \* Excellent knowledge of English (spoken and written)

We offer:

\* A stimulating, collaborative and open research environment \* Access to State-of-the-Art research facilities (incl. in-house laboratories, HPC, etc.) \* A long-standing collaborative network and close involvement (incl. external visits) with researchers at the Naturhistoriska Riksmuseet Stockholm (Sweden) and RIKEN (Japan) \* Healthy work-life balance (incl. 30 days paid leave each year) \* Competitive remuneration corresponding to TV-L (E13) with company pension scheme \* Exciting opportunity to join us in one of the most dynamic, livable and free spirited capital cities of Europe.

Application process: Please apply using the following link <https://jobs.museumfuernaturkunde.berlin/jobposting/-8154f5be04ad4a1a77e0c741dc24fc0e6bd163df0> Application requirements: Please include the following

\* A 1-2 page cover letter detailing your research background and interests \* Your curriculum vitae (CV) \* Academic transcripts and certificates \* Names and contact details of two academic referees

Application deadline: 11.06.2025 (Only shortlisted candidates will be contacted for interviews shortly after this date)

Informal inquiries about the position are welcome and can be directed to Dr. Mozes Blom ([mozes.blom@mfn.berlin](mailto:mozes.blom@mfn.berlin))

Mozes Blom Leibniz Junior Research Group leader Museum für Naturkunde Berlin Invalidenstrasse 43, Berlin

“Blom, Mozes” <[Mozes.Blom@mfn.berlin](mailto:Mozes.Blom@mfn.berlin)>

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## Netherlands AvianMicrobiomesImmunity

\*\*\*\* PhD position: avian reproductive microbiomes and immunity \*\*\*\*

The Rowe Group in the Department of Animal Ecology

at the Netherlands Institute of Ecology (NIOO-KNAW) offers a fully funded PhD position in avian microbiomes and immune function. The PhD candidate will work on an ERC-Consolidator grant project where the overarching aim is to determine whether reproductive microbiomes impact host fitness in wild animals and reveal the role of host genetics and immune functioning in shaping reproductive microbiome variability.

**\*\* Project description \*\*** Animal hosts may be under strong selection to control their microbiota; A host can benefit from monitoring the species in its microbiome and shaping microbiome composition towards a beneficial (or at least neutral) community by promoting or hindering the proliferation of certain taxa. Mounting evidence suggests that the immune system plays a central role in host control of the microbiome, although currently this work is focused primarily on the microbial communities in the gut.

In this project, the PhD will investigate the potential role of the local immune system in shaping (‘controlling’) the ejaculate microbiome of male house sparrows and link variation in the microbiome to sperm quality. They will perform both correlational studies using wild birds and in vitro experiments to test: (a) whether antimicrobial activity in the ejaculate shapes the ejaculate microbiome, and (b) if variation in the microbiome impacts sperm quality. The successful candidate will also be expected to develop additional complementary research questions in line with their own interests.

**\*\* Duties of the position \*\*** The PhD position will involve fieldwork on wild birds to collect samples for analysis of microbiomes, immune function, and sperm quality, as well as performing in vitro studies to experimentally validate the impact of bacteria on avian sperm quality and the impact of antimicrobial proteins on bacterial community growth and composition. The position will also involve laboratory work, including processing of microbiome samples, immune assays, analysis of sperm quality, and bacterial culturing. The successful candidate will also be responsible for bioinformatic and statistical analysis of data, reading and writing scientific papers, supervision of students, and contributing to the scientific life at the Department. As there is scope for the candidate to develop complementary avenues of research, additional skills and tasks may also be required.

**\*\* What are we looking for \*\*** We are looking for a highly motivated, independent, and productive person, who thrives in a collaborative and international environment and is willing to work in the field and the lab and contribute intellectually to the project. The candidate should hold a MSc degree in ecology/evolution, molecu-

lar biology, microbial ecology, or a related discipline by the time of starting the position. The candidate must have excellent communication skills, including writing and presentation of research, and must be fluent in English, as this is the working language of the group.

Prior experience in the following areas is highly desirable: avian field research, immunity, sperm biology, microbiomes, and microbiology. The candidate should have an interest in bioinformatics, be comfortable working with big datasets, and have some experience with R statistical software. Possession of a valid driver's license is preferred.

**\*\* More information \*\*** Informal inquiries can be made to: Melissah Rowe, [m.rowe@nioo.knaw.nl](mailto:m.rowe@nioo.knaw.nl) Information on the Netherlands Institute of Ecology (NIOO-KNAW) and the Department of Animal Ecology can be found at the website: <http://www.nioo.knaw.nl/> . **\*\* Application procedure \*\*** The deadline for applications is June 29, 2025.

For further information and to apply please see: <https://nioo.knaw.nl/en/vacancies/phd-position-on-avian-reproductive-microbiomes-and-immunity> "Rowe, Melissah" <[M.Rowe@nioo.knaw.nl](mailto:M.Rowe@nioo.knaw.nl)>

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## NTNU Norway BiodiversityOfDarkTaxa

PhD Opportunity: Unveiling Dark Taxa at the Department of Natural History, NTNU

The Department of Natural History at the University Museum of NTNU (Norwegian University of Science and Technology) is excited to offer a PhD position in the exploration of Dark Taxa the often overlooked species that represent an under explored frontier in biodiversity research. This unique PhD opportunity invites candidates with innovative research ideas that push the boundaries of evolutionary biology, ecology, and molecular methods to help illuminate the ecological roles and evolutionary trajectories of these enigmatic organisms.

Key Information:

Location: NTNU, Trondheim, Norway

Focus Area: Dark Taxa, biodiversity, evolutionary ecology, and novel molecular or ecological methodologies

Requirements: A strong academic background, a deep interest in evolutionary theory, and a passion for advancing the understanding of poorly understood taxa within ecosystems.

Funding: 3-year PhD position, contingent on the successful selection of your project idea.

How to Apply: Interested candidates should reach out to Dr. Emily Hartop ([emily.hartop@ntnu.no](mailto:emily.hartop@ntnu.no)) to discuss potential research concepts related to Dark Taxa and to receive guidance on developing a robust, innovative project proposal. This position is part of a competitive, open-call process, and the position will be awarded only if your project idea is selected based on its scientific merit and alignment with current research goals.

Deadline for project proposal submission: 15 August 2025

We are looking for motivated, creative, and skilled individuals who are eager to explore evolutionary patterns and ecological dynamics within the understudied, yet diverse, realm of Dark Taxa. This is an exciting opportunity to contribute to transformative research that will expand our understanding of biodiversity through evolutionary lenses.

We look forward to hearing your ideas!

Official job posting: <https://www.jobbnorge.no/en/available-jobs/job/280575/two-phd-candidates-within-cultural-and-natural-history> Department webpage with more information on the open call: <https://www.ntnu.edu/museum/phd-positions-at-the-ntnu-university-museum> Emily Hartop <[emily.hartop@ntnu.no](mailto:emily.hartop@ntnu.no)>

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## StockholmU PlantPhylogeneticsMadagascar

PhD student position on "Reconstructing Madagascar's biome history using plant phylogenetics". You will join my new research group focusing on evolutionary biogeography at the DEEP department of Stockholm University. 4-year job with salary & benefits.

Info & application here: <https://su.varbi.com/en/what:job/jobID:826108/where:4/> General info on doctoral studies at SU: <https://www.su.se/english/-education/top-reasons-to-choose-su/our-courses-and-programmes/phd-studies-at-stockholm-university->



**1.690164** Don't hesitate to contact me for questions!

Jan Hackel

Associate Professor/Universitetslektor Evolutionary and Systematic Botany Department of Ecology, Environment and Plant Sciences (DEEP) Stockholm University < <https://www.su.se/english/profiles/-jaha4643> > < <https://www.su.se/english/research/-research-groups/group-hackel> >

Jan Hackel <jan.hackel@su.se>

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### **TrentU Canada ConservationGenomics**

Graduate Positions - Muskox and Bison Conservation Genomics

Background: The Kyle laboratory, in close collaboration with partner institutions and agencies (e.g., Parks Canada) is working to understand the adaptive resiliency of large northern ungulates in context of rapid environmental change and acute selective pressures from disease. Current study systems include muskox and American bison, where archived and ongoing collections of specimens will be examined, comparing host genomic variation (specifically the immunome) and microbiome variation relative to disease status, stress indicators and other phenotypic data (e.g., body condition metrics). We are recruiting several PhDs and graduate students to assist with this research. There will be some flexibility to adapt projects to candidate interests with opportunities for field and lab work.

Location: Successful candidates will join the Kyle lab group at Trent University in Peterborough, ON, and will have access to networking and training opportunities with collaborators at U. Montreal, U. Calgary, Parks Canada, among other partners and stakeholders.

Qualifications and Eligibility: successful candidates must have a degree(s) relevant to projects described.

Compensation: PhDs: 30-35K CAD/year (with graduate teaching assistantship), MScs 25-28K CAD/year (with graduate teaching assistantship) where additional grants/scholarships available at Trent U. could supplement stipends.

To Apply: Please send an email to Christo-

pherkyle@trentu.ca) including: a brief statement outlining research interests, previous experience and training relating to this project, C.V., and contact information for two references.

Applications will be reviewed as they are received.

Start Date: Summer / Fall 2025, negotiable

Dr. CJ Kyle, Professor

Forensic Science Department Environmental and Life Sciences Bldg Trent University, Peterborough Ontario, Canada, K9J 7B8 christopherky@trentu.ca 705-748-1011 x 7055

Christopher Kyle <christopherky@trentu.ca>

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### **TrinityC Dublin AncientGenomics**

Link title: TrinityCollegeDublin.AncientGenomics

Text: We are seeking highly motivated PhD students for a research project on ancient human and pathogen genomics at the insular edges of Eurasia. For more details about the position, please visit: <https://www.findaphd.com/phds/project/ancient-human-and-pathogen-genomics-at-the-insular-edges-of-eurasia/?p184967> Shigeki Nakagome, PhD School of Medicine Faculty of Health Sciences Trinity College Dublin Tel: +353-1-896-3260 E-mail: nakagoms@tcd.ie

Shigeki Nakagome <NAKAGOMS@tcd.ie>

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### **UAuckland PlantMicrobePollinatorInteractions**

PhD Scholarship - Ecology & Evolution of interactions between floral microbes, pollinators and plant reproductive fitness Supervisors: Dr Manpreet Dhani and Professor Jacqueline Beggs Closing date: 15/05/2025 Location: Manaaki Whenua Landcare Research in Lincoln, New Zealand. Start date: Immediately, upon enrollment via the University of Auckland Background: Flower-

associated microbes can alter the pollination success of the plant, by modifying nectar composition and chemistry. This project is focused on understanding how certain microbes may alter the nectar chemistry of Kowhai (*Sophora* spp.) flower nectar. Kowhai flowers produce a large volume of nectar, which is an especially important resource for birds and insects. We have identified the key microbes that dominate Kowhai nectar. But it remains unknown whether these microbes have any impact on the production of nectar, its quality in the flowers and its consumption by pollinators. Project scope: The student will develop questions investigating the role of floral microbes in shifting the value of Kowhai nectar resources to potential pollinators and whether this affects the reproductive fitness of Kowhai trees. The student will develop new understanding of these multi-partite interactions to contribute to the growing body of research on the ecology and evolution of the role microorganisms play in mediating pollination. Qualifications & skills: The applicant should hold a first class honours degree, or Masters in Biological Sciences or Microbiology, with a strong background in Ecology or Evolutionary Biology. The applicant should have skills in microbiology, ecology, biochemistry, statistics and competent with the use of R and other analytical environments. The candidate satisfies the PhD enrolment requirements as described here: <https://www.auckland.ac.nz/en/-study/applications-and-admissions/apply-now.html> Personnel specifications: The applicant should be curious, self-driven and able to work effectively independently and in a team environment. The applicant is able to disseminate their research in written and spoken English, effectively and communicate with others well. Proven ability to conduct and publish research, experience with field work and/or lab work, sterile methods or basic molecular methods (DNA extraction, PCR, genome resequencing) are desirable. The applicant will work collaboratively with scientists, technicians, postdocs and While this position is open to international applicants, preference will be given to candidates already residing in NZ with valid permission to work or study. Stipend: Tax-free stipend of NZ\$35,000 per annum for 3 years and PhD fees are covered. Additional support towards research operating expenses available. How to apply: Applications should include evidence of qualifications and research experience, together with a curriculum vitae and contact details of two academic referees who can be contacted. Applications should be supported by a cover letter that states a) why you are interested in continuing your studies to obtain a PhD; b) what specific aspects of this particular PhD attracted you; c) how your qualifications and experience would map onto the proposed research; and d) your GPE as calculated here: <https://www.gpecalculator.auckland.ac.nz/>. Please email com-

plete applications to [dhamim@landcareresearch.co.nz](mailto:dhamim@landcareresearch.co.nz) before 15th May 2025. Preferred candidates would then need to apply to study at the University of Auckland and meet the institutional criteria for entry prior to the scholarship being confirmed. Contact: All enquiries may be directed to Manpreet Dhama [dhamim@landcareresearch.co.nz](mailto:dhamim@landcareresearch.co.nz)

Manpreet Dhama

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## UCollege London EvolutionProjects

For those who wish to go on to do a PhD in an evolutionary focused topic, choose to complete a year-long Masters by Research (MRes) project in The Centre of Life's Origins and Evolution at University College London, UK.

We are at the forefront of research focusing on understanding the processes that govern organismal evolution across the tree of life, from deep time, through to understanding how biodiversity evolves in the Anthropocene. Research labs offer projects to students using an array of approaches, from statistical and theoretical methods, through data science, modelling and deep learning to high-throughput experimental approaches, genomics tools, and palaeobiology.

Examples of research topics covered by this stream include (but are not limited to) the following themes:

§Origin of life, bioenergetics and paleoenvironments (Pr. Nick Lane, Pr. Bridget Wade, Dr. Florencia Camus)

§Origin of multicellularity and major evolutionary transitions in plants, animals and protists (Pr. Chris Thompson, Pr. Max Telford)

§Role of hybridisation and whole genome duplication in evolution (Pr. Duncan Greig, Dr. Ferdinand Marlétaz)

§Origin and evolution of sex, altruism and parental care (Pr. Max Reuter, Dr. Florencia Camus, Dr. Rahia Mashoodh, Pr. Chris Thompson)

§Patterns of diversification across the tree of life using molecular phylogeny and fossils (Pr. David Murrell, Pr. Julia Day, Pr. Hernan Burnano, Dr. Stephen Pates)

§Dynamics of microbial populations (Pr. Wenying Shou)

§Emerging of biological complexity and novelty through evolution of development (Pr. Paola Oliveri, Dr. Ferdi-

nand Marlétaz).

You can choose an evolutionary topic in the most relevant research group and spend the year developing advanced research skills. The course structure closely matches that of a first year PhD and helps you develop the generic and specialised skills to launch your research career. More details can be found here <https://www.ucl.ac.uk/biosciences/mres-biosciences/evolution-and-origins-life-stream> With the evolutionary programme being part of the umbrella MRes Biosciences the overview of the course structure can be found here <https://www.ucl.ac.uk/biosciences/mres-biosciences> Details of how to apply are found here <https://www.ucl.ac.uk/prospective-students/graduate/taught-degrees/biosciences-mres> And please make clear in your cover letter that you are interested in the Evolution and Origins of Life stream

Questions on the programme can be directed to either Dr. Ferdinand Marlétaz Email [f.marletaz@ucl.ac.uk](mailto:f.marletaz@ucl.ac.uk) or Professor David Murrell [d.murrell@ucl.ac.uk](mailto:d.murrell@ucl.ac.uk)

Professor David Murrell Centre for Biodiversity and Environmental Research, Department of Genetics, Evolution and Environment, University College London, Medawar Building Gower Street London WC1E 6BT United Kingdom

Programme Lead for MRes Biosciences <https://www.ucl.ac.uk/biosciences/study/masters/mres-biosciences> Personal research website [http://www.homepages.ucl.ac.uk/~ucbtdjm/Site/Murrell\\_Group.html](http://www.homepages.ucl.ac.uk/~ucbtdjm/Site/Murrell_Group.html) Telephone: 020 31087696

Email: [d.murrell@ucl.ac.uk](mailto:d.murrell@ucl.ac.uk)

“Murrell, David” <[d.murrell@ucl.ac.uk](mailto:d.murrell@ucl.ac.uk)>

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## UEdinburgh OnlineBreedingAndGenetics

Dear colleagues (apologies for any double-posting),

We are excited to announce the launch of our new post-graduate online programme in Data-Driven Breeding and Genetics, set to begin in September 2025. This programme is led by academics from The Roslin Institute and the Division of Global Agriculture and Food Systems at the University of Edinburgh.

Our programme is part-time and thus offers flexible learning paths, from individual credit-bearing PPD courses a full MSc, catering to the diverse needs of professionals seeking to upskill in the field without having to leave their current positions.

Full information on the programme and how to apply is available here: [edin.ac/pgt-data-driven-breeding-genetics](http://edin.ac/pgt-data-driven-breeding-genetics)

We would appreciate if you could help us disseminate this information to those that might benefit from it.

For enquiries, you can reach us at [DDBG@ed.ac.uk](mailto:DDBG@ed.ac.uk)

In brief:

This is a globally-unique online programme that will train the next generation of breeders and geneticists in the statistical and computational skills to design and implement sustainable genetic improvement programmes for key aquacultural and agricultural animal and plant species across global food systems, raw material, heat, and power production.

The programme will equip graduates with practical, applied statistical and computational skills to manage, analyse and interpret large, real-world data and address context-specific genetic challenges using specialised skills in genetics, data science, and underpinning technologies.

By bringing together animal and plant species, this programme opens-up career prospects.

By engaging with colleagues in industry and institutions such as ILRI and CTLGH, the programme will give a diverse range of global perspectives and representation of systems across Global North and South and prepare students with key transferable skills valued by employers.

Graduates from this programme will be equipped to address the shortage of data scientists in the Agri-Tech

sector globally and locally, strengthening the pipeline into industry research and development, academia, governmental and non-governmental organisations (GOs and NGOs) amongst others, and will serve as advocates for the importance of coordinated international efforts in tackling global challenges equitably.

Thank you very much for your support with dissemination. Pau

Pau Navarro, PhD, SFHEA My pronouns are she/her Senior Lecturer in Quantitative Genetics and Group Leader Data-Driven Breeding and Genetics programme director The Roslin Institute and the Division of Global Agriculture and Food Systems, University of Edinburgh

The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336. Is e buidheann carthannais a th' ann an Oilthigh Dh'n ?ideann, cl?raichte an Alba, ?reamh cl?raidh SC005336.

Pau Navarro <Pau.Navarro@ed.ac.uk>

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## UFrenchGuiana eDNA AmazonianPlants

Hello everyone,

We are looking for a motivated candidate to apply for the following PhD position: "Development and deployment of innovative environmental genomics approaches for monitoring plant diversity in the Amazon rainforest", based at the University of Guyane (Cayenne, French Guiana).

This is an ambitious, multidisciplinary project combining genomics, fieldwork, and bioinformatics. The research will be carried out in close collaboration with the Universidad Nacional Mayor de San Marcos in Peru. The goal of the project is to develop an environmental DNA (eDNA) method that will enable Amazonian countries to monitor their plant biodiversity over the long term.

The application deadline is Friday, May 30. Mathieu Chouteau Chargé de recherche CNRS USR MIXTE 3456 LEEISA Centre de Recherche de Montabo 275 Route de Montabo 97300 Cayenne CEDEX Guyane Française 0694 40 39 61 ( 5h de moins que la France Métropolitaine) <https://mathieuchouteau.weebly.com/> Remplacer le '#' par 'y' car le mail cnrs filtre.

CHOUTEAU Mathieu <mathieu.chouteau@cnrs.fr>

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## UGeneva SocailBeeGutMicrobes

Fully funded 4-year PhD position at the University of Geneva, Switzerland

The Microbiota-gut-brain axis and behaviour laboratory at the Department of Genetics and Evolution, led by Dr. Joanito Liberti, invites applications for a PhD position. We are seeking a creative and collaborative scientist to join our dynamic, interdisciplinary team to explore the interplay between gut symbionts, neurophysiology, and behaviour in bees.

Background: Our research investigates the bi-directional communication between the gut microbiota and animal behaviour, aiming to uncover the proximate mechanisms and evolutionary significance of microbiota-host interactions. We work across different social bee species to understand how microbes influence behavioural complexity in animal societies.

Research focus: The project will be developed in line with the successful candidate's interests and skills. Possible directions include investigating the role of the gut microbiota in regulating bee neurophysiology and behaviour, building on our recent work (see Liberti et al. (2022) Nature Ecology & Evolution, <https://www.nature.com/articles/s41559-022-01840-w>; Liberti et al. (2024) mBio, <https://journals.asm.org/doi/10.1128/mbio.01034-24>), or exploring how sociality shapes microbiome dynamics. These studies can be complemented by analyses of the underlying molecular mechanisms (e.g., using microscopy, metagenomics, metabolomics, transcriptomics, proteomics and/or epigenomics).

Start date: between September and December 2025.

Qualifications: - MSc in evolutionary biology, behavioural ecology, microbiology, molecular biology, or a related field - Experience in experimental design and behavioural studies - Knowledge of NGS technologies and associated bioinformatics pipelines - Familiarity with R, Python and/or Bash, and Linux operating systems - Skills in statistical data analysis and scientific writing - Experience working with bees is an advantage but not essential

The University of Geneva (UNIGE) is world-renowned for its research and ranks among the top 1% of universities worldwide. We offer an attractive research environment and salaries according to Swiss standards.

What we offer: - A friendly and inspiring international research environment - Access to state-of-the-art technologies: automated behavioural tracking, next-generation sequencing, advanced microscopy, and a fully equipped microbiology and molecular biology laboratory - Opportunities for collaboration within UNIGE and with international partners - Access to courses through the PhD Program in Ecology and Evolution (<https://lifesciencesphd.unige.ch/program/ecology-and-evolution>) - Competitive salary according to university regulations

Application process: informal inquiries about the position are welcome. To apply, please send your application package as a single PDF file to Dr. Joanito Liberti at: joanito.liberti[at]unige.ch.

Deadline: the closing date for applications is May 25th, 2025. Shortlisted candidates will be contacted for interviews shortly after this date.

The application should include: - A 1-page cover letter detailing your research interests and relevant experience - Your curriculum vitae (CV) - Academic transcripts and certificates - Names and contact details of two academic referees

By joining our team, you will contribute to cutting-edge research on the proximate and ultimate mechanisms linking gut microbes, brain function, and behaviour in animals. We look forward to receiving your application!

Joanito Liberti <Joanito.Liberti@unige.ch>

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## ULille France SpeciationInSilene

Two PhD  $\frac{1}{2}$  positions are available in the university of Lille (France), in Evo-Eco-Paleo lab. PhD will start on  $\frac{1}{2}$  Oct. 2025 for a duration of 3 years.

- the first subject < [https://eep.univ-lille.fr/wp-content/uploads/2025/02/-PhD\\_advert\\_eep-TOUZET\\_SeCSSi\\_2025.pdf](https://eep.univ-lille.fr/wp-content/uploads/2025/02/-PhD_advert_eep-TOUZET_SeCSSi_2025.pdf) > concerns the implication of sex chromosomes in reproductive isolation in  $\frac{1}{2}$  the otites section of *Silene*.

- the second subject < [https://eep.univ-lille.fr/wp-content/uploads/2025/02/-PhD\\_advert\\_EEP\\_UGSF\\_Touzet\\_Cenci\\_PIE.pdf](https://eep.univ-lille.fr/wp-content/uploads/2025/02/-PhD_advert_EEP_UGSF_Touzet_Cenci_PIE.pdf) > concerns the study of cytonuclear genetic incompatibilities in *Silene nutans*.

The deadline to apply is April 21st 2025. Interviews will occur in the first week of May 2025.

Best regards, Pascal Touzet

Pascal Touzet Professor Evo-Eco-Paleo, Univ. Lille, UMR-CNRS 8198 tel: 03-20-43-40-32 <https://eep.univ-lille.fr/> Pascal Touzet <pascal.touzet@univ-lille.fr>

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## UManchester PhageEvolution

Title:PhD: How do the interactions between temperate and lytic phages shape microbial communities? (University of Manchester)

Bacteriophages, the viruses that infect bacteria, are the most abundant biological entities on Earth. These phages often compete for the same resources - bacterial hosts -but still find ways to coexist. This is particularly interesting for two types of phages: obligately lytic phages, which infect and kill bacterial cells to release new virions, and temperate phages, which can either follow the lytic pathway or enter a dormant state by integrating into the bacterial genome as a prophage. The dormant prophage maybe at risk if the host is infected by another lytic phage, which would destroy both the



host and the resident prophage. However, other resident prophages may also be activated and kill the host. Such complex interactions likely influence phage ecology and evolution, as evidenced by phages carrying mechanisms to avoid superinfection by other phages. Yet, we have a very limited understanding of phage interactions and their influence on microbial communities.

This project aims to understand how phages, particularly temperate and lytic phages, interact and coexist within bacterial communities. We will combine ecological theory, mathematical modelling, bioreactor experiments, and synthetic engineering to develop a predictive model of phage dynamics. Building on our previous theoretical work, we will develop novel mathematical models that incorporate phage ecology and evolution, then use continuous culture experiments in bioreactors to test and iteratively refine our mathematical predictions. Engineered phages with fluorescent markers and OD measurements will allow us to track prophage and bacterial populations in real-time, while qPCR and plating will provide co-resident prophage and free phage numbers. By iterating between mathematical simulations and bioreactor experiments, we will refine our theory on phage interactions and microbial community dynamics. This research will provide novel insights into the dynamics of phage infections and offer practical tools for manipulating microbial communities, such as fostering healthy microbiomes and managing microbial infections. The results can be applied to human health, conservation, and agriculture/food security.

This project offers an exciting opportunity for interdisciplinary research, where participants will acquire diverse skills, including computational modelling, mathematical theory, microbiological experimentation, machine learning, and synthetic engineering. The successful applicant will be funded (tuition and stipend) by the UK Engineering and Physical Sciences Research Council and by the University of Manchester.

For information on how to apply, please visit <https://www.findaphd.com/phds/project/epsrc-dtp-how-do-the-interactions-between-temperate-and-lytic-phages-shape-microbial-communities/?p185126>. If you have questions, email the advisory team at [claudia.igler@manchester.ac.uk](mailto:claudia.igler@manchester.ac.uk) (Claudia Igler), [katharine.coyte@manchester.ac.uk](mailto:katharine.coyte@manchester.ac.uk) (Kat Coyte), and/or [tucker.gilman@manchester.ac.uk](mailto:tucker.gilman@manchester.ac.uk) (Tucker Gilman).

R. Tucker Gilman (he/him)

Department of Earth and Environmental Sciences University of Manchester Office: C.1249a Michael Smith Building Tel: +44 (0)161 275 1544 Twitter: @Gilman-Tucker Zoom: <https://zoom.us/join/tucker.gilman> Tucker Gilman <[tucker.gilman@manchester.ac.uk](mailto:tucker.gilman@manchester.ac.uk)>

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## UMemphis BearAdaptation

The Puckett Lab in the Department of Biological Sciences at the University of Memphis is recruiting a highly motivated student for a PhD position in Evolutionary Genomics. The Puckett Lab utilizes population and comparative genomics to understand the evolutionary history of bears with a particular emphasis on translating work for conservation and management decision makers. The successful applicant will contribute towards projects on the genomic basis of adaptive traits in bears. Specifically, the project will utilize comparative transcriptomics to investigate tissue-specific gene regulation.

**Required Qualifications:** Academic interests in evolution, genetics/genomics, and/or bioinformatics. Candidates should be organized, persistent, a team-player, and have strong writing skills. Availability to begin graduate school in August 2025.

**Preferred Qualifications:** A Master's degree, 2 years work experience, or a post-bac. Experience analyzing transcriptomic data. Experience working within Unix/Linux or a programming language (R, perl, python, etc).

Students will receive five years of stipend support via TA-ships and tuition waivers. To learn more about the graduate program and intellectual community within the department, visit: <http://www.memphis.edu/biology/> Due to funding constraints, this position is only open to US applicants.

Please email Emily Puckett ([Emily.Puckett@memphis.edu](mailto:Emily.Puckett@memphis.edu)) with application materials (person statement including relevant experience and future goals, CV, and contact information for two references) as a single pdf. Applications will be reviewed on a rolling basis until May 28, 2025 for entrance to the program in Fall/August 2025. The successful applicant will then be asked to fill out the formal University of Memphis application.

Emily E. Puckett, PhD University of Memphis Memphis, TN 38152 <https://puckettresearch.org/> [Emily.Puckett@memphis.edu](mailto:Emily.Puckett@memphis.edu)

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## Umontpellier Two SexualSelectionPlants

A fully-funded three-year position is opened to work on sexual selection in plants with a special focus on pollen-pistil interactions, under the supervision of Dr. Jeanne Tonnabel ( <https://isem-evolution.fr/membre/-tonnabel/> ) in the context of the SEXIPLANTS project funded by the ERC.

Project goals ? Sexual selection is generally thought to apply to all sexually reproducing organisms and should therefore include plants. Yet, general predictions from sexual selection theory remains untested for the plant kingdom. This PhD aims at testing the most fundamental predictions of sexual selection theory, including female choice models (Fisherian and good-genes models) with a special focus on pollen and pistil traits. Indeed, cryptic female choice in plants might stem from simple morphological pistil traits or from the physiology of pistil tissues, which is known to actively provide nutritive and guidance molecules to pollen tubes. The PhD will benefit from a unique material developed for plants: the output of experimentally evolved lines of *Brassica rapa* 'fast plants' which have been maintained for 18 generations in monogamy vs. polygamy. The PhD candidate will study the evolution of pollen and pistil traits in these experimental evolution lines, but also paternity biases induced by those traits and the genetic correlations between them through quantitative genetics.

For whom? We are looking for candidates with a MSc degree in biology (or equivalent) with strong motivation both for understanding and testing general concepts in evolutionary biology and for conducting experimental work. Knowledge on sexual selection and/or plant evolution and experience on experimental evolution/quantitative genetics/paternity analyses would be an advantage but is not required.

Where? The PhD student will join a stimulating working atmosphere comprising enthusiastic researchers working on sexual selection in plants in the context of the SEXIPLANTS project with high collaboration opportunities (Agneil,  $\frac{1}{2}$  euro s Mignot, FrancRousset, Tim Janicke). The PhD student will work at the Institut des Sciences de l'Evolution de Montpellier (ISEM, UMR 5554). Montpellier offers a stimulating scientific environment for evolutionary biologists with many seminars

and opportunities to interact with many renowned scientists. The working language will be English but some notions of French will come in handy in the daily life.

Working contract? The PhD contract will consist three-year contract funded by the ERC SEXIPLANTS led by Jeanne Tonnabel. The gross monthly salary is around 2 200 euros. The contract includes health insurance and 44 days of annual leave.

When? The ideal starting date of PhD would be October 1 st 2025 but starting date is negotiable.

How to apply? All applications must be sent by email to Jeanne Tonnabel ( [jeanne.tonnabel@umontpellier.fr](mailto:jeanne.tonnabel@umontpellier.fr) ) and in parallel submitted to the CNRS platform ( <https://emploi.cnrs.fr/Offres/CDD/UMR5554-JEATON-009/Default.aspx> ) before July 10th. Applications should include 1) a motivation letter describing research interests, relevant experience and motivation for applying to this PhD position, 2) a CV and 3) contact information for two referees.

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A fully-funded three-year position is opened to work on sexual selection in plants with a special focus on its effect on plant fitness, under the supervision of Dr. Jeanne Tonnabel ( <https://isem-evolution.fr/membre/-tonnabel/> ) in the context of the SEXIPLANTS project funded by the ERC.

Project goals ? Sexual selection is generally thought to apply to all sexually reproducing organisms and should therefore also operate in plants. Yet, general predictions from sexual selection theory remain largely untested in the plant kingdom. This PhD project aims at testing one of the most fundamental predictions of sexual selection theory: that both male-male competition and female choice favor individuals of higher genetic quality and thereby positively impacting population fitness. To address this, the project will combine three complementary approaches: (1) experimental evolution, by testing whether plant populations of *Brassica rapa* populations evolved under monogamy vs. polygamy for 20 generations differ in mutational load and abilities to respond to stress; (2) quantitative genetics, by testing whether plant traits related to mates and gametes are genetically correlated with other fitness components, and (3) a meta-analysis quantifying the strength of sexual selection across species and testing for angiosperm-wide associations with demographical trends and plant traits.

For whom? We are looking for candidates with a MSc degree in biology (or equivalent) with strong motivation both for understanding and testing

This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

## UOttawa FungalEpiGenomics

### PhD in Fungal Comparative (Epi)Genomics

A PhD is available in the laboratory of Dr. Nicolas Corradi at the University of Ottawa (ON, Canada).

The PhD position would be fully funded for 4 years, with possibilities of extensions.

The successful applicant will join a fun and inclusive lab supervised by Dr. Nicolas Corradi. The lab is located in the Department of Biology at the University of Ottawa (Ottawa, Ontario, Canada).

**Project:** the PhD or Postdoctoral trainee will help us continue to push boundaries in understanding the complex genetics and genomics of multinucleate plant symbionts called arbuscular mycorrhizal fungi (AMF). In particular, the candidate's work is expected to further highlight the intricate relationships between AMF genomics and those of their hosts through epigenomic analyses. For recent breakthroughs in this area, see representative publications below and our website (<https://corradiab.weebly.com/our-work.html>).

### Application Process:

Generally, we seek someone who is excited about tackling questions that relate to complex genetic systems and genetic interactions between fungal symbionts and their plant hosts and learn new methods. Previous good knowledge of the following areas will be considered assets: Transcriptomics/Comparative genomics, Phylogenomics or Programming skills for the Life Sciences.

A complete application package includes 1) a CV, 2) Cover Letter with a short (half a page) description of past research accomplishments/future goals and 3) the names and e-mail addresses of at least two references. Complete applications can be sent to Dr. Nicolas Corradi: [ncorradi@uottawa.ca](mailto:ncorradi@uottawa.ca). N.B: Applications sent without the complete above-mentioned documents and/or background will not be evaluated.

### Starting date and eligibility

September 1st, 2025 (Flexible). Evaluation of applications starts immediately until a suitable candidate is found. Preference will be given to applications from

Canadian citizens and Permanent residents. However, exceptional International applicants are welcomed to apply.

**Location:** The University of Ottawa is a large, research-intensive university, hosting over 40,000 students and located in the downtown core area of Canada's capital city (<https://www2.uottawa.ca/en>). Ottawa is a vibrant, multicultural city with a very high quality of life (<https://ottawatourism.ca/en>).

Representative Publications and Preprints for the PhD position:

JIN Oliveira, C Lane, K Mugambi, G Yildirim, AM Nicol, V Kokkoris, et al. Analyses of transposable elements in arbuscular mycorrhizal fungi support evolutionary parallels with filamentous plant pathogens. *bioRxiv*.

Sperschneider J. \*, Yildirim Y. \*, Rizzi, Y., Malar C. M., Mayrand Nicol A., Sorwar E., Chen E.C.H., Brauer E.K., Bosnich W., Gutjahr C. and N. Corradi. Arbuscular mycorrhizal fungi heterokaryons have two nuclear populations with distinct roles in host-plant interactions. *Nature Microbiology* (8) 2142-5

Yildirim G. \*, Sperschneider J. \*, Malar MC, Chen ECH., Iwasaki W., Cornell, C. and N. Corradi. Long reads and Hi-C sequencing illuminate the two-compartment genome of the model arbuscular mycorrhizal symbiont *Rhizophagus irregularis*. *New Phytologist*. 223, 1097-1107

Malar M.C., Krüger M., Krüger C. \*, Wang Y., Stajich J.E., Keller J., Chen C.H., Yildirim G., Villeneuve-Laroche M., Roux C.R., Delaux P.M. and Corradi N. The genome of *Geosiphon pyriformis* reveals ancestral traits linked to the emergence of the arbuscular mycorrhizal symbiosis. *Current Biology*. 31, 1570-1577.e

Kokkoris V., Chagnon P.L., Yildirim G., Clarke K., Goh D., MacLean A.M., Dettman J., Stefani F. and Corradi N. Host identity influences nuclear dynamics in arbuscular mycorrhizal fungi. *Current Biology*. 31, 1531-1538.e6

Vasilis V., Dettman J., Dalpé Y., Stefani F. and N. Corradi. Nuclear Dynamics in the Arbuscular Mycorrhizal Fungi. 2020. *Trends in Plant Science* 25 p. 41-48.

Yildirim G., Malar M.C., Kokkoris V. and N Corradi. 2020. Parasexual and Sexual Reproduction in Arbuscular Mycorrhizal Fungi: Room for Both. *Trends in Microbiology* 28 (7), 518-52

Ropars J., Kinga Sêdziewska Toro K. Noel J., Pelin A., Charron P., Farinelli L., Marton T., Krüger M., Fuchs J., Brachmann A., and N. Corradi. Evidence for the sexual origin of heterokaryosis in Arbuscular Mycorrhizal Fungi. *Nature Microbiology* 1(6): 16033, 2016.

Nicolas Corradi

Professor and Chair in Microbial Genomics - Professeur et Chaire en Génomique Microbienne Department of Biology - Département de Biologie University of Ottawa - Université de Ottawa

Room GNN 257 - Phone: 613 562-5800 (ext 6563) - Website: <https://corradilab.weebly.com/> Nicolas Corradi <[ncorradi@uottawa.ca](mailto:ncorradi@uottawa.ca)>

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## UParma PrimateEvolutionaryGenomics

Graduate Position: UniParma. PrimateEvolutionaryGenomics. PhD. ExpressionOfInterest

Do you have a robust background in computational biology applied to evolutionary genomics? Would you be interested in a three-year PhD project in primate population genomics? Will you be willing to moving to Parma, Italy?

If your answers to these questions are three motivated and well justified “Yes”, please get in touch with me (including your CV) for an initial meeting:

[cristian.capelli@unipr.it](mailto:cristian.capelli@unipr.it)

Cristian CAPELLI <[cristian.capelli@unipr.it](mailto:cristian.capelli@unipr.it)>

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## UppsalaU MolecularEvolution

PhD student in Molecular Evolution

Are you interested in working with molecular data, with the support of competent and friendly colleagues in an international environment? Are you looking for an employer that invests in sustainable employeehip and offers safe, favourable working conditions? We welcome you to apply for a PhD position at Uppsala University.

The Department of Cell and Molecular Biology is divided into seven research programs, each focusing on different areas within cell and molecular biology: computational

biology and bioinformatics, microbiology and immunology, molecular biology, molecular biophysics, molecular evolution, molecular systems biology, and structural biology. The scientific foundation of what we do lies in biology, but our research overlaps with other fields such as medicine, computer science, mathematics, chemistry, engineering, and physics. The department has over 200 employees, including around 60 doctoral students. Please read more about our work at <https://icm.uu.se>. The position is placed in the Molecular Evolution program, with main supervisor Jennifer James

**Project Description** This PhD position will be entirely computational, focusing on the large-scale bioinformatic analysis of proteome data from a wide range of existing species. The research will focus on understanding mutational robustness. Mutational robustness is the capacity of individuals within populations to express similar phenotypes despite the existence of underlying genetic variation. The project will uncover how mutational robustness relates to phenotypic diversity, and whether mutational robustness promotes evolvability. The project could also expand in scope to the consideration of DNA data. Further specific projects will be developed collaboratively with the successful candidate, depending on their project findings and research interests.

**Duties** At the start of the project, the successful candidate will create a protein dataset collaboratively with other group members, collecting amino acid sequence data from across multiple fully sequenced genomes. The student will conduct a variety of measures of protein phenotypic diversity, in the form of variation in protein structure and function, using simple measures such as overall hydrophobicity, in addition to modern protein structural prediction techniques.

The student will then be responsible for estimating measures of mutational robustness. These measures could include the relative proportion of amino acid changing mutations per codon, and the proportion of changes that result in a radical versus conservative amino acid change, i.e., what proportion of mutations will lead to an exchange between dissimilar amino acids as opposed to similar amino acids.

To investigate the relationship between phenotypic diversity and mutational robustness, the student will conduct a variety of statistical analyses. Further projects could include assessing whether adaptive substitution rates relate to degree of mutational robustness, and whether levels of genetic diversity relate to levels of phenotypic diversity.

**Requirements**

To meet the entry requirements for doctoral studies, you must: - hold a Master's (second-cycle) degree in a field of biology, or - have completed at least 240 credits in higher education, with at least 60 credits at Master's level including an independent project worth at least 15 credits, or - have acquired substantially equivalent knowledge in some other way.

Candidates must be able to express themselves fluently in spoken and written English. The applicant should have a strong grasp of key concepts in evolutionary biology. The applicant should also have an interest in learning, or previous experience in, computer programming, particularly using languages such as Python. The ideal candidate is driven and a creative thinker, with a passion for discovery. We are looking for a person with excellent communication skills who will thrive in a collaborative environment but is also able to work on their own initiative. We're excited to support you in developing your skills and following your scientific interests.

**Additional qualifications** Prior experience in computational biology, bioinformatics or generally in computer programming is desirable. Experience working in population genetics and evolutionary biology/genomics or proteomics is also desirable. Experience with statistical analyses will be considered advantageous. Rules governing PhD students are set out in the Higher Education Ordinance chapter 5, §§ 1-7 and in Uppsala University's rules and guidelines.

**About the employment** The employment is a temporary position according to the Higher Education Ordinance chapter 5 § 7. Scope of employment 100%. Starting date 2025-05-05 or as agreed. Placement: Uppsala

For further information about the position, please contact: Jennifer James, [jennifer.james@icm.uu.se](mailto:jennifer.james@icm.uu.se).

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## USunshineCoast KoalaGeneticsAndManagement

<https://unisc-cp.enquire.cloud/round/RND-0000049/-894> Measuring success of management strategies of

a threatened species, koalas, in highly anthropogenic landscapes

Complete your PhD on in the areas of conservation genetics, conservation management, landscape ecology, disease (chlamydia), koalas

Open for application 27/5/2025 9:00 AM

Applications Close 13/6/2025 11:55 PM

Summary of the project

The team at Detection Dogs for Conservation, University of the Sunshine Coast, Australia is looking for a wildlife passionate, conservation minded, kind and dedicated PhD candidate to join us for a fully funded project. The ideal candidate would have a strong interest in statistics and genetics ; and enjoy doing field work in urban/semi urban areas (not remote) in Redlands Coast, Australia.

Summary of Position

Activities within the position include:

- Working within the Detection Dogs for Conservation team at the University of the Sunshine Coast (Sippy Downs Campus), a team of ~ 15 with other students and staff - Going in the field to lead weekly koala tracking and scat collection, and assist (drone) or lead (dog) surveys using detection dogs and/or drones, of a population with almost 10 years of long term monitoring data - Engaging the community with new technology and tools for conservation management such as Bluetooth solar-powered ear tags - Doing molecular analyses of non-invasive scat samples - Statistical analyses eg genetics, wildlife hospital data sets - Exploring the field of measuring conservation management success: (How) can we quantify and qualify the success of conservation management strategies?

Possible research chapters include, but are not exclusive to:

What measures are available to monitor koalas conservation status? (focusing on genetic methods, and looking at repeats, sample size, certainty, precision) How well can we measure ecological impact currently - including public datasets (hospital data, citizen science); comparison between ecological field / hospital data? How can citizen help monitoring koalas?

**Ideal Candidate**

Is self motivated has a background in fields of / similar to / including some of: genetics, ecology, zoology, biology, veterinary science has a scientific mindset, adheres to our values of inclusivity, kindness, compassion and equity, and Is competitive, e.g., Honours first class, publication(s), etc.



**Inclusions & Eligibility**

Stipend of \$35 482 per annum - paid in fortnightly instalments. Tax Free for full time students Tuition offset scholarship \$28 000 per annum \$2 000 Allowance for relocation per scholarship conditions Support is for 3 years to align with thesis submission (possible extension in line with relevant policies and procedures)

Include in your application

CV Academic Transcripts Two potential referees short cover letter

The preferred candidate will be invited to apply for PhD program at UniSC and must meet entry requirements to be formally offered scholarship.

For more information

For additional questions contact Romane and Katrin on DDC@usc.edu.au

Social Media links

Facebook - Detection Dogs For Conservation

Instagram - Detection Dogs for Conservation

More Information on the UniSC website:

Detection Dogs for Conservation (University of the Sunshine Coast, Australia)

Dr. Katrin Hohwieler (she/her) Conservation Scientist

90 Sippy Downs Drive, Sippy Downs 4556 m: 0435 350132 | e: khohwie1@usc.edu.au Postdoctoral Research Fellow, University of the Sunshine Coast

Please note: I only work Mondays, Tuesdays, and Wednesdays. Please be patient if I don't respond immediately.

Katrin Hohwieler <khohwie1@usc.edu.au>

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## UZurich Switzerland PopulationGenomics

**Open PhD position in Population Genomics**

A fully funded PhD position is available in the Human Genetic and Cultural Evolution group at the University of Zurich. Our research focuses on reconstructing the demographic history of ancient and modern human populations to understand how various evolutionary pro-

cesses - both biological and cultural - shape genetic and linguistic diversity.

Cultural practices, while fluid and ever-changing, can alter a population genetic landscape by influencing social structures and mating patterns. At the same time, genetic variation provides the foundation for cognition, language development, and cultural behaviors. To explore this complex interplay, our lab investigates fundamental questions, such as: How were early human populations structured? What processes led to the current mosaic of human genetic and linguistic variation? What demographic factors drive language diversification, diffusion, and extinction? How does migration and admixture impact our genomes and languages?

Join our group to investigate the impact of demography in the evolution and diffusion of languages and other cultural traits. The project will involve modelling and the analysis of large datasets, including newly generated genomes. You will have the opportunity to participate in sample collection in Africa and to be involved in the development of new approaches to study the interplay between genetic and linguistic evolution.

I am looking for a student with a strong background in population genetics, genomics, bioinformatics, computational biology, statistics, or related fields, and an interest in linguistic and cultural evolution. Good communication skills in English are required.

As the newly appointed Professor of Genetic and Linguistic Evolution starting at the University of Zurich (UZH) in September 2025, I invite you to work with me and enroll in the PhD Program in Evolutionary Biology (<https://www.evobio.uzh.ch/en.html>). The UZH offers excellent infrastructure and opportunities to expand your scientific and transferable skills. You will be part of an international, diverse, and inclusive community of researchers, and have the support of a PhD advisory committee. Additionally, you will become a member of the National Centre of Competence in Research (NCCR) 'Evolving language', contributing to the Diversification project (<https://evolvinglanguage.ch/-diversification-project/>). In these settings, you will benefit from a highly collaborative and interdisciplinary research environment.

To apply, please send the following documents to [sroliveiraa@gmail.com](mailto:sroliveiraa@gmail.com): - A motivation letter (max. 2 pages) outlining your qualifications, interest in the project, and relevant experience. - A CV including contact details for 2 to 3 referees. - A copy of your Master's thesis, if available.

The application deadline is June 30, 2025. The planned start is October 2025, with the project duration of

four years and a competitive salary following UZH standards ( <https://www.lifescience-graduateschool.uzh.ch/en/application/faq.html#C5>). For questions, do not hesitate to contact me at: [sroliveiraa@gmail.com](mailto:sroliveiraa@gmail.com).

Sandra Oliveira <https://orcid.org/0000-0002-1133-7130>  
Assistant Professor for Genetic and Linguistic Evolution  
(starting September 2025) Department of Evolutionary  
Biology and Environmental Studies University of Zurich  
Sandra Oliveira <[sroliveiraa@gmail.com](mailto:sroliveiraa@gmail.com)>

(to subscribe/unsubscribe the EvolDir send mail to  
[golding@mcmaster.ca](mailto:golding@mcmaster.ca)<<mailto:golding@mcmaster.ca>>)

## UZurich Switzerland SexualSelectionDrosophilaProlongata

We are seeking a highly motivated PhD candidate to investigate how operational sex ratios shape long-term evolutionary adaptations in reproductive strategies. The project leverages *Drosophila prolongata* populations experimentally evolved over 60 generations under male- or female-biased OSR regimes. This work addresses critical gaps in understanding how competition and mate choice drive the evolution of male and female mating strategies in dynamic social environments.

Your responsibilities: This fully funded project of 4 years combines large-scale experimental evolution with cutting-edge deep-learning tools for automated, high-throughput phenotyping of behavioral and morpholog-

ical traits. This approach allows rigorous testing of hypotheses about adaptive benefits of evolved strategies in mixed social contexts.

Your profile: - Master's degree in evolutionary biology, ecology, animal behavior, or a related field - Good knowledge of sexual selection theory and evolutionary ecology - Experience with statistical analysis using R or similar - Enthusiasm for lab-based experimental work using a unique *Drosophila* species - Ability to work independently and collaboratively in an interdisciplinary team - Strong written and verbal communication skills in English

Prior experience with behavioral assays, insect experimentation, or deep-learning is a plus though not essential. We prioritize candidates with a commitment to learning these techniques.

Information on your application: Please submit your application through the following form:

<https://ohws.prospective.ch/public/v1/application/-faede58f-a691-4a13-9d4c-346aac46d0b5?lang=en> Your application should include: - Motivation letter (1-2 pages) describing your expertise and interests, as well as why you see yourself as a good fit for this project - CV with publication list (if available) and contacts of 2-3 referees - Academic transcripts

Interviews will start on 9 June 2025.

Please direct any questions regarding this position to:

Prof. Dr. Stefan Lupold Department of Evolutionary Biology and Environmental Studies University of Zurich-Irchel Winterthurerstrasse 190 8057 Zurich Switzerland

E-mail: [stefan.luepold@uzh.ch](mailto:stefan.luepold@uzh.ch) Web: <https://-www.lupoldlab.net>

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## AarhusU Bioinformatics

Dear all,

We have an open position as Tenure-Track Assistant Professor or Associate Professor in bioinformatics at the Bioinformatics Research Centre (BiRC), Department of Molecular Biology and Genetics (MBG), Aarhus University, Denmark.

Application deadline is June 1, 2025 with an expected start September 1 or shortly thereafter.

<https://international.au.dk/about/profile/vacant-positions/job/tenure-track-assistant-professor-associate-professor-in-bioinformatics-at-aarhus-university-denmark-1> We seek a highly motivated researcher in bioinformatics to complement and expand our current research portfolio and teaching activities. We welcome applicants within all areas of bioinformatics with a strong focus on development of computational and statistical methods, particularly within machine learning and artificial intelligence. The applicant must have earned a PhD degree and have demonstrated excellence in research and scholarship within the field of interest.

Please forward to anybody who might be interested.

Best Regards, Thomas Bataillon

Thomas Bataillon <tbata@birc.au.dk>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

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## GEOMAR Kiel MarineEvolGenomics

The GEOMAR Helmholtz Centre for Ocean Research Kiel, and Kiel University, Germany, jointly invite applications for a 3+3 yr (non tt)

Junior professorship (W1) "Marine Evolutionary Genomics"

The junior professorship is initially for a period of 3 years and will be extended for another 3 years upon successful evaluation. The post is located at the GEOMAR Helmholtz Centre for Ocean Research Kiel

([www.geomar.de](http://www.geomar.de)) and embedded into the research unit "Marine Evolutionary Ecology" (head Thorsten B.H. Reusch).

We are expecting applications from early career researchers with a very good doctoral degree in the area of genetics of aquatic organisms, evolutionary biology, evolutionary genomics or related areas, ideally with a few years of postdoctoral experience. The successful applicant will have in-depth knowledge in evolutionary genomics and bioinformatics and intends to or has already started to develop an independent research line after their doctorate, best demonstrated through excellent scientific publications. The research area should be in an innovative field of marine evolutionary biology and genomics, involving multicellular marine animals, algae or plants (no microbes).

The successful applicant is expected to have deep proficiency in population genetics and ecological genomics, as well as in bioinformatic scripting, which also forms the basis for the associated teaching commitments. Teaching will mainly take place within the Master's program "Biological Oceanography" at GEOMAR.

Highly desirable would be a track record of successful third-party funding acquisition as well as experience in teaching topics such as genetics, genomics, evolutionary biology or marine biology. Experience in supervising students would be advantageous.

We offer support of technical staff and support scientists in marine cultivation and bioinformatics. Through the Kiel Marine Organism Culture Center KIMOCC at GEOMAR (<http://www.futureocean.org/de/kimocc/>), state-of-the-art cultivation facilities are available that allow the combination of evolutionary genomics with experimental work. Preferred access to high-performance computing and the sequencing centre at Kiel University (<https://cega.uni-kiel.de>) is provided.

Applications (curriculum vitae, copies of academic degree certificates, list of publications and third-party funding, short research and teaching perspective (max 2 pages each) should be sent by 6 June 2025 to the Dean, Faculty of Mathematics and Natural Sciences, Kiel University, Germany, in electronic form in a single PDF file to bewerbung (at) mnf.uni-kiel.de

Starting date: 1 October 2025 or later (negotiable)

For more information pls visit the complete position description:

<https://www.geomar.de/en/karriere/job-single-en/-junior-professorship-w1-in-marine-evolutionary-genomics-1> Further informal inquiries can be addressed to: treusch(at)geomar.de

Thorsten Reusch <treusch@geomar.de>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

## Greifswald Germany Biomathematics

Dear colleagues,

We are seeking a highly motivated candidate for an ASSISTANT PROFESSORSHIP IN BIOMATHEMATICS.

So if you know anyone who would be a suitable candidate to join our institute, please don't hesitate to forward this job ad!

Greifswald is one of the biomaths hubs in Germany, research opportunities here are fantastic. Biomathematicians get the great opportunity to also teach the very subject they are passionate about as we offer a unique biomaths study program for our students. Plus, it's of course a bonus to work in a small historic town directly at the Baltic Sea (and yes, we do have a nice beach €).

Knowledge of the German language would be helpful, but is not strictly required.

Details can be found here: <https://www.uni-greifswald.de/universitaet/-information/stellenausschreibungen/professuren/-stellenausschreibung/n/juniorprofessur-w1-fuer-biomathematik-ohne-tenure-track-238641/> If you have any questions, please go ahead and contact me!

Kind regards, Mareike Fischer

Prof. Dr. Mareike Fischer

Biomathematics and Stochastics

Institute for Mathematics & Computer Science Greifswald University Walther-Rathenau-Str. 47 Office 3.15 17487 Greifswald GERMANY

+49 (0) 3834 420 46 43

mareike.fischer@uni-greifswald.de

“Prof. Dr. Mareike Fischer” <mareike.fischer@uni-greifswald.de>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

## KunmingInstZool Multiple Evolution

The Kunming Institute of Zoology in Kunming, China is recruiting senior and junior faculty and postdoctoral fellows across all its research fields, which include evolution, genetics, ecology, and conservation.

We have particular interest in recruiting a senior PI who can lead a team to develop scalable biodiversity monitoring, for both basic and applied science.

Kunming is a very liveable city with the ideal climate combination of high altitude (1900 m) in the subtropics.

To make informal queries regarding applications at the Senior PI and Young Investigator levels, especially from non-Chinese nationals, please feel free to email me at [dougwyu@mac.com](mailto:dougwyu@mac.com).

We will begin assessing applications on 12 August 2025.

I will post this announcement multiple times over the next two months. The formal announcement is below.

Douglas Yu

About KIZ

The Kunming Institute of Zoology (KIZ) is directly affiliated to the Chinese Academy of Sciences (CAS). Located at the head of the Indo-Burma biodiversity hotspot, KIZ is dedicated to research in the fields of evolution, genetics, human disease mechanisms, ecology, and biodiversity conservation. KIZ provides a fertile environment for scientific innovation and vibrant interactions, offering competitive remuneration packages and high-quality training programmes for graduate students and postdoctoral fellows. The Institute currently has 40 research groups and attracts postgraduate students from around the world. It is home to several major research platforms, including the State Key Laboratory of Genetic Evolution & Animal Models, the National Research Facility for Phenotypic and Genotypic Analysis of Model Animals (our primate facility), and the Kunming National High-level Biosafety Primate Research Centre (Level-3 Lab). For more information, see [www.kiz.ac.cn](http://www.kiz.ac.cn) or <http://english.kiz.ac.cn/> KIZ welcomes applications for (1) Senior Principal Investigators, (2) Young Investigators, and (3) Postdoctoral Fellows from interested individuals of all nationalities and ethnicities.

Positions:

1. Senior Principal Investigators To lead large research teams that tackle high-risk/high-reward questions in one or more of the research fields listed above.

Qualifications: You will have made significant contributions in one or more of the research fields listed above, have shown the ability to independently fund and lead a research team, and have demonstrated a high degree of scientific integrity and interest in collaborative research.

Support: Senior PIs will receive full support from KIZ to establish a research team of research technicians, post-doctoral fellows, and graduate students. In addition, KIZ will provide excellent research facilities, attractive start-up funding, and competitive salary, benefits, and housing subsidy.

2. Young Investigators To establish an independent research programme in one or more of the research fields listed above.

Qualifications: 1) Candidates should have a PhD degree in a relevant field. 2) Candidates should have excellent scholastic achievements and exhibit the potential to develop into an independent scientist. 3) Candidates should demonstrate a strong team spirit and a high degree of scientific integrity.

Support: Young investigators will be supported with the resources necessary to establish an independent research programme, including start-up funds, laboratory space, and a salary and benefits, and housing subsidy. A mentorship committee of three senior investigators will provide guidance in research direction and laboratory management.

3. Postdoctoral Fellows To join one of the well-funded research laboratories in KIZ, contributing your expertise in evolutionary biology, genetics, molecular and cell biology, ecology, bioinformatics, and/or statistics.

Qualifications: 1) Candidates should have a PhD degree in a relevant field. 2) Candidates should demonstrate promising scholastic achievements, commitment to a high degree of scientific integrity, and be ambitious and self-motivated. 3) Candidates should have the ability to work both independently and as a team member and are encouraged to carry out independent research projects.

How to Apply (send to [kizfsc@mail.kiz.ac.cn](mailto:kizfsc@mail.kiz.ac.cn)) - Cover letter (please specify your target position) - CV (include birthdate, nationality, and full publication list) - Research proposal (3 pages outlining your vision and alignment with KIZ's research foci) - Contact information for 3 references

Deadline: We will begin assessing applications on 12 August 2025. Ready to advance your career at the intersection of life sciences and global sustainability?

Contact: [kizfsc@mail.kiz.ac.cn](mailto:kizfsc@mail.kiz.ac.cn) Explore: [www.kiz.ac.cn](http://www.kiz.ac.cn) or [english.kiz.ac.cn](http://english.kiz.ac.cn)

The law locks up the man or woman / Who steals the goose from off the common

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at <http://life.biology-mcmaster.ca/~brian/evoldir.html>

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## Marseille 1yr ModellingPopDynamics

POSITION TITLE: Research engineer - modeling population dynamics and connectivity in fragmented landscapes

1-General information - Workplace: IMBE, Aix-en-Provence workplace - Institution: Aix Marseille Université;  $\frac{1}{2}$  - Date of publication: 01/06/2025 - Duration of the contract: 1 year - Hiring date: 01/09/2025 - Working time: 100% of the time - Desired level of study: Engineer diploma or PhD - Desired experience: none

2-Missions The research engineer will join a team that contributes to the modeling of ecological continuities as part of various research projects with an objective of conservation and/or land management. The person will carry out spatially explicit individual-based modeling (via the RangeShifter platform) and graph-based approaches for species representative of various environments. In particular, the person will take part in 1) a fundamental research project on the impacts of landscape planning on the dynamics and genetics of populations of the European red squirrel (*Sciurus vulgaris*) in fragmented landscapes in the south of France; 2) a participative scenario-building and integration project for renaturation actions to reinforce ecological continuities in an area of Ile de France. He/she will ensure the biological relevance of his/her modeling outputs. He/she will write up the results in the form of scientific reports and articles in collaboration with the project teams. He/she may also present his/her results at a scientific conference. Finally, he/she may contribute to the collection of spatial data on red squirrels (e.g. GPS data) currently underway in our team, which will enable the model to be validated.

3-Activities Numerical simulations, data analysis, valorisation of modelling work. 4-Skills Good modelling

skills (spatially-explicit individual-based models) and use of numerical tools. Basic knowledge in population genetics and landscape ecology Good level of scientific English Team work Plus: interest for field work, previous knowledge of RangeShifter.

**5-Context of work** The loss and fragmentation of natural habitats is a major threat to biodiversity. On the one hand, there is a strong consensus that conserving biodiversity requires preserving a large amount of natural habitats, while on the other hand, the spatial configuration (or arrangement) of habitats to conserve biodiversity has been the subject of intense debate since the 1970s. More precisely, for a certain quantity of habitats in a landscape, are there spatial configurations that are really more favourable than others for maintaining biodiversity? This debate is extremely lively in the current literature, with two opposing scientific communities: those who defend the fact that managing the spatial configuration of habitats is essential for conservation versus those who assert that managing the configuration is of little interest and that conservation only requires the preservation and restoration of natural habitats. The two phenomena, habitat loss and fragmentation, are not independent: when the amount of habitat in a landscape decreases, the remaining 'pieces' of habitat become smaller and more widely spaced, making the debate difficult to resolve. Given the high land pressure around the world today, the opportunities to maintain or restore habitats in large quantities are limited. Designing territories to optimise the spatial configuration of habitats and the resistance of the landscape matrix (i.e. the difficulty organisms have in crossing the spaces between habitat areas) appears in this context to be the only option for conserving biodiversity. In this context, the host team of this position is involved in the SCALED (<https://www.scaled-erc.eu>) and FAR (<https://erable.archi.fr/-projets/fictions-danticipation-de-renaturation>) research projects, which respectively aim to: 1) identify the respective roles of habitat quantity and configuration on movements (gene flow) in red squirrels (*Sciurus vulgaris*), 2) develop renaturation scenarios for a dense urban area and understand their impacts on biodiversity.

## 6-Constraints

Some fieldwork sessions or meetings involving potential travelling.

**7-Work details** Gross monthly salary: 2357 euros. Work team: The person will be located at the IMBE, in Aix-en-Provence, France. They will work with Cécile Albert (IMBE) and Aurélie Coulon (MNHN-CESCO and CEFE).

**8-Application** Send a resume and a cover letter CV to Cécile Albert ([cecile.albert@imbe.fr](mailto:cecile.albert@imbe.fr)) and Aurélie Coulon

([aurelie.coulon@mnhn.fr](mailto:aurelie.coulon@mnhn.fr)) by June 21st, 2025.

Aurélie Coulon, PhD Maître de Conférences (Associate Professor) du Muséum national d'Histoire naturelle

Centre d'Ecologie et des Sciences de la Conservation (CESCO) UMR 7204

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## NaturalHistoryMuseum Denmark Paleontology

The Natural History Museum Denmark wishes to appoint a Tenure-track Assistant Professor and Curator in Paleontology with a great vision for natural history museums in a changing world. Duties are divided equally between collection-based research and other museum duties including curation and digitization of relevant parts of the geological collections, research-based teaching and supervision of students, and public engagement/exhibition/interpretation work, and to act as the museum's liaison with relevant Danish natural history communities.

The successful candidate will be expected to establish and develop an externally funded collection-based research program/group and publish in influential journals. We particularly encourage applications from candidates with a research specialization in vertebrate paleontology. The successful candidate will be expected to curate the museums vertebrate paleontology collections (+18.000 specimens) as well as participate in curation of other paleontology collections (primarily 1 million invertebrate specimens).

We value collaboration across disciplines and professions. All applicants are expected to demonstrate interdisciplinary thinking and a commitment to working together to create solutions to global challenges. This also goes for collection work. Curators develop the collections that they are responsible for through research, field work, loan activities, digitization, acting as scientific host for visiting researchers, and increasing accessibility for everyone.

The museum is a member of Geocenter Denmark, a



national center of geoscientific research, education, consulting and innovation that enables close cooperation with other Danish university departments and the Geological Survey of Denmark and Greenland.

All curators at the Natural History Museum Denmark are expected to take a leading role in society as advocates for science and nature, creating impact at all levels while actively promoting the museum's Vision and Values (<https://snm.dk/en/about-museum>). Further details of qualifications required for appointment at the museum are detailed below.

The position is available starting 1 January 2026 or as soon as possible thereafter. The deadline for applications is 18 May 2025, 23:59 GMT+2.

**Qualifications** Applicants at the Tenure-track Assistant Professor level are expected to have an academic record demonstrating the potential to deliver high profile internationally competitive research in the area of specialization. They should be a scientific specialist in one of the collection areas of the museum and have experience with collection-based research. Previous curatorial and university teaching experience would be advantageous but is not a requirement at the time of hiring for Tenure-track Assistant Professors. A documented interest in and a vision for public engagement and community-based activities, such as citizen science, is essential.

#### Assessment of candidates

Assessment of applicants will primarily consider their level of documented, internationally competitive research as well as their curatorial experience and potential to curate one or more of the museum's collections. The ability to attract external funding will be considered together with outreach qualifications. Teaching qualifications are not mandatory, but documented teaching qualifications and teaching experience will be considered. The overall fit for the Natural History Museum will also be considered.

Candidates will have one or more of the following qualifications: - An outstanding reputation for high quality research within paleontology - A proven track record of interdisciplinary research - Scientific expertise that ensures ability to curate both vertebrate and invertebrate paleontology collections held by the museum - Curatorial experience of natural history collections - Experience from a natural history museum or similar - A record of scientific use of museum collections and/or data - A vision for how digital, genomic, and other new technologies will drive advances in natural history science - A proven ability to work at a strategic level - A proven track record of public engagement and cre-

ating impact beyond academia - Experience working on museum exhibitions - Experience in fundraising and ability to grow research funding from external sources - Supportive and performance-oriented people skills and commitment to an inclusive workplace that celebrates diversity and respect for everyone with equality and opportunity for all - A passion for the vision and values of the Natural History Museum of Denmark - Excellent written and oral communication skills - Confidence in ability to provide advocacy for the Museum with multiple stakeholders

About the Natural History Museum Denmark The Natural History Museum Denmark is the Danish national museum for nature. We work to empower citizens to connect with nature with the aim to

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

## NorthernNewMexicoC TeachingEvol LabManager

Northern New Mexico College, Espanola, NM, USA Full time Compensation: \$51,096.00/annually Compensation Type: Exempt Employment Type: Regular Scheduled Weekly Hours: 40

**Position Summary:** Laboratory manager is a position that provides important support to the Department of Biology, Chemistry and Environmental Sciences (BCES) located in the Espanola campus of Northern New Mexico College (NNMC). The lab coordinator will be overall responsible for maintaining teaching laboratories, organizing and conducting laboratory classes, supporting students and coordinating with instructors for laboratory classes. BCES offers laboratory classes in disciplines like Biology, Chemistry and Environmental Sciences.

#### Duties & Responsibilities

Performs general upkeep of laboratory and maintenance of laboratory equipment.

Ensures laboratory safety and verifies that all laboratory participants have completed applicable safety training; monitors activities to ensure compliance to established safety standards and executes appropriate interventions when necessary.



Maintains and/or oversees maintenance and testing of equipment and instruments to ensure accuracy, efficiency, and safety of performance as frequently as needed.

Maintains supplies and equipment inventories; orders laboratory supplies and equipment.

Coordinates with NNMC receiving section for receiving laboratory reagents and/or equipment.

Coordinates with Departmental Admin to process purchase requisition forms and update invoices against purchase orders.

Assists in the annual Dept. budget planning process and regularly monitors laboratory expenditures.

Participates in student recruitment initiatives and/or events, as appropriate to departmental requirements, which may include practical demonstrations, laboratory tours, and/or other associated activities.

#### Minimum Job Requirements:

Bachelor's degree in the field of Biology or, Chemistry or, Environmental sciences. A candidate pursuing a Bachelors can also be considered if they have an Associates degree in the field of Biology or, Chemistry or, Environmental sciences.

#### Knowledge, Skills and Abilities:

Basic knowledge of laboratory supplies and equipment.

Ability to communicate effectively, both orally and in writing.

Basic knowledge of chemical, hazardous waste, industrial hygiene, and/or environmental health standards.

Ability to read and understand equipment manuals and utilize, calibrate, configure and/or troubleshoot laboratory systems and instruments.

#### Physical Demands:

Light to Moderate physical effort which may require lifting up to 40 pounds and/or some standing or walking. Effort applies to no more than two (2) hours per day.

Work environment may involve continuous exposure to physical risks, such as working with chemicals.

Work may involve moderate exposure to unusual elements, such as extreme temperatures, dirt, dust, fumes, smoke and/or unpleasant odors.

Best consideration date: June 30, 2025

**APPLICATION PROCEDURE:** A complete application must include 1) a cover letter addressing how the candidates experiences match the position requirements, 2) curriculum vitae, 3) unofficial transcripts conferring

required or preferred degree, and 4) names, addresses, phone numbers and email addresses of three (3) professional references. Incomplete applications will not be reviewed. Required application materials should be uploaded to the Resume Drop Box of your application.

References will be contacted in conjunction with interviews.

Northern New Mexico College provides all training required by OSHA to ensure employee safety.

EEO STATEMENT: NNMC is an equal opportunity employer.

Apply: [https://chess.wd1.myworkdayjobs.com/-NNMCJobs/job/Northern-New-Mexico-College-Espanola-NM/Lab-Manager\\_JR108710](https://chess.wd1.myworkdayjobs.com/-NNMCJobs/job/Northern-New-Mexico-College-Espanola-NM/Lab-Manager_JR108710) Note to recipient: To protect sensitive information, please refrain from sending Social Security numbers, credit card details, or other confidential data through email. Consider alternative communication methods for such information.

Rhiannon West <rhiannon.west@nnmc.edu>

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## QueenMaryLondon TeachingBioinformatics

The Department of Biology at Queen Mary University of London is looking for a teaching fellow to cover our postgraduate teaching in Bioinformatics and AI for the biosciences. The Biology department at Queen Mary focusses on ecological, evolutionary and developmental processes, at the scale of DNA up to ecosystems. We have particular research strengths in Evolutionary Genetics and Genomics.

This is a fixed term 3-year contract starting as soon as September. We are looking for candidates with a PhD, and a keen interest in teaching and supervising Master research projects in data science applied to biological data, ideally in genomics.

The advert is available at: <https://qmul-jobs.tal.net/-vx/appcentre-ext/brand-4/candidate/so/pm/1/pl/3/-opp/6278-Teaching-Fellow-in-Bioinformatics/en-GB> and will close on June 4th.

Informal inquires can be addressed to [sbbs-doe@qmul.ac.uk](mailto:sbbs-doe@qmul.ac.uk)

Matteo Fumagalli <m.fumagalli@qmul.ac.uk>

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## Stuttgart Germany ConservationGenomics

Dear EvolDir Community,

This is a kind reminder that the application deadline for the Junior Group Leader position in Conservation Genomics at the State Museum of Natural History Stuttgart (SMNS) is approaching less than one month remains.

Please note that the application package has been updated ( <https://tinyurl.com/biodivgen>) to include a 3-page research program contextualizing your past and future research within the SMNS framework. This should be submitted along with your cover letter, CV, list of three academic references (references will be requested after shortlisting), and relevant certificates (Masters and PhD). Applications or updates should be sent to biodiversity@smns-bw.de by June 15th, 2025.

To learn more about the mission of our Biodiversity Monitoring Department, please visit: <https://www.naturkundemuseum-bw.de/en/research/-biodiversity-monitoring> Should you have any questions, please do not hesitate to contact me at ricardo.pereira@smns-bw.de.

For your convenience, I have included the previous announcement below, with the updated application requirements.

Best regards, Ricardo J. Pereira Head of Department of Biodiversity Monitoring State Museum of Natural History Stuttgart and University of Hohenheim

### announcement ### The State Museum of Natural History Stuttgart (SMNS) invites applications for a dynamic Junior Group Leader in Conservation Genomics (m/f/d) to join its newly established Biodiversity Monitoring Department.

Our department focuses on understanding the evolutionary drivers of genomic diversity within species, enabling their persistence amid environmental changes. Leveraging our extensive museum and monitoring collections alongside state-of-the-art genomic methods, we aim to integrate foundational insights from evolutionary genomics with practical conservation outcomes ([https://](https://biodiversitysmns.wixsite.com/rpereiralab)

[biodiversitysmns.wixsite.com/rpereiralab](https://biodiversitysmns.wixsite.com/rpereiralab)). We are committed to creating a hub for dedicated scientists to establish independent research programs exploring the evolutionary processes that shape multiple levels of biodiversity.

This position supports the development of a collection-based research program focused on Conservation Genomics, Museomics, and related fields, bridging the gap between evolutionary genetics research and practical conservation strategies in response to the global biodiversity crisis. The position offers an initial three-year contract with the possibility of renewal, and applications are due by June 15th, 2025.

Position Details: - Lead innovative research that bridges evolutionary genetics and conservation. - Publish impactful manuscripts and secure external funding. - Foster interdisciplinary collaborations within SMNS. - Mentor students and researchers to translate findings into tangible conservation actions.

Requirements: - Ph.D. in Conservation Biology, Genetics, Bioinformatics, or a related discipline. - Strong publication record in relevant fields. - Experience with next-generation sequencing and bioinformatics. - Proficiency in relevant analytical methods and programming languages. - Proficiency in English.

Desirable: - Experience across diverse study systems. - Experience collaborating with conservation agencies. - Proven track record in funding acquisition.

We Offer: - Mentorship for a “Habilitation” degree. - Strong collaborative network with departments at SMNS and the University of Hohenheim. - Leadership role within an interdisciplinary team. - Annual research budget of 5,000 EUR. - Salary according to E13 TV-L.

Applications in English should be submitted as a single PDF (max. 10 MB) including a cover letter, CV, 3-page research program contextualizing your past and future research at the SMNS, three academic references, and relevant certificates to biodiversity@smns-bw.de by June 15th, 2025.

For inquiries, please contact Prof. Dr. Ricardo Pereira at ricardo.pereira@smns-bw.de. SMNS is committed to diversity and encourages applications from all qualified individuals.

More info: <https://tinyurl.com/biodivgen> Prof. Dr. Ricardo Pereira Abteilungsleitung Biodiversitätsmonitoring, Head of the Department of Biodiversity Monitoring

Naturkundemuseum Stuttgart | Natural History Museum Stuttgart

Rosenstein 1, 70191 Stuttgart, Germany

+49 711 8936-2814

Raum F167 | Room F167

ricardo.pereira@smns-bw.de

[www.naturkundemuseum-bw.de](http://www.naturkundemuseum-bw.de) Bleiben Sie informiert:  
Abonnieren Sie unseren Newsletter!

Unterstützen Sie das Museum und werden Sie Mitglied im Förderverein! Informationen zur Verarbeitung personenbezogener Daten nach der DSGVO durch das SMNS finden Sie hier.

“Pereira, Ricardo” <ricardo.pereira@smns-bw.de>

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To read the entire message look it up at <http://life.biology-mcmaster.ca/~brian/evoldir.html>

## TrinidadWestIndies GuppyPaidResearchInternships

Paid Research Internships - The Guppy Project Research interns are needed to assist in a multi-disciplinary, multi-investigator, experimental study of the evolution of species interactions in Trinidad, West Indies. The research is led by Professors David Reznick (University of California, Riverside), Joseph Travis (Florida State University), Tim Coulson (University of Oxford), and Ron Bassar (Auburn University). We seek to integrate multiple biological fields for the study of these interactions in experimental populations of guppies and killifish in Trinidad. Duties include assisting in monthly censuses of guppy and killifish populations in montane streams and helping to execute experiments in on-site artificial streams. The monthly censuses include long hours in the field and laboratory.

Interns will be required to spend a minimum of 3 months in Trinidad, with possibility of extension, and/or promotion to field site manager. There are potential start dates in June 2025 and every month thereafter until September 2025. We will pay a monthly stipend (\$700 USD per month for first time interns), cover travel (up to \$900 USD), and provide housing.

Qualifications: We seek interns who are entertaining the possibility of pursuing graduate studies in some area of ecology and evolution and who wish to gain some

additional field research experience before doing so. Research will take place in semi-remote areas of Trinidad, sometimes under bad weather conditions. Applicants must be able to live and work well with others. Research will involve carrying heavy packs over slippery and steep terrain. Applicants must be in good physical condition and be able to meet the demands of field research under these conditions. Ability to drive a standard transmission vehicle is desirable but not required. Applicants with first-aid/first responder training, skills in automobile maintenance, and construction skills are highly desirable. Please address these skills when applying.

Please see our website <[www.theguppyproject.weebly.com](http://www.theguppyproject.weebly.com)> for more information on the project and access to reprints. Be sure to check out our video menu, which includes a “guppy censuses” as submenu VII. It details the main tasks associated with the internship.

Applicants should send a cover letter, CV, and the names and e-mail addresses of three or more professional references to David Reznick (gupy@ucr.edu). At least two of the references should be academics.

Ron Bassar Assistant Professor Department of Biological Sciences Auburn University

Personal Webpage: [www.ron-bassar.squarespace.com](http://www.ron-bassar.squarespace.com) Guppy Project Webpage: [www.theguppyproject.weebly.com](http://www.theguppyproject.weebly.com) Ronald Bassar <rdb0057@auburn.edu>

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## UGuyane FrenchGuiana NouraguesSciStation

Hello everyone,

We are looking for a motivated candidate to apply for the following PhD position: “Development and deployment of innovative environmental genomics approaches for monitoring plant diversity in the Amazon rainforest”, based at the University of Guyane (Cayenne, French Guiana).

This is an ambitious, multidisciplinary project combining genomics, fieldwork, and bioinformatics. The research will be carried out in close collaboration with the Universidad Nacional Mayor de San Marcos in Peru. The goal of the project is to develop an environmen-

tal DNA (eDNA) method that will enable Amazonian countries to monitor their plant biodiversity over the long term.

The application deadline is Friday, May 30. Mathieu Chouteau Chargé de recherche CNRS USR MIXTE 3456 LEEISA Centre de Recherche de Montabo 275 Route de Montabo 97300 Cayenne CEDEX Guyane Française 0694 40 39 61 ( 5h de moins que la France Métropolitaine) <https://mathieuchouteau.weebly.com/> Remplacer le '#' par 'y' car le mail cnrs filtre.

CHOUTEAU Mathieu <mathieu.chouteau@cnrs.fr>

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### ULisbon LabTech Evolutionary Agroecology

The Evolutionary Agroecology Lab at Univ. Lisbon is recruiting a laboratory technician (full-time position) to work within the project HotPest (ref: 2022.04172.PTDC).

Research within the EA group explores the eco-evolutionary responses of organisms to both biotic and abiotic selection pressures in an agricultural context. We use spider mites as a research model, small arthropods that cause severe damage to several crop plants (tomato, bean, etc). We do a combination of behavioural and ecological lab experiments, coupled with field sampling and Experimental Evolution. The HotPest project explores the impact of heat on the adaptation of crop pests to pesticides and novel crops.

We seek a highly motivated candidate who is interested in working with both herbivores and plants. The candidate should be a team player, able to adapt to changing circumstances and new tasks, and open to collaborating with colleagues from different backgrounds. The work plan includes 1) assisting the research team in their regular tasks (e.g., plant rearing, spider mite rearing and experiments involving plant and spider mite manipulation); 2) collecting and analysing data; 3) ensuring the proper functioning of the laboratory in general, namely the maintenance of stocks and all material associated with the project.

#### I. Admission Requirements

- a) Having a Master's degree in Biology or similar areas
- b) Experience with laboratory procedures, namely ex-

perience in plant biology and/or entomology and/or molecular biology

#### II. Preferential Requirements

- a) Proficiency in Portuguese and English (written and spoken); b) Relevant scientific and/or professional training in Evolutionary Biology; d) Experience in data processing and analysis, namely with the R program; e) Good organizational, multitasking and teamwork skills.

To apply, please follow this link: <https://www.euraxess.pt/jobs/340175> Deadline of submission: 29/05/2025

Starting date: August 2025

For any queries, please contact Leonor Rodrigues (alrodrigues[at]fc.ul.pt)

For more information about the EA group:

<https://www.ce3c.pt/research/research-groups/-evolutionary-perspectives-in-a-changing-world/evolutionary-agroecology> <https://mitesquad.weebly.com/> Leonor Rodrigues <alrodrigues@fc.ul.pt>

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### UMelbourne Australia Geneticists Genomicist

The School of BioSciences at the University of Melbourne, Australia is seeking an enthusiastic and collaborative academic colleague with expertise in genetics/genomics/ and/or epigenetics.

To address the under representation of women in our School's genetics program and pursuant to a special measure under Section 12 (1) of the Equal Opportunity Act 2010 (VIC), this position is only open to female-identifying candidates. We are open to applicants using any study system but particularly encourage applicants with interests aligned with current School strengths. Applicants should have strong quantitative skills and a strong modelling or bioinformatics element to their research programs. Applicants may also have a wet-lab component to their research.

Position Number: 0065841 Location: Melbourne, Australia (Parkville Campus) Role type: Full-time; Continuing (permanent) position Faculty: Faculty of Science Department/School: School of BioSciences Salary: Level



B: AUD \$122,212 to \$145,121 p.a. or Level C: AUD \$149,701 to \$172,613 p.a. or Level D: AUD \$180,254 to \$198,584 p.a. plus 17% super (retirement savings system/pension scheme) Level of appointment is subject to qualification and experience.

\* Teach and mentor the next generation of biologists  
 \* Apply now to drive innovative genetics research and cultivate a diverse scientific community at a world-class institution  
 \* Investing in you - benefits package including salary packaging, health and wellbeing programs, discounted services, and professional development opportunities

More Details: <https://jobs.unimelb.edu.au/en/job/-920074/lecturer-senior-lecturer-associate-professor-in-genomics> Charles Robin <crobin@unimelb.edu.au>

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## UOtago NewZealand Two EvolEcol ConservationBiol

2500432; Lecturer - Evolutionary Ecology < <https://otago.taleo.net/careersection/2/jobdetail.ftl?lang=en&job%00432> > DEPARTMENT OF ZOOLOGY | TE TARI MĪŪ<sup>1</sup>/<sub>2</sub>TAI KARAREHE DIVISION OF SCIENCES | TE ROHE A AHIKAROA UNIVERSITY OF OTAGO, DUNEDIN, NEW ZEALAND

Who we are / Ko wai mĪŪ<sup>1</sup>/<sub>2</sub>tou The Division of Sciences is one of the four divisions in the University, the others being Health Sciences, Commerce, and Humanities. The Division of Sciences represents a broad range of disciplines in 15 Departments and a number of interdisciplinary programmes. The Department of Zoology has a strong international reputation in whole-organism biology, with research strengths in areas including conservation biology, genetics/genomics, parasitology, entomology, environmental physiology, wildlife management, neurobiology and statistical modeling, as well as in molecular, functional, population, community, freshwater and behavioural ecology. We have well-established links to the Departments of Botany and Marine Science, the cross-disciplinary Ecology Programme, the Genetics and Neuroscience Programmes, and other centres at the University of Otago, providing a collaborative environment and resources for innovative interdisciplinary research. Our staff have international reputations in their areas of expertise and make major contributions to

answering fundamental questions in basic and applied research. The Department of Zoology is committed to affording students the opportunity to engage with knowledge of animals from a te ao MĪŪ<sup>1</sup>/<sub>2</sub>ori world view, and to strengthening its curriculum and research in relation to kaupapa MĪŪ<sup>1</sup>/<sub>2</sub>ori and mĪŪ<sup>1</sup>/<sub>2</sub>tauranga MĪŪ<sup>1</sup>/<sub>2</sub>ori, the University of Otago MĪŪ<sup>1</sup>/<sub>2</sub>ori Strategic Framework and Pacific Strategic Framework, and Te Tiriti o Waitangi (the Treaty of Waitangi).

The role / Te mahi Applications are invited for the permanent position of Lecturer/PĪŪ<sup>1</sup>/<sub>2</sub>kenga in Evolutionary Ecology. We are seeking a person with a relevant completed or nearly completed doctorate and demonstrated potential to develop as an outstanding researcher and teacher in advancing the study of evolution, ecology, and zoology. Applicants are encouraged to identify the manner in which they could complement existing strengths in the Department and develop new and innovative directions in research and teaching. A range of approaches would be considered including behavioural, physiological, population and community perspectives, with research interests in evolutionary ecology taking a multidisciplinary approach, and some or all of; applied genetics/genomics, ecophysiology, applied ecological theory, ecological modelling, disease ecology, being an advantage. Applicants with a willingness to incorporate and develop Indigenous perspectives in their research and teaching are strongly encouraged.

Your skills and experience / KĪŪ<sup>1</sup>/<sub>2</sub> PĪŪ<sup>1</sup>/<sub>2</sub>keka me KĪŪ<sup>1</sup>/<sub>2</sub> Wheako - A completed or nearly completed PhD with an established research focus in any area of evolutionary ecology. - Demonstrated experience and ability in delivering high-quality teaching and research in any aspect of evolutionary ecology. - An ability to contribute to teaching and learning environments that support the engagement of students and staff with evolutionary ecology research interests. - Be committed to and/or have established connections or a track record of working with international and/or national researchers. - Be committed to being a productive collaborator with a track record of working collegially. - Be committed to upholding the University's core values related to support and success of MĪŪ<sup>1</sup>/<sub>2</sub>ori and Pacific students, aligned with the University's MĪŪ<sup>1</sup>/<sub>2</sub>ori Strategic Framework and Pacific Strategic Framework.

Further Details / PĪŪ<sup>1</sup>/<sub>2</sub>roko This is a permanent, full-time (1 FTE) position based in ŪŪ<sup>1</sup>/<sub>2</sub>tepoti, Dunedin. A Lecturer level appointment is equivalent to Assistant Professor in the North American system. The successful candidate is expected to take up duties by 1 February 2026. Further details and job description are available on our website: 2500432; Lecturer - Evolutionary Ecology < <https://otago.taleo.net/careersection/2/->



[jobdetail.ftl?lang=en&job%00432](#) >

[University of Otago] JACQUELINE FRASER  
(she/her) Operations Lead | Kaii<sub>2</sub>rahi Whakahaerenga,  
Whakaratonga Wi<sub>2</sub>hanga me te Whakaritenga

Zoology & Botany Departments, Ecology Programme;  
School of Physical Education, Sport & Exercise Science

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This message has been arbitrarily truncated at 5000 characters.  
To read the entire message look it up at <http://life.biology-mcmaster.ca/~brian/evoldir.html>

## UOulu Finland FreshwaterBiodiversity

Tenure Track Assistant or Associate Professor in Freshwater Biodiversity

Please apply via: <https://oulunyluopisto.varbi.com/-what:job/jobID:811771/> Multidisciplinary recruitment  
The University of Oulu is a multidisciplinary, international research university, with about 3,600 employees who produce new knowledge based on high-standards research and provide research-based education to build a more sustainable, smarter, and more humane world. The University of Oulu community has about 17,000 people in total. Our northern scientific community operates globally and creates conditions for the emergence of innovations.

We are now looking for a

Tenure Track Assistant or Associate Professor in Freshwater Biodiversity

to join us in the interdisciplinary research program “SAFIRE: Safeguarding Biodiversity through Interdisciplinary Research on Habitat Restoration” < <https://www oulu fi/en/research/biodiverse-arctic-and-global-resilience/safeguarding-biodiversity-through-interdisciplinary-research-habitat-restoration-safire> > at the University of Oulu (Finland).

We are looking for a motivated and talented researcher with a strong background in freshwater biodiversity and research on or relevant to habitat/environmental restoration to join our interdisciplinary Research Council of Finland Profi8 programme. SAFIRE is a new strategic research programme which brings together the faculties of Sciences, Humanities, and Information Technology

and Electrical Engineering. SAFIRE’s focus is the production of scientifically excellent and actionable knowledge on habitat restoration, especially in the Arctic regions. SAFIRE aims to develop transdisciplinary processes to improve habitat restoration through basic and applied science, engaging and co-producing knowledge and solutions with societal actors, and the integration of advanced modelling approaches, both at the level of individual projects and at an institutional level within the University of Oulu SAFIRE will also advance research and discussion concerning the multiple environmental and societal contributors to ecosystem restoration and will strengthen the collaborative role of the natural sciences, social sciences, and the humanities, and engineering, in current political and scientific debates about the environment, especially but not limited to the Arctic. Through three linked tenure track appointments and significant investment in transdisciplinary collaboration between research disciplines and with societal actors, SAFIRE will promote inter- and transdisciplinary and citizen-engaged studies of the environment and raise the University’s profile as an international leader in restoring inter-related ecological and social systems. SAFIRE is part of a wider Profi8 program at the University of Oulu, funded by the Research Council Finland, and it is co-led by the Faculties of Science and Humanities at the University of Oulu.

About the job As an Assistant/Associate Professor, you will:

- \* -â€œand sustain a distinctive program of research and creative scholarly initiatives leading to academic publications, research funding applications, and public-facing outreach initiatives;
- \* -â€œtransdisciplinary research partnerships in Finland and internationally;
- \* -â€œwith the relevant faculties at the University of Oulu to further the aims of SAFIRE;
- \* -â€œin national and international scientific organizations;
- \* -â€œresearch results to academic community, user groups and general public;
- \* -â€œin administrative tasks related to the position at the faculties and the university;
- \* -â€œand lead undergraduate and graduate level courses, especially in the fields of Aquatic Biodiversity and Ecosystem Restoration;
- \* -â€œgraduate research students (MA and PhD levels) and postdocs;
- \* -â€œskills or the motivation to learn Finnish is an asset;

\* -â€œâ€œâ€œâ€œâ€œthe strategic aim to renew the scientific profile of the university and to promote multi- and interdisciplinary research approaches;

\* -â€œâ€œâ€œâ€œâ€œon funding calls and project management

Who are you?

— / —

This message has been arbitrarily truncated at 5000 characters.  
To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

## USouthCarolina EcolEvolution

Colleagues,

My department is searching for a non-tenure track faculty member with a specialty in ecology & evolution.

The link to apply: <https://uscjobs.sc.edu/postings/-186357> (emphasis in Ecology/Evolution). We also have a similar position in Cell/Molecular Biology (posting #185517).

Job Description: The faculty of the Department of Biological Sciences at the University of South Carolina, Columbia campus invites applications for a full time, professional-track position at the rank of Instructor to begin August 16, 2025. The position is a 9-month appointment with a teaching load of 8 courses in Introductory Biology with an emphasis on Ecology/Evolution over the 9-months (or the equivalent of 12 credit hours of courses each academic semester). This is an annual appointment that may be renewed contingent upon Dean's approval, satisfactory performance, departmental needs, and the availability of funding.

The successful candidate will teach multiple sections of introductory biology, which may include a combination of BIOL 101 (Biological Principles I; Introductory

survey of macromolecules, cell structure and function, genetics and molecular biology), BIOL 102 (Biological Principles II; Introductory survey of plant and animal development, physiology, ecology, and evolution), and/or BIOL 110 (General Biology; Basic biological concepts and issues for non-biology majors). The 4:4 teaching load is equivalent to teaching 12 credit hours of courses each semester. These 12 hours can be any combination of lectures as needed by the department.

The Department of Biological Sciences is a multidisciplinary unit of approximately 1,800 undergraduate students, 70 graduate students, 35 tenure-line, and 22 professional-line faculty representing a broad range of research areas ([www.biol.sc.edu](http://www.biol.sc.edu)). USC ([www.sc.edu](http://www.sc.edu)) is comprised of the state's flagship university in Columbia (founded in 1801 and currently one of the top 50 "Best Colleges" according to U.S. News and World Report).

Applications must include: (1) a cover letter, (2) a curriculum vita, (3) a statement of teaching interests, experience, and expertise (1-2 pages), and (4) the names and email addresses of 3 references. Professional references will be contacted directly by the Chair of the Search Committee, and letters will be requested on the candidate's behalf.

Review of applications will begin on 05/01/2025 and will continue until the position is filled.

Inquiries about this position may be directed to Dr. Amanda P. Zeigler, Undergraduate Director, Department of Biological Sciences [polsona@mailbox.sc.edu](mailto:polsona@mailbox.sc.edu); phone 803-777-2518).

Cheers,

Jeff

Jeffrey L. Dudycha Professor Dept. of Biological Sciences University of South Carolina Columbia, SC 29208 [dudycha \[at\] biol.sc.edu](mailto:dudycha[at]biol.sc.edu) <http://www.tangledbank.org> tw: JLDudycha

"Dudycha, Jeff" <[DUDYCHA@biol.sc.edu](mailto:DUDYCHA@biol.sc.edu)>

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## EvolutionMeeting AssistantMeetingOrganizer

The Society for the Study of Evolution (SSE), on behalf of the Joint ASN/SSB/SSE council, seeks one or two members of one or more of our societies to help plan and run our annual scientific conference - the Evolution meetings. The meetings are coordinated by one or more Chief Meeting Officers (CMOs), academics who oversee all aspects of the meeting and who are responsible for final decisions about schedules, activities and venues, in consultation with a tri-society Joint Meeting Committee (JMC) and the larger ASN/SSB/SSE Joint Council. The CMOs also act as the principal liaisons with a Professional Conference Organizer (PCO), whose responsibilities include executing the logistics of conference management, interactions with vendors and service providers, and helping identify and negotiate contracts with future meeting venues.

**Duties:** Specific duties will be determined by the CMO and the JMC, in consultation with the AMO, and are expected to be for a combination of the in-person and virtual conferences. General duties & time commitment include interfacing with society councils and other stakeholders; producing the scientific program; providing academic insight to help guide the work of the PCO; regular electronic communication and virtual meetings with co-organizers; at conference assistance for both the in-person and virtual conferences.

The time commitment is variable but is expected to average a few hours per week, ramping up at certain times depending on particular tasks and in the month preceding the meeting.

Assistants normally serve a 3-year term and, if interested, may transition into the lead CMO role at some point, with approval of the JMC.

**Stipend:** Helping run our meetings is an important and valuable service to our societies and our field which is largely a volunteer effort, but the AMO will be given a stipend of \$5000/year (USD) in appreciation. All meeting attendance costs will also be covered, as well as any other costs associated with carrying out meeting responsibilities.

**Qualifications:** This position is best suited to someone who has attended several of our recent meetings, has academic organizational and leadership experience, enjoys teamwork, and would find it rewarding to serve the societies by fostering dynamic and high-quality meetings.

**How to apply:** Please email expressions of interest to [evolution.meetings@gmail.com](mailto:evolution.meetings@gmail.com) with 'AMO position' in the subject and include any relevant experience and a CV. These will be reviewed starting on June 6, 2025, so that potential new AMOs can be interviewed at the 2025 meeting (to be held in Athens, GA from June 20-24, 2025). The new AMO(s) is/are expected to begin working in July following the 2025 meetings. There are no geographic restrictions, nor citizenship or residency requirements, but attendance at the 2026 and subsequent meetings (during tenure as an AMO) is expected and in-person attendance at the 2025 meeting would be an asset.

Alex Wong <[AlexWong@cunet.carleton.ca](mailto:AlexWong@cunet.carleton.ca)>

(to subscribe/unsubscribe the EvolDir send mail to [gold-ing@mcmaster.ca](mailto:gold-ing@mcmaster.ca))

## List EcolEvolMarineLabs RecruitingGrad

Hello Listers -

If you are a PI in ecology/evolution/marine biology looking to recruit a PhD student for a Fall 2026 start please consider advertising your opening through this form: <https://forms.gle/-2XTHBP6CZGEn3D1t9> It populates a view-only spreadsheet which you can also share with prospective students [https://docs.google.com/spreadsheets/d/-1P2s4n5oA0\\_SF\\_0L8RmrwdDdtKVfWfUx7Q\\_no00muk8/-edit?resourcekey=&gid=1719965013#gid=1719965013](https://docs.google.com/spreadsheets/d/-1P2s4n5oA0_SF_0L8RmrwdDdtKVfWfUx7Q_no00muk8/-edit?resourcekey=&gid=1719965013#gid=1719965013) Thanks for helping the next generation,

Carly

Dr. Carly D. Kenkel (she/her) Wilford and Daris Zinsmeyer Early Career Chair in Marine Studies Department of Biological Sciences University of South-

ern California 3616 Trousdale Parkway, AHF 231 Los Angeles, CA 90089-0371 Office: +1 (213) 821-1705 Email: ckenkel@usc.edu Twitter: @DrCarlsHorn <http://dornsife.usc.edu/carlsfab> ckenkel@usc.edu

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## Software DAMBE UpdateOnNewMacComputers

Dear All,

Responding to popular requests, I have added instructions on how to install and run DAMBE on new MAC computers (with Apple Silicon M1, M2, ..., processors):

[https://dambe.bio.uottawa.ca/DAMBE/-dambe\\_install\\_mac.aspx](https://dambe.bio.uottawa.ca/DAMBE/-dambe_install_mac.aspx) Please let me know if you encounter any problems.

(DAMBE is a comprehensive software workbench in molecular biology and evolution.)

Best. Xuhua Xia Professor, Department of Biology University of Ottawa [https://scholar.google.ca/citations?hl=en&user=fbAS\\_FcAAAAJ&view\\_op=list\\_works](https://scholar.google.ca/citations?hl=en&user=fbAS_FcAAAAJ&view_op=list_works) Xuhua Xia <Xuhua.Xia@uottawa.ca>

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## SSB MentorshipProgram 2025

The Society of Systematic Biologists is recruiting new mentees and mentors to participate in the Mentorship Program for 2025-2026!

The Program helps facilitate new professional relationships between graduate students and postdocs with more-established members of the systematics community, such as faculty, curators, teachers, researchers, etc. Mentoring pairs typically meet virtually once per month throughout the year. It's a great way to find your community, meet new people, support your colleagues, and get a fresh perspective on systematics research.

Visit <https://www.systbio.org/mentorship-program.html> to learn more about the program.

Apply by completing this form: <https://forms.gle/-QtD22C9dtfRFCs7a7>. Applications are open until June 10th, 2025. Please contact mentorship@systematicbiologists.org with any questions or comments.

The SSB Mentorship Program Team Michael Landis, Laura Kubatko, Alonso Delgado, Ixchel Gonzalez-Ramirez

Michael Landis Assistant Professor Department of Biology Washington University in St. Louis michael.landis@wustl.edu <https://landislab.org> "Landis, Michael" <michael.landis@wustl.edu>

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## Sweden SiberianJay VolFieldAssist

Field volunteer position for a project investigating climate change adaptations of Siberian jays in Sweden, 10 August to 31 October 2025.

Opportunity: Field Volunteer (Expenses Paid)

We are seeking one highly motivated field volunteer to support a long-term ecological research project led by Dr. Michael Griesser (University of Konstanz) and Dr. Miya Warrington (Oxford Brookes University). This is an expenses-paid position, offering hands-on experience in bird ringing and behavioural data collection.

Our research investigates how animals adapt to changing environments, with a particular focus on the role of social interactions in enhancing resilience. In the upcoming field season, we will examine how habitat structure and forestry practices influence life history traits and social dynamics within animal groups.

An overview over our past work can be found here: <https://www.youtube.com/watch?v=JaH6wjAYAiE>

Position Summary: We are seeking a motivated field volunteer to support the collection of baseline ecological and species-specific data. The successful candidate will assist with a range of field activities, including mist-netting and colour-ringing birds, recording morphometric measurements, collecting blood samples, conducting behavioural observations, and managing associated data.

This opportunity is well-suited for individuals interested in pursuing further studies in wildlife conservation, ornithology, or ecology, as well as those seeking to develop

or enhance practical field research skills.

**Field Conditions:** This is a fully immersive field position. Volunteers will be expected to work approximately 8 hours per day in variable weather conditions, provided it is safe to do so. Daily activities may involve walking up to 15 km. Please note that towards the end of the field season, daytime temperatures may drop to -20°C; cold-weather layers are available for loan.

**Qualifications:** 1) Bird ringing and mist-netting experience 2) Field work experience, if possible involving behavioural observations and experiments 3) Driver's license (manual transmission) 4) Ability to work independently and in small team 5) Sociable personality, with an ability to share living spaces 6) Working knowledge of English

Further information can be found here: <https://sites.google.com/view/c-wild-griesser/home> We will provide the volunteer with a stipend to contribute towards food and travel expenses to and from the study site. Accommodation for the duration of the project will be provided at the associated field station.

Applications, including a CV, letter of motivation (1 page), and the name of two referees, should be sent to Michael Griesser [michael.griesser@uni-konstanz.de](mailto:michael.griesser@uni-konstanz.de), preferably in a single PDF.

Review of applications will start 9 June 2025, position will remain open until filled.

Michael Griesser <[michael.griesser@uni-konstanz.de](mailto:michael.griesser@uni-konstanz.de)>  
(to subscribe/unsubscribe the EvolDir send mail to [golding@mcmaster.ca](mailto:golding@mcmaster.ca))

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## AmsterdamVU Two InsectFungalEvolution

Postdoctoral position on the chemical ecology of insect-fungal symbiosis

The Berasategui Lab at Vrije Universiteit Amsterdam invites applications for a full-time ERC-funded Postdoctoral Researcher to investigate the chemical and functional genomics of defensive fungal symbionts associated with beetles. This project will focus on identifying and characterizing the bioactive compounds produced by a diverse set of fungal mutualists, using a metabologenomics approach to link chemical profiles with biosynthetic gene clusters. The successful candidate will also conduct targeted bioassays to determine which compounds contribute to beetle defense, providing functional insights into the ecological roles of these symbioses.

The position is expected to begin in early 2026. It is initially offered as a one-year appointment, with the possibility of extension for up to a total of three years based on performance.

Candidate Requirements: - A PhD in Chemistry, Biology, Ecology & Evolution, Genomics, or a closely related field - Demonstrated experience with analytical chemistry - Strong bioinformatics skills (highly desirable) - Excellent communication and interpersonal skills - Willingness to collaborate in a multidisciplinary team environment

Applicants should submit the following materials in a single PDF file: 1. A cover letter describing previous research experience, interests, and motivation for applying 2. A current CV 3. Contact information for three academic referees

Full consideration will be given to applications received by June 6th, but the position will remain open until filled. Informal inquiries can be directed to Dr. Aileen Berasategui ([a.berasateguilopez@vu.nl](mailto:a.berasateguilopez@vu.nl)).

Assistant Professor in Ecology and Evolution Amsterdam Institute for Life and Environment (A-LIFE)

Section Ecology and Evolution Faculty of Science

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Postdoctoral position on insect-fungal mutualisms and plant pathology

Many plant pathogens rely on insect partners for transmission and dispersal, often providing mutualistic benefits in return. The Berasategui Lab at Vrije Universiteit Amsterdam invites applications for a full-time ERC-funded Postdoctoral Researcher to investigate how mutualistic interactions between phytopathogens and insect vectors influence pathogen virulence. This project will focus on tortoise leaf beetles, their fusarial defensive symbionts, and a shared plant host system to explore whether these mutualisms constrain or promote pathogen virulence.

The position is expected to begin in early 2026. It is initially offered as a one-year appointment, with the possibility of extension for up to a total of three years based on performance.

Candidate Requirements: - A PhD in Biology, Ecology & Evolution, Genomics, or a closely related field - Demonstrated experience with plant-microbe systems - Strong bioinformatics skills (highly desirable) - Excellent communication and interpersonal skills - Willingness to collaborate in a multidisciplinary team environment

Applicants should submit the following materials in a single PDF file: 1. A cover letter describing previous research experience, interests, and motivation for applying 2. A current CV 3. Contact information for three academic referees

Full consideration will be given to applications received by June 6th, but the position will remain open until filled. Informal inquiries can be directed to Dr. Aileen Berasategui ([a.berasateguilopez@vu.nl](mailto:a.berasateguilopez@vu.nl)).

“Berasategui Lopez, A. (Aileen)”  
<[a.berasateguilopez@vu.nl](mailto:a.berasateguilopez@vu.nl)>

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## BiologyCentre Czech ProtistProteomics

ERC-funded postdoctoral position in proteomics and data analysis of a kleptoplastidic protist

Background of the project: Plastid endosymbiosis has transformed our planet, introducing photosynthesis to eukaryotes and triggering the evolution of a massive diversity of algae and plants. Yet we do not know how it works - mainly because most endosymbiotic events took place such a long time ago. Kleptoplastidic microbes, which steal and transiently retain plastids from their algal prey for photosynthesis, offer the unique possibility to investigate plastid endosymbiosis while it is happening. Overall rare in eukaryotes, kleptoplastidy has evolved relatively frequently in dinoflagellates, a species-rich lineage of unicellular eukaryotes that is nevertheless understudied in its diversity. The Evolution of Protist Symbioses Laboratory utilizes known and newly isolated kleptoplastidic dinoflagellates as models to study the process of plastid endosymbiosis. For this specific project, one of the very few kleptoplastidic lineages in culture, the Ross Sea Dinoflagellate (RSD), will be employed in spatial and quantitative proteomic experiments to investigate several aspects of early plastid endosymbiosis.

The project: The project integrates experimental and bioinformatic approaches to explore the long-term kleptoplastidic association in RSD. The successful candidate will, together with our collaborators at the University of Cambridge, develop a (hyper)LOPIT protocol for this lineage, complement this approach with quantitative proteomic experiments and analyze the resulting data to help resolve the following fundamental questions: What is the composition of the plastid proteome in a kleptoplastidic lineage? How does the kleptoplast and control of the kleptoplast change during integration? Do endosymbiosis-associated gene transfers impact other compartments of the cell besides the plastid?

The workplace: The work locations will be the Biology Center of the Czech Academy of Sciences in Ceske Budejovice (<https://www.bc.cas.cz/en/homepage/>) and the University of Cambridge, UK. The successful candidate will spend approximately one year in the UK in the laboratory of our collaborator, Prof. Ross Waller, to establish the spatial proteomics workflow. The candidate will be an integral member of the international research

group led by Dr. Elisabeth Hehenberger, who has recently been awarded an European Research Council Consolidator Grant. The candidate will have excellent opportunities to advance their scientific career in a supportive research team that has built an extensive network of national and international collaborators across Europe, Japan and North America. The lab is located in a newly built open space research center that houses three other labs focusing on various evolutionary aspects of microbial eukaryotes.

České Budejovice is located >2 hours south of the capital city, Prague, and 2 hours north of the Austrian Alps. Situated on the confluence of the Vltava and Malse rivers, it offers over 750 years of tradition and history. Visit the Guide for Expats (<https://www.bc.cas.cz/en/-employees/>) to read about life in the city and the Czech Republic.

Requirements: We are seeking an early-career researcher with a PhD in biology or molecular/cellular biology who: - is an enthusiastic scientist with proven research abilities that include persistence in resolving technical issues. Ideally, with expertise in one or more of the following methodologies/fields: proteomics, mass spectrometry or bioinformatics/large datasets. Previous experience with dinoflagellates is a plus. - is organized, accurate and responsible - possesses excellent communication skills that contribute to a pleasant working atmosphere

Our offer: A fully funded position with a competitive salary for 3 years, with the possibility for extension. Starting date: July 1st 2025 or soon after A general understanding of a healthy work/life balance

About the selection process: The Biology Centre of the Czech Academy of Sciences holds the HR Excellence in Research Award. Our selection process is transparent, open, non-discriminating, and fair. For more information about the recruitment policy for researchers at our institution, see OTM-R (<https://www.bc.cas.cz/en/employees/candidates/otm-r/>). At the deadline, we will review all applications and select 3-5 of the best candidates to interview online.

How to apply: Application deadline is Saturday, May 31, 2025. Please submit your CV along with a motivational letter explaining your research passions and why you are uniquely qualified to join our research group HERE: <https://jobs.bc.cas.cz/en/detail/250> You are invited to submit the names

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## BiologyCentre CZ PlantPhytochemicalDiversity

Postdoctoral Position in Plant Chemical Ecology We are inviting applications for a postdoctoral researcher to join our project exploring the drivers and functional roles of phytochemical diversity in plants.

**Project Overview** Our research investigates the remarkable diversity of plant metabolites and their correlations with biotic and abiotic stressors at a global scale. To test our hypotheses, we focus on the Salicaceae family that represents a unique model system, being globally distributed in diverse environments. The project combines field observations with advanced metabolomics techniques. The successful candidate will enhance these efforts through laboratory-based experiments to test the functional roles of phytochemical diversity in plant defence. A key part of this work involves conducting feeding experiments with model herbivores to determine how different facets of chemical diversity influence insect behaviour and performance.

**Responsibilities include:** \* Preparing plant extracts from plant species with varying chemical profiles \* Rearing insect herbivores for feeding trials using diets infused with extracts or analytical standards \* Conducting fieldwork in Europe and overseas to collect additional plant samples \* Analysing and interpreting the data and results \* Leading the preparation of manuscripts for publication While the project has defined goals, we welcome candidates with initiative and interest in broadening its scope through independent hypothesis testing.

**Required Qualifications and Skills:** \* PhD in a relevant field (required for postdoctoral eligibility) \* Strong interest in chemical ecology, plant-insect interactions, or entomology \* Experience in both field and laboratory research \* Proficiency in insect rearing and basic analytical chemistry techniques \* Solid background in biostatistics \* Excellent written and spoken English \* Ability to work both independently and collaboratively

**About the Host Institution** The successful applicant will join the Laboratory of Evolutionary Ecology led by Dr. Martin Volf at the Institute of Entomology, Biology Center of the Czech Academy of Science. The candidate will live in Ceske Budejovice (Czech Republic) where the laboratory experiments will take place and conduct fieldwork in Europe and overseas. Our department is a

diverse, international team studying ecology, evolution and biogeography, and a world-class centre for interaction network research with regular publications in leading journals.

**Position Details:** \* Application deadline: June 25, 2025 \* Interviews: early July 2025 \* Start date: November 1, 2025 \* Duration: August 31, 2027 \* The position is fully funded. \* Applicants from all countries are welcome to apply.

**How to Apply** Please send the following to Dr. Martin Volf (volf@entu.cas.cz): \* Your CV \* A cover letter outlining your qualifications, relevant experience, and motivation \* Contact information for three referees

**External Links** Volf lab: <https://www.volfab.com/>  
Czech Academy of Science : <https://www.entu.cas.cz/en/homepage/> Ceske Budejovice : [https://en.wikipedia.org/wiki/%C4%8Cesk%C3%A9\\_Bud%C4%Bjovice](https://en.wikipedia.org/wiki/%C4%8Cesk%C3%A9_Bud%C4%Bjovice) Volf Martin <volf@entu.cas.cz>

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## ColumbiaU SpeciationBehaviorGenomics

ONE FULLY FUNDED POSTDOCTORAL POSITION AVAILABLE

Delmore lab (delmorelab.com)

Ecology, Evolution, and Environmental Biology (E3B), Columbia University

DESCRIPTION

The Delmore lab in the Department of Ecology, Evolution, and Environmental Biology (E3B) at Columbia University invites applications for a position at the rank of Postdoctoral Research Scientist. The successful candidate will contribute to research on behavioral and speciation genomics.

As a first step, the candidate will lead a project linking structural variants to both seasonal migration and reductions in hybrid fitness. The main study system for this project is a hybrid zone between Swainson's thrushes that differ in their migratory behavior. Preliminary data for this project have already been collected (e.g., individual-level tracking data for hundreds of birds is available along with both short- and long-read se-

quencing data). We hope the applicant will use this project as a stepping stone for additional work in the system (e.g., we also have quite a few additional 'omic' datasets that can be used to complement results from structural variants).

#### QUALIFICATIONS

PhD in biology, bioinformatics, or related fields.

Previous experience with next-generation sequencing is highly desirable.

A track record of research excellence is essential (e.g., first-author pubs and/or grants), as are excellent written and oral communication skills.

Experience with birds is not necessary.

#### START DATE

Flexible but prefer by end of summer. Two-year contract with potential to extend.

#### SALARY AND FUNDING

Salary will be commensurate with experience, starting at \$71,000.

Project is part of NIH MIRA grant for which we have 5 years of research funding.

#### TO APPLY

Please email a cover letter and CV to [ked2195@columbia.edu](mailto:ked2195@columbia.edu). The cover letter should outline your research interests, motivation, and experience. The CV should include the names and emails of at least two references.

Kira Delmore | Associate Professor Department of E3B | Columbia University 1014A Schermerhorn Extension | 1200 Amsterdam Avenue | New York, NY 10027 1 (979) 900-2129 | [ked2195@columbia.edu](mailto:ked2195@columbia.edu) | [delmorelab.com](http://delmorelab.com)

\* My working hours may not be your working hours. Please do not feel obligated to reply outside of your normal work schedule. \*

Kira Delmore <[ked2195@columbia.edu](mailto:ked2195@columbia.edu)>

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## EarlhamInst UK Metagenomics

### Postdoctoral Research Scientist in Metagenomics

Applications are invited for a Postdoctoral Research Scientist to join the Laboratory of Dr Hildebrand and Prof Quince in the Research Faculty of the Earlham Institute, based in Norwich, UK.

#### Background:

This post is part of the OpenCLIM.LANDS project, that aims at providing the insights needed to put the UK on a path to achieving net-zero emissions by 2050, achieved through climate resilient soil health, food security, and biodiversity net gain. In this multi-centre project, we will combine climate forecasting with latest advances in soil science to enable a unique perspective into land use under forecasted climate change scenarios.

#### The role:

In this post, we will address the following questions: How do soil microbes establish, contribute and maintain healthy, biodiverse macro- & micro-communities, and how are these impacted by different land use scenarios? How can we use machine learning to predict soil microbiomes from either pristine or agriculturally used soils, predict their functional capacity (e.g. carbon storage)? What practices can help microbial soil communities recover? To answer these and more questions the OpenCLIM.LANDS multi-centre project was established.

The project holder will use metagenomics (similar to doi:10.1038/s41586-018-0386-6, 10.1111/1462-2920.15314) to profile both taxonomic and functional compositions of 3,000 newly sequenced soil sites. Using machine learning we will build comprehensive profiles of typically expected microbial profiles across soil sites (similar to doi: 10.1016/j.chom.2023.05.024) and their relation to soil health and carbon storage. Using a combination of robotics and third-generation sequencing, we will use predictive microbial modelling to improve land use on existing agricultural sites. Long-term, this work will enable microbially-informed agriculture, combating the impact of climate change and understanding how healthy soil microbiomes are established & maintained.

#### The environment:

The Hildebrand group uses metagenomics to research the diversity, community interactions, and evolution of

microbes in communities using custom software solutions. The Quince group explores environmental and host-associated microbiomes using statistics and machine learning. Both groups are situated at the Norwich Research Park (NRP) UK, that integrates the 4 BB-SRC Institutes, University of East Anglia (UEA), 15 companies, 3,000 researchers and clinicians, and 17,000 students. Norwich ranked in the top 10 of UK cities with a historical town centre and an active food & coffee aficionado scene.

OpenCLIMLANDS is a multi-centre UK collaboration between Earlham & Quadram Institutes, UEA, University of Leeds, Newcastle University, UK Centre for Ecology & Hydrology, among others. The applicant will have direct access to established PacBio/ONT, Hi-C and single cell sequencing facilities, as well as one of UK's largest HPC cluster on-site.

The ideal candidate:

The applicant needs to hold a PhD (or equivalent) in biology, bioinformatics, computer science or a related discipline with a background and/or interest in at least one of the following subjects:

- Microbiomes & biodiversity - Metagenomics & patient cohorts - Ecology & evolution

The ideal candidate will have experience in conducting scientific experiments independently, writing papers, presenting work and grant writing. Basic statistics and programming skills (either R, python, Perl, C++, or equivalent) is expected. Specialised skills will be taught and developed through mentorship and collaborations. The applicant is expected to help in the supervision of junior group members and to represent the group at trainings.

Additional information:

Salary on appointment will be within the range 36,720 to 42,000 per annum depending on qualifications and experience. This is a full-time post with an expected end date of September 2027, with the potential for extension.

For further information and details of how to apply, please visit our website <http://jobs.earlham.ac.uk/> or contact the Human Resources team on 01603 450814 or [nbi.recruitment@nbi.ac.uk](mailto:nbi.recruitment@nbi.ac.uk) quoting reference 1004892.

This role meets the criteria for a visa application, and we encourage all qualified candidates to apply. Please contact the Human Resources Team if you have any questions regarding your application or visa options.

As a Disability Confident employer, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy.

The closing date for applications will be 8 June 2025. Interviews will likely be held around 17 and/or 18 June 2025.

Kind regards Laura

Laura Booth Associate CIPD

HR Advisor (Recruitment) Human Resources

Personal Pronouns: She/Her

NBI Partnership, Norwich Research Park, Colney, Norwich, NR4 7UH

Tel: 01603 450308 or Ext 2308

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## Goettingen Germany RedDeerGenomics

The Department of Wildlife Sciences at the Faculty of Forestry and Forest Ecology at the Georg August University of Göttingen is seeking to fill a position as a research associate (f/m/d) in a third-party funded project on landscape genomics of red deer.

This is a 100 % position with regular weekly working hours (currently 39.8 hours) for an initial period of three years. Remuneration will be based on salary group 13 TV-L (German public service agreement). The position should start no later than February 1, 2026.

**Job Description** The successful candidate will conduct a landscape genomic study for red deer (*Cervus elaphus*) in Lower Saxony and neighboring areas. The occurrence of red deer in Germany is limited to a few spatially isolated subpopulations. Population fragmentation has already led to a loss of genetic diversity. However, to date, all genetic studies on red deer in Germany have been carried out using microsatellites.

For the project, approximately 2,000 samples will be collected and analyzed by partners at the University of Giessen using microsatellites. These same samples will then be used for SNP-based analysis in our department. Sequencing will be performed by an external service provider using either an existing SNP array for red deer, or via RADseq, ddRAD, or Genotyping By



Sequencing. The bioinformatic steps will run either on the University of Göttingen's High Performance Computing Cluster (see <https://gwdg.de/en/hpc/>) or via a cloud service provider. The focus of the position is on bioinformatics and the population and landscape genetic analysis of SNP data. The goal is to quantify the neutral and adaptive genomic diversity of red deer populations, their genetic exchange, genetically effective population sizes, and inbreeding, as well as to identify possible landscape influences on these parameters. The SNP-based results will then be compared with those from the microsatellites.

In addition to the samples from Lower Saxony, an interesting dataset of over 900 red deer samples from across Germany is available, which have already been sequenced in an external laboratory using an Illumina NovaSeq 6000 S4 PE150. This dataset can also be analyzed for landscape genetics as part of the project. For comparison purposes, a dataset with 14 microsatellites is already available for the same samples.

There is also the opportunity to participate in a project in which a SNP chip is used to calculate relationships within a red deer population using a genomic relatedness matrix (GRM).

Your Profile - Completed master's degree in bioinformatics, genetics, evolution, ecology, biology, or a similar field - Experience in the preparation and analysis of SNP datasets and the required bioinformatics methods - Experience in working with high-performance/remote computing clusters - Good knowledge of population genetic concepts and methods - Good knowledge of landscape genetic or genomic concepts and methods - Knowledge of spatial data analysis (e.g., modeling resistance landscapes for gene flow) in R and/or a GIS - Good programming skills in R, Perl, and/or Python - Very good written and spoken English skills - Experience in scientific writing, demonstrated by (co-)authorship of peer-reviewed articles in scientific journals

Further advantages include a doctorate in a field relevant to the project, knowledge of calculating genomic kinship matrices, experience in collaborative projects, and knowledge of other programming languages (e.g., Python). Java, MatLab, Julia, LaTeX, Mathematica, C, SAS). We are seeking an enthusiastic and productive individual who is independent but also a good team player. You should be motivated to advance and shape future landscape genomics research in the department.

The work location is Göttingen.

The University of Göttingen strives to increase the proportion of women in fields where women are under-represented and therefore strongly encourages qualified

women to apply. It is a family-friendly university and promotes the compatibility of science/work and family. The university is particularly committed to supporting employees with severe disabilities and therefore welcomes applications from people with severe disabilities. In cases of equal qualifications, applications from people with severe disabilities will be given preference. To safeguard interests, any disability or equal opportunity must be included in the application.

Please send your comprehensive, English-language application (a letter of motivation with the usual supporting documents) electronically as a single PDF document to Niko Balkenhol (nbalken@gwdg.de) by June 29, 2025. In your letter of motivation, you should primarily describe your experience in working with SNP datasets, bioinformatics, and landscape genetic and genomic analyses.

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## Lausanne Switzerland ProteinEvolution

Dear colleagues,

I currently have an opening for a postdoctoral position in my group at EPFL (Ecole Polytechnique Federale de Lausanne, Switzerland).

We mainly focus on modeling evolution and extracting information from evolutionary data, from molecules to microbial populations. We develop approaches based on mathematical and physics-based modeling, statistical inference and machine learning (especially protein language models). The primary topic for this position is protein evolution, but there is flexibility.

To apply, please send a cover letter, a complete CV and copies of transcripts to [anne-florence.bitbol@epfl.ch](mailto:anne-florence.bitbol@epfl.ch) by June 6.

The start date is flexible. More information is available at <https://www.epfl.ch/labs/bitbol-lab/join-us/> Best regards, Anne-Florence Bitbol

Anne-Florence Bitbol <[anne-florence.bitbol@epfl.ch](mailto:anne-florence.bitbol@epfl.ch)>

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## LundU FunctionalGenomics

I am searching for a postdoc to take up a 3-year position with me (possibility of 1 year extension). The idea is to use gene editing to work out why birds struggle with climate warming and how that maps onto fitness. The project is part of a larger initiative dealing with birds in a hotter world, funded by the European Research Council.

The ideal candidate is a molecular biologist with keen interest in evolutionary questions. A background working on birds is helpful, though not essential. Details about the position and instructions for how to apply are available on this link.

Best wishes, Andreas

Dr. Andreas Nord Associate Professor Department of Biology Lund University SE-223 62 Lund, Sweden Board Member Young Academy of Sweden Member Reference Group for Science Communication

Phone: +46 704 953 262 E-mail: Andreas.Nord@biol.lu.se Personal website Google Scholar

Andreas Nord <andreas.nord@biol.lu.se>

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## Montpellier France DeepSeaBiodiversity

A post-doctoral position is available at UMR MARBEC-Ifremer Sîl<sub>2</sub>te (France) to work on Deep-sea benthic communities and environmental drivers in and around hydrothermal vents of the Mid-Atlantic Ridge, explored by multi-marker metabarcoding of environmental DNA“.

The project is based on the analysis of environmental DNA data from generated by the Lifedeep project (<https://lifedeep.ifremer.fr/>) and collected during the BICOSE3 cruise on the Mid Atlantic Ridge, particularly in and around areas associated with exploration

mining permits, including active and inactive hydrothermal fields and the abyssal environment. Details of the project and how to apply are available from the link below. I will reply to emails from applicants who would like more details before applying.

Applications must be submitted by June 20th.

<https://www.hw-recruteur.com/offer/joboffer/offre-57306-aHecZw> Sophie Arnaud-Haond Ifremer-UMR Marbec Montpellier-Sîl<sub>2</sub>te

Sophie Arnaud Haond <sophie.arnaud-haond@umontpellier.fr>

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## Naturalis Leiden IslandBirds

Postdoctoral fellow studying birds on islands

We are looking for a postdoc to work on a project on biogeography, genomics, and conservation of birds on land-bridge islands, based at Naturalis Biodiversity Center (Leiden, Netherlands), and part of an international team.

You will be working on a NWO-funded project led by Dr. Lui<sub>2</sub>s Valente, which aims to study the biogeography, population genomics and evolution of bird species on land-bridge islands around the world. The project has a global focus, but it will also zoom-in on the bird fauna of the tropical island of Bioko (Equatorial Guinea). You will perform bioinformatic, macroecological and morphometric analyses. For the bioinformatics, you will analyse sequence-capture genomic data (ultraconserved elements, UCEs) from museum specimens of birds. For the macroecological analyses, you will compile a new global database and use it to investigate global patterns of avian diversity on land-bridge islands. For the morphometric analyses, you will measure museum specimens and analyse them in combination with the UCE data.

Beyond the scientific components above, the project involves an educational and conservation programme on the island of Bioko, in collaboration with the National University of Equatorial Guinea, and the Bioko Biodiversity Protection Program (NGO). You will contribute to this by engaging with our partners in Equatorial Guinea, as well as local students from the island of Bioko. The project does not involve fieldwork on birds,

but you will have the opportunity (if you so wish) to join field expeditions to the tropical rainforest of Bioko as part of our monitoring and educational program.

Within the Naturalis research group Biodiversity Hotspots, you will work closely with Dr. Luís  $\frac{1}{2}$ s Valente. You will also work together with Dr. Martim Melo (FitzPatrick Institute of African Ornithology, South Africa) and Prof. Sonya Clegg (University of Oxford, UK). The project is a collaboration with Prof. Liliana D'Alba (Naturalis), Prof. Maximiliano Fero (University of Equatorial Guinea), the Bioko Biodiversity Protection Program (BBPP) and Dr. Luke Powell (CIBIO, Portugal).

You can find the description of the position here: <https://www.naturalis.nl/en/about-us/job-opportunities/-postdoc-birds-on-islands> Luís  $\frac{1}{2}$ s Lima Valente <luis.valente@naturalis.nl>

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## NortheasternU Boston Genomics

### Job Summary

A postdoctoral research associate is available at the Lotterhos Lab at Northeastern University. The postdoc will be based at Northeastern University's Marine Science Center and will work closely with PI Kathleen Lotterhos. NUMSC a strong research presence in evolution and ecology research and there are many opportunities for interaction and collaboration both there and in the greater Boston area.

**Key Responsibilities** The Postdoc will have the opportunity to develop self-directed research within the scope of existing lab projects on the ecological genomics of oysters, genomic forecasting, evolution of structural variants, and population genomics. More information on lab projects can be found in our lab publication record and our lab website: <https://sites.google.com/-site/katielotterhos/home> **Qualifications**

Must have a Ph.D.; be able to undertake substantially full-time research or scholarship; work under the supervision of a senior scholar. Applicants will be expected to develop and lead projects. Ideal candidates will have knowledge of population genomics, machine learning, and evolutionary theory. Candidates should have a strong track record of publication; be able to manage and analyze large datasets; have strong organizational,

written, and oral communication skills; and be able to work both independently and as part of a collaborative team. The initial appointment is for 12 months with the opportunity to extend the position for up to 24 months, dependent on funding.

### Application Materials

In a single PDF: cover letter with three references, CV, two examples of a research publication (at least one that has completed the peer review process)

### Additional Information

Northeastern University considers factors such as candidate work experience, education and skills when extending an offer. Northeastern has a comprehensive benefits package for benefit eligible employees. This includes medical, vision, dental, paid time off, tuition assistance, wellness & life, retirement- as well as commuting & transportation. Visit <https://hr.northeastern.edu/benefits/> for more information. All qualified applicants are encouraged to apply and will receive consideration for employment without regard to race, religion, color, national origin, age, sex, sexual orientation, disability status, or any other characteristic protected by applicable law.

Please email me if you would like to discuss the position. Review of applications will begin in mid-July.

K. E. Lotterhos, PhD Department of Marine and Environmental Sciences Coastal Sustainability Institute Northeastern University Marine Science Center Nahant, MA 01908

"Lotterhos, Katie" <k.lotterhos@northeastern.edu>

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## OhioStateU PhenotypicPlasticity

### The Ohio State University- Phenotypic plasticity

The Hellmann Lab at The Ohio State University seeks a Post Doctoral Scholar to contribute to a project investigating how developmental and transgenerational plasticity shapes individual responses to both natural and human-induced environmental change, using fish as model organisms. The successful candidate will have flexibility in determining the specific direction of the project; please see the lab website (<https://jehellmann45.wixsite.com/home>) for information about current research. The Post Doctoral Scholar should take

advantage of current fish colonies (threespined stickleback, mangrove rivulus) at OSU. Developing a strong field, genomic, or theoretical component would be welcome. This position will also supervise and mentor graduate and undergraduate students, analyze data, lead writing peer-reviewed publications, and participate in various lab duties and activities.

Required: Ph.D. degree in a field of biological sciences. Strong research experience in evolutionary biology, ecology, animal behavior, or related field(s). A record of conference presentations and/or peer-reviewed publications in academic journals.

The start date for this position is flexible, but ideally sometime in Summer 2025. Funding is for up to two years.

Applicants will please submit the following: (1) A cover letter describing relevant experience, research interests, and future goals. (2) A curriculum vitae. (3) Contact information (telephone number and email address) for three professional references. Please feel free to contact the PI (Jennifer Hellmann-Hellmann.13@osu.edu) with any questions. Applications received by May 30, 2025 will be prioritized. [https://osu.wd1.myworkdayjobs.com/OSUCareers/job/-Columbus-Campus/Post-Doctoral-Scholar\\_R128140](https://osu.wd1.myworkdayjobs.com/OSUCareers/job/-Columbus-Campus/Post-Doctoral-Scholar_R128140)

Jennifer Hellmann Assistant Professor Department of Evolution, Ecology, and Organismal Biology The Ohio State University Hellmann lab website Pronouns: she/her/hers

“Hellmann, Jennifer” <hellmann.13@osu.edu>

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## Prague MacroEvol DataAnalyst

We are hiring a Data Analyst postdoc to join our new team in Prague for a 2+years, see here for details: [https://www.researchgate.net/job/-1021667\\_Postdoctoral\\_data\\_scientist\\_in\\_macroecology\\_and\\_macroevolution\\_2\\_years\\_in\\_Prague](https://www.researchgate.net/job/-1021667_Postdoctoral_data_scientist_in_macroecology_and_macroevolution_2_years_in_Prague). Position Summary (for convenience):

Focus: Macroecology, macroevolution and biorhythms of avian parental care, fear (also urbanisation), and song

BULLAB Start date: September 2025 (negotiable) Duration: 2 years (with potential for extension) Application deadline: June 15, 2025.

Martin Bulla <bulla.mar@gmail.com>

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## PrincetonU ComputationalBiology

### Application for Postdoctoral Research Associate

Dr. Bridgett vonHoldt is seeking to hire a postdoctoral associate (or other senior research) in the areas of evolutionary and ecological analyses of large genome datasets, modelling and simulation biology, conservation genomics, and population genomics of admixture, introgression, and species concepts for North American canid species. This research is in collaboration with Colossal Foundation, a non-profit organization that uses science and technology to help preserve endangered species and ecosystems.

Candidates are required to have a Ph.D. or equivalent in evolutionary biology, genomics, or related fields. Candidate must have excellent computational and bioinformatic skills; abilities for developing simulation models (like SLiM) will be highly valued; experience with ancient DNA genomic datasets is encouraged but not required. Excellent writing ability in English is essential as well as creativity, energy, and the desire to work in an interactive and inter-disciplinary environment.

The Term of appointment is at the postdoctoral rank for one year with the possibility of renewal for two additional years, pending satisfactory performance and continued funding.

Research staff are entitled to University benefits. This position is subject to the University's background check policy. The work location for this position is in-person on campus at Princeton University.

Applicants must apply online at: <https://www.princeton.edu/acad-positions/position/38661>

and submit a curriculum vitae, a one-page statement of research experience and interests, and a cover letter that includes names and contact information of three references. References will only be contacted if the candidate is a finalist.

Princeton University is an equal opportunity/affirmative action employer, and all qualified applicants will receive consideration for employment without regard to age, race, color, religion, sex, sexual orientation, gender identity or expression, national origin, disability status, protected veteran status, or any other characteristic protected by law. Requisition No: D-25-EEB-00004

Bridgett vonHoldt, Ph.D. Professor Princeton University Ecology & Evolutionary Biology 106A Guyot Hall Princeton, NJ 08544-2016 Office:609-258-7021 vonholdt@princeton.edu <http://vonholdt.princeton.edu> <http://canineancestry.princeton.edu> [www.gulfcoastcanineproject.org](http://www.gulfcoastcanineproject.org) “Bridgett M. vonHoldt” <vonholdt@princeton.edu>

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## PurdueU EpigeneticClocks

Postdoc on Epigenetic Clocks at Purdue University (West Lafayette, IN, USA) — Closing date: 20th May 2025 or until the position is filled — A postdoc position is available immediately in Andrew DeWoody’s lab at Purdue University (West Lafayette, Indiana, USA). The successful applicant will develop, calibrate, and employ epigenetic clocks for use in demographic and evolutionary studies pertaining to wildlife and/or fisheries management. Requisite skills include DNA extractions (ideally from noninvasive sources), PCR, sequencing and basic statistical modeling (e.g., simple regression). Desired skills include qPCR, ddPCR, and/or bisulfite sequencing as well as elastic net regression or other statistical techniques suitable for use with high-dimensionality data. The initial appointment is for 12 months with the possibility of an extension.

Prospective applicants should first review this out-of-date webpage (<https://www.purdue.edu/fnr/sites/-dewoody/lab-members/potential-students/>), then contact Andrew DeWoody via email (please attach a current CV) to see if a video chat is warranted.

“Purdue University is a public research institution demonstrating excellence at scale. Ranked among top 10 public universities and with two colleges in the top four in the United States, Purdue discovers and disseminates knowledge with a quality and at a scale second to none. More than 105,000 students study at Purdue across modalities and locations, including nearly 50,000 in person on the West Lafayette campus. Committed to affordability and accessibility, Purdue’s main campus has frozen tuition 13 years in a row. See how Purdue never stops in the persistent pursuit of the next giant leap including its first comprehensive urban campus in Indianapolis, the new Mitchell E. Daniels, Jr. School of Business, and Purdue Computes.”

“DeWoody, James Andrew” <dewoody@purdue.edu>

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## RBI Zagreb Croatia AdaptiveEvolInCaves ShortDeadline

Postdoc in Molecular and Evolutionary Mechanisms of Cave Adaptation Ruder Boskovic Institute, Division of Molecular Biology, Zagreb, Croatia

We invite applications for a postdoctoral researcher to join our group in the Division of Molecular Biology at the Rudjer Boskovic Institute in Zagreb, Croatia. Our lab specializes in comparative evolutionary biology, with a focus on rapid adaptation and evolution in extreme environments, using cave-dwelling animals as model systems. We investigate the evolutionary mechanisms underlying adaptation to subterranean life by combining a diverse range of model organisms and multidisciplinary approaches. Our research integrates fieldwork, organismal biology, and wet lab techniques including developmental biology, molecular genetics, gene editing, imaging, and bioinformatics to address two central themes: The mechanisms driving loss of pigmentation across different cave-adapted animal phyla The role of phenotypic plasticity in cave colonization and the evolution of specialized adaptations Our goal is to uncover both the proximate mechanisms (e.g., genetic, developmental, and physiological processes) and the evolutionary drivers (e.g., selection, plasticity, constraint) that shape adaptations of cave animals. Our current grant focuses on the role of maladaptive plasticity in eye degeneration in the Mexican cavefish (*Astyanax mexicanus*). More about this project can be found on our lab website (<https://bilandzija.irb.hr/Projects-and-Funding>), and previous research on the topic is published here: doi: 10.7554/eLife.51830 and doi: 10.24272/j.issn.2095-8137.2022.528. In addition to working on this project, the postdoc will have opportunities to: Contribute to other ongoing research projects Analyse existing NGS datasets and prepare manuscripts for publication

Position Details: Funding is secured until December 2026. A 6-month trial period will be required at the start of employment. Extension is possible based on performance, collaboration quality, and mutual interests. Salary and Benefits: Gross salary: approx. 3000 EUR/month, depending on qualifications. Excellent benefits including health insurance, travel support, and



holiday bonuses

Required Qualifications PhD in Biology or a related discipline. Proficiency in English. Strong interest in basic research in evolutionary biology. Preferred Qualifications Experience with next-generation sequencing (NGS) data analysis. A solid background in statistics and/or R. Hands-on wet lab experience, especially staining and imaging techniques. Experience working with laboratory animals, particularly fish

We Offer A collaborative and supportive research environment (English-speaking) Access to excellent research infrastructure at Rudjer Boskovic Institute, including a dedicated *Astyanax mexicanus* facility and animal caretaker Opportunities for skill development via workshops (e.g., bioinformatics, data analysis) No teaching obligations, but teaching/supervision opportunities are available Funding for travel to conferences and workshops

Application Instructions Please refer to the full application details here: <https://euraxess.ec.europa.eu/jobs/-338545> .Application Deadline: Friday, May 23 at 23:00 CET Your motivation letter should include: Your research interests and career goals Relevant experience and qualifications Why you are interested in joining our lab and how you can contribute to our research

Helena Bilandija <Helena.Bilandzija@irb.hr>

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## Regensburg Germany BeeVirusMolEvol

PostDoc Position on host pathogen evolution in bees and viruses - ERC Project BeePath

We are looking for a postdoc to join us on the ERC consolidator project BeePath, where we study how the acquisition of vector-borne transmission via the Varroa mite has impacted on the epidemiology and evolution of an important bee pathogen, Deformed Wing Virus. The project integrates evolution in natural populations of honeybees and bumblebees with experimental viral evolution in the lab, fitness assays in the virus and its hosts and modelling to understand the ultimate drivers of pathogen and host fitness. The project team currently includes a post-doc and a PhD student and labwork is supported by an experienced technician dedicated to this project. Some background on

this system:doi:10.1111/ele.13323; doi:10.1038/s41467-025-57314-7; dot: 10.1098/rsbl.2023.0600 < <https://doi.org/10.1098/rsbl.2023.0600> >

The focus of this position should be on the molecular evolution of the virus and host populations from the field, based largely on existing samples and data (although more field work on for example the Channel Islands is an option). We are therefore looking for a candidate with experience in bioinformatics and molecular evolution and an interest in host-pathogen co-evolution. Expertise or an interest in working with our collaborator Prof Mike Boots (UC Berkeley) on mathematical models would also be welcome.

The position will be held at the University of Regensburg, where we will move this summer. For this position, you will join a diverse group working with various social insects on questions of disease transmission, behaviour, and adaptation. The position is open from the 1st of September 2025. Until March 2027, it is financed in part by the ERC grant. The position can then be extended for multiple years in accordance with the German Wissenschaftszeitgesetz. Please note that from April 2027, there is a (modest) teaching requirement which will include some teaching (such as practical supervision) in German. The position means that you are eligible to apply for full research grants as a PI or CoPI, and this would very much be encouraged.

For further information and applying, please contact Prof. Dr. Lena Wilfert [lena.wilfert@uni-ulm.de](mailto:lena.wilfert@uni-ulm.de). More information can be found on our website <https://www.uni-ulm.de/nawi/evolutionary-ecology-and-conservation-genomics/prof-dr-lena-wilfert/>The closing date is the 2nd of June 2025.

Lena Wilfert <[lena.wilfert@uni-ulm.de](mailto:lena.wilfert@uni-ulm.de)>

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## RoslinInst Edinburgh Two BreedingSimulation

Two postdocs: breeding simulation software development and biometrics/applied statistics

Two three-year postdoc positions are available within the HiPerBreedSim project at Edinburgh's Roslin Institute. With HiPerBreedSim, we are going to deliver new tools and resources to the breeding community and boost research in evolutionary genomics. The project is funded through a BBSRC BBR grant to Prof Gregor Gorjanc, Daniel Tolhurst, and Hannes Becher.

Postdoc 1 will work on genomic simulations and simulation software development working under Hannes Becher. They will extend our selective breeding simulator AlphaSimR and improve interoperability with the tree sequence (ancestral recombination graph) ecosystem. They will also add additional functionality for polyploids to the coalescent simulator msprime. Programming skills in R and Python are required as well as a background in genetics. More information and application link here: <https://elxw.fa.em3.oraclecloud.com/hcmUI/CandidateExperience/en/sites/CX.1001/-jobs/preview/12513> Postdoc position 2 is for a biometrician / applied statistician working under Daniel Tolhurst. They will develop novel extensions of AlphaSimR and FieldSimR to introduce complex phenotypes arising from multiple data streams, e.g. high-throughput and hyper-spectral longitudinal data. The post holder will help push the forefront of state-of-the-art data generation in breeding programmes to match the rising amount of data generated in the field. More information and application link here: <https://elxw.fa.em3.oraclecloud.com/hcmUI/CandidateExperience/en/sites/CX.1001/job/12535>

Both positions come with ample opportunities for publication and other dissemination.

Hannes Becher, Daniel Tolhurst, Gregor Gorjanc

For informal requests, contact [h.becher@ed.ac.uk](mailto:h.becher@ed.ac.uk), [dtolhurst@ed.ac.uk](mailto:dtolhurst@ed.ac.uk), or [gregor.gorjanc@roslin.ed.ac.uk](mailto:gregor.gorjanc@roslin.ed.ac.uk)

Hannes Becher <[hannesbecher@gmx.de](mailto:hannesbecher@gmx.de)>

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## TexasStateU MicrobialGenomicsPhylogenetics

The Sobol Ecology and Evolution of Early Life Lab (<https://sobollab.wp.txstate.edu/>) at Texas State University is looking to hire a Postdoctoral Scholar to begin Fall 2025.

**Position Summary:** As a postdoc in our lab, you'll apply your expertise in microbial 'omics analysis and phylogenetics to explore the biological, ecological, and environmental drivers contributing to the evolution of microbial life and their metabolisms. Applicants should have interests broadly in the fields of microbial ecology and evolution, geomicrobiology, and/or astrobiology.

You will be given substantial intellectual freedom to develop your own research projects, with possible directions including: 1) Gene regulatory network evolution, 2) Mechanisms of gene divergence and neofunctionalization, 3) Discovery of novel taxa and novel genes/pathways, 4) Unlocking eco-evolutionary drivers of metabolic evolution, or other related ideas.

You will be expected to be involved in the supervision of PhD, Master and Bachelor students. We're looking for someone excited to mentor students in computational approaches, whether through informal guidance or structured in-lab tutorials and workshops. Additionally, you will contribute to manuscript preparations and present your research at conferences.

**Qualifications:**

You hold a PhD in microbiology/microbial ecology or similar and have experience in bioinformatic methods for analyzing microbial sequence data (metagenomes, amplicons, whole genomes). Experience with collecting environmental samples, extracting microbial DNA, preparing sequencing libraries and any other wet lab experience is a big plus.

**Duration:** The position is available for up to two years pending satisfactory progress during the first year, with a 3% raise in the second year. Starting salary is \$60,000. Start date is somewhat flexible but should be between 8/1/25 and 12/31/25.

You must submit the following documents, in one single PDF, to Dr. Morgan Sobol ([msobol@txstate.edu](mailto:msobol@txstate.edu)) to be considered for the position:

A brief cover letter describing your interests and how

they align with the lab, your career goals, and what you expect from your experience in our lab.

Your CV with clear evidence of your skills in microbial 'omics data analysis.

A list of up to three references with contact information. We will contact references directly during the candidate selection process. Application review will start immediately and will continue until the position is filled. Questions and inquiries can be directed to Dr. Morgan Sobol.

“Sobol, Morgan S” <msobol@txstate.edu>

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### TrentU Canada MuskoxBisonConservation

Postdoctoral Fellow (PDF) - Muskox and Bison Conservation Genomics

Background: The Kyle laboratory, in close collaboration with partner institutions and agencies (e.g., Parks Canada) is working to understand the adaptive resiliency of large northern ungulates in context of rapid environmental change and acute selective pressures from disease. Current study systems include muskox and American bison, where archived and ongoing collections of specimens will be examined, comparing host genomic variation (specifically the immunome) and microbiome variation relative to disease status, stress indicators and other phenotypic data (e.g., body condition metrics). We are recruiting several PDFs and graduate students to assist with this research. There will be some flexibility to adapt projects to candidate interests with opportunities for field and lab work.

Location: Successful candidates will join the Kyle lab group at Trent University in Peterborough, ON, and will have access to networking and training opportunities with collaborators at U. Montreal, U. Calgary, Parks Canada, among other partners and stakeholders.

Qualifications and Eligibility: successful candidate must have PhD with relevant experience such as bioinformatic processing of genomic data, metabarcoding, or metagenomics.

Compensation:: no less than 60K CAD/year (negotiable based on experience). One year of funding is guaranteed with contract extensions based upon satisfactory

progress.

To Apply: Please send an email to Christopherkyle@trentu.ca including: a brief statement outlining research interests, previous experience and training relating to this project, C.V., and contact information for two references.

Applications will be reviewed as they are received.

Start Date: Summer / Fall 2025, negotiable

Christopher Kyle <christopherkyle@trentu.ca>

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### TrentU EnvMicrobialGenomics

Postdoctoral Fellow in Environmental Microbial Genomics

The Ecosystems and Global Change Group ([www.ecosystemchange.com](http://www.ecosystemchange.com)) at Trent University jointly led by Prof Andrew Tanentzap (Canada Research Chair in Climate Change and Northern Ecosystems) and Dr Erik Emilson (Research Scientist, Canadian Forest Service sector of Natural Resources Canada, <https://glfc-wet.github.io>) is recruiting a Postdoctoral Fellow to start immediately. The initial appointment will last for two years with a possibility for renewal.

The project: Permafrost thaw risks releasing microbes into the natural environment that have been isolated from modern ecosystems for millennia with unknown consequences for people and wildlife. We are searching for an experienced researcher to characterise microbial community composition, functioning, and evolution in thawing North American permafrost, with a particular focus on environmental pathogens and the application of single-cell sequencing approaches. Our research group also holds large sequencing datasets from freshwaters and soils that are often coupled with untargeted metabolomics data, offering substantial opportunities for focused data mining. The appointed candidate will have completed the requirements for a PhD by their start date and have evidence of an emerging publication record using state-of-the-art bioinformatics tools to analyse metagenomics sequencing data. The ideal candidate will have some knowledge relevant to long-read sequencing, single-cell microbial genomics, and whole genome assembly. The candidate will be expected to

mentor junior team members, so leadership experience will be advantageous.

What we can offer: Our research training environment features some of the most advanced environmental research infrastructure in Canada, including access to a Fourier-transform ion cyclotron resonance mass spectrometer, short- (Illumina) and long-read (Oxford Nanopore) sequencing facility with dedicated HPC, radioisotope and stable isotope labs, and eddy covariance systems, with extensive support for field research (ATVs, snowmobiles, autonomous surface vessel). As our team partners with government scientists, you will have a unique opportunity to influence environmental policy and make connections outside of academic to bolster your career.

We offer competitive wages (starting \$55k/yr) plus enhanced health and dental benefits. Peterborough is one of the most affordable and desirable places to live in Ontario, offering the best of urban (70 mins to Toronto) and rural living all under 30 minutes to the heart of the Kawarthas that boasts endless lakes and forests to explore. Our group supports flexible working arrangements and encourages applicants from diverse backgrounds as we strive to build a more equitable, diverse, and inclusive workplace. Overseas applicants will be supported in applying for a Work Permit.

How to apply: Please email Andrew Tanentzap (atanentzap@trentu.ca) with a CV and brief cover letter describing what you hope to get out of working with us, how your research interests are a good fit to our group, and how your past experiences make you suitable for this position. The position will remain open until filled.

Andrew Tanentzap <atanentzap@trentu.ca>

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## UCambridge TransmissibleCancer

Postdoctoral Research Associate: Chromosomal instability in marine transmissible cancers

An exciting new postdoctoral opportunity has become available in the Bivalve Transmissible Neoplasia Group ([www.zoo.cam.ac.uk/btn](http://www.zoo.cam.ac.uk/btn)), a small, interactive and international research team at the University of Cambridge, with strong collaborative links with other groups in Europe and the US. The group's research is focused on the genetics and evolution of a recently discovered family

of clonally transmissible cancers which affect several species of marine bivalves.

The new position is part of an ERC-funded project examining genome evolution in hundreds of samples from multiple independent marine transmissible cancer clones. A poorly understood aspect of these cancers is the phenomenon of extreme chromosomal instability, whereby individual cancer cells in a single animal may present a dynamic spectrum of karyotypes ranging from ~10 to ~350 chromosomes per cell (<https://doi.org/10.1038/s43018-023-00641-9>).

Our team is looking for a highly motivated postdoctoral researcher to lead new research into the mechanisms enabling such exceptional levels of chromosomal instability, as well as the long-term evolutionary consequences of this phenomenon, using a combination of single-cell genome sequencing and classical cytogenetics.

The role will involve: - Developing new methods for inference of copy number alterations from single-cell DNA sequencing data - Analysing patterns of single-cell copy number variation to identify mechanistic signatures of chromosomal instability - Learning and applying cytogenetic methods for generation and analysis of chromosome imaging data - Interacting with international experts in single-cell sequencing, cytogenetics, somatic evolution, and comparative cancer genomics - Possible scope for field work involving marine bivalves.

The ideal candidate will be self-motivated, passionate about cancer genome biology and somatic evolution, and willing to learn, develop and apply state-of-the-art molecular and computational approaches. They will hold a PhD in a relevant subject, have a solid computational background, and be able to curate, analyse and interpret complex single-cell data sets. Experience in molecular biology or cytogenetics is desirable but not essential.

Both the start date and the duration of this position are flexible.

Informal enquiries are encouraged and should be directed to Dr Adrian Baez-Ortega <ab2324@cam.ac.uk>.

For more details and how to apply: <https://www.jobs.cam.ac.uk/job/51236/> Adrian Baez-Ortega <ab2324@cam.ac.uk>

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## UColorado Denver TranscriptionalPlasticity

University of Colorado, Denver: Postdoctoral position in comparative transcriptomics and population genetics

The Ragland lab in the Department of Integrative Biology at the University of Colorado, Denver is seeking a postdoc to lead projects on the evolution of transcriptional plasticity and to contribute to analysis and interpretation of clinal, population genomic data sets. The primary project will involve 1) analysis of RNA sequencing data from experiments examining thermal plasticity of expression across *Drosophila* species from varying thermal environments, and 2) performing experiments to understand the thermal sensitivity of the gene regulatory landscape, also in a comparative framework. There are also opportunities to contribute to analysis and interpretation of clinal, genomic variation in populations of the fly *Rhagoletis pomonella* undergoing speciation with gene flow, and potentially to other ongoing projects in the lab (see below).

Initial appointment is for 12 months, with the possibility of extension.

Though the preference is for onsite, a hybrid on-site/remote model may be possible.

Required qualifications:

1) a PhD in a biological, or biology-adjacent sub-discipline 2) a solid background in either comparative/evolutionary physiology or evolutionary genetics 3) a solid background in statistics 4) an on the \*nix command line and experience working with next generation sequencing data 5) a proficiency in R

Preferred qualifications:

1) with wet lab molecular biology 2) a proficiency in one or more programming languages OR extensive experience with statistical models underlying analyses of gene expression, population genetic data, or phylogenetic comparative data

Salary:

Salary will be set on the current NIH postdoc pay scale with an excellent and flexible benefits package through CU.

The lab:

The Ragland lab is broadly interested in comparative and evolutionary physiology, the genomic architecture of rapid adaptation, and adaptation in variable environments (see <https://raglandlab.wordpress.com>). We are a friendly and diverse group who ask questions that cross biological disciplines and collaborate broadly to tackle these questions from multiple angles.

CU Denver and Integrative Biology:

The University of Colorado, Denver, the department of Integrative Biology, partner institutions (e.g., Denver Museum of Nature and Science, Denver Botanic Gardens), and nearby universities in the Front Range collectively provide a broad research community including infrastructure (e.g., sequencing and imaging facilities, high performance computing) and opportunities for collaboration. Denver is a vibrant city and serves as a gateway to world class outdoor recreation.

The review process:

Application review will begin 30 May and continue until the position is filled. Please submit a pdf file including 1) A brief cover letter outlining your experience, goals, and fit for the position, 2) CV, and 3) 1 - 2 representative publications or pre-prints to Greg Ragland at [gregory.ragland@ucdenver.edu](mailto:gregory.ragland@ucdenver.edu). Informal inquiries are welcome, I am happy to talk through more specifics about pre-existing data and planned experiments.

GREGORY.RAGLAND@UCDENVER.EDU

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## UCopenhagen 2yr NarwhalPopulationGenomics

Postdoc in narwhal population genomics and demography at Globe Institute, Faculty of Health and Medical Sciences, University of Copenhagen

We are looking for a highly motivated, competent, independent, and dynamic researcher for a 2-year Postdoctoral fellowship, with demonstrated experience in relevant areas of population genomic research. The position will commence on 1 October 2025, or as soon as possible hereafter.

The full-time postdoc position is funded by the Danish Independent Research Fund (DFF) 'BRIDGE – bridging



fundamental science and applied conservation in polar research', as part of their 2024 thematic research call in 'Arctic research - Climate change and sustainable arctic communities'.

Our research and work environment This postdoc position is a joint project between the Globe Institute at University of Copenhagen and Pinnngortitaleriffik (Greenland Institute of Natural Resources). The successful candidate will thus be part of both research environments.

The Molecular Ecology and Global Climate Change group at the Globe Institute is led by Professor Eline Lorenzen. The Lorenzen group integrates biomolecular data to understand patterns and drivers of eco-evolutionary change in mammal populations. We are an international group of PhD students and postdocs - currently from - China, Denmark, New Zealand, South Africa, and the US. Our work is interdisciplinary and highly collaborative, and we value a diverse, inclusive, supportive, and team-oriented work environment that fosters creativity. We are based in the Section for Molecular Ecology and Evolution, one of six research sections at Globe Institute.

Professor Mads Peter Heide-Jørgensen from the Greenland Institute of Natural Resources has extensive experience in marine mammal studies in Greenland, including narwhals. Mads Peter is responsible for the biopsy sampling program for narwhals in Scoresby Sound, which has been conducted annually since 2005 and is the foundation of this postdoc.

Senior researcher Marie Louis at the Greenland Institute of Natural Resources has a background in population genomics, ecology and evolution, with a focus on marine mammals, and has worked extensively on narwhal populations around Greenland.

The Greenland Institute of Natural Resources conducts research into Arctic ecosystems, monitors the living resources and the environment in Greenland, and advises the Government of Greenland and other authorities on sustainable exploitation of living resources and safeguarding the environment and biodiversity.

Your job Your research will focus on investigating patterns of demographic change in narwhals in Scoresby Sound, across the past 20 years, based on genetic analysis of a unique time series of 200 tissue samples collected by the Greenland Institute of Natural Resources since 2005.

Narwhals are considered the most sensitive Arctic marine mammal to climate change, due to their adaptations to a narrow sea-temperature niche, dependence on sea ice, specialised feeding habits, restricted range, and low

plasticity in migratory patterns. They are the first Arctic marine mammals that at a population level show clear signs of the effects of habitat loss. A recent letter in the journal *Science* by Heide-Jørgensen et al. (2020) served as a clarion call that narwhals require targeted conservation to ensure the survival of individual sub-populations, each of which has its own ecological niche, migratory routes, and exploitation history.

Over the past two decades in Scoresby Sound, a vital area for Inuit subsistence hunting, narwhals have experienced an alarming level of decline. Due to their extreme site fidelity and niche-conservative behaviour, the loss of sub-populations will likely be permanent, and recolonization is unlikely. The extirpation of this top predator from Scoresby Sound, one of the largest and longest fjord systems in the world, would widely affect the trophic cascades of the ecosystem, and in addition have major impacts on Inuit communities relying on them for subsistence and their cultural heritage.

This project will use genome-wide data to identify the demographic consequences of a rapidly decreasing population in this top predator. We hypothesise the decline has resulted in an increase in relatedness and a change in population composition in recent years. Hence, the project will (i) estimate changes in abundance since sampling of the narwhals in Scoresby Sound was initiated in 2005; (ii) identify individuals and their relatedness through time; (iii) infer changes in population composition and kinship using estimates of sex and relatedness.

Your findings will provide crucial insights into the status of not just this population, but also the food web and trophic cascades of which narwhals are an integral part, at timescales of direct relevance to conservation and management efforts.

Your work will include laboratory work for DNA data generation, and

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**UEdinburgh**  
**EvolutionaryMicrobiology**

A postdoctoral research position is available at the Institute of Ecology and Evolution, University of Edinburgh,

in the lab of Helen Alexander (<https://biology.ed.ac.uk/-alexander>). The postdoc will investigate emergence of antibiotic resistance in bacterial populations, using in vitro experiments. Candidates should have experience in experimental work with microbes, knowledge of evolutionary/ecological concepts, and good skills in experimental design, data processing and statistics. The position is for 16 months, ideally starting around Sept./Oct. 2025 but with considerable flexibility in start date. The closing date for applications is June 2nd. Full details and a link to apply available at: <https://tinyurl.com/-ws7s5dmb> The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336. Is e buidheann carthannais a th' ann an Oilthigh Dh'n ?ideann, cl?raichte an Alba, ?ireamh cl?raidh SC005336.

Helen Alexander <Helen.Alexander@ed.ac.uk>

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## UJyväskylä Finland AvianMicrobiomeSelection

Postdoctoral Researcher: Contribution of genetic background and gut microbiome on thermal physiology

A post-doctoral Researcher position is available at the Department of Biological and Environmental Sciences, University of Jyväskylä, Finland, in the group of Dr. Suvi Ruuskanen. The post-doctoral researcher will work on an ERC-funded project where the overarching aim is to understand the significance of the gut microbiome in thermal adaptations in birds within and across generations, and species. Application deadline is 15.7.2025, and starting date is very flexible, preferably between Nov 2025-Jan 2026.

### PROJECT DESCRIPTION

All animals on our planet carry microorganisms in their gut. The gut microbiome has recently been shown to be strongly linked to health in humans and model animals and there is a complex two-way interaction between gut microbiome and host physiology. For example, our group recently showed how temperature-induced variation in gut microbiome can have causal effects on host thermal physiology. However, we still have limited knowledge on the relative contribution of gut microbiome on host traits and the interplay with host genetic background. In this project the post-doctoral research will study the

contribution of host genetics and microbiome on cold tolerance by creating selection lines on thermal physiology, combined with microbiome-disturbance experiments, in an avian model system, the Japanese quail. In addition, the post-doc can contribute to other work on physiology, and gut microbiome and in the research group. The work is conducted at the University of Jyväskylä, with data collection at the Konnevesi Research Station, and collaborators include Dr. Barbara Tschirren (University of Exeter).

### DUTIES

The post-doctoral researcher position will involve setting up and running selection lines of Japanese quails, leading and conducting physiological data and sample collection, contribution to laboratory analyses (physiological and molecular), bioinformatic analyses of 16s rRNA data, manuscript preparation and supervision of students.

### QUALIFICATIONS

- Suitable candidates should have a PhD in evolutionary biology, (eco)physiology, molecular biology or related field by the time of starting the position, strong interest in animal physiology, host- microbiome research and bioinformatics.
- We are seeking a highly motivated, innovative, productive person, with good problem-solving and project management skills.
- The candidates should have experience of working with animals, some experience in laboratory analyses and strong analytical skills.
- The candidate is also expected to contribute intellectually to the project development.

The duties, qualification requirements, and language skills of a postdoctoral researcher are stipulated by the University of Jyväskylä Regulations and language skills guidelines. The PhD degree required for the position must have been completed before the starting date. A trial period of six months will be used in the beginning of the employment.

### WE OFFER

- Funding for 3 years at the University of Jyväskylä.
- International, enthusiastic working environment (working language is English) in a friendly research group with a large collaborator network.
- Possibility to join workshops etc to improve specific skills in e.g. bioinformatics, data analysis.
- Excellent research infrastructure at Jyväskylä (incl Konnevesi research station with animal caretaker), labs and state-of-the-art scientific equipment, software, access to journals and scientific databases.
- Resources for travel to conferences or workshops abroad.
- Possibility to teach and supervise students

At the University of Jyväskylä, you are a recognized

member of our community with a unique opportunity to influence international research. You get to participate in our international and multidisciplinary community where the welfare of each individual is important. At the University of Jyväskylä, we offer a great and lively campus area with opportunities to maintain an active and healthy lifestyle. Finland has a high standard of living, with free schooling (also in English), affordable childcare, good family benefits, and healthcare. Jyväskylä is located in central Finland in the Finnish lakeland and has excellent opportunities for different nature, outdoor, and sports activities. The city of Jyväskylä is a major educational center and the city has a large student population. As such there is a vibrant cultural scene in the city. To find useful information about the University of Jyväskylä, the City of Jyväskylä and living in Finland, see the University's International Staff Guide. The salary for a Postdoctoral Researcher is determined based on the task-specific demand level 5-6 of the university salary system for teaching and research

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## ULausanne BacterialGenomics

Join the Evolutionary Epidemiology group to work at the intersection of evolutionary theory, microbial ecology and public health.

We use mathematical and statistical modelling to draw insights from genomic and epidemiological data; address problems in public health; and answer fundamental questions about bacterial ecology and evolution.

We are looking for two postdoctoral researchers with experience in bacterial genomics (e.g. phylogenetics, phylodynamics, molecular evolution, pangenome analysis) to join our team. If you are interested in combining genomics and modelling, we are particularly keen to hear from you. There is scope to collaboratively shape the project, with possible directions including: - The evolutionary dynamics of antibiotic resistance. - The role of horizontal gene transfer in bacterial ecology and evolution. - Multi-locus models of pangenome evolution.

The Evolutionary Epidemiology group is based at the University of Lausanne's Computational Biology De-

partment. We are also affiliated with the NCCR Microbiomes, providing fantastic opportunities for collaborations with experimental, clinical and other modelling groups. The group is very friendly, with people from diverse backgrounds working on a range of projects relating to microbial evolution and dynamics. We're looking for curious, collaborative and thoughtful researchers. If you like our papers, we want to hear from you!

Essential information: - Duration: 2 years (initial contract for 1 year, but funding is available for 2 years) - Potential for further extension depending on funding - Start date: ideally October 2025, but there is flexibility in both directions - Apply by 31.05.2025

Your profile: - A PhD in a relevant topic, such as evolutionary theory, computational biology, bacterial genomics, by the start date. - Expertise in bacterial genomics. - Interest in mathematical modelling (experience is a bonus). - Excellent written and oral communication skills in English.

What we offer: - An exciting opportunity to shape your research in a supportive and stimulating environment. - Exceptional scope for collaboration through the NCCR Microbiomes network. - Access to top-notch resources and possibilities for independent funding and fellowships. - Excellent support for further learning and professional development. - Plenty of opportunities to attend conferences and to build your scientific network. - Attractive salary, beautiful location and excellent quality of life in a great city.

For more information and to apply: <http://tinyurl.com/n34vzsuz> Sonja Lehtinen <sonja.lehtinen@unil.ch>

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## UOslo NHM EvolutionaryBiology

The Natural History Museum, University of Oslo, is recruiting a 3y postdoctoral fellow in a self-developed project: <https://www.jobbnorge.no/en/available-jobs/-job/280531/postdoctoral-fellow-self-developed-project> Job description With this competitive three-year postdoctoral fellowship, the Natural History Museum, University of Oslo (NHM), aims to bring in a talented researcher to enhance our strategic research environment (<https://www.nhm.uio.no/english/research/groups/stadis/>).

Starting date: October 1st 2025, or as soon as possible

thereafter.

About the position and work environment The fellowship opportunity involves engaging in a self-developed and innovative research project. To foster collaboration, the successful candidate for this position will work in close collaboration with staff members of at least two of NHM's research groups (<https://www.nhm.uio.no/english/research/groups/>). The position comes with an independent research budget of 100,000 NOK per year.

Candidates should contact prospective NHM research groups to develop the proposal together. The ideal project will effectively utilize NHM's extensive physical and digital collections, either separately or in combination. This fellowship presents an exciting prospect to contribute to the advancement of knowledge and leverage NHM's resources in a meaningful way.

At our research environment, we seek to understanding the origins and processes governing stability and discontinuity of biological and geological systems at different levels of organization from the genome/atom to the ecosystem, including questions associated to:

- \* What characterizes a stable biological and geological system?
- \* How is it discontinuous from other biological or geological systems (stable or unstable)?
- \* How is stability and discontinuity of the system maintained?
- \* What happens with the system when stability and discontinuity break down?

NHM is located in Oslo's Botanical Garden, which is very close to the city center, and at Åkern. The Botanical Garden and the city of Oslo provide a vibrant environment for both work and personal life, with proximity to the forest, the Oslofjord and mountain areas.

For almost 200 years, specimens of animals, fungi, plants, rocks, minerals and fossils have been collected, studied and preserved at NHM. With over 6 million specimens, NHM has the largest natural history collection in Norway, including zoology, botany, mycology, paleontology, and mineralogy collections, in addition to a DNA bank. The improvement, maintenance and use of scientific collections is central to our work. The museum provides excellent research facilities in-house, with outstanding in-house expertise in DNA-based and molecular biology methods, microscopy and visualization, and analytical methods for the characterization of inorganic materials.

NHM has ten research groups that pursue research and education within basic and advanced biosystematics and biodiversity as well as geological studies. NHM is part of the University of Oslo (UiO), which is Norway's oldest and highest ranked educational and research institution. With its broad range of academic disciplines and internationally recognized research communities both

at NHM and UiO, both are important contributors to society.

Expectations and requirements for the project and host A fundable project shall:

- \* be innovative
- \* enhance the strategic research environment
- \* focus on bio- and/or geo-diversity
- \* be hosted by at least two of NHM's research groups
- \* enhance and/or use NHM's physical and digital collections, ideally both

Expectations of the postdoc:

- \* Carry out the project proposed in the application within the employment period
- \* Participate and contribute actively in the strategic research environment

Expectation for the Hosts:

- \* Primary and secondary hosts must be from different research groups at NHMO (<https://www.nhm.uio.no/english/research/groups/>)
- \* The primary host shall provide office space and administrative support

Qualification requirements The candidate must:

- \* have a degree equivalent to a Norwegian doctoral degree (PhD). For candidates not having finished their doctoral degree, the doctoral dissertation must have been submitted for evaluation by the closing date of the call. An appointment is dependent on the defense of the doctoral dissertation being approved
- \* have excellent communication skills (including written and spoken English) .

It is preferable that the candidate has (and can document):

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## UOttawa FungalComparativeGenomics

Postdoctoral position in Fungal Comparative (Epi)Genomics

A Postdoctoral Fellow position is available in the laboratory of Dr. Nicolas Corradi at the University of Ottawa (ON, Canada).

Postdoctoral (PDF) position would be initially funded for two years, and possibilities to extend the contract via



external funding are strongly encouraged and supported (e.g. Human Frontiers, Global Marie-Curie or NSERC Postdoctoral Fellowships).

The successful applicant will join a fun and inclusive lab supervised by Dr. Nicolas Corradi. The lab is located in the Department of Biology at the University of Ottawa (Ottawa, Ontario, Canada).

**Project:** the PhD or Postdoctoral trainee will help us continue to push boundaries in understanding the complex genetics and genomics of multinucleate plant symbionts called arbuscular mycorrhizal fungi (AMF). In particular, the candidate's work is expected to further highlight the intricate relationships between AMF genomics and those of their hosts through epigenomic analyses. For recent breakthroughs in this area, see representative publications below and our website (<https://corradiab.weebly.com/our-work.html>).

#### Application Process:

Generally, we seek someone who is excited about tackling questions that relate to complex genetic systems and genetic interactions between fungal symbionts and their plant hosts and learn new methods. Previous good knowledge of the following areas will be considered assets: Transcriptomics/Comparative genomics, Phylogenomics or Programming skills for the Life Sciences.

A complete application package includes 1) a CV, 2) Cover Letter with a short (half a page) description of past research accomplishments/future goals and 3) the names and e-mail addresses of at least two references. Complete applications can be sent to Dr. Nicolas Corradi: [ncorradi@uottawa.ca](mailto:ncorradi@uottawa.ca). N.B: Applications sent without the complete abovementioned documents and/or background will not be evaluated.

#### Starting date and eligibility

September 1st, 2025 (Flexible). Evaluation of applications starts immediately until a suitable candidate is found. Preference will be given to applications from Canadian citizens and Permanent residents. However, exceptional International applicants are welcomed to apply.

**Location:** The University of Ottawa is a large, research-intensive university, hosting over 40,000 students and located in the downtown core area of Canada's capital city (<https://www2.uottawa.ca/en>). Ottawa is a vibrant, multicultural city with a very high quality of life (<https://ottawatourism.ca/en>).

**Representative Publications and Preprints for the PhD position:**

JIN Oliveira, C Lane, K Mugambi, G Yildirim, AM Nicol, V Kokkoris, et al. Analyses of transposable elements

in arbuscular mycorrhizal fungi support evolutionary parallels with filamentous plant pathogens. *bioRxiv*.

Sperschneider J. \*, Yildirim Y. \*, Rizzi, Y., Malar C. M., Mayrand Nicol A., Sorwar E., Chen E.C.H., Brauer E.K., Bosnich W., Gutjahr C. and N. Corradi. Arbuscular mycorrhizal fungi heterokaryons have two nuclear populations with distinct roles in host-plant interactions. *Nature Microbiology* (8) 2142-5

Yildirim G. \*, Sperschneider J. \*, Malar MC, Chen ECH., Iwasaki W., Cornell, C. and N. Corradi. Long reads and Hi-C sequencing illuminate the two-compartment genome of the model arbuscular mycorrhizal symbiont *Rhizophagus irregularis*. *New Phytologist*. 223, 1097-1107

Malar M.C., Krüger M., Krüger C. \*, Wang Y., Stajich J.E., Keller J., Chen C.H., Yildirim G., Villeneuve-Laroche M., Roux C.R., Delaux P.M. and Corradi N. The genome of *Geosiphon pyriformis* reveals ancestral traits linked to the emergence of the arbuscular mycorrhizal symbiosis. *Current Biology*. 31, 1570-1577.e

Kokkoris V., Chagnon P.L., Yildirim G., Clarke K., Goh D., MacLean A.M., Dettman J., Stefani F. and Corradi N. Host identity influences nuclear dynamics in arbuscular mycorrhizal fungi. *Current Biology*. 31, 1531-1538.e6

Vasilis V., Dettman J., Dalpé Y., Stefani F. and N. Corradi. Nuclear Dynamics in the Arbuscular Mycorrhizal Fungi. 2020. *Trends in Plant Science* 25 p. 41-48.

Yildirim G., Malar M.C., Kokkoris V. and N. Corradi. 2020. Parasexual and Sexual Reproduction in Arbuscular Mycorrhizal Fungi: Room for Both. *Trends in Microbiology* 28 (7), 518-52

Ropars J., Kinga Sédziewska Toro K. Noel J., Pelin A., Charron P., Farinelli L., Marton T., Krüger M., Fuchs J., Brachmann A., and N. Corradi. Evidence for the sexual origin of heterokaryosis in Arbuscular Mycorrhizal Fungi. *Nature Microbiology* 1(6): 16033, 2016.

Nicolas Corradi

Professor and Chair in Microbial Genomics - Professeur et Chaire en Génomique Microbienne Department of Biology - Département de Biologie University of Ottawa - Université de Ottawa

Room GNN 257 - Phone: 613 562-5800 (ext 6563) - Website:

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TURCOTTE@pitt.edu

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## UPittsburgh PlantEvolution

Interested in the evolutionary and ecological impacts of whole genome duplication?

The Ashman and Turcotte labs at the University of Pittsburgh are looking to hire a postdoc that will leverage our experimental duckweed system *Spirodela polyrrhiza* a very rapidly reproducing floating aquatic plant. Using replicated experimental manipulations of genotype and environment, the postdoc will test what drives the competitive outcomes between diploids and polyploids using techniques from Modern Coexistence Theory. This population-level approach will test long standing hypotheses concerning the role of abiotic and biotic stresses, functional traits and phenotypic plasticity in promoting polyploid persistence. This postdoc is funded by an NSF DEB grant.

The postdoc will be: - co-mentored by both PIs in research, professional development, and outreach - active members of the vibrant community at Pitt and that of Biological Integrative Institute on Polyploidy (BII PI~3) [www.pi3biology.org](http://www.pi3biology.org) - supported in development of various experimental and analytical skills in an exciting emerging model plant system - major contributors to the focal projects and provided opportunities to develop independent lines of related research - supported in mentoring junior researchers including those who participate regularly in Ashman/Turcotte labs - participate in various broader impact activities

Requirements - Applicants should have (or will soon) a Ph.D. in a relevant field such as Ecolog, Evolutionary Biology, or Botany - Ideal candidates will have training in evolution and ecology and experience conducting experiments

Apply here: <https://shorturl.at/IIsUQ> And please include: 1) Cover letter: brief summary of your past research experience and why you are interested in the position 2) C.V. (or resume) 3) Contact information for three references

Application review will begin immediately; applications must be submitted by June 13th, 2025, to receive full consideration.

If you have any questions please don't hesitate to contact Drs. Tia-Lynn Ashman ([tia1@pitt.edu](mailto:tia1@pitt.edu)) and Martin Turcotte ([turcotte@pitt.edu](mailto:turcotte@pitt.edu))

## URegensburg+Germany InsectBioticInteractions

The Wilfert lab is looking for a postdoc to join us at the University of Regensburg, where we will be part of a new center for organismic biology focusing on biotic interactions. Our group works on a wide range of topics from the evolution of invertebrate immune systems to the drivers of biodiversity loss, with a focus on host-pathogen evolution and ecology in pollinators - more information on our research can be found here <https://www.uni-ulm.de/nawi/evolutionary-ecology-and-conservation-genomics/prof-dr-lena-wilfert/>. There are a range of ongoing and planned projects that you can join. The position will also allow you to develop your own research, in collaboration with our group and aligning with the center's focus. This means that you are eligible to apply for full research grants as a PI or CoPI, which is highly encouraged. Our lab offers a variety of options to investigate your research questions, as we integrate fieldwork, experiments, and genetic approaches. We primarily work with bumblebees, honeybees, ants, and *Drosophila*, but we are open to exploring other systems.

The position (E13, 100%) is initially for 4 years, starting from the 1st of September (based on the German Wissenschaftszeitgesetz). Importantly, the position comes with a (moderate) teaching load (5 SWS), but involves some teaching in German. Therefore, in addition to a PhD and research experience, you need to have at least some level of proficiency in German for this position (non-native speakers absolutely welcome!).

For further information and applying, please contact Prof. Dr. Lena Wilfert [lena.wilfert@uni-ulm.de](mailto:lena.wilfert@uni-ulm.de). More information can be found on our website closing date is the 2nd of June 2025.

Prof. Dr. Lena Wilfert University of Ulm Institute of Evolutionary Ecology and Conservation Genomics Albert-Einstein Allee 11 D-89069 Ulm Germany Tel.: 0049-731-5030615 Fax: 0049-731-5022683

email: [lena.wilfert@uni-ulm.de](mailto:lena.wilfert@uni-ulm.de) Website: <https://www.uni-ulm.de/nawi/evolutionary-ecology-and-conservation-genomics/prof-dr-lena-wilfert> Lena

Wilfert Ulm <lena.wilfert@uni-ulm.de>

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## UVienna GenomeTopology-CephalopodEvoDevo

Two postdoc (3yr) + technician (2yr) positions at U Vienna: Genome topology dynamics in cephalopod development and evolution

Two postdoc (3 years each) and a technician (2 year) positions available at the Department for Neuroscience and Developmental Biology at the University of Vienna in the group of Oleg Simakov (<https://neurodevbio.univie.ac.at/simakov-research/>), starting earliest from November 2025. The group's long-standing interests center around comparative genomics of animals and, more recently, emergence of evolutionarily irreversible genomic configurations and their role in shaping animal regulatory genome architectures (summarized here <https://link.springer.com/article/10.1186/s13227-025-00242-w>).

The first postdoc position, funded by a WEAVE grant with Eve Seuntjens (KU Leuven) and Simon Sprecher (U Fribourg), will be strongly embedded into the collaborative network of the three labs with the other members of the international teams in Belgium and Switzerland. The project will study changes in regulatory landscape during neuronal development across several cephalopod species. The second postdoc position (funded by an FWF grant) will study the regulatory landscape behind the symbiotic light organ development and evolution in the Hawaiian bobtail squid *Euprymna scolopes* and will also be embedded into a larger existing collaborative environment of the squid-Vibrio community. Both postdocs should have background in (or very strong interest for) evolutionary biology, with, optimally, expertise in comparative and/or evolutionary genomics and, ideally, with experimental experience in multiomics, HiC or similar techniques.

Additionally, a 2 year technician position is funded to support the lab in rearing cephalopod cultures. Prior animal husbandry and, optimally, basic molecular biology experience are advantageous.

Interested applicants should send their CV and letters of recommendation (or contacts) directly to Oleg Simakov ([oleg.simakov@univie.ac.at](mailto:oleg.simakov@univie.ac.at)) and Nina Znidaric

([nina.znidaric@univie.ac.at](mailto:nina.znidaric@univie.ac.at)) mentioning "PDFWF" in the subject. Deadline for applications is June 30th 2025. Monthly salary grades for postdoc and technician positions (including social and health insurance) are found at <https://www.fwf.ac.at/en/funding/steps-to-your-fwf-project/further-information/personnel-costs> Location of work will be at the University Biology Building and Vienna Zoo in Vienna (Austria).

Oleg Simakov <[oleg.simakov@univie.ac.at](mailto:oleg.simakov@univie.ac.at)>

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## UWesternAustralia PDF PhD MarineBiodiversity

Fully funded, deep-sea biodiversity and vision research opportunities

PhD, Postdoc & Program Manager positions available.

The School of Biological Sciences and the University of Western Australia Oceans Institute (Perth) are offering several research opportunities in the context of species evolution, delimitation and description, behaviour, physiology, and functional morphology of visual and other sensory systems in deep sea (midwater) invertebrates.

The project is supported by the Ocean Shot project (Sasakawa Peace Foundation) "Discovery in the largest frontier: advance imaging and genomics of open ocean animals"

The project is run in collaboration with Tohoku University, Sendai, Japan and Monterey Bay Aquarium Research Institute, Moss Landing, CA. Our aim is to accelerate the process of species discovery, classification, and documentation in the largest and least explored habitat on earth - the deep, open ocean or midwater. We have four primary objectives. 1. Expediting species discovery. 2. Fast and accurate classification. 3. Understanding the role of newly discovered species in oceanic processes. And 4. building collaboration within the midwater science and engineering community.

We will gather high-quality, biologically meaningful data about the morphology and sensory systems (with a focus on vision) of novel specimens using innovative in situ and ex situ imaging and sampling systems. Genome sequencing will produce reference libraries for a wide diversity of midwater invertebrates. At UWA we will develop and apply approaches such as bioinformatics,

modelling, anatomy (including 3D microCT), electrophysiology, and behaviour to identify, document and describe novel species and their midwater communities.

We are looking to assemble a dynamic and diversely skilled team to work together on this opportunity. We are looking for a program manager with an interest in deep sea biology, to bind it all together.

Positions available at University of Western Australia:

- Project/data manager (1+1+1 yrs)
- Midwater invertebrate behavior postdoc (1+1+1 yrs)
- PhD students (3.5 yrs)

Contact for further information: Prof Jan Hemmi  
jan.hemmi@uwa.edu.au

– Karen Osborn Research Zoologist/Curator of Polychaetes, Peracarids and Plankton Department of Invertebrate Zoology w 202.633.3668 osbornk@si.edu <http://orcid.org/0000-0002-4226-9257> Mail: Department of Invertebrate Zoology, Smithsonian National Museum of Natural History, MRC-163

P.O. Box 37012, Washington, D.C. 20013-7012 USA

Courier Address: Smithsonian Institution, MR 0163, Natural History, West Loading Dock, 10th and Constitution Ave NW, Washington, D.C. 20560

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\*\*

“Osborn, Karen” <OsbornK@si.edu>

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## WageningenU ModellingPhageEvolution

Postdoc position (2 years): Interacting scales in phage-host-superhost evolution

Laboratory of Phytopathology and Laboratory of Genetics, Wageningen University, the Netherlands

We are looking for a postdoctoral researcher that is eager to use spatially explicit modelling to study coevolution between phages, bacteria, and a eukaryote superhost, focusing on how feedback within and between these three ecological layers impacts bacteriophages virulence.

For this project, you need to have experience in mathematical modelling and/or eco-evolutionary simulations, and to be willing and able to closely collaborate with experimental biologists.

Project Eukaryote superhosts restructure environments, therewith favoring or opposing specific bacterial species and thus changing the availability of phage hosts. Moreover, phages and bacteria can hitchhike on mobile multicellular hosts and this movement may allow phages to access more distant bacterial hosts, which impacts selection pressures on phage virulence. In turn phage pressure on bacterial populations shapes the superhosts microbiome, potentially limiting the superhosts influence. In this project you will determine how specific patterns of migration, microbiome composition and environmental restructuring brought on by different superhosts (nematode, insect or plant) impact virulence in phage-bacteria coevolution. Different aspects of phage virulence, such as the ability to enter bacteria, range of bacteria that can be infected, and phage activation rate, will be described explicitly and left free to evolve in the model. This project runs parallel to and in close collaboration with experimental evolution studies of host-phage coevolution in nematodes and insects. Model runs will lead to hypotheses on likely adaptations in phage pathways, and on the correlation of phage abundance with host abundance, that can be tested in these experimental model systems. Thereby, you will contribute to fundamental understanding of feedback loops in host-parasite-superhost coevolution.

Job profile \* You have a PhD degree in a relevant field (preferably in evolutionary biology with hands-on experience in modelling or in mathematical/computational biology with a strong interest in evolutionary questions); \* You have demonstrable experience in mathematical modelling and/or eco- evolutionary simulations; \* You have programming experience (e.g., python, C++, or another language); \* You are enthusiastic to work on fundamental biological questions in close collaboration with experimental biologists and bioinformaticians; \* You are willing to supervise/guide undergraduate and MSc students; \* You contribute to an open and inclusive atmosphere.

Offer We offer a one year contract that will be extended for another year if there is mutual enthusiasm. Depending on experience, you will receive a gross salary of up to €3.707,- for a full-time working week of 38 hours. Benefits include: \* (Partially) paid parental leave; \* Holiday bonus (8%) and End-of-year bonus (8,3%); \* Flexibility in working hours and location to allow for healthy work- life balance;

More information For questions: hilje.doeke@wur.nl

To apply: [https://www.wur.nl/en/vacancy/-](https://www.wur.nl/en/vacancy/-postdoctoral-researcher-interacting-scales-in-host-pathogen-superhost-coevolution.htm) <hilje.doeke@wur.nl>

[postdoctoral-researcher-interacting-scales-in-host-pathogen-superhost-coevolution.htm](https://www.wur.nl/en/vacancy/-postdoctoral-researcher-interacting-scales-in-host-pathogen-superhost-coevolution.htm) “Doeke, Hilje”

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### Barcelona EMBO EvolMulticellularity Oct9-11

Dear colleagues,

We would like to announce the EMBO workshop “Evolution and origins of multicellularity across the tree of life” (<https://meetings.embo.org/event/25-multicellularity>) that we are organizing this October (9-11 Oct) in Barcelona, Spain.

Multicellular life formsâas animals, plants, and fungiâindependently and uniquely evolved across various branches of the tree of life. Are there any common principles that underlie the organization of these multicellular organisms? What factorsâ, genetic, ecologicalâthe trajectories of multicellular evolution?

To explore these questions, we are hosting a three-day workshop that brings together researchers studying diverse multicellular systems, from bacteria to organoids. In addition to invited talks, the program will include

oral and poster presentations selected from general submissions.

For more details on the program and invited speakers, please visit: <https://meetings.embo.org/event/25-multicellularity> You can also register for the event through this website.

If you have any interest in the evolution of multicellularity, we warmly encourage you to join us. We would also greatly appreciate it if you could share this information with anyone else who might be interested.

Travel support is available for students, and we especially welcome active participation from student attendees.

We will be happy to see you in our beautiful venue of the PRBB or online. The deadline for abstract application is June 1st. If you need more time, email us at [multicellverse-org@ibe.upf-csic.es](mailto:multicellverse-org@ibe.upf-csic.es) and we will try to adjust our timelines.

Feel free to spread the news among your contacts.

If you have any questions regarding the organization or scientific agenda, let us know.

Best,

Multicellverse Team (multicellverse-org@ibe.upf-csic.es)

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éâ'ç<< / Koryu Kin

éâ©âââ' / Juntendo University â>>â'é  
çââ'ç¬¬¬¬¬¬¬¬¬¬/Department of Biochemistry II, Faculty of Medicine  
/Department of Biochemistry and Systems  
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## Barcelona ESEB Coevolution Genomics Aug20

Call for Poster Submissions - ESEB 2025 Satellite Symposium: Ecological Genomics of Coevolution

We are pleased to announce the ESEB 2025 Satellite Symposium "Ecological Genomics of Coevolution", taking place on 20th August 20, 2025 at the International Convention Centre of Barcelona (CCIB) Venue: Google Maps link.

This one-day event will bring together researchers at the interface of ecology, evolution, and genomics to explore coevolutionary processes across diverse systems.

Program: - 2:00 - 2:10 PM - Welcome & Opening Remarks - 2:10 - 2:40 PM - Ellen Leffler (University of Utah) - Talk + Q&A - 2:40 - 3:25 PM - Young Researcher Talks 1-3 - 3:25 - 3:40 PM - Coffee Break - 3:40 - 4:10 PM - Joy Bergelson (New York University) - Talk + Q&A - 4:10 - 4:40 PM - Young Researcher Talks 4-5 - 4:40 - 5:40 PM - Poster Session & Networking

Poster Submissions Are Now Open!

We warmly invite early-career researchers to present their work during the poster session & networking hour. Submit your abstract here: <https://forms.gle/-3JXDCeBDvA1Cyabu7> Notes: \*This submission is separate from the main ESEB 2025 abstract call and deadline, as this is a satellite workshop. This is entirely normal for satellite events. \*Oral presentation slots have already been allocated by invitation and are not part of this call. \*People must have registered at the ESEB conference 2025 to apply for a poster here.

Please feel free to circulate this opportunity to colleagues

or students who may be interested. We look forward to your contributions!

The Organizing Committee

Amandine Cornille, Ph.D. She/Her/Hers

Assist. Prof. / Assistant Professor of Biology, NYU Abu Dhabi

Saadiyat Island campus

P.O. Box 129188 Abu Dhabi, United Arab Emirates

Twitter: @CornilleAmand or

@PommierVerger Bluesky: @CornilleAmand.bsky.social

Google Scholar profile

Group page (new to be announced soon)

To schedule a brief meeting with me, please use my appointment calendar.

Any message I send outside regular working hours does not require an immediate response.

Amandine Cornille <amandine.cornille@nyu.edu>

(to subscribe/unsubscribe the EvolDir send mail to goldring@mcmaster.ca)

## Barcelona ESEB Genomics Coevolution Aug20

\*Call for Poster Submissions - ESEB 2025 Satellite Symposium: Ecological Genomics of Coevolution\*

We are pleased to announce the ESEB 2025 Satellite Symposium \*"Ecological Genomics of Coevolution"\*, taking place on \*20th \*\*August 20, 2025\* at the \*International Convention Centre of Barcelona (CCIB) Venue: Google Maps link < <https://g.co/kgs/fm1NBaC> >.

This one-day event will bring together researchers at the interface of ecology, evolution, and genomics to explore coevolutionary processes across diverse systems.

ï\* Program\*:

- 2:00 - 2:10 PM - Welcome & Opening Remarks  
- 2:10 - 2:40 PM - \*Ellen Leffler\* (University of Utah) - Talk + Q&A  
- 2:40 - 3:25 PM - Young Researcher Talks 1-3  
- 3:25 - 3:40 PM - Coffee Break  
- 3:40 - 4:10 PM - \*Joy Bergelson\* (New York University) - Talk + Q&A



- 4:10 - 4:40 PM - Young Researcher Talks 4-5
- 4:40 - 5:40 PM - Poster Session & Networking

\*Poster Submissions Are Now Open!\*

We warmly invite early-career researchers to present their work during the \*poster session & networking hour\*. \*Submit your abstract here\*: <https://forms.gle/-3JXDCeBDvA1Cyabu7> \*Notes: \*

\*\*This submission is separate from the main ESEB 2025 abstract call and deadline, as this is a satellite workshop. This is entirely normal for satellite events.\*

\*\*Oral presentation slots have already been allocated by invitation and are not part of this call.\*

\*\*People must have registered at the ESEB conference 2025 to apply for a poster here.\*

Please feel free to circulate this opportunity to colleagues or students who may be interested.

We look forward to your contributions!

â€œThe Organizing Committee

\*Amandine Cornille, Ph.D.\* She/Her/Hers Associate Professor of Biology, NYU Abu Dhabi Saadiyat Island campus P.O. Box 129188 Abu Dhabi, United Arab Emirates

Twitter: @CornilleAmand < <https://x.com/-cornilleamand?lang=en> > or @PommierVerger < <https://x.com/pommierverger> > Bluesky: @CornilleAmand.bsky.social Google Scholar profile < <https://scholar.google.com/citations?user=EqIE2h8AAAAJ&hl=fr> >

Group page < <http://moulon.inrae.fr/en/equipes/-eclectic/> > (new to be announced soon)

\*To schedule a brief meeting with me, please use my appointment calendar < <https://calendar.app.google/-Ljeuk5Fmm5bgoUS6A> >.\* \*Any message I send outside regular working hours does not require an immediate response\*\*.\*

Amandine Cornille <amandine.cornille@nyu.edu>

(to subscribe/unsubscribe the EvolDir send mail to [golding@mcmaster.ca](mailto:golding@mcmaster.ca)<<mailto:golding@mcmaster.ca>>)

## Barcelona OriginMulticellularity Oct9-11

EMBO Workshop: Evolution and origins of multicellularity across the tree of life

The EMBO Workshop “Evolution and origins of multicellularity across the tree of life” will take place from 9-11 October 2025 and will be hosted by the Institute of Evolutionary Biology (IBE; CSIC-UPF).

The study of the origins and evolution of multicellularity in different lineages has recently captured the attention of many research groups and is fueling the generation of numerous innovative research articles. Can we identify universal principles of multicellularity and/or fundamental differences intrinsic to each lineage? Also, can we improve or modify our approaches and formulate new questions and hypotheses? In this workshop, we bring together researchers interested in different multicellular lineages, including complex multicellular plants, animals, and fungi as well as multicellular algae, protists, and prokaryotes. We will discuss the origins of cell differentiation and germ-soma segregation, genome evolution, modelling and mechanics of complex systems. We will also cover the topic of the evolutionary impacts of multicellularity, including potential downsides like the emergence of tumors.

This international workshop is designed for researchers from diverse disciplines and career stages who are interested in the evolutionary transition to multicellularity.

2025 | 9th-11th October

PRBB Auditorium

Learn more here

SPEAKERS:

Aurora M. Nedelcu - University of New Brunswick, CA  
Dolf Weijers - University of Wageningen, NL  
Elizabeth Ostrowski - Massey University, Auckland, AU  
Emma Hammarlund - Lund University, DK  
Gohta Goshima - Nagoya University, JP  
Hiroshi Suga - Prefectural University of Hiroshima, JP  
Jordi Paps - University of Bristol, UK  
Katrin Hammerschmidt - Christian-Albrechts-University Kiel, DE  
László Nagy - HUN-REN Szegedi Biológiai Kutatóközpont, HU  
Laura Nuño de la Rosa - Complutense University of Madrid, ES  
Maja Adamska - The Australian National University, AU  
Marco La Fortezza - ETH Zürich, CH  
Nicholas Irwin - Gregor

Mendel Institute of Molecular Plant Biology, AT NÄoria  
 Ros-Rocher - Institute Pasteur, FR Philip Donoghue -  
 University of Bristol, UK Ricard Solé - Institut de Biolo-  
 gia Evolutiva, ES Susana Coelho - Max Planck Institute  
 for Biology Tübingen, DE Tomislav Domazet LoÄo -  
 RuÄer BoÄkoviÄ Institute, HR Vikas Trivedi - EMBL  
 Barcelona, ES William Ratcliff - Georgia Institute of  
 Technology, US

Abstract submission: 1st June

Registration deadline: 20th July2025

Register here

CONTACT & VENUE:

Email: multicellverse@ibe.upf-csic.es

PRBB Auditorium Dr. Aiguader, 88 08003 Barcelona,  
 Spain

Feel free to share and/or forward this information to  
 anyone that might be interested.

Contact us:comunicacio@ibe.upf-csic.es

Institut de Biologia Evolutiva (CSIC-UPF) Dr.  
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 Barceloneta, 39 - 47,08003 Barcelona <http://ibe.upf-csic.es> | +34 932 309 645 | comunicacio@ibe.upf-csic.es

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## Copenhagen

### PopGenHighThroughputData

#### Aug4-8

Summer course in analysis of high throughput data for  
 population genetics

The course is a comprehensive introduction to a number  
 of topics and common research tools used in analyses of  
 next-generation sequencing (NGS) data. Topics include:  
 genetic drift, natural selection, population structure, re-  
 cent and ancient admixture, f-statistics and demographic  
 inference. We will cover the theoretical concepts but

the main focus is practical use of the methods. Lectures  
 will be combined with hands-on computer exercises.

Date: August 4-8, 2025 Place: Copenhagen, Denmark  
 (virtual option available) Organized by: The Depart-  
 ment of Biology and GLOBE, University of Copenhagen  
 Instructors: Martin Sikora, Shyam Gopalakrishnan, Ka-  
 tia Bougiouri, Fernando Racimo, Anders Albrechtsen,  
 and Ida Moltke

Price: On site: Free for all PhD students at Danish,  
 Faroese and Greenlandic universities. 200 Euro for all  
 other students. Virtual: Free

Price Includes: On site: All teaching. Food and accom-  
 modation are NOT included in the course fee. Virtual:  
 includes steaming, server access, and online teaching  
 assistants.

Sign up: [https://docs.google.com/-  
 forms/d/e/1FAIpQLSe-YM5Xjp-  
 xZpognNT5khZaWjV7ai0cHrGGWph1xzx4NnGjSw/-  
 viewform?usp=header](https://docs.google.com/forms/d/e/1FAIpQLSe-YM5Xjp-xZpognNT5khZaWjV7ai0cHrGGWph1xzx4NnGjSw/-viewform?usp=header) Contact: Credit and diploma:  
 The course is 2.5 ETCS credits and you will receive  
 a diploma. Africa BioGenome Project participants:  
 The course will be offered as part of the African  
 BioGenome Project Open Institute East and Central  
 Africa Regional Workshop.

Intended Learning Outcome

After the course the student should be able to: - Use pop-  
 ulation genetic theory to infer basic population genetics  
 characteristics from genetic data - Be able to infer ances-  
 try and population structure based on genetic data - Use  
 NGS data including low depth for population genetic in-  
 ference. - Select the optimal strategy for selection scans  
 depending on the population genetics characteristics  
 of the sample population, including taking population  
 structure into account - Interpret and discuss the results  
 of own analyses and results in the scientific literature

For more information and sign up visit: [https://-  
 website.popgen.dk/summer/](https://-website.popgen.dk/summer/) For questions write to cph-  
 summercourse@gmail.com

Patriĭ<sub>2</sub>cia Chrzanoviĭ<sub>2</sub> Pecneroviĭ<sub>2</sub>  
 <patricia.pecnerova@bio.ku.dk>

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## FrenchAlps PredictiveGenomics Sept8-12

Dear colleagues,

We are pleased to announce that registration is open for the fifth edition of the Software and Statistical Methods for Population Genomics(SSMPG) summer school, to be held in Aussois, France, September 8 - 12, 2025. Max 50 participants.

For this fifth edition, we will once again provide a comprehensive overview of software and statistical methods for detecting genes involved in local adaptation and predicting population risk of maladaptation to climate change.

As in previous editions, the program will feature keynote lectures, tutorials, and a data challenge, where participants will collaborate in teams to analyze simulated or real datasets. Attendees will also have the opportunity to present their own research during poster sessions.

The summer school will be held in the scenic village of Aussois, within the Vanoise National Park (French Alps), fostering interaction between mentors and participants and encouraging synergies among young researchers.

This year's instructors include:

Brenna Forester (U.S. Fish & Wildlife Service, USA)

Christian Rellstab (Swiss Federal Research Institute, Switzerland)

Orly Razgour (University of Exeter, UK)

Simon Boitard (INRAE, Montpellier, France)

Juliette Archambeau (INRAE, Université de Bordeaux, France)

Philippe Cubry (IRD, Université de Montpellier, France)

Mathieu Gautier (INRAE, Montpellier, France)

Olivier François (Université Grenoble Alpes, France)

Thibaut Capblancq (Université Grenoble Alpes, France)

For more details on the program and registration, please visit the school website:<https://-ssmpg2025.sciencesconf.org/> We hope to see you there!

Best wishes, Thibaut & Olivier

THIBAUT CAPBLANCQ <[thibaut.capblancq@univ-grenoble-alpes.fr](mailto:thibaut.capblancq@univ-grenoble-alpes.fr)>

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## FUBerlin ProgrammingForEvolBiol Feb17-Mar6

Course on Programming for Evolutionary Biology

When: 2026 February 17th - March 6th 2026

Location: Berlin, Germany

Application deadline: June 10th 2025

Detailed information about the course content and how to apply: <http://evop.bioinf.uni-leipzig.de/> Founded in 2012, our well established course is back with novel content! In this intensive 16 days course, students will learn how to survive in a Linux environment, get hands-on experience in two widely used programming languages (Python and R), and statistical data analysis. The classes will be given by experts in the field and consist of lectures and exercises with the computer. The aim of the course is to provide the students with the necessary background and skills to perform computational analyses with a focus on solving research questions related to genomics and evolution. The philosophy of the course will be "learning by doing", which means that the computational skills will be taught using examples and real data from evolutionary biology for the exercises. During the course, students will also propose projects of their own interest and perform them as final projects in small groups under the supervision of a teaching assistant. This course is open for students from all countries and targeted toward PhD students and postdocs of evolutionary biology or related research fields with no or little programming experience who want to become proficient in computational evolutionary biology in a couple of weeks.

The course takes place at the Free University of Berlin. For any questions related to the course, please send an email to: [evop@bioinf.uni-leipzig.de](mailto:evop@bioinf.uni-leipzig.de)

Katja Nowick Professorin für Humanbiologie Freie Universität Berlin Königin-Luise-Straße 1-3 14195 Berlin

<http://www.nowick-lab.info/> My working hours may not be your working hours. Please do not feel obligated to reply outside of your normal work schedule.

Katja Nowick <[katja.nowick@fu-berlin.de](mailto:katja.nowick@fu-berlin.de)>

(to subscribe/unsubscribe the EvolDir send mail to

golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

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## Krakow Poland Computational Genomics Jun7-12

Join us for the 4th East European Bioinformatics and Computational Genomics (EEBG) Workshop, June 7-12!

Hurry up and register this week for EEBG at MCB in Krakow. The application is free, and the early applications are eligible for scholarships.

Early Registration and Scholarship Application deadline extended till May 19th!

The application is free! Registration fees are due only after acceptance for on-site participation! The Scholarship waives the early registration fee and includes lodging and food in Krakow.

Read more: <https://lnkd.in/dmZsYCMN> Day 1: Frontiers in Computational Biology/Bioinformatics lectures & Galaxy workshop

Day 2: Metagenomics lectures & Metagenomics data analysis workshop

Day 3: Omics in Personalized Medicine lectures & Phylogenomics Using Geneious Software workshop

Day 4: Oxford Nanopore Technologies Day with lectures and a workshop

Day 5: Transcriptomics lectures & Transcriptomic data analysis workshop

Day 6: NVIDIA workshop

Lectures by: André G. Uitterlinden (Erasmus Univ, NL), Joaquin Dopazo (FPS, ES), Stephan Ossowski (Univ Tübingen, DE), Ugur Sezerman (Acibadem Univ, TR), Mariia Pavlovska (NASC, UA), Audrey Majeske (Oakland University, USA), Taras Oleksyk (Oakland University, USA), Serghie

Mangul (USC, USA), Alexander Lucaci, Ph.D. (WCM, USA), Joanna Polanska (SUT, PL), Tomasz Kościółek (Sano, PL), Guillem Ylla (FBBB UJ, PL) Krzysztof Szade (FBBB UJ, PL), Kinga Zielinska (MCB UJ, PL), Mateusz Sikora (MCB UJ, PL), Paweł P. abaj (MCB UJ, PL), ...

Dates: July 7-12, 2025 Location: Krakow, Poland (in-person and remote participation available)

Don't miss this fantastic opportunity to expand your

skills and network with the bioinformatics community.

Make sure you've submitted your application! Learn more and apply here: <https://eebg2025.edu.pl/> Taras K. Oleksyk, Ph.D.

Associate Professor Department of Biological Sciences Oakland University Dodge Hall, Rm. #367 118 Library Dr Rochester, MI 48309-4479 office: +1 (248) 370-3359 fax: (248) 370-4225 [oleksyk@oakland.edu](mailto:oleksyk@oakland.edu) <https://-oakland.edu/biology/directory/oleksyk> Taras Oleksyk <[oleksyk@oakland.edu](mailto:oleksyk@oakland.edu)>

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## Mainz Germany EvolutionAgeing Sep30-Oct2

Hi,

We are hosting an evolution of ageing workshop:

<https://gutenberg-workshops.uni-mainz.de/evolution-ageing/> Dr Edward Ivimey-Cook

Research Associate Monaghan Lab School of Biodiversity, One Health & Veterinary Medicine University of Glasgow Website: <https://eivimeycook.github.io/> President of SORTEE Interested in Open, Reliable, and Transparent Science? You might be interested in joining SORTEE!

Edward Ivimey-Cook <[Edward.Ivimey-Cook@glasgow.ac.uk](mailto:Edward.Ivimey-Cook@glasgow.ac.uk)>

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## Online BiodiversityData Jun9-13

Dear all,

We're excited to announce our upcoming online course: Analysing Biodiversity Through Time and Space Using R

Dates: 9-13 June 2025 Course website: ( <https://www.physalia-courses.org/courses-workshops/-biodiversity-in-r/> )

This hands-on course will guide you through building reproducible workflows for acquiring, cleaning, and analysing biodiversity data from both modern and fossil records. You'll explore how diversity patterns vary across space and time, and learn to address common sampling challenges using powerful R tools and packages.

By the end of the course, participants will be able to:

Access and clean biodiversity occurrence data from major databases (GBIF, PBDB, IUCN).

Analyse biodiversity patterns across spatial and temporal scales.

Visualise biodiversity data and estimate diversification rates using appropriate R tools.

Integrate palaeontological and neontological datasets for comprehensive biodiversity analysis. For the full list of your courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/-biodiversity-in-r/>)

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
info@physalia-courses.org mobile: +49 17645230846  
(<https://www.linkedin.com/in/physalia-courses-a64418127/>)

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## Online ConservationGenomics Jul2124

Dear colleagues,

We are pleased to announce the online course: Conservation Genomics.

Dates: 21-24 July

Course website: (<https://www.physalia-courses.org/courses-workshops/course62/>)

This course will provide a practical introduction to how population genomics can be applied to conservation. Participants will learn how to design studies, process raw genomic data, and perform analyses related to pop-

ulation structure, local adaptation, effective population size ( $N_e$ ), inbreeding, and relatedness.

Participants should have some basic background in evolution and population genetics. Previous experience in UNIX-based command line and R is required. Hands-on exercises will be run in a Linux environment on remote servers and data analysis and visualization will be run in R using RStudio.

For the full list of our courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/-course62/>)

Best regards, Carlo

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

info@physalia-courses.org

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(<https://www.linkedin.com/in/physalia-courses-a64418127/>)

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## Online DataAnalysisWithR Jun2-4

Dear all,

We're running an online course titled "A Practical Hands-On Introduction to R with the tidyverse" from 2-4 June and there a few seats left.

This course is aimed at researchers (with or without prior programming experience) who want to gain confidence in using R and tidyverse for data analysis and visualization. Over three days, we'll cover data wrangling, plotting with ggplot2, and creating reproducible reports with Quarto. The focus will be on interactive, hands-on learning using tools from the tidyverse ecosystem.

For more information, please visit: (<https://www.physalia-courses.org/courses-workshops/r-tidyverse/>)

For the full list of our courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/>)

Feel free to get in touch if you have any questions. Best



wishes,

Carlo

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR info@physalia-courses.org  
mobile: +49 17645230846 ( <https://www.linkedin.com/in/physalia-courses-a64418127/> )

"info@physalia-courses.org" <info@physalia-courses.org>

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ics interested in ecological applications. Basic experience with Unix commands and R is recommended.

Best regards, Carlo

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( <https://www.linkedin.com/in/physalia-courses-a64418127/> )

"info@physalia-courses.org" <info@physalia-courses.org>

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## Online eDNAMetabarcoding Jul14-18

Dear all,

We are pleased to announce the upcoming Physalia online course: Eukaryotic (eDNA) Metabarcoding

Dates: 14-18 July 2025 Format: Online Course website: ( <https://www.physalia-courses.org/courses-workshops/-course4/> )

This hands-on course offers an in-depth overview of metabarcoding techniques for the qualitative and quantitative assessment of biodiversity in natural communities. Participants will explore practical pipelines using short (Illumina)- and long (Nanopore)- data, and gain the skills to design and analyze their own metabarcoding projects.

By the end of this course, participants will be able to:

Understand the principles and workflow of DNA metabarcoding, including technical replication, sequencing depth, and methodological biases Recognize good laboratory practices for sample collection, DNA extraction, PCR, and library preparation Apply the AP-SCALE pipeline and BOLDigger for raw read processing and taxonomic assignment Use TaxonTableTools (TTT) for data filtering, alpha and beta diversity analysis, and result visualization Explore eDNA metabarcoding using Nanopore sequencing and understand its advantages and limitations in environmental applications Build local reference databases and design metabarcoding primers for custom applications

Confidently troubleshoot and design their own metabarcoding projects with expert support This course is intended for researchers in ecology, biodiversity, evolution and community biology, as well as those in bioinformat-

## Online ExploringBiodiversityPatterns Jun23-27

Dear colleagues,

Transmitting Science is offering a new course that may be of interest: "Macroecology in R: Exploring Biodiversity Patterns at Large Scales." It combines historical components of geographic patterns, phylogenies, and ecology to provide a comprehensive overview of evolutionary macroecology.

Places are limited to 16 participants.

Dates and schedule: Online live sessions from June 23rd to 27th, 2025, from 10:00-14:30 (Madrid time zone).

Course webpage: <https://www.transmittingscience.com/courses/ecology/-macroecology-in-r-exploring-biodiversity-patterns-at-large-scales/> COURSE OVERVIEW

This course provides a primer on Macroecology, focusing on geographic patterns of biodiversity and how those patterns are affected by species evolution and adaptation over time.

The course has a strong practical component in R. Students will learn to manipulate large geographic databases in R, grid-map biodiversity in various forms, conduct analyses of biogeographic regionalization incorporating evolutionary history, and estimate phylogenetic turnover and historical dispersal in geographic space. The practical sessions also cover common metrics in community phylogenetics and diversification, focusing on large geographic scales.

At the end of this course, participants will be able to:

\* Generate geographic maps of biodiversity (species diversity, trait diversity, etc.). \* Use phylogenies to incorporate evolution into geographic patterns of diversity. \* Construct biogeographic regions while accounting for the evolutionary relationship of species. \* Map historical patterns of diversification, historical dispersal, and phylogenetic turnover. \* Calculate and map in-situ diversification, the age of assemblages, and new tip-based metrics of trait evolution. \* Associate geographic patterns of biodiversity with ecological predictors. \* Integrate tools of macroevolutionary dynamics, such as estimating ancestral areas and ancestral traits, with community phylogenetic metrics.

Several datasets will be provided to illustrate the application of these methods. Participants are encouraged to bring their own datasets to analyze and discuss with the instructor.

If you have any doubts or questions, do not hesitate to write to [courses@transmittingscience.com](mailto:courses@transmittingscience.com)

Best wishes

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science [www.transmittingscience.com/courses](http://www.transmittingscience.com/courses) Bluesky @soledeesteban.bsky.social X @SoleDeEsteban Orcid: <https://orcid.org/0000-0002-2049-0890> Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to [info@transmittingscience.com](mailto:info@transmittingscience.com) or <http://transmittingscience.com/additional-terms>. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at [www.aepd.es](http://www.aepd.es). Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction.

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— / —

This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

## Online GenomeAnnotation May19-22

Dear all,

there are still 3 seats available for our upcoming Physalia online course: Introduction to Genome Annotation, taking place 19-22 May. More info and registration: ( <https://www.physalia-courses.org/courses-workshops/-genome-annotation/> ) This practical course will guide participants through key aspects of annotation workflows, including:

Sample quality and sequencing platform selection

Transcriptome assembly (ab initio and de novo)

Evidence-guided gene prediction (e.g., BRAKER, Augustus)

Building and assessing gene models

Approaches to genome-specific challenges By the end of the course, participants will be able to:

Set up and run a full annotation pipeline

Apply best practices to address annotation challenges

Use standard tools for gene prediction and evaluation For the full list of our courses and workshops, please visit: ( <https://www.physalia-courses.org/courses-workshops/-genome-annotation/> )

Feel free to share this with colleagues who may be interested.

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR

info@physalia-courses.org mobile: +49 17645230846  
( <https://www.linkedin.com/in/physalia-courses-a64418127/> )

“info@physalia-courses.org” <info@physalia-courses.org>

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## Online GenomeAnnotation May27-29

The Computational Biology Core at the University of Connecticut is hosting virtual bioinformatics workshops this spring! We still have space available in our Genome Annotation Workshop (virtual but live instruction - May 27-29). This hands-on workshop will cover genome assembly validation, annotation using tools such as Helixer, BRAKER, and EASEL, and evaluation of annotation results. Participants will gain practical experience with real datasets and learn how to generate high-quality genome annotations.

Learn more & register here: <https://bioinformatics.uconn.edu/cbc-workshops/> WHERE: Virtual (Zoom) WHEN: 10:00 AM - 2:00 PM EST COST: \$400 (UConn affiliates) â€€â€\$500 (External participants)

Registration is first come, first served.

Questions? E-mail cbcsupport@helpspotmail.com

“Lambert, Karelyn” <zsc25001@uconn.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

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## Online GWAS Jun23-27

Dear all,

there are only a few seats left for the upcoming Physalia online course on “Introduction to Genome-Wide Association Studies (GWAS)”, taking place from 23 to 27 June. Course page: ( <https://www.physalia-courses.org/-courses-workshops/course49/> )

Whether you're a student, researcher, or professional

looking to build a strong foundation in GWAS analysis, this course is designed to equip you with the core tools and knowledge needed to confidently approach GWAS data and workflows.

Over five days, the course will guide you through a comprehensive, module-based program. Each day features a combination of clear, engaging lectures and interactive discussions to reinforce key concepts. These will be followed by hands-on practical sessions, including both guided exercises with our instructors and independent tasks to deepen your understanding. You'll also have opportunities to discuss and interpret your results collaboratively with peers.

Participants should ideally have a background in biology, especially genetics. While basic familiarity with R and Unix is recommended, the course is structured to support learners with varying levels of experience. For a complete overview of our training programme, please visit: ( <https://www.physalia-courses.org/courses-workshops/> )

Best regards, Carlo

Carlo Pecoraro, Ph.D Director, Physalia-coursesinfo@physalia-courses.org +49 176 45230846

“info@physalia-courses.org” <info@physalia-courses.org>

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## Online Inclusion May15-16

“Hi all,

My colleagues in the Animal Behavior Society and I are organizing a Supporting Inclusion in Graduate Networks and Leadership (SIGNAL) community and career development workshop that will be held on May 15th and 16th this year. Our keynote speakers are Dr. Charissa Owens, the director of Diversity, Equity, Inclusion and Belonging at the Yale School of Nursing, and Dr. Cesar Estien, an urban ecologist working at Second Nature Design, who helped start the EEB Language Projection using more inclusive terminology in ecology and evolution.

SIGNAL is a fantastic opportunity to network with scientists in academic and non-academic careers, as well as students and staff at other institutions. The deadline to apply is May 9th on the SIGNAL website (<https://->

[signal-ab.weebly.com/](http://signal-ab.weebly.com/)).

Undergraduate students, post-bacc researchers, and lab technicians working in any research area related to the intersection of evolution and animal behavior are highly encouraged to apply. Participants will hear from keynote and panel speakers who work in traditional academic, alternative academic, and industry careers.

Please disseminate this information to anyone in your respective networks who may be interested!

Grace Smith-Vidaurre, PhD (she/her) 1855 Assistant Professor Department of Integrative Biology Department of Computational Mathematics, Science, and Engineering Michigan State University

"Smith Vidaurre, Grace" <[smithvid@msu.edu](mailto:smithvid@msu.edu)>

(to subscribe/unsubscribe the EvolDir send mail to [goldring@mcmaster.ca](mailto:goldring@mcmaster.ca))

## Online IntroPalaeogenomics May21-27

Dear colleagues,

Transmitting Science has opened registration for the online course "Introduction to Palaeogenomics".

Date and schedule: Online live sessions on May 21st, 22nd, 23rd, 26th, and 27th, 2025; from 16:00 to 21:00 (Madrid time zone).

Course webpage: <https://www.transmittingscience.com/courses/genetics-and-genomics/introduction-to-palaeogenomics-concepts-methods-and-applications-of-ancient-dna-data/> Course Overview:

Ancient DNA (aDNA) research, defined as the retrieval and analysis of DNA sequences from various degraded biological materials, has been evolving as a research field for four decades.

DNA extracted from archaeological samples, and museum specimens has proven useful to study species and life on earth from the genomic perspective. It has made it possible to measure changes in genetic diversity through time, test hypotheses about the association of environmental phenomena and genetic changes in natural populations, and to resolve long-standing questions about the evolutionary relationships between species.

In a combination of interactive lectures and hands-on

practical sessions, this course will provide a theoretical overview of molecular biology laboratory techniques for the retrieval of aDNA from ancient samples from different species and an introduction to the bioinformatic pipelines for the analysis of palaeogenomic data.

Students will be introduced to the standard bioinformatic methods often used in palaeogenomic projects for the analysis of aDNA data from human and non-human samples.

We will also review the history and developments of the field to understand how it came to be what it is today and consider and discuss the practical problems of ancient DNA recovery, the theoretical problems associated with the interpretation of palaeogenomic data, and the ethical implications embedded in this type of research.

At the end of the course, students will have gained a general understanding of common key methods and tools used in palaeogenomics projects: from the basics in the field to the interpretation of the results, as well as ethical and responsibility aspects and implications of aDNA research.

If you have any questions, please do not hesitate to write to [courses@transmittingscience.com](mailto:courses@transmittingscience.com)

Best wishes

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science [www.transmittingscience.com/courses](http://www.transmittingscience.com/courses) Bluesky @soledeesteban.bsky.social X @SoleDeEsteban Orcid: <https://orcid.org/0000-0002-2049-0890> Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to [info@transmittingscience.com](mailto:info@transmittingscience.com) or <http://transmittingscience.com/additional-terms>. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at [www.aepd.es](http://www.aepd.es). Confidentiality. -

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Soledad De Esteban-Trivigno  
<soledad.esteban@transmittingscience.com>

(to subscribe/unsubscribe the EvolDir send mail to gold-ing@mcmaster.ca)

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## Online MappingTraitEvolution, May26-Jun4

Dear colleagues,

There are a few places available for the online course MAPPING TRAIT EVOLUTION (8th edition!).

Dates and schedule: Online live sessions on May 26th, 28th, and 30th & June 2nd and 4th, 2025, from 14:00 to 18:00 (Madrid time zone).

Instructor: Jeroen B. Smaers (Stony Brook University, USA).

Course webpage: <https://www.transmittingscience.com/courses/-evolution/mapping-trait-evolution/> or writing courses@transmittingscience.com

### COURSE OVERVIEW

The course provides a comprehensive overview of the state-of-the-art methods in mapping phenotypic trait evolution and will provide participants with a springboard to using these methods to answering their own research questions.

We focus on analyses that use a phylogenetic tree and observed trait information from tip taxa (extant and/or extinct) to describe how traits have changed along the branches of a phylogeny. The course covers methods

that estimate and test patterns related to changes in mean, covariation, and rate. Applications for continuous and categorical, and univariate and multivariate research designs are discussed.

At the end of this course, participants will have developed an understanding of: (1) Brownian motion and Ornstein-Uhlenbeck models of evolution. (2) How these models can be applied to estimate and test patterns of trait evolution. (3) What the advantages and disadvantages are of different models/methods. (4) How to recognize which model/method is most appropriate given a particular dataset and research question.

We provide several data sets that will be used to exemplify the application of these methods. We do, however, encourage participants to work with their own data so as to get direct experience with analysing precisely what they expect to analyse.

Methods from the following R packages will be discussed: ape, geiger, phytools, evomap, I1ou, bayou, surface, OUwie, mvMORPH, geomorph (this list may change as new packages become available).

Important note: Please bear in mind that this course is not about reconstructing (building) phylogenetic trees, the methods we cover in this course assume that a phylogeny is known.

If you have any doubts or questions do not hesitate to write to courses@transmittingscience.com

Best wishes

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science [www.transmittingscience.com/courses](http://www.transmittingscience.com/courses) Bluesky @soledeesteban.bsky.social X @SoleDeEsteban Orcid: <https://orcid.org/0000-0002-2049-0890> Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona)



or sending an email to [info@transmittingscience.com](mailto:info@transmittingscience.com) or <http://transmittingscience.com/additional-terms>. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at [www.aepd.es](http://www.aepd.es). Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction. Disclaimer of liability. - The sending of this communication does not imply any obligation on the part of the sender to control the absence of viruses, worms, Trojan horses and/or any other harmful computer program, and it corresponds to the recipient to have the necessary hardware and software tools to guarantee both the security of its information system and the detection and elimination of harmful computer programs. TRANSMITTING SCIENCE SL shall not be liable.

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(to subscribe/unsubscribe the EvolDir send mail to [goldring@mcmaster.ca](mailto:goldring@mcmaster.ca))

## Online MappingTraits May26-Jun4

Dear evoldir members,

A few spots are still available for the Transmitting Science course: "Mapping Trait Evolution" (8th edition).

The course provides a comprehensive overview of the state-of-the-art methods in mapping phenotypic trait evolution and will provide participants with a springboard to using these methods to answering their own research questions.

Max capacity: 16 participants Format: Live online sessions Dates: May 26th, 28th, and 30th & June 2nd and 4th Schedule: 14:00-18:00 (Madrid time)

Instructors: Dr. Jeroen B. Smaers (Stony Brook University, USA)

Learn more and register here: <https://www.transmittingscience.com/courses/evolution/-mapping-trait-evolution/> Course overview:

We focus on analyses that use a phylogenetic tree and observed trait information from tip taxa (extant and/or extinct) to describe how traits have changed along the

branches of a phylogeny. The course covers methods that estimate and test patterns related to changes in mean, covariation, and rate. Applications for continuous and categorical, and univariate and multivariate research designs are discussed.

If you have any questions do not hesitate to contact us at [courses@transmittingscience.com](mailto:courses@transmittingscience.com)

Best regards,

Haris

Check the full list of upcoming courses here: <https://www.transmittingscience.com/courses/> Haris Saslis, PhD Course Coordinator Transmitting Science [www.transmittingscience.com](http://www.transmittingscience.com) [1]

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Links:

[1] <http://www.transmittingscience.com> [2] <http://www.es> Haris Saslis - Transmitting Science  
<haris.saslis@transmittingscience.com>

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## Online MultiOmicsIntegration Jun9-11

Dear all,

We are thrilled to announce our upcoming course on Machine Learning for Multi-Omics Integration, taking place online from June 9-11! This is your chance to dive into the world of biological Big Data and harness the potential of cutting-edge machine learning techniques to uncover hidden insights from diverse Omics datasets.

Multi-Omics integration is the key to unlocking synergies across datasets, helping us reveal novel biological pathways and better understand cellular behavior. With machine learning, we can take this integration to the next level, making sense of complex data to drive forward breakthroughs in biology and medicine.

Course website: ( <https://www.physalia-courses.org/-courses-workshops/multiomics/> )

In this hands-on course, you'll explore: Machine learning methodologies for integrating large biological datasets. Supervised and unsupervised approaches to Omics integration. Deep learning techniques tailored to multi-omics data. Best practices and tools for single-cell Omics integration. For the full list of our courses and workshops, please visit: ( <https://www.physalia-courses.org/-courses-workshops> )

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
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## Online ReproducibilityInBioinformatics Jul7-9

Dear all,

We are excited to announce the Physalia upcoming online course on Reproducibility in Bioinformatics, taking place from July 7-9, from 2-8 PM (Berlin time) Course website: ( <https://www.physalia-courses.org/courses-workshops/bioinformatics-reproducibility/> ) This hands-on course will introduce key strategies to make your bioinformatics workflows more reproducible and transparent. You will learn to use containers, virtual environments, version control, and workflow management systems like Snakemake and Nextflow. Topics include:

Best practices in data organization and documentation

Version control with Git

Using and building containers (Docker/Singularity)

Setting up reproducible workflows (Snakemake, Nextflow)

Running pipelines across different computing environments For the full list of our courses and workshops, please visit: ( <https://www.physalia-courses.org/courses-workshops/> )

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
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( <https://www.linkedin.com/in/physalia-courses-a64418127/> )

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## Online SpeciesCommunityAnalysis Sep15-19

ONLINE COURSE - Multivariate Analysis Of Ecological Communities Using R With The VEGAN

package (VGNR08) <https://www.prstats.org/course/-multivariate-analysis-of-ecological-communities-using-r-with-the-vegan-package-vgnr08/> 15th - 19th September 2025 Please feel free to share!

We encourage attendees to bring their own data, you will receive opportunities to discuss your data with the instructor throughout the course, if you would like guidance on how to organize your data prior to the course please ask [oliverhooker@prstatistica.com](mailto:oliverhooker@prstatistica.com) This course is suitable for researchers (PhD and MSc students, post-docs, primary investigators) and environmental professionals who are interested in implementing best practices and state-of-the-art methods for modelling species' distributions or ecological niches, with applications to biogeography, spatial ecology, biodiversity conservation and related disciplines.

This 5-day course will cover R concepts, methods, and tools that can be used to analyze community ecology data. The course will review data processing techniques relevant to multivariate data sets. We will cover diversity indices, distance measures and distance-based multivariate methods, clustering, classification and ordination techniques using the R package VEGAN. We will use real-world empirical data sets to motivate analyses, such as describing patterns along gradients of environmental or anthropogenic disturbances, and quantifying the effects of continuous and discrete predictors. We will emphasise visualisation and reproducible workflows as well as good programming practices. The modules will consist of introductory lectures, guided computer coding, and participant exercises. The course is intended for intermediate users of R who are interested in community ecology, particularly in the areas of terrestrial and wetland ecology, microbial ecology, and natural resource management. You are strongly encouraged to use your own data sets (they should be clean and already structured, see the document: "recommendation if you participate with your data").

Classes will run from 08:00 - 13:00 for the morning lecture and 14:00 - 16:00 for the practical (UK time) with an evening time session tbc for US, Canada etc. attendees. The course will be recorded and made available each day and will remain available for 28 days after the course for you to revisit any lectures. DAY 1 - Module 1: Introduction to community data analysis, basics of programming in R - Module 2: Diversity analysis, species-abundance distributions

DAY 2 - Module 3: Distance and transformation measures - Module 4: Clustering and classification analysis

DAY 3 - Module 5: Unconstrained ordinations: Principal Component Analysis - Module 6: Other unconstrained ordinations

DAY 4 - Module 7: Constrained ordinations: RDA and other canonical analysis - Module 8: Statistical tests for multivariate data and variation partitioning

DAY 5 - Module 9: Overview of Spatial analysis, and recent Hierarchical Modeling of Species Communities (HMSC) methods - Modules 10: Special topics and discussion, analyzing participants' data.

Email [oliverhooker@prstatistics.com](mailto:oliverhooker@prstatistics.com) with any questions. – Oliver Hooker PhD. PR stats

Oliver Hooker <[oliverhooker@prstatistics.com](mailto:oliverhooker@prstatistics.com)>

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## Online VariantDetection May20-22

The Computational Biology Core at the University of Connecticut is hosting virtual bioinformatics workshops this spring! We still have space available in our Variant Detection Workshop (virtual but live instruction - May 20-22). This hands-on workshop will cover genome preparation, sequencing quality control, sequence alignment, and variant detection using tools such as FreeBayes, GATK, and bcftools. Participants will also explore functional annotation and data visualization using real datasets.

Learn more & register here: [bioinformatics.uconn.edu/cbc-workshops/](http://bioinformatics.uconn.edu/cbc-workshops/)

WHERE: Virtual (Zoom) WHEN: 10:00 AM - 2:00 PM EST COST: \$400 (UConn affiliates) €€\$500 (External participants)

Registration is first come, first served.

Questions? E-mail [cbcsupport@helpspotmail.com](mailto:cbcsupport@helpspotmail.com)

"Lambert, Karelyn" <[zsc25001@uconn.edu](mailto:zsc25001@uconn.edu)>

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## StAndrews MLGenomics Jun24-27 AbstDeadlineMay13

\*\*\* Call for Participation and Abstracts\*\*\*

We are happy to announce the workshop “Short and long timescales in speciation genomics: Machine Learning approaches” (ML Speciation Genomics) to be held on 24th-27th June 2025 at University of St Andrews/Scotland. We have extended the deadline for abstract submission to \* May 13th\*.

\*\*\*About the Workshop \*\*\*

How new species emerge is one of the big questions in evolutionary biology. Speciation genomics investigates the genetic basis of this process. Until recently researchers were only able to sequence a few individuals at a single time-point. Yet, with the growing affordability of genome sequencing, it is now possible to consider multiple individuals at multiple points in time.

These multiple time-points could include samples from Natural History Museums, they could be multiple generations of a population housed in controlled laboratory environments or diverse samples collected from the wild. This workshop will bring researchers together to make the best use of the new data. We will have introductory lectures, contributed talks as well as hands-on sessions on museum genomics, phylogenomics and machine learning methods.

We have conference rates for students of £12.50 and £17.50 for all academics and industry participants. Reduced rate conference accommodation can be booked at Agnes Blackadder Hall.

\*\*\* Faculty \*\*\*

Nick Bailey, Rui Borges (University of St Andrews); Svitlana Braichenko (University of Edinburgh); Martin Kapun (Natural History Museum of Vienna); Carolin Kosiol (St Andrews); Manolo Perez (Imperial College London); Antonio Pacheco, Mike Ritchie (St Andrews); Alexander Suh and Christoph Mayer (Research Museum Koenig Bonn) among others.

\*\*\* Important Dates \*\*\*

Registration opens: 17th March 2025 Abstract submission: 13th May 2025 (please send an email to: [MLSpeciationGenomics@gmail.com](mailto:MLSpeciationGenomics@gmail.com))

Reduced rate accommodation: 24th April 2025 Registration closes: 2nd June 2025 Conference: 24th- 27th June 2025

For registration and more information see

<https://www.eventsforce.net/standrews/264/home>

<https://ckosiol.github.io/MLSpeciationGenomics/>

Looking forward to seeing you in St Andrews!

Dr Carolin Kosiol Reader in Bioinformatics Centre for Biological Diversity School of Biology University of St Andrews St Andrews, Fife KY16 9TF, UK [ck202@st-andrews.ac.uk](mailto:ck202@st-andrews.ac.uk)

<https://biology.st-andrews.ac.uk/kosiol-lab/> Carolin Kosiol <[ck202@st-andrews.ac.uk](mailto:ck202@st-andrews.ac.uk)>

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Instructions: To be added to the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; Workshops/Courses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). In addition, if it originates from ‘blackballed’ addresses it will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email [evoldir@evol.biology.McMaster.CA](mailto:evoldir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. ... plain old

ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

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