

# An Introduction to Bioinformatics

WEILONG HAO



## **Bio-Informatics**

- ◆ **To use computers for the management and analysis of biological information**
- ◆ **Internet + Programs + Data**

# **DNA and Protein**

**A T C G**

# DNA and Protein

<b>Ala A</b>	<b>Leu L</b>
<b>Arg R</b>	<b>Lys K</b>
<b>Asn N</b>	<b>Met M</b>
<b>Asp D</b>	<b>Phe F</b>
<b>Cys C</b>	<b>Pro P</b>
<b>Glu Q</b>	<b>Ser S</b>
<b>Gln Q</b>	<b>Thr T</b>
<b>Gly G</b>	<b>Trp W</b>
<b>His H</b>	<b>Tyr Y</b>
<b>Ile I</b>	<b>Val V</b>

# A Protein Sequence

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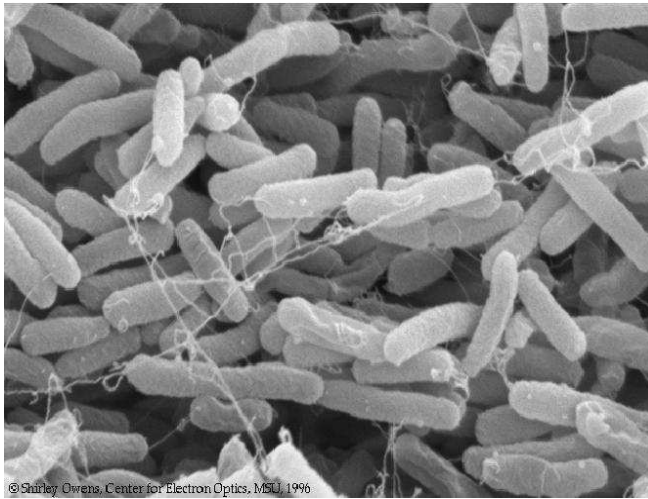
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# DNA Sequence

## ORIGIN

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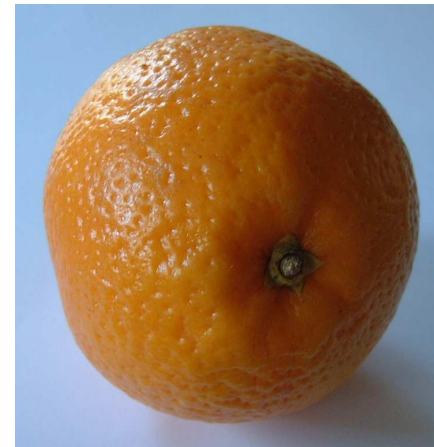
***E. coli* K12 genome is 4,639,675 bp    Human is about 3,000,000,000 bp**

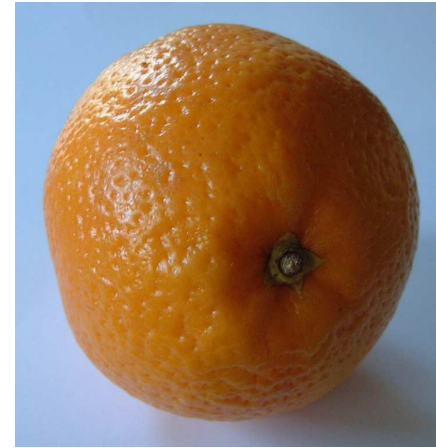
## How to analyze the sequences

- >Sample1 MAKAAIGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPS
- >Sample2 TMAKAAISIDLGTTYSCVGVFQHGKVEIANDQGNRTTPS
- >Sample3 MAKAAIGIDLGTFITYSCVGVFQHGKVEIANDQGNRTTPS

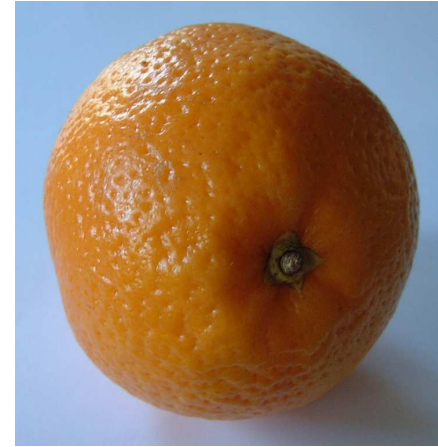


**Which two are more closely related?**





?



?

# Alignment

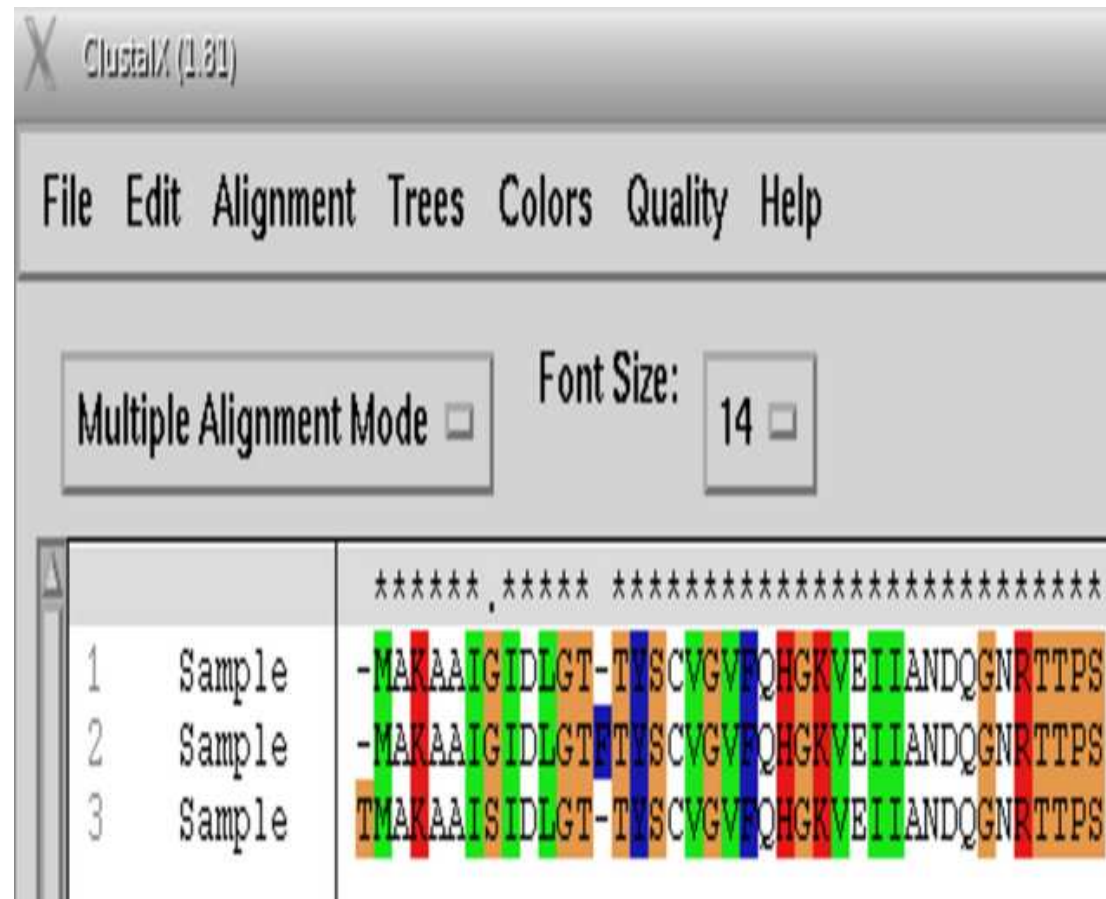
ClustalX (1.81)

File Edit Alignment Trees Colors Quality Help

Multiple Alignment Mode ☐ Font Size: 14 ☐

		*****.***** *****
1	Sample	-MAKAAIGIDLGT-TYSCVGVEQHGKVEIIANDQGNRTTPS
2	Sample	-MAKAAIGIDLGT-TYSCVGVEQHGKVEIIANDQGNRTTPS
3	Sample	TMAKAAISIDLGT-TYSCVGVEQHGKVEIIANDQGNRTTPS

# Alignment



**Difference → Distance**

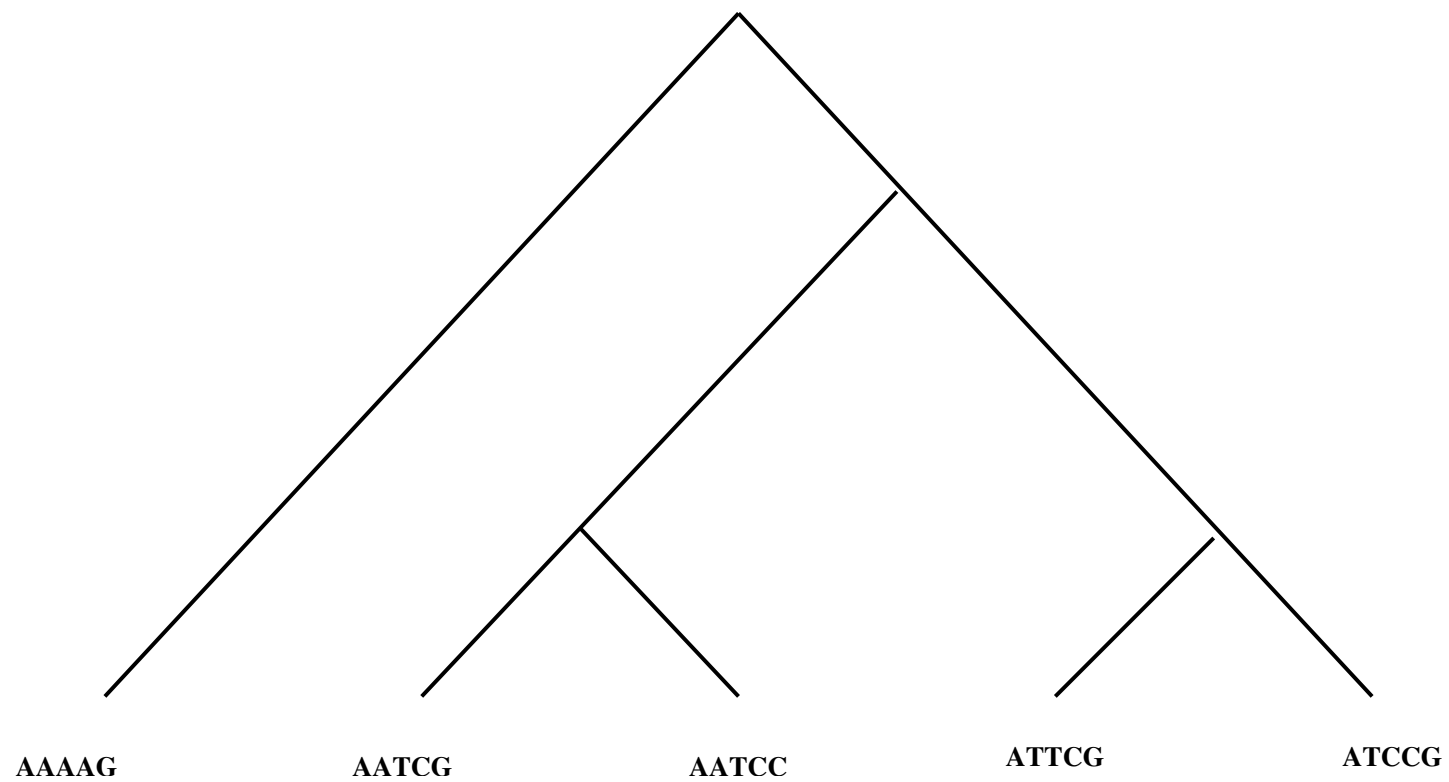
**Distance  $\rightarrow$  Tree**

## Parsimony Tree

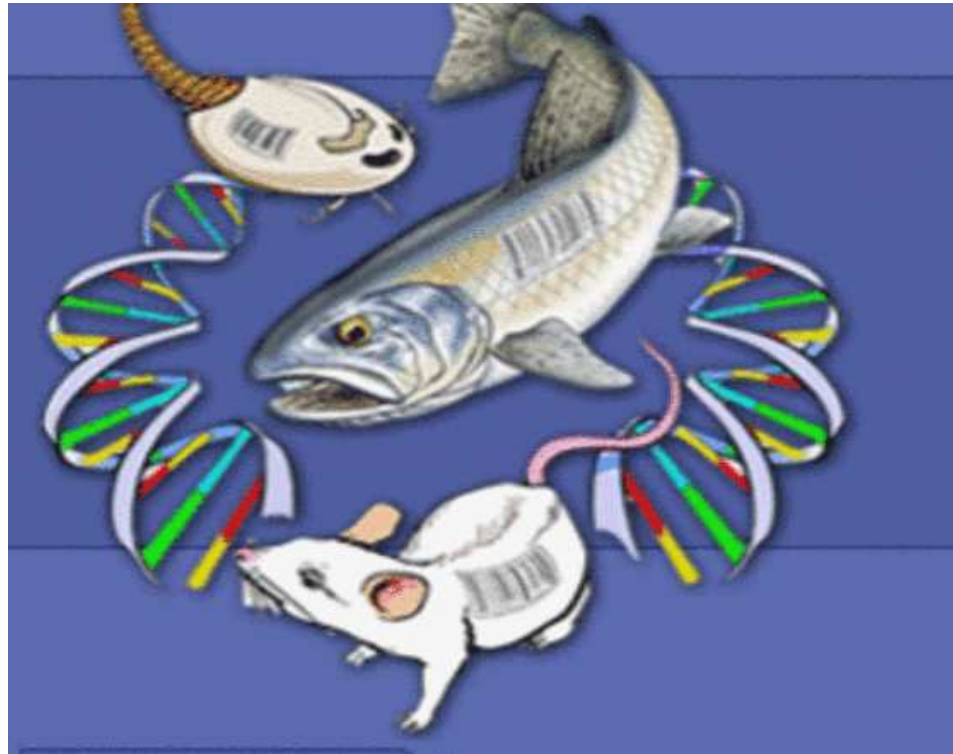
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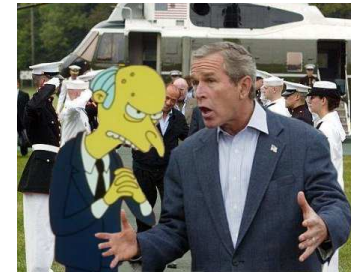
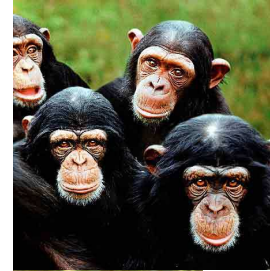
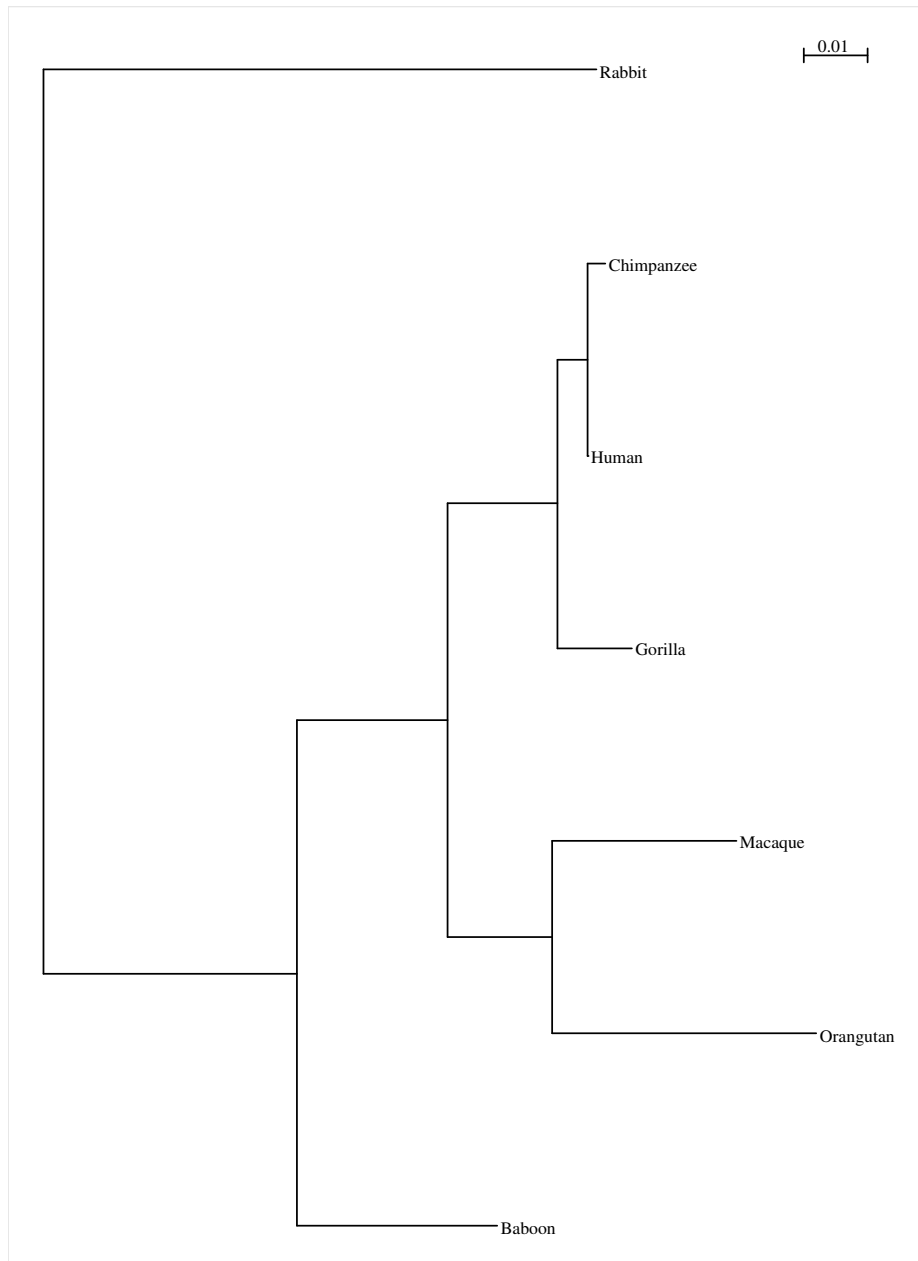


## Parsimony Tree

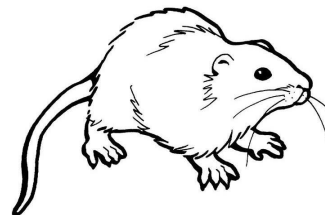
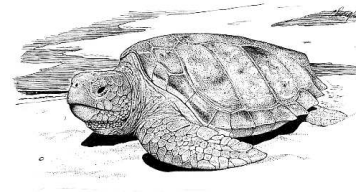


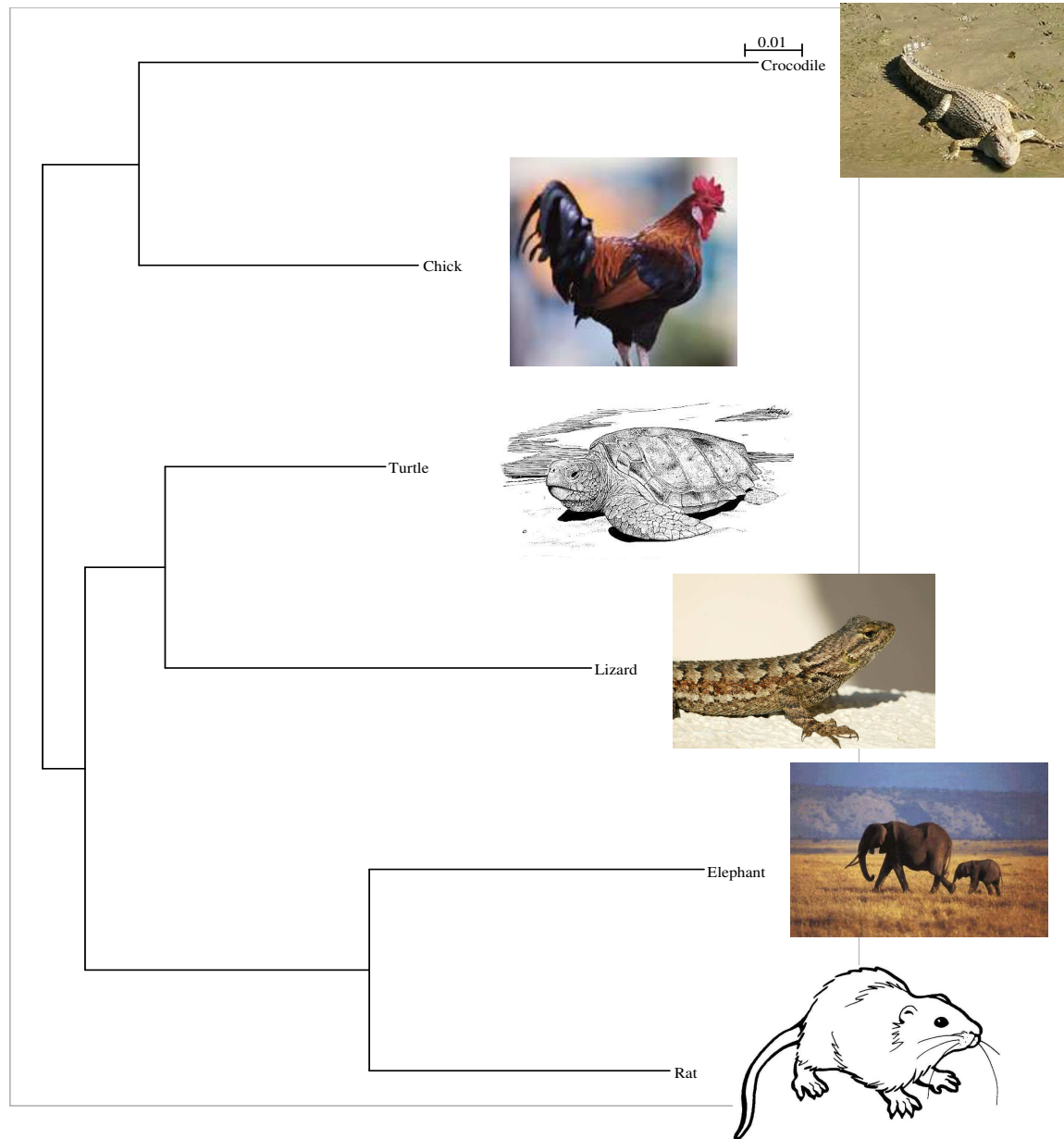
## One application





# Relationship?





## **Something to think about**

**Why should we do the alignment before we compare genes?**

**How do we get the relationship of genes?**

**More applications...**