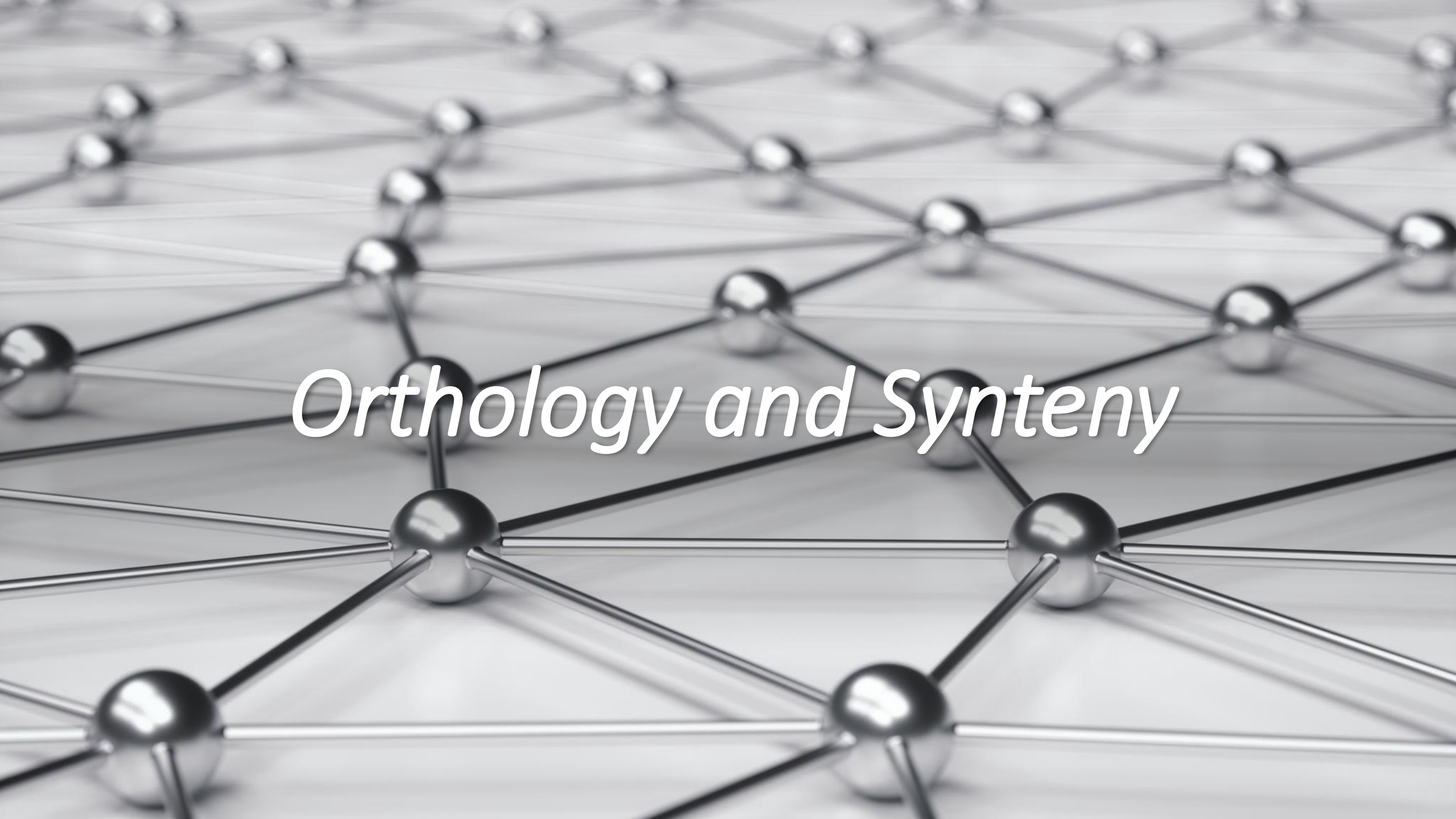
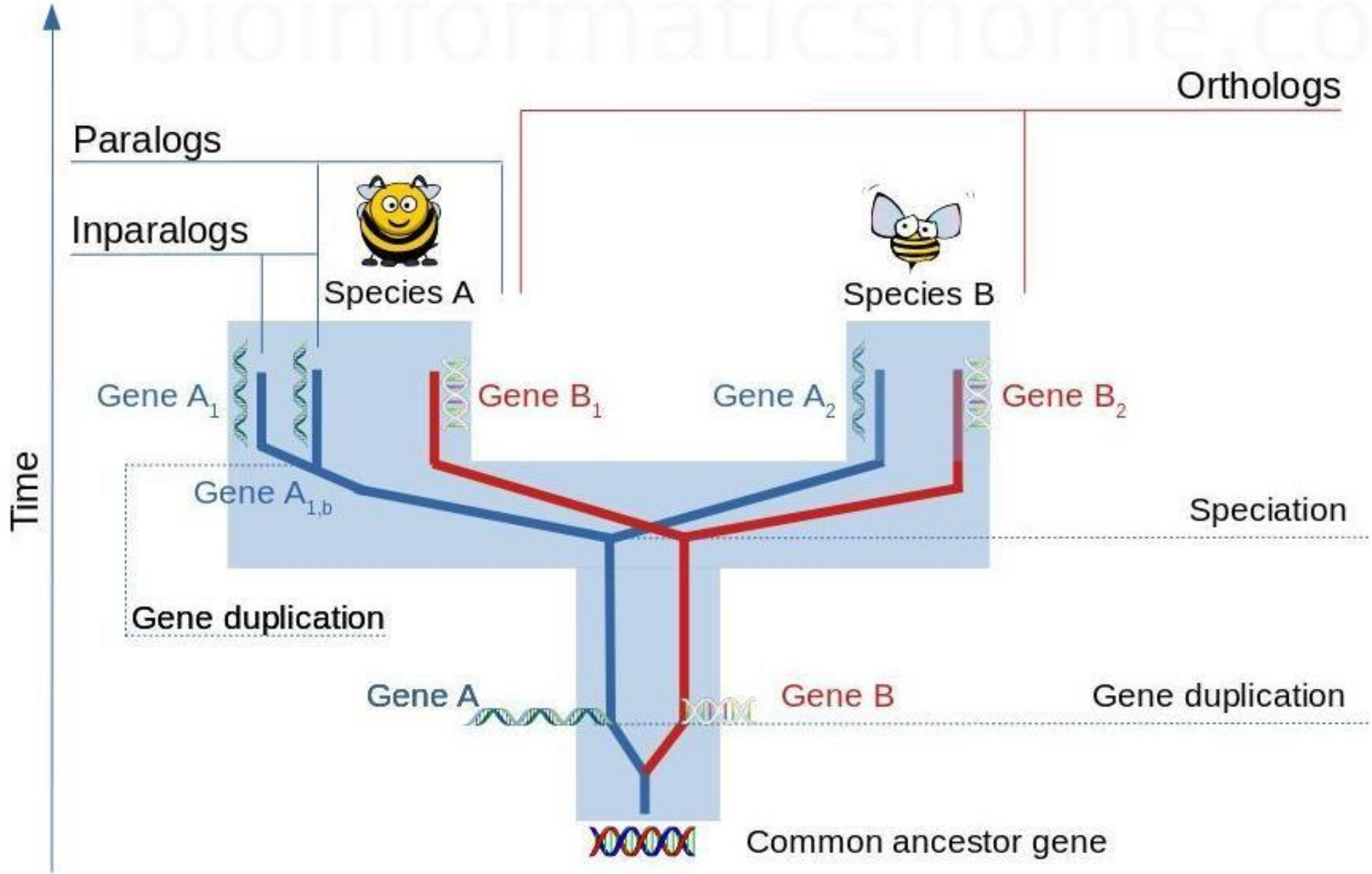
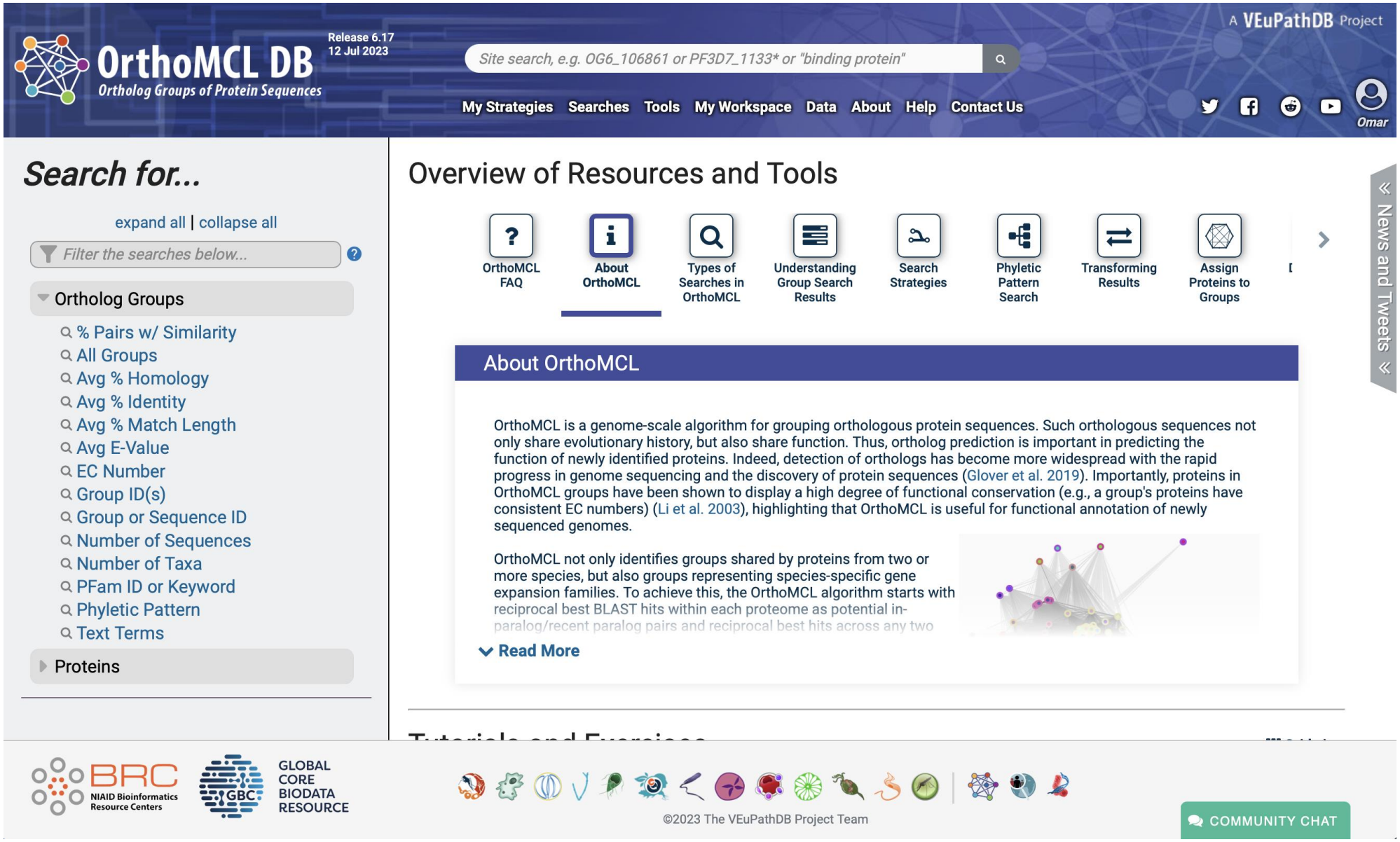

Orthology and Synteny



https://bioinformaticshome.com/bioinformatics_tutorials/sequence_alignment/homology.html

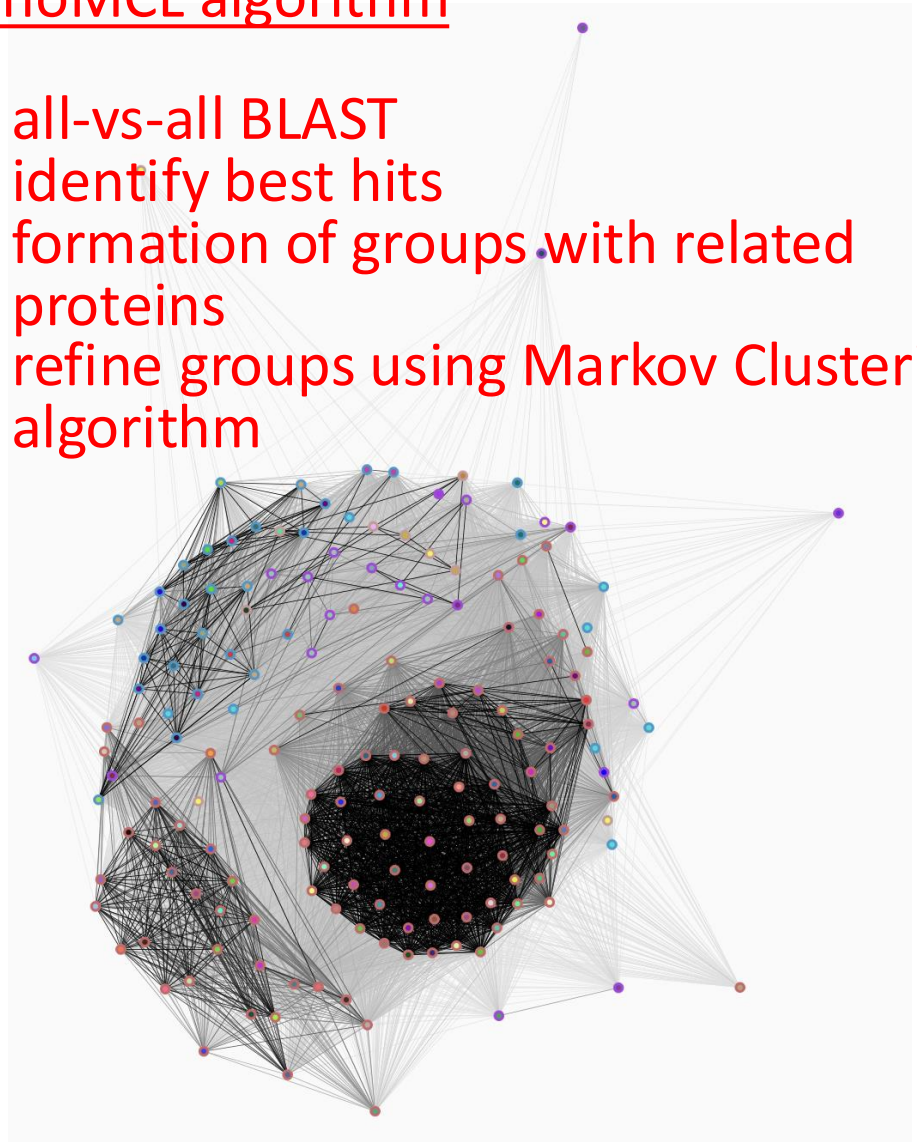
OrthoMCL: identifying ortholog groups



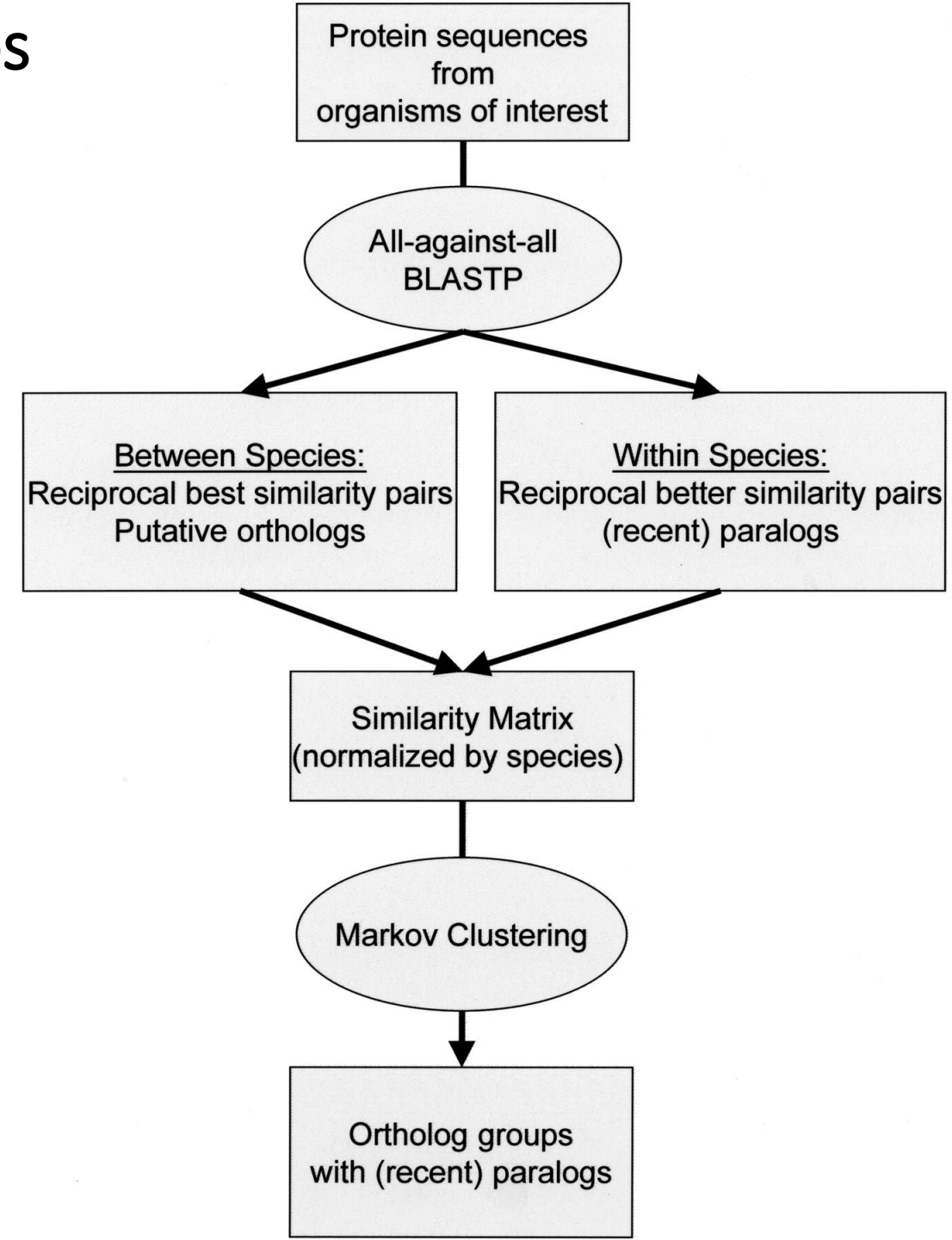
OrthoMCL: identifying ortholog groups

OrthoMCL algorithm

1. all-vs-all BLAST
2. identify best hits
3. formation of groups with related proteins
4. refine groups using Markov Clustering algorithm



https://orthomcl.org/orthomcl/app/static-content/OrthoMCL/about.html



Why is orthology useful?

- *Learn about your favorite gene using the gene's orthologs.*
- *An example:*

***Candida auris* B9J08_000022**

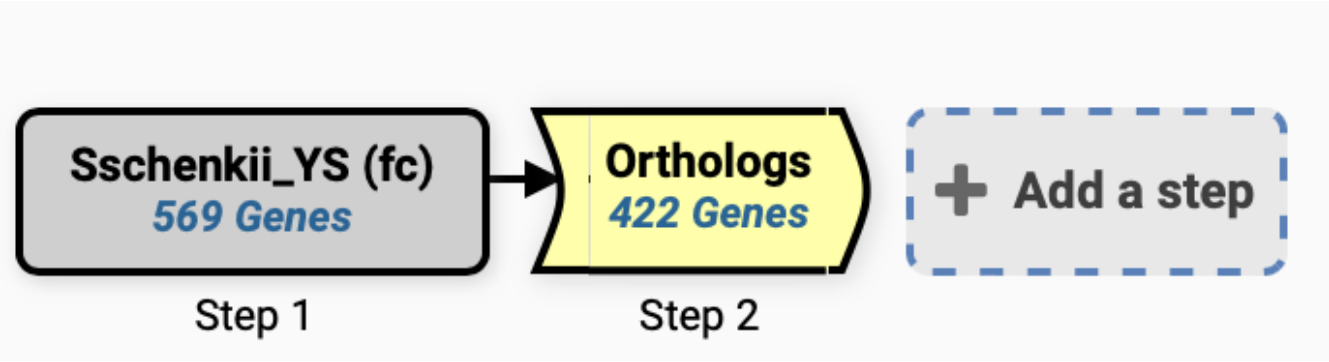
Description: hypothetical protein

Examine B9J08_000022 orthologs to learn about:

1. **conservation**
   a. Are there orthologs in other fungi?
   b. Are there orthologs in metazoan?
   c. What about bacteria or archaea?
2. **function** (below are putative functions of orthologs)
   a. Are these orthologs with know function?
   b. What about functional domains?

Why is orthology useful?

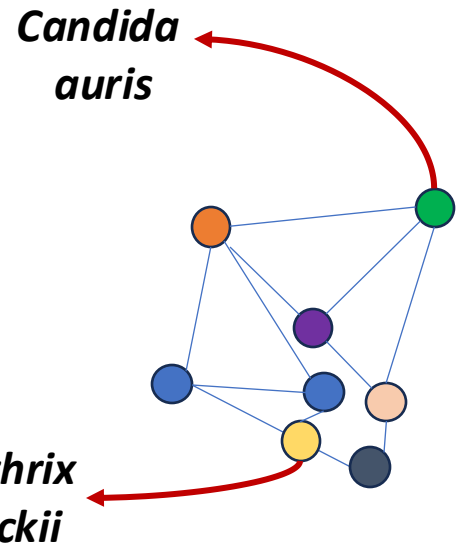
- *Leverage data across species - Transform orthologs from one species to another*



Sporothrix schenckii

Candida auris

Orthology Transformer



Why is orthology useful?

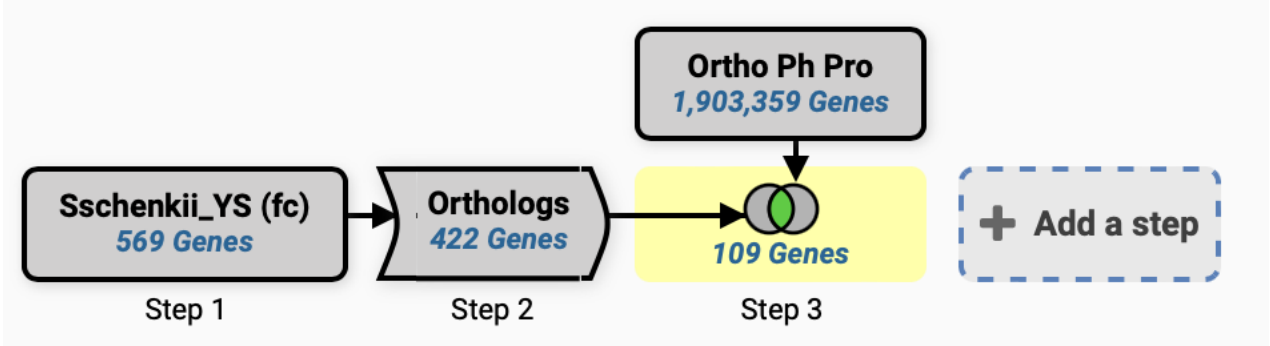
- *Define phylogenetic profile of genes of interest*

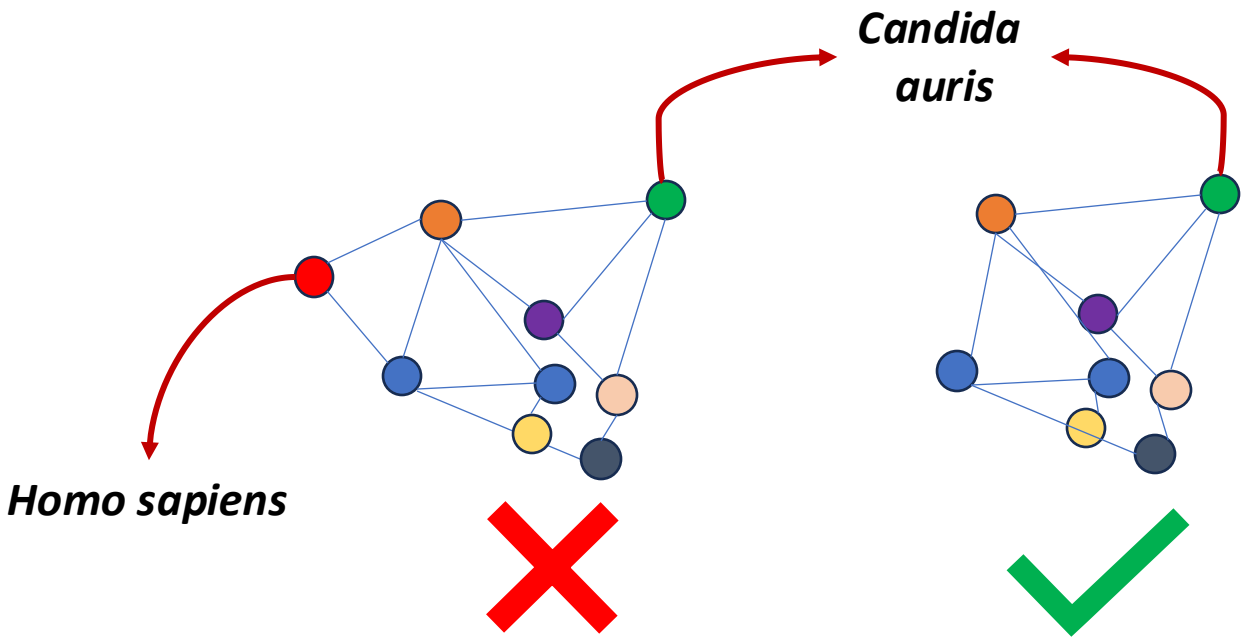
Click on ● to determine which organisms to include or exclude in the orthology profile.
(● = no constraints | ✔ = must be in group | ✖ = must not be in group | ✲ = mixture of constraints)

expand all | collapse all

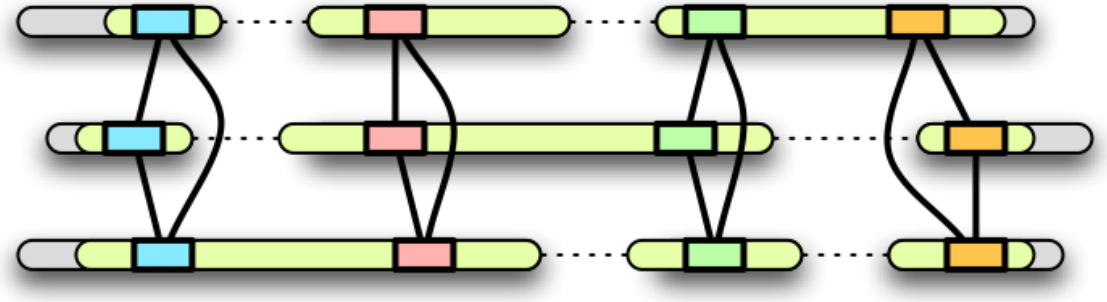
- ✲ **All Organisms**
  - ● *Bacteria* (BACT)
    - ● *Firmicutes* (FIRM)
    - ● *Proteobacteria* (PROT)
    - ● *Other Bacteria* (OBAC)
  - ● *Archaea* (ARCH)
    - ● *Nitrosopumilus maritimus (strain SCM1)* (nmar)
    - ● *Euryarchaeota* (EURY)
    - ● *Crenarchaeota* (CREN)
    - ● *Nanoarchaeota* (NANO)
    - ● *Korarchaeota* (KORA)
  - ✲ *Eukaryota* (EUKA)
    - ● *Alveolates* (ALVE)
    - ● *Amoebozoa* (AMOE)
    - ● *Euglenozoa* (EUGL)
    - ● *Viridiplantae* (VIRI)
    - ● *Fungi* (FUNG)
    - ✲ *Metazoa* (META)
      - ● *Nematodes* (NEMA)
      - ● *Arthropoda* (ARTH)
      - ✲ *Chordata* (CHOR)
        - ● *Branchiostoma floridae (Florida lancelet) (Amphioxus)* (bflo)
        - ● *Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)* (xtro)
        - ● *Actinopterygii* (ACTI)
        - ● *Aves* (AVES)
        - ✖ *Mammalia* (MAMM)
        - ● *Tunicates* (TUNI)
      - ● *Other Metazoa* (OMET)
    - ● *Other Eukaryota* (OEUK)

Not in Mammals





Synteny



- Attempt to identify evolutionary relationships within and between multiple genomes
- The term "syntenic" is often used to describe regions of multiple genomes that are believed to have evolved from the same region in an ancestral genome.
- In VEuPathDB, synteny refers to Co-linearity of homologues regions coupled with shading of genes by orthology.

https://www.biostat.wisc.edu/~cdewey/mercator/

Synteny: compare arrangement of genes between genomes