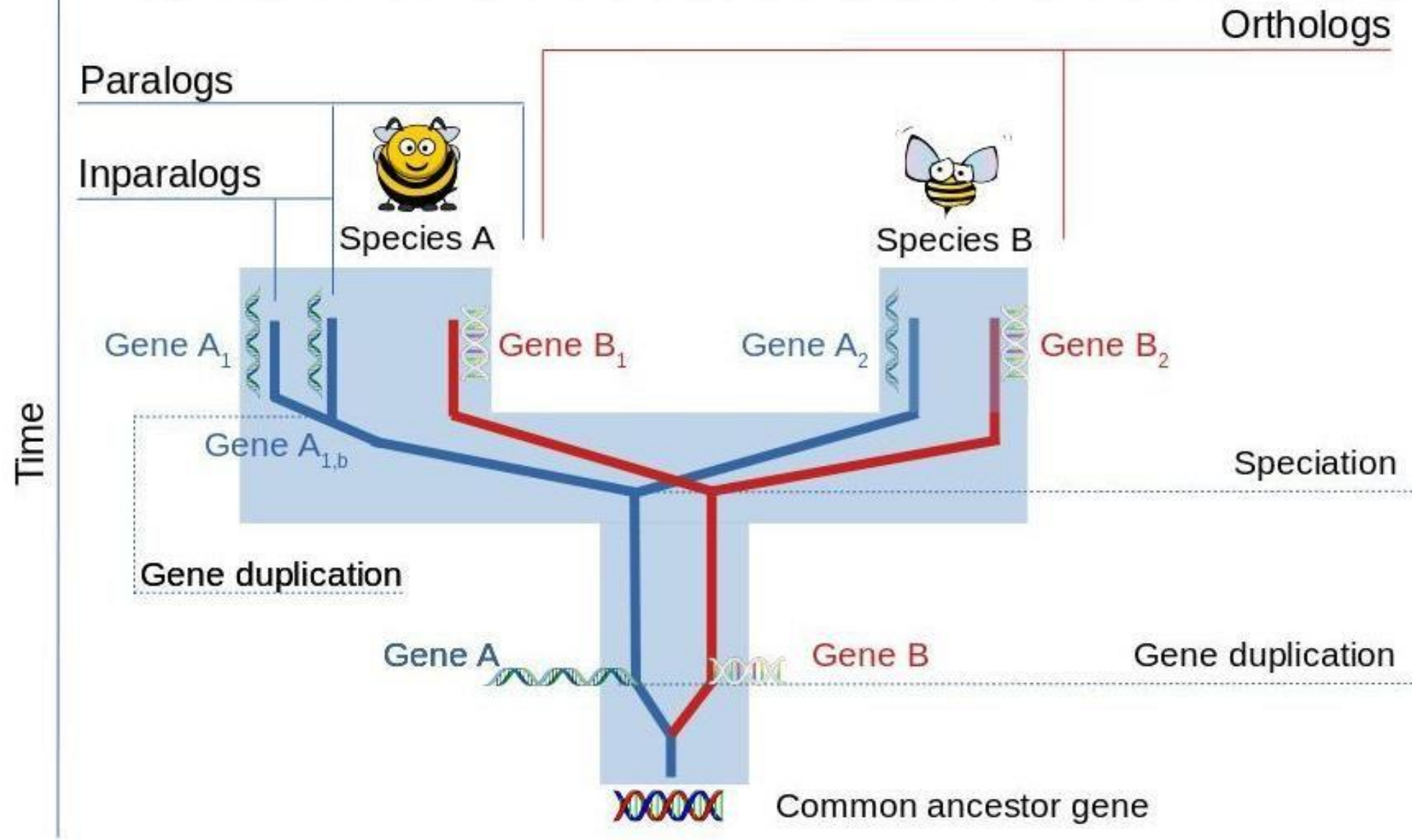



The background of the image is a 3D network of metallic spheres connected by thin rods, forming a complex geometric pattern. The spheres are arranged in a way that creates a series of interconnected triangles and polygons, giving the impression of a molecular structure or a network graph. The lighting is soft, highlighting the metallic texture of the spheres and the lines connecting them.

Orthology and Synteny



OrthoMCL: identifying ortholog groups





**OrthoMCL DB**
Ortholog Groups of Protein Sequences

Release 6.17
12 Jul 2023

A VEuPathDB Project

Site search, e.g. OG6_106861 or PF3D7_1133* or "binding protein"

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Omar

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Ortholog Groups

☐ % Pairs w/ Similarity

☐ All Groups

☐ Avg % Homology

☐ Avg % Identity

☐ Avg % Match Length

☐ Avg E-Value

☐ EC Number

☐ Group ID(s)

☐ Group or Sequence ID

☐ Number of Sequences

☐ Number of Taxa

☐ Pfam ID or Keyword

☐ Phyletic Pattern

☐ Text Terms

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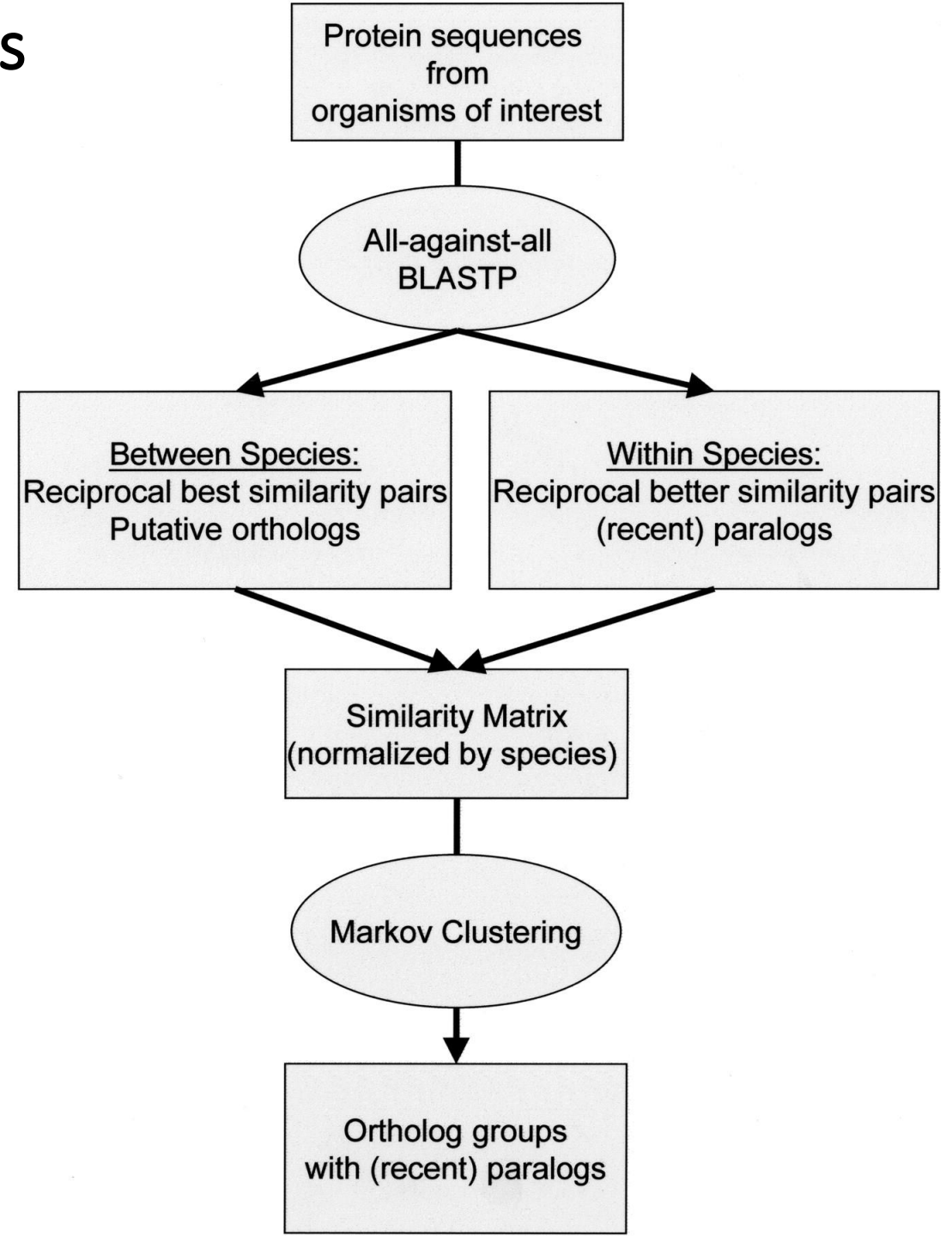
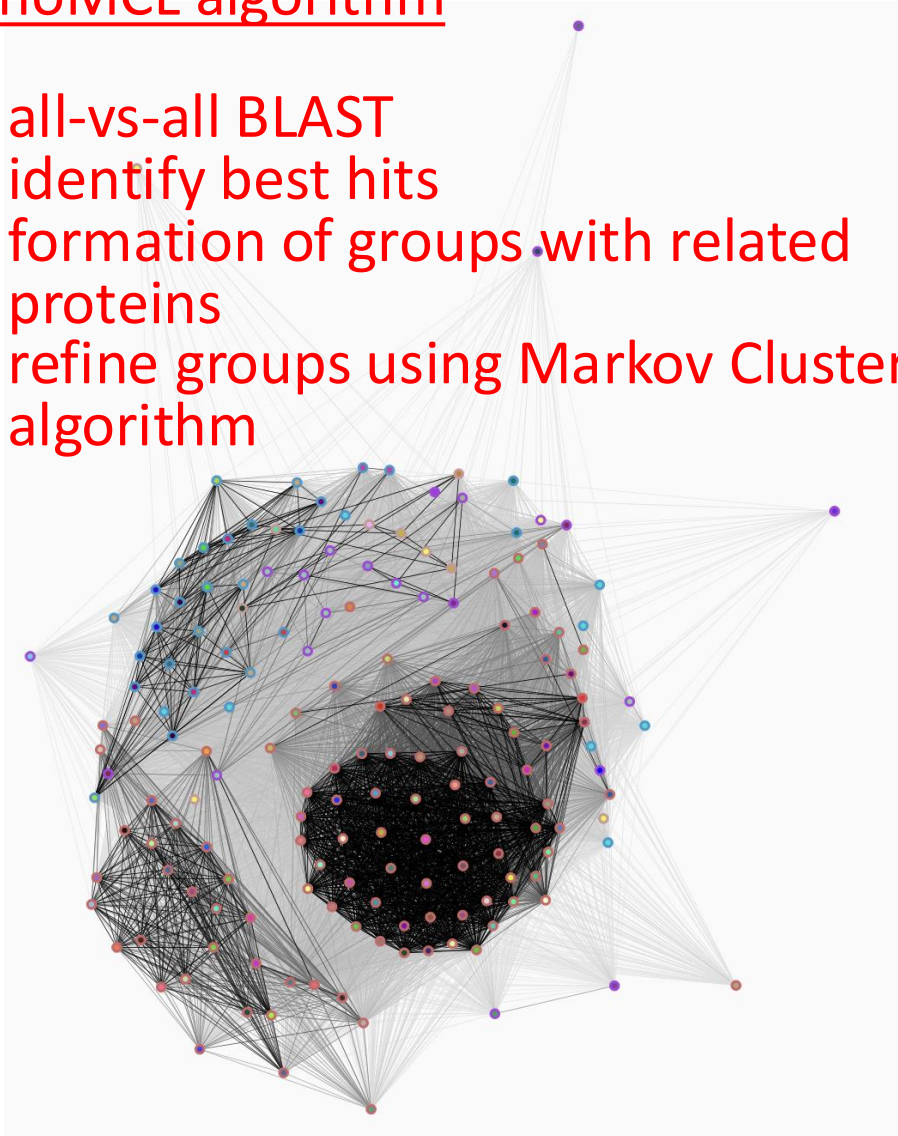
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 **COMMUNITY CHAT**

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



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

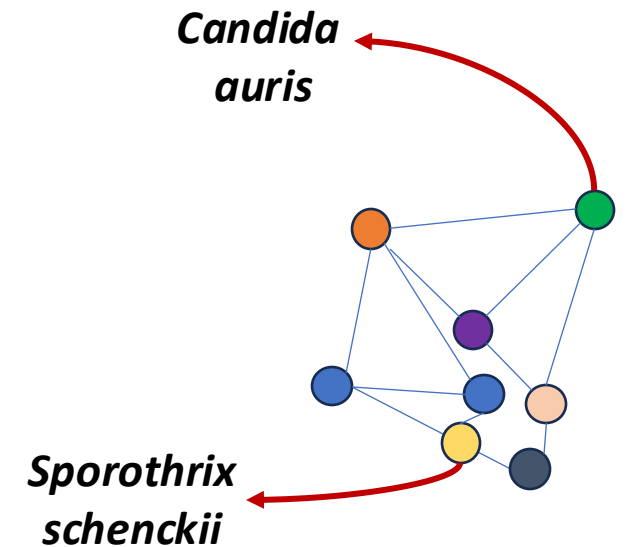
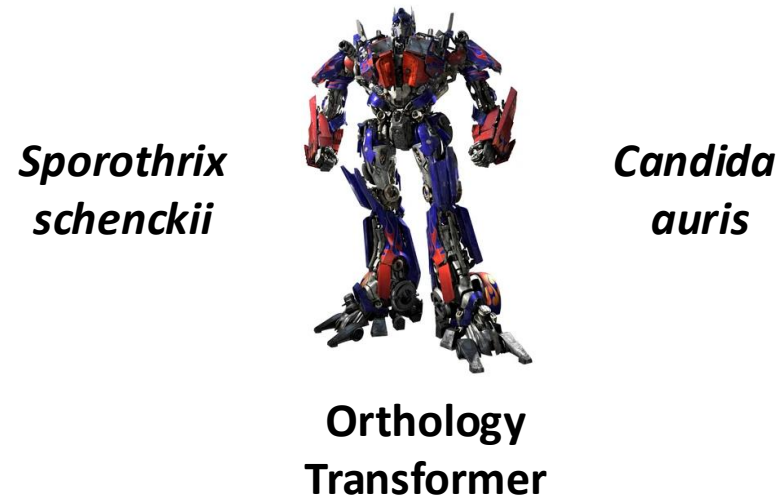
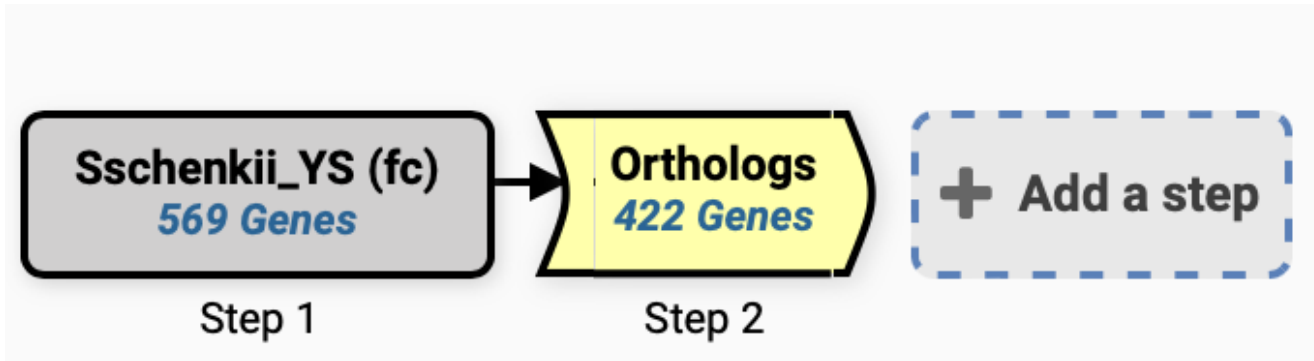
- a. Are there orthologs in other fungi?
- b. Are there orthologs in metazoan?
- c. What about bacteria or archaea?

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*



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)

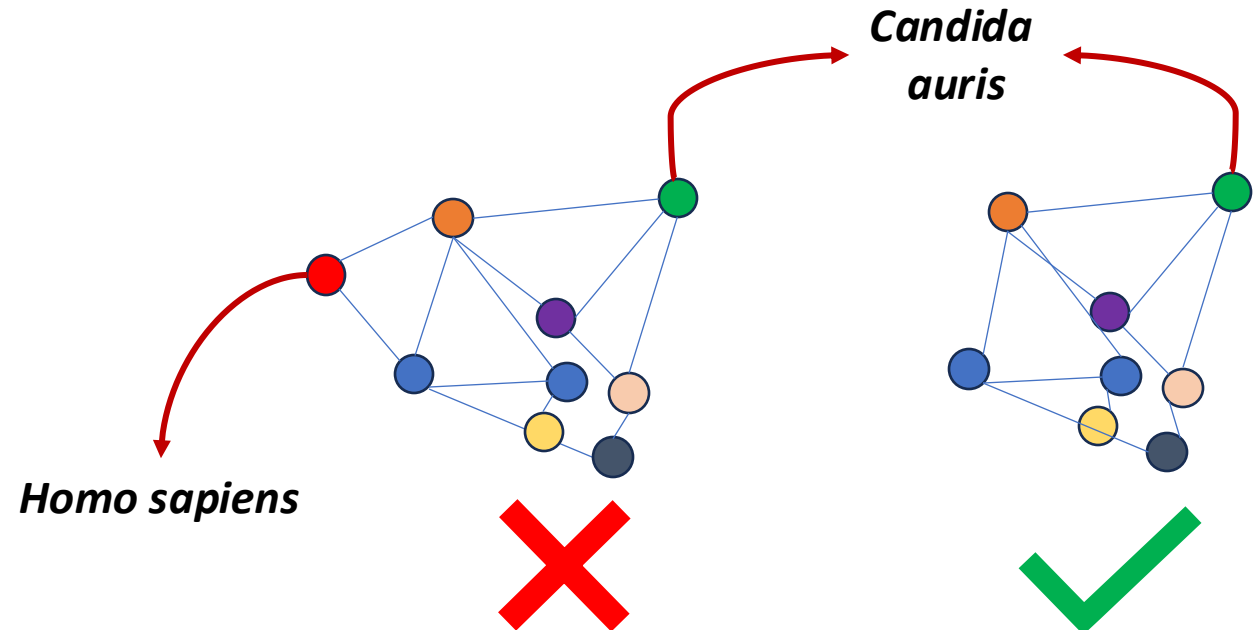
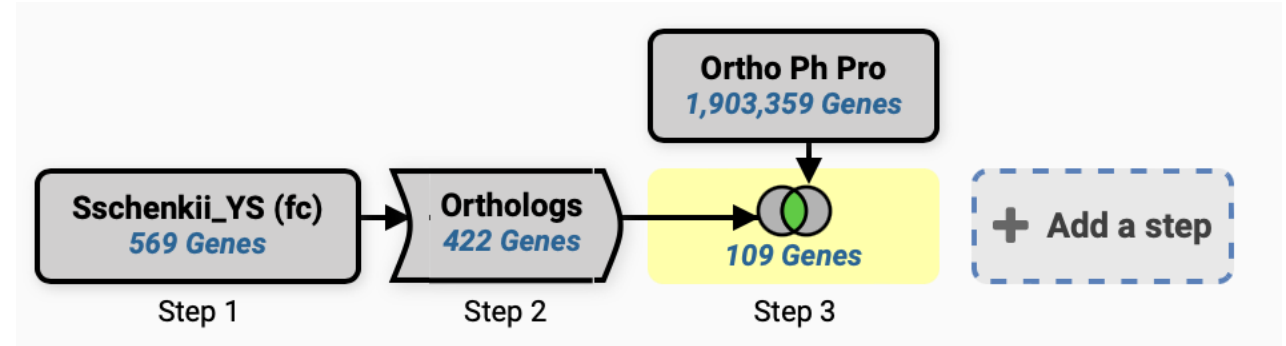
▼ * Eukaryota (EUKA)

- ▶ ● Alveolates (ALVE)
- ▶ ● Amoebozoa (AMOE)
- ▶ ● Euglenozoa (EUGL)
- ▶ ● Viridiplantae (VIRI)
- ▶ ● Fungi (FUNG)

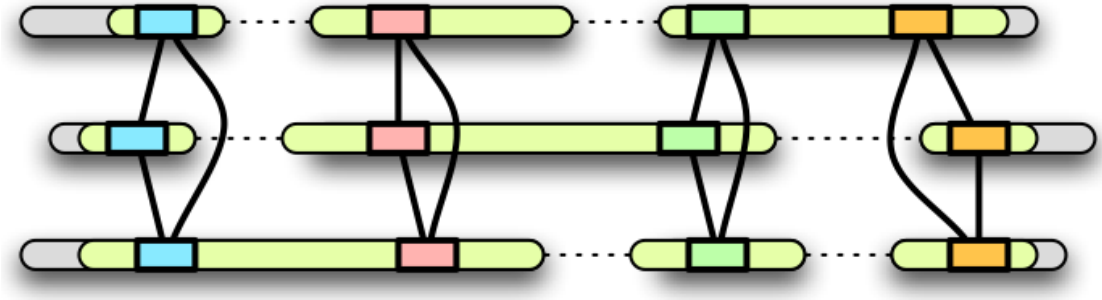
▼ * Metazoa (META)

- ▶ ● 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.

Synteny: compare arrangement of genes between genomes

