

A complex network diagram with numerous nodes of varying sizes (dark blue, light blue, and grey) connected by thin grey lines. Some nodes are highlighted with larger concentric circles. The background is a light blue-grey gradient.

OrthoFinder

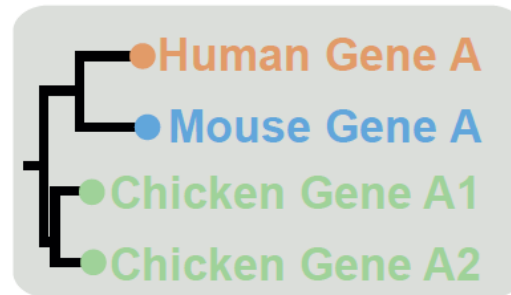
Niloofer Ghadam, May 31st 2023

Mol.981

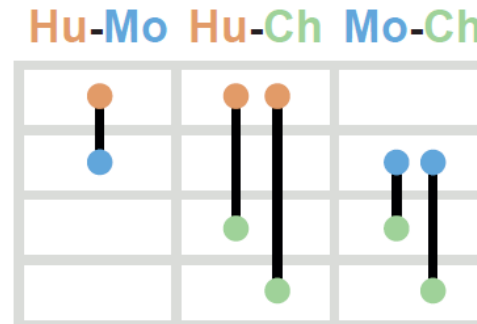
What are Orthologs?

- **Orthologs** are genes present in different species that have evolved from a common ancestral gene through speciation events.
- The **biological functions** of orthologous genes are generally the **same** across different species.

Orthogroup



Orthologues



OrthoFinder

A diagram showing the OrthoFinder workflow. A vertical blue bar on the left contains the text 'OrthoFinder'. A horizontal line extends from this bar to the right, where it connects to a vertical line. From this vertical line, four horizontal lines branch out to the right, each pointing to an orange rectangular box. The boxes contain the following text from top to bottom: 'Orthologues And Orthogroups', 'Infers gene trees for all orthogroups', 'Infers a rooted species tree for the species being analyzed', and 'Comprehensive statistics for comparative genomic analyses.'

Orthologues And Orthogroups

Infers gene trees for all orthogroups

Infers a rooted species tree for the species
being analyzed

Comprehensive statistics for comparative
genomic analyses.

OrthoFinder



FAST



ACCURATE



**COMPREHENSIVE
ANALYSIS**



SIMPLE

How to perform an OrthoFinder analysis?

1. Download the amino acid sequences in FASTA format for the species you want to analyze.
2. Optionally, rename the files to simpler names since they will be used as species identifiers in the results.
3. Place all the FASTA files in a single directory.
4. Use the OrthoFinder tool to perform a complete analysis by running the command:
 - `orthofinder -f fasta_files_directory [-t number_of_threads]`

OrthoFinder Results

Orthogroup files

- Orthogroups.csv
- Orthogroups_UnassignedGenes.csv
- Orthogroups.txt.

Single-copy orthogroups & gene counts

- SingleCopyOrthogroups.txt
- Orthogroups.GeneCount.csv

Orthogroup Statistics files

- Statistics_Overall.csv
- Statistics_PerSpecies.csv
- Orthogroups_SpeciesOverlaps.csv

The background is a complex network of thin grey lines connecting various circular nodes. The nodes are in different sizes and colors: dark blue, light blue, and grey. Some nodes are highlighted with larger concentric circles. The overall aesthetic is modern and technological.

Thank You For Your Attention!