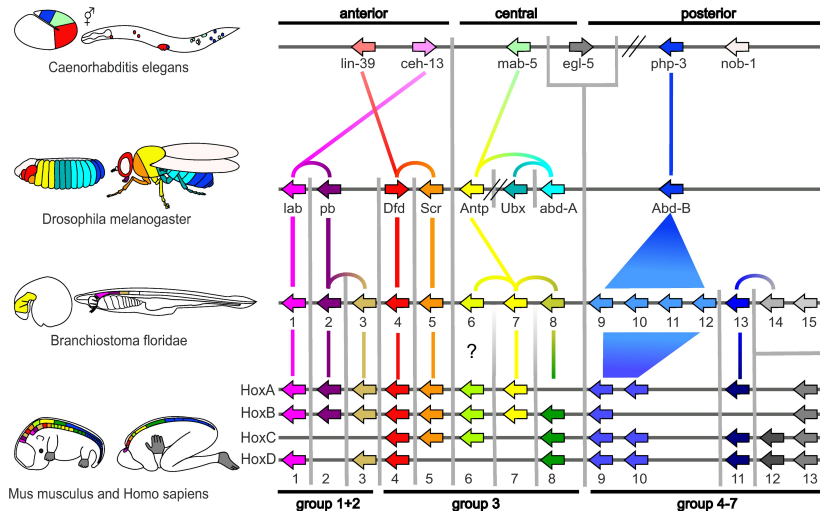


Automated Synteny Computation and Use

Karl Kaether

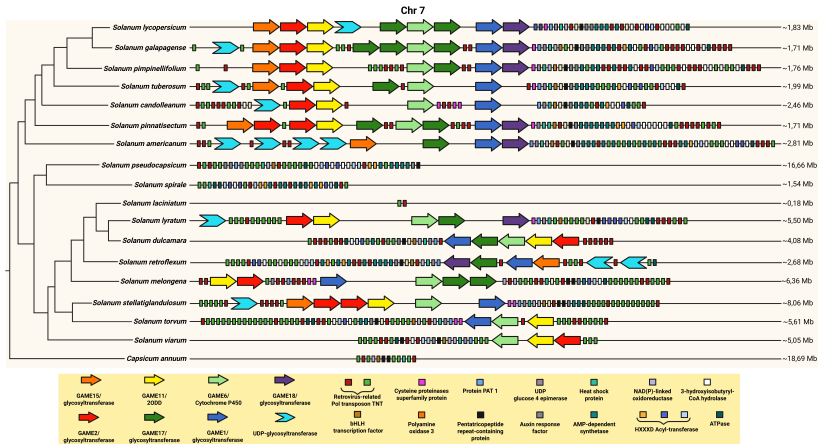
Bioinformatics Group Leipzig

Synteny



Stefanie D. Hueber, Georg F. Weiller, Michael A. Djordjevic, Tancred Frickey, CC BY 4.0,
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Synteny



Webserver

Species Analysis Webserver

Unpublished Content and History Deleted

HomeSpeciesNewSubmit JobHelp

Upload Files (optional if species selected already)

Input File Requirements

Upload Clustal Outgroup Nucleotide Genomes as FASTA

Browse...

No file selected

Upload TSV File (one separated NCI annotations on genomes)

Browse...

No file selected

Processing Options

☐ Private results (password-protected access)

☐ Complete anchors only (no full analysis)

Check this to only compile anchors for the submitted species without running the full species analysis. (default for preparing data for future analysis.)

Please submit single-species submissions

When submitting only one species, genomic alignments cannot be computed. Such submissions are automatically processed as anchor-only jobs, computing and storing anchors for future multi-species analysis. You will receive a downloadable anchor containing the computed anchors.

Analysis Mode

Automatic (recommended)

Manual (advanced parameters)

Submit Job for Analysis

Species Analysis Webserver

Unpublished Content and History Deleted

HomeSpeciesNewSubmit JobHelp

Available Species Sets

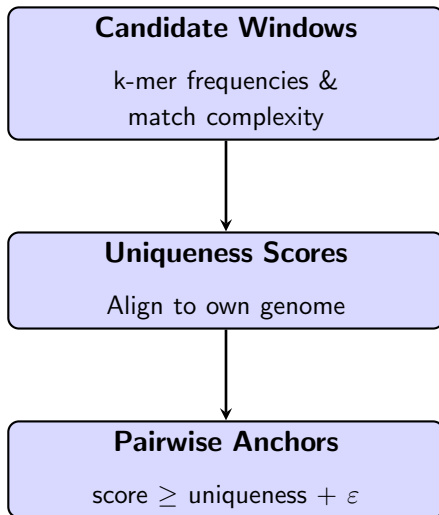
Download completed analysis results

Completed Sets (7 total)

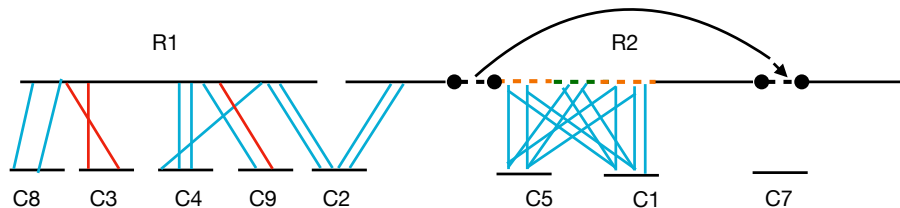
Set Name	Species Count	Completed	Actions
comp_pam_dreadl_peds_reuse_36077	2 species	Nov 16, 2025 12:46	Download View Results
2010206_86176	2 species	Nov 16, 2025 10:40	Download View Results
hatali_47717	2 species	Nov 16, 2025 02:13	Download View Results
tax_hata_49883	4 species	Nov 16, 2025 02:10	Download View Results
494_49947	2 species	Nov 16, 2025 00:58	Download View Results
64c_49996	2 species	Nov 16, 2025 00:23	Download View Results
hata_47516	2 species	Nov 15, 2025 23:47	Download View Results

© 2024 Species Analysis Webserver

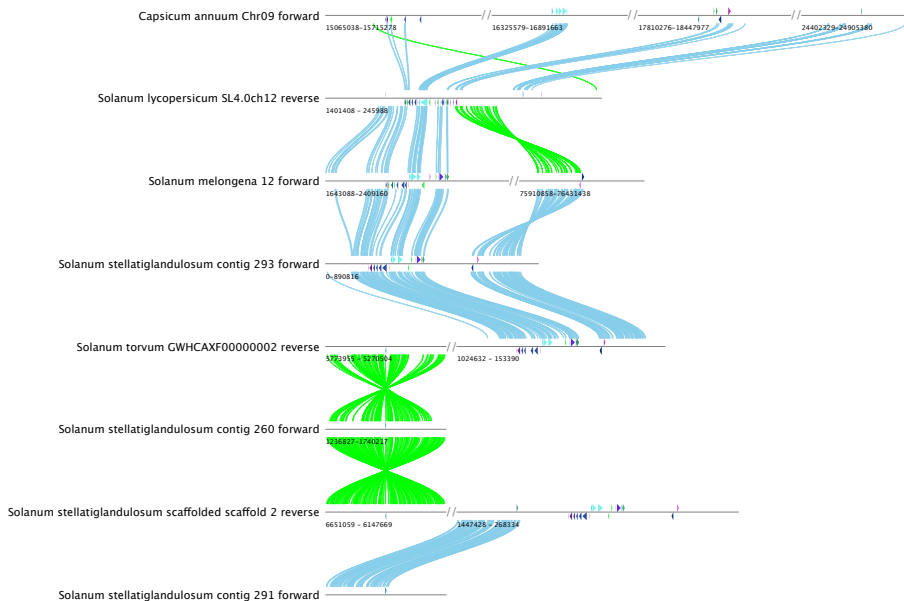
Synteny



Application: Homology-based scaffolding

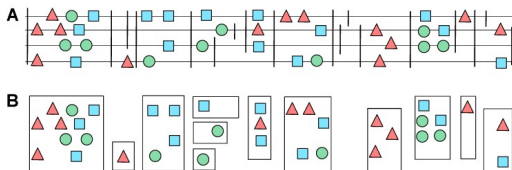


Application: Homology-based scaffolding

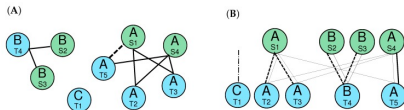


Application: Enhanced orthology inference

- 1 partition of genomes into anchor-separated regions with homologs



- 2 initial orthology graph construction (sequence similarity, cograph editing)
- 3 rearrangement-aware refinement

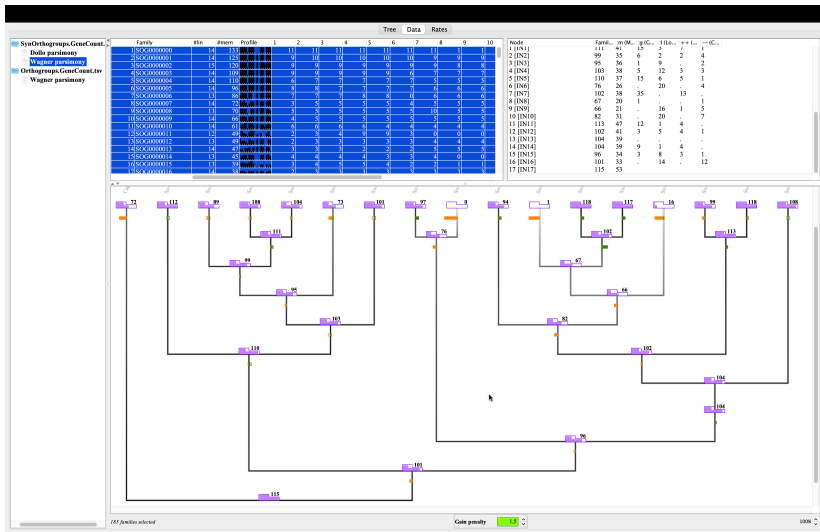


$$D_{ij} = \min \begin{cases} D_{i-1,j-1} + \delta(t_i^a, t_j^b) \\ D_{i-1,j} + \delta(t_i^a, -) \\ D_{i,j-1} + \delta(-, t_j^b) \\ D_{i-1,j-2} + \lambda(t_i^a, t_j^{-1}b, t_j^b) \\ D_{i-2,j-1} + \lambda(t_i^{-1}a, t_i^a, t_j^b) \end{cases}$$

Marc Hellmuth et al. "Orthology relations, symbolic ultrametrics, and cographs". In: *Journal of mathematical biology* 66.1 (2013), pp. 399–420

Sarah J Berkemer et al. "Smore: Synteny modulator of repetitive elements". In: *Life* 7.4 (2017), p. 42

Application: Enhanced orthology inference



Thank you!

<https://anchored.bioinf.uni-leipzig.de/>