Multiple Alignments and Phylogenies

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3/29/2012

Comprehending our BLAST results

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- We have a bunch of sequences that look similar to our query
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- What does that mean, anyway?

Nomenclature

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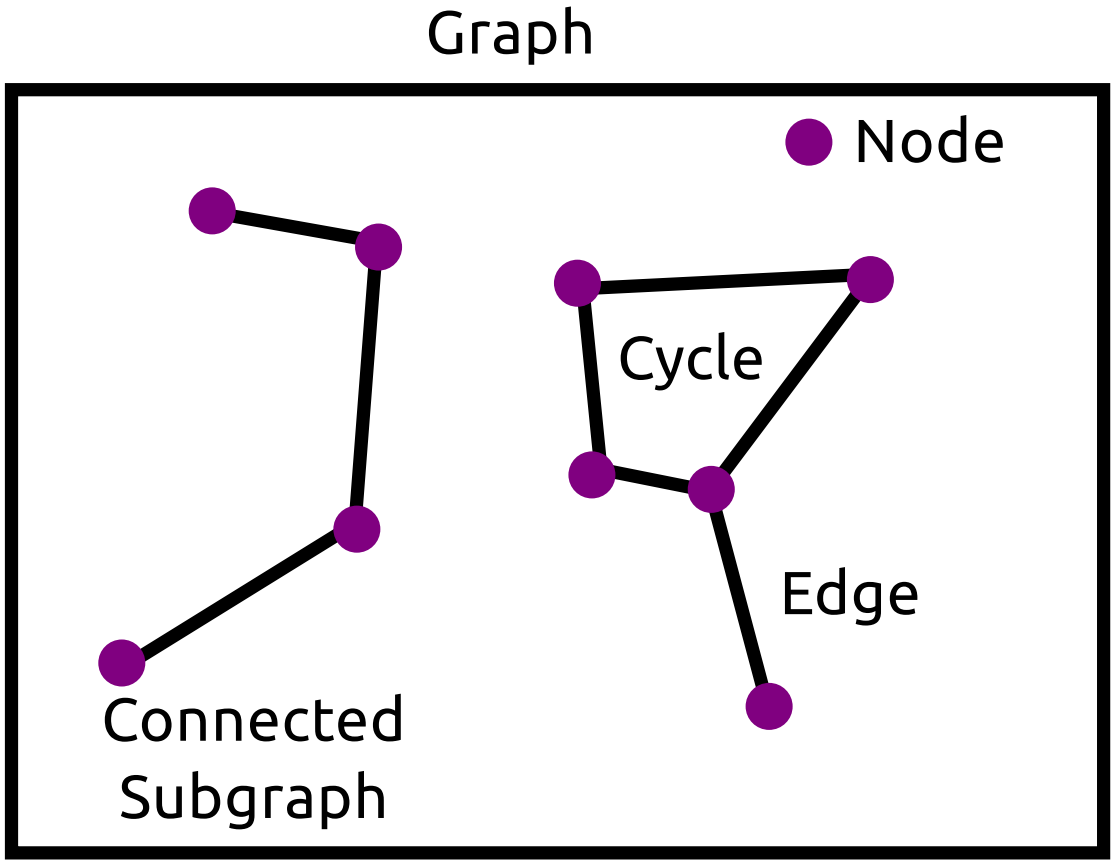
Orthologs homologs arising from speciation.

Paralogs homologs arising from duplication and divergence within a single genome.

Xenologs homologs arising from horizontal transfer.

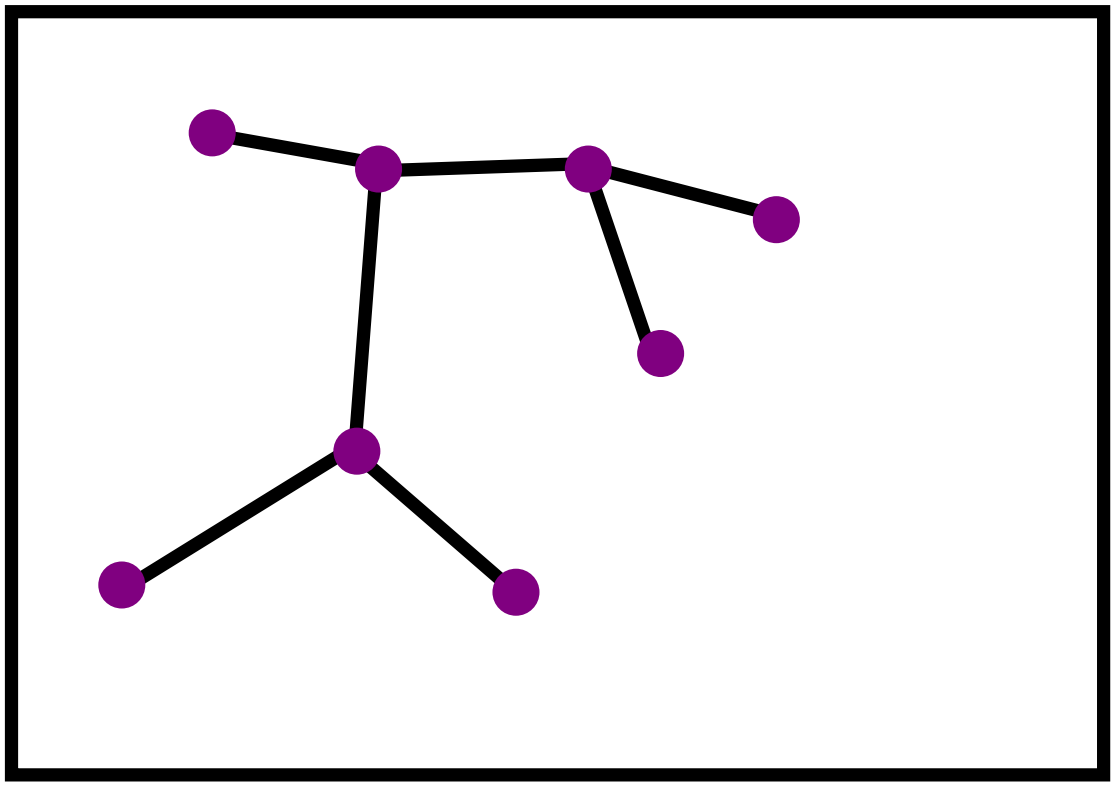
Onologs homologs arising from whole genome duplication.

Nomenclature

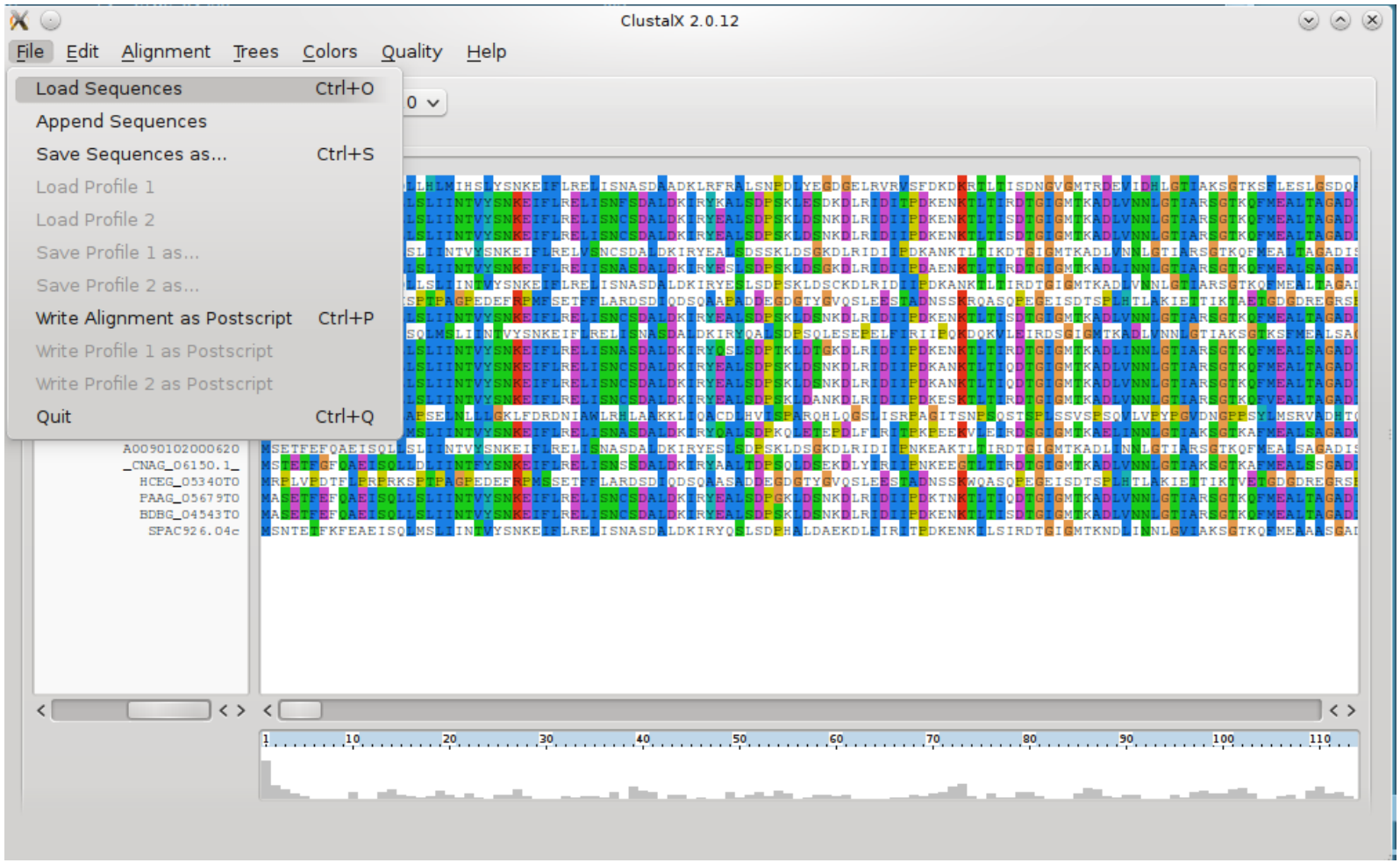


Nomenclature

Tree = Connected Graph with no Cycles



Generating a multiple alignment in CLUSTALX



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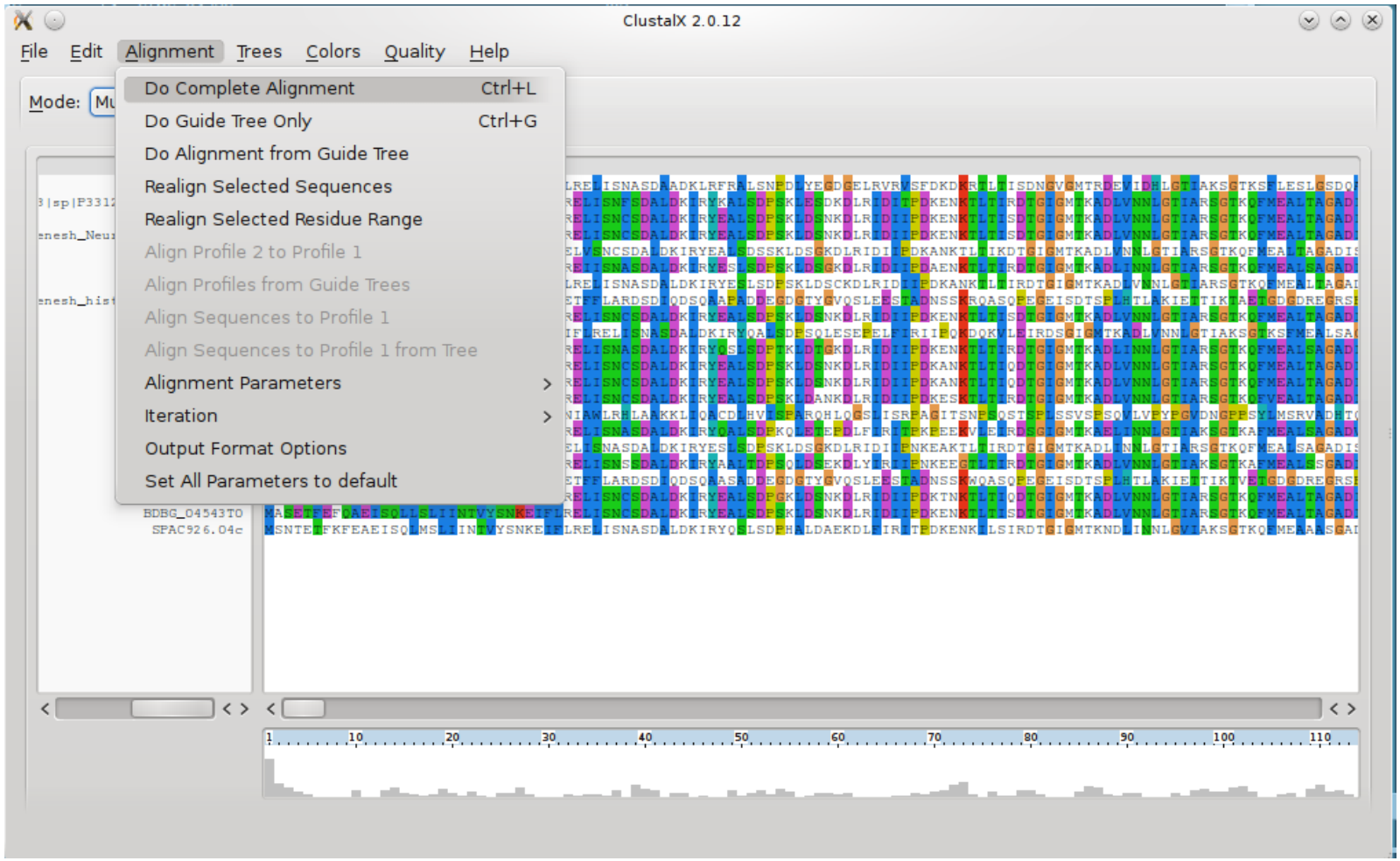
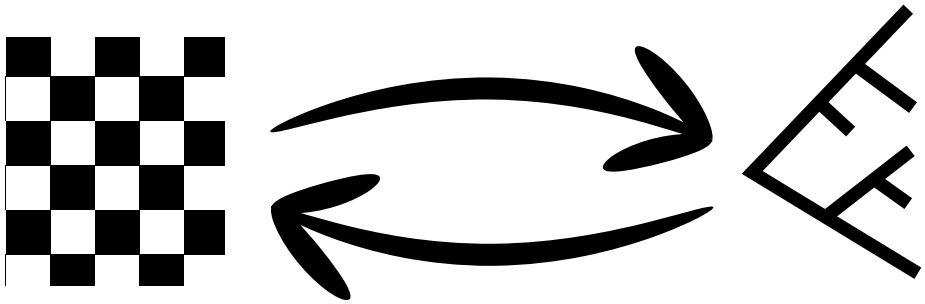


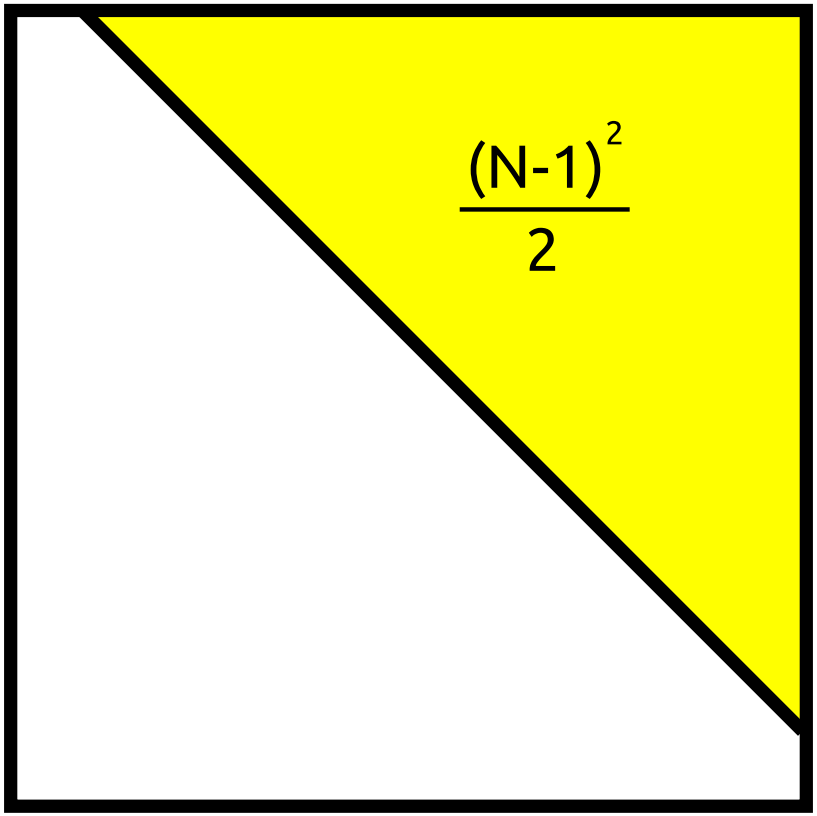
Evolution implies a self-consistent model



Distances
(Pairwise relationships)

Topology
(Evolutionary history)

Measure all pairwise distances by dynamic programming



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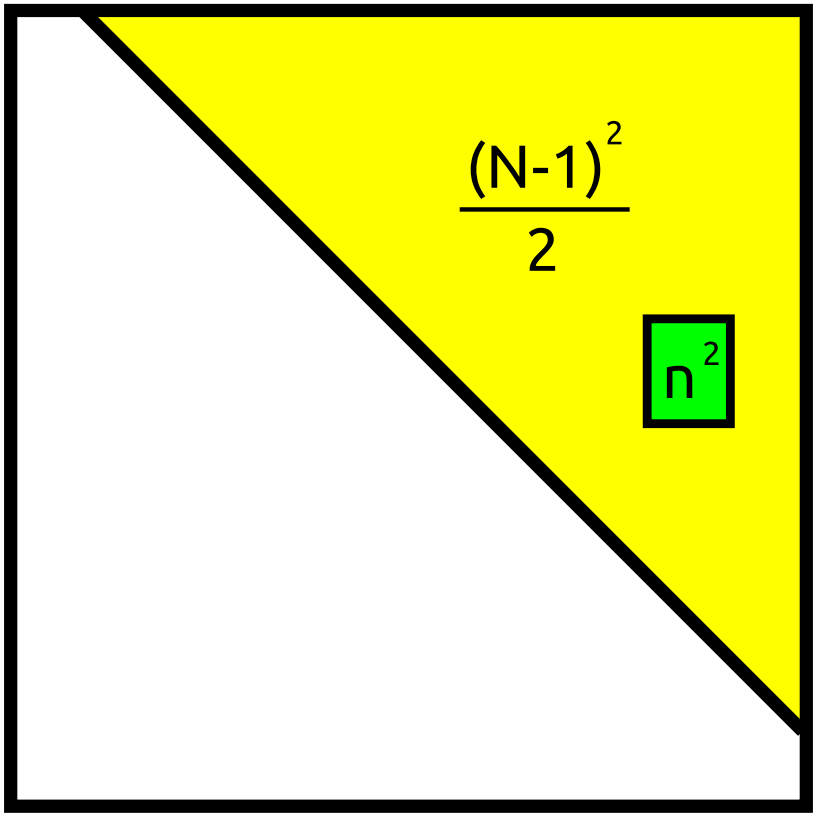
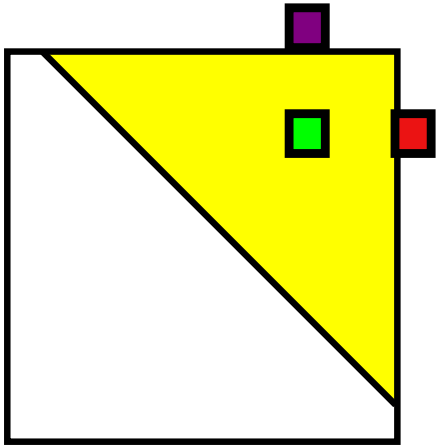
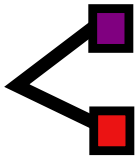


Generate a guide tree by UPGMA





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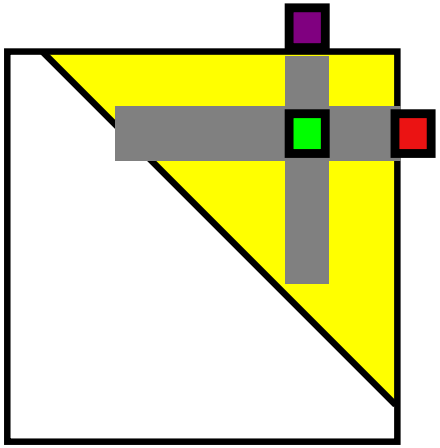

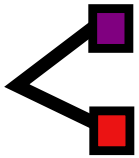

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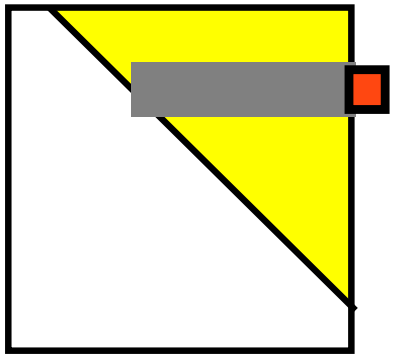

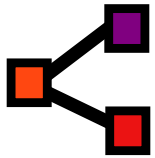

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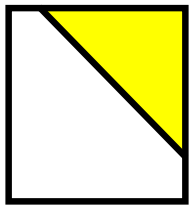

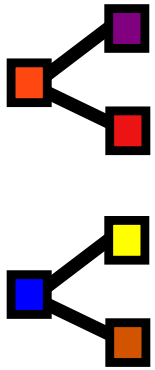

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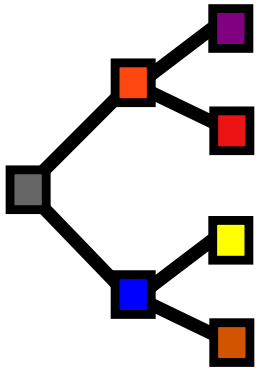
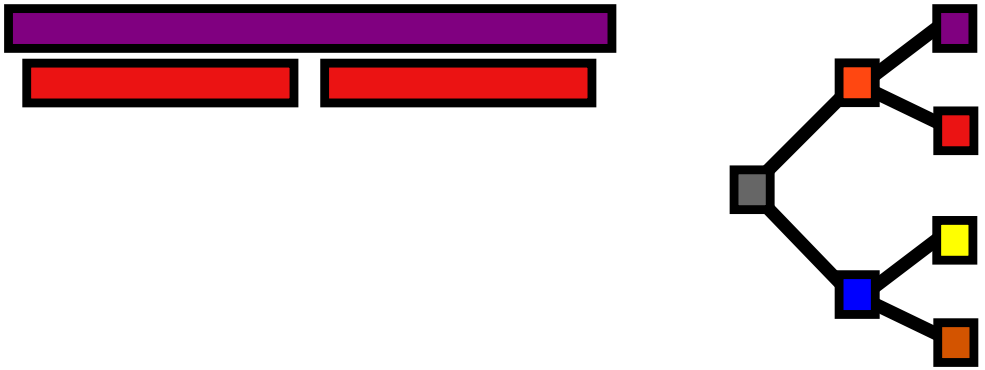


Progressive alignment following the guide tree



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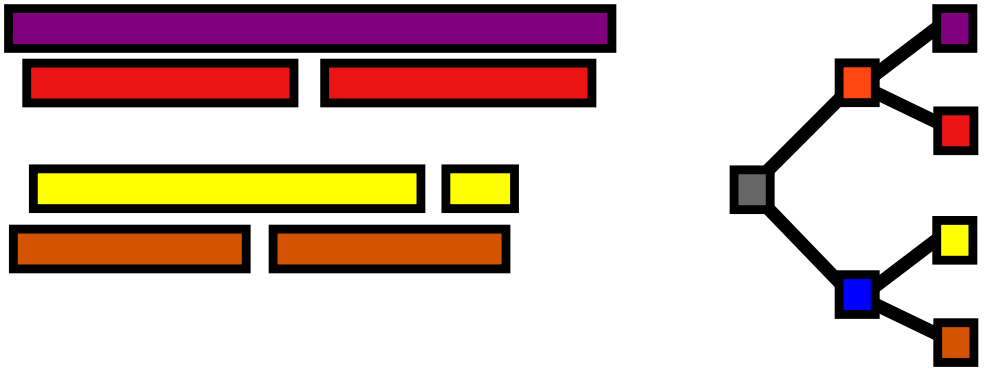

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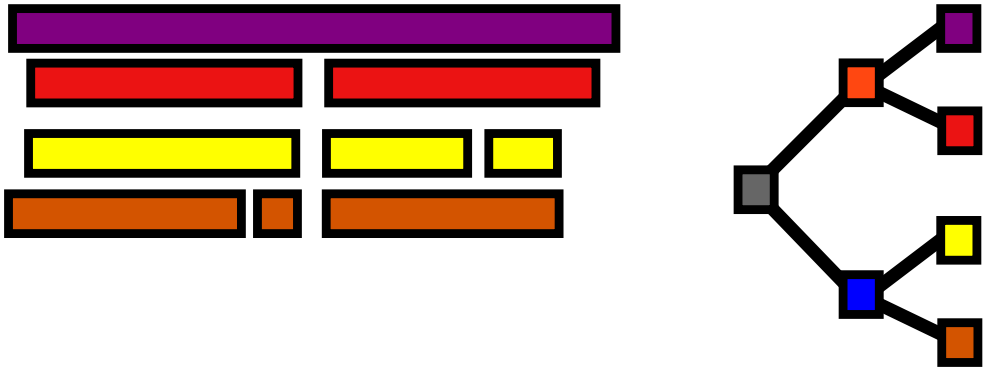
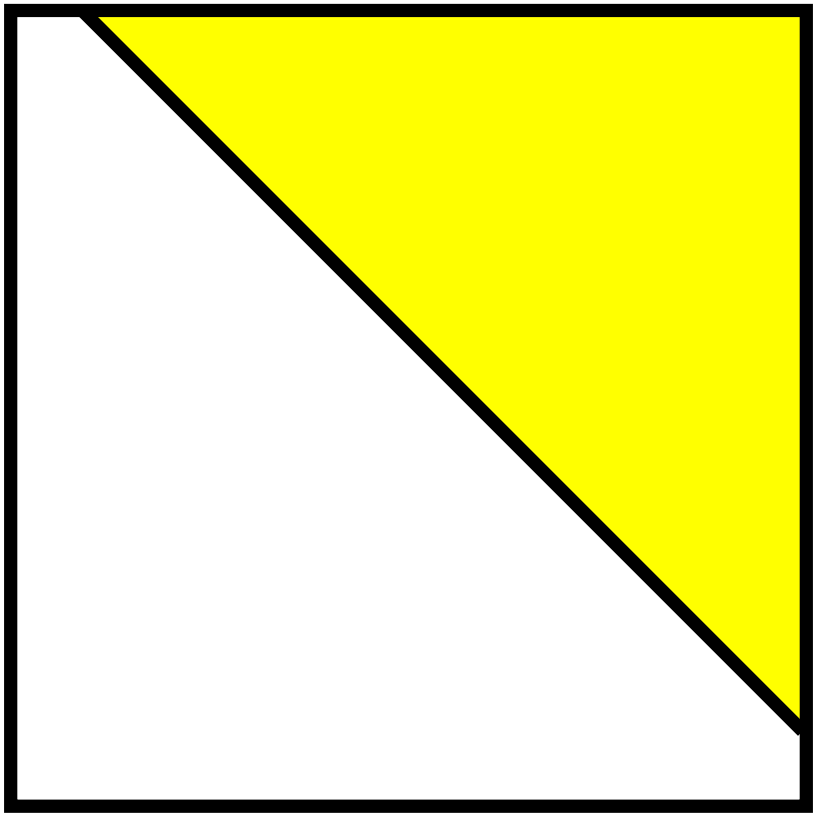
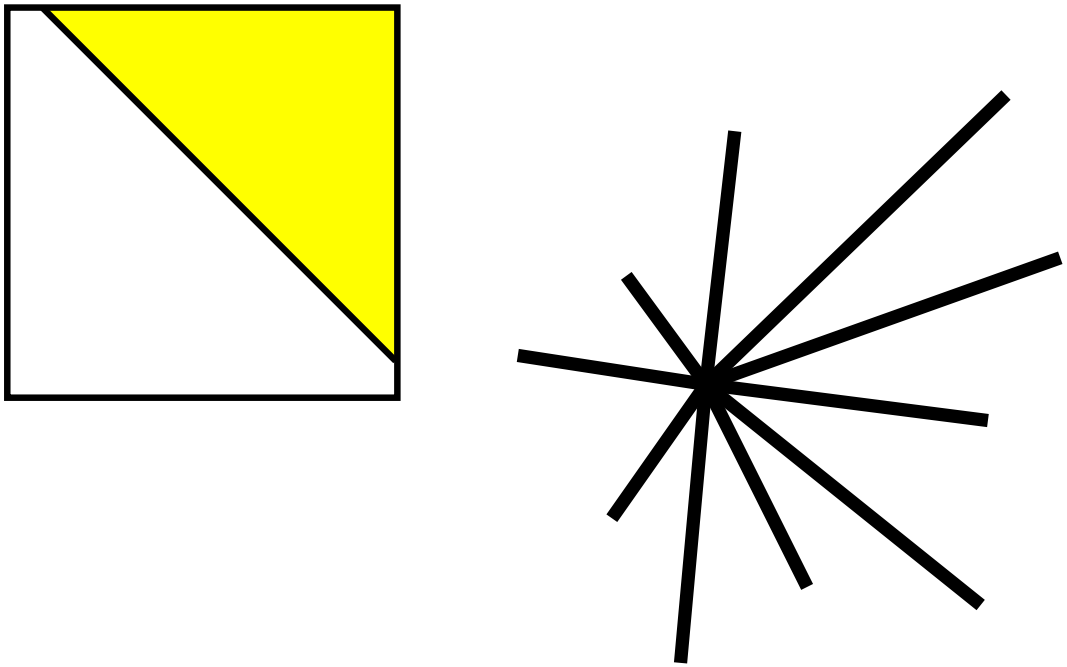


Measure distances directly from the alignment



Generate neighbor-joining tree from new distances



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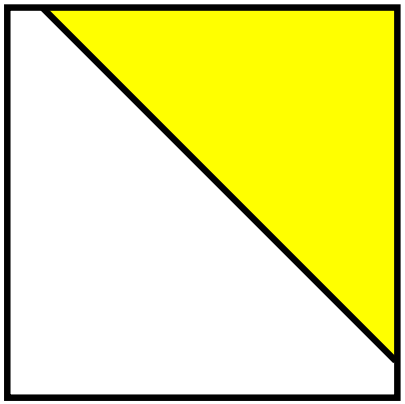

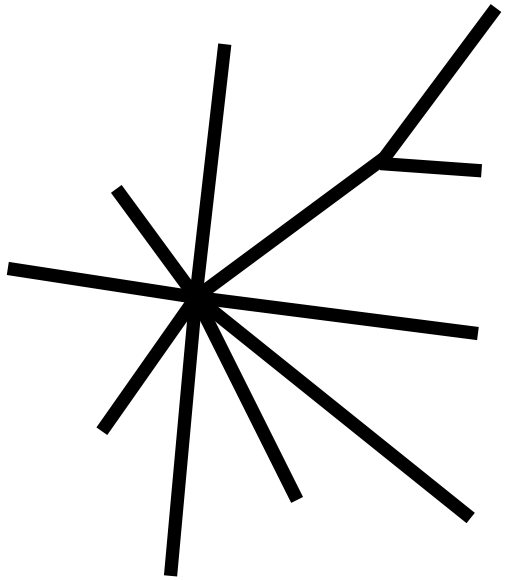

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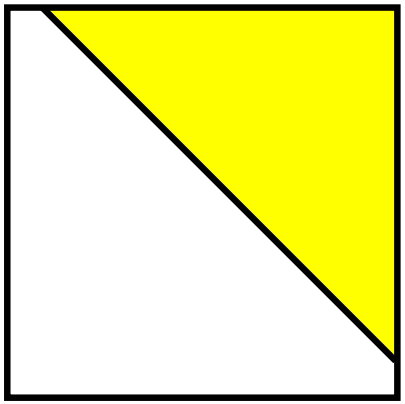
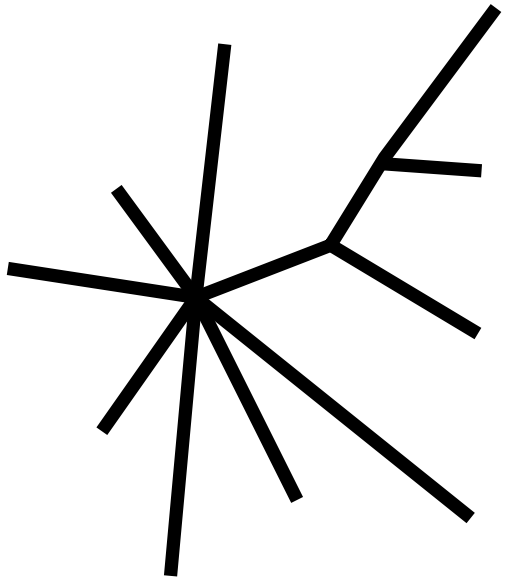
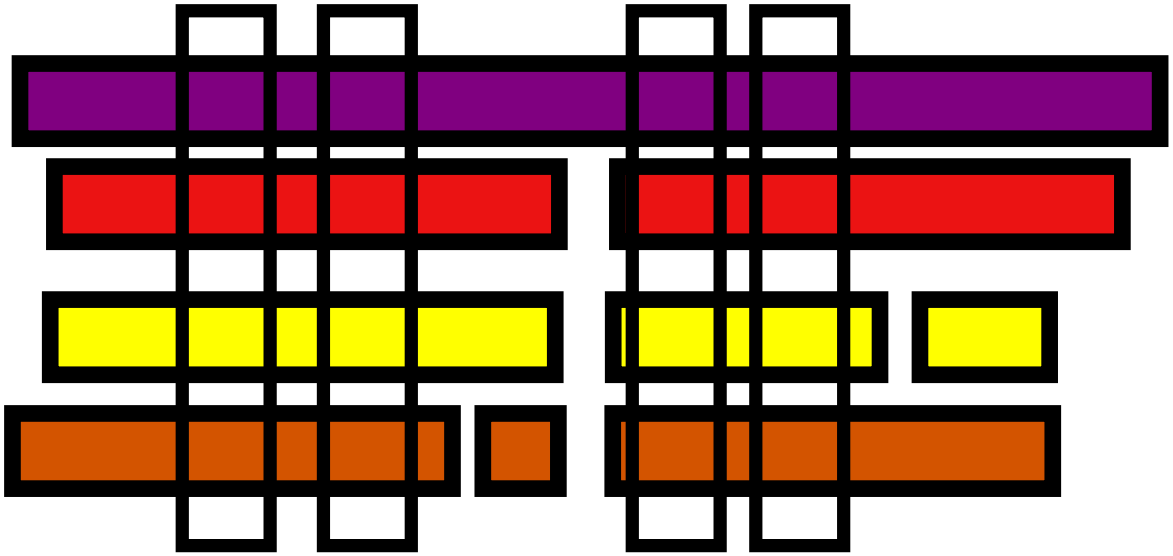
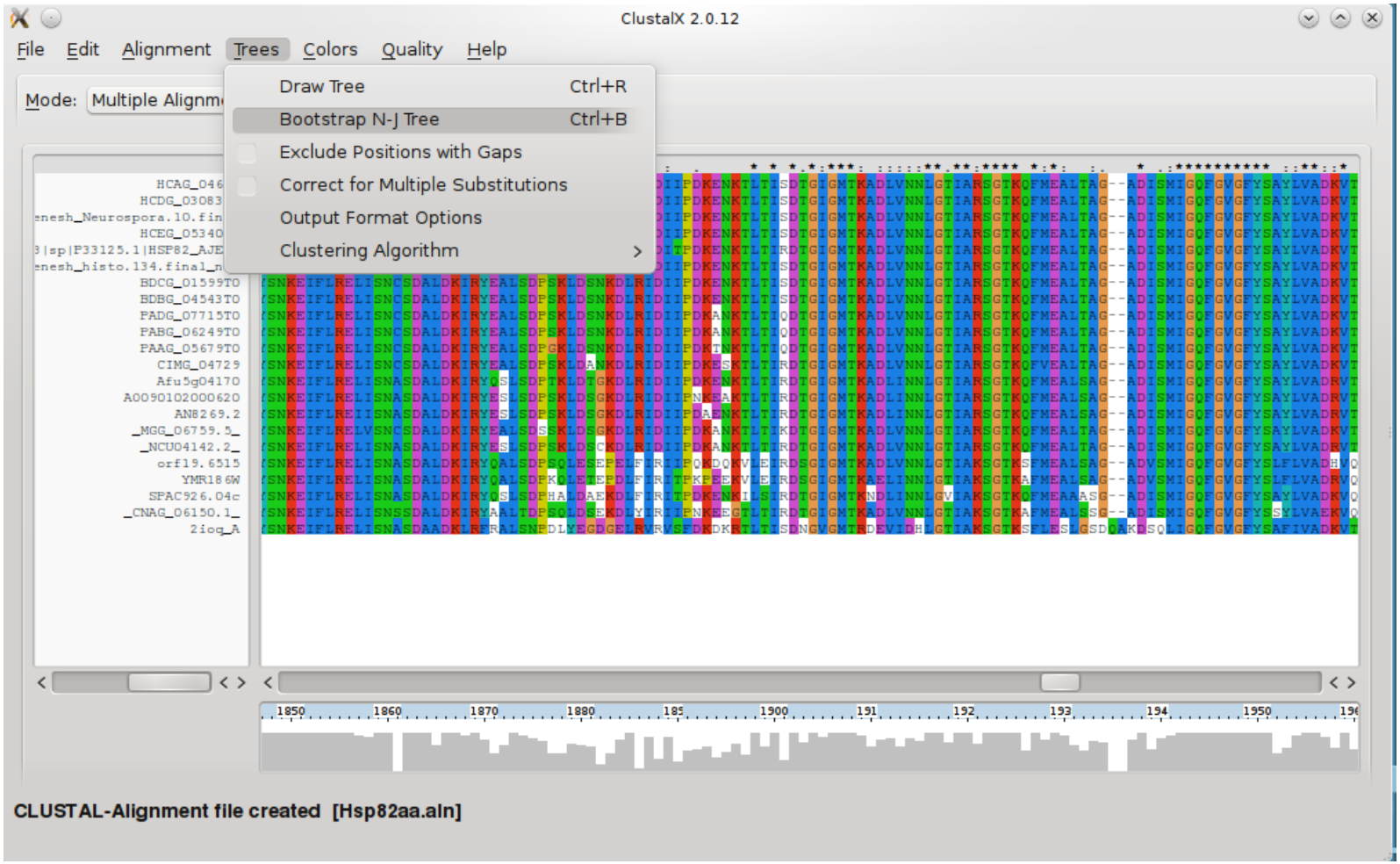




Generate bootstrap values from subsets of the alignment



Generating a neighbor joining tree in CLUSTALX

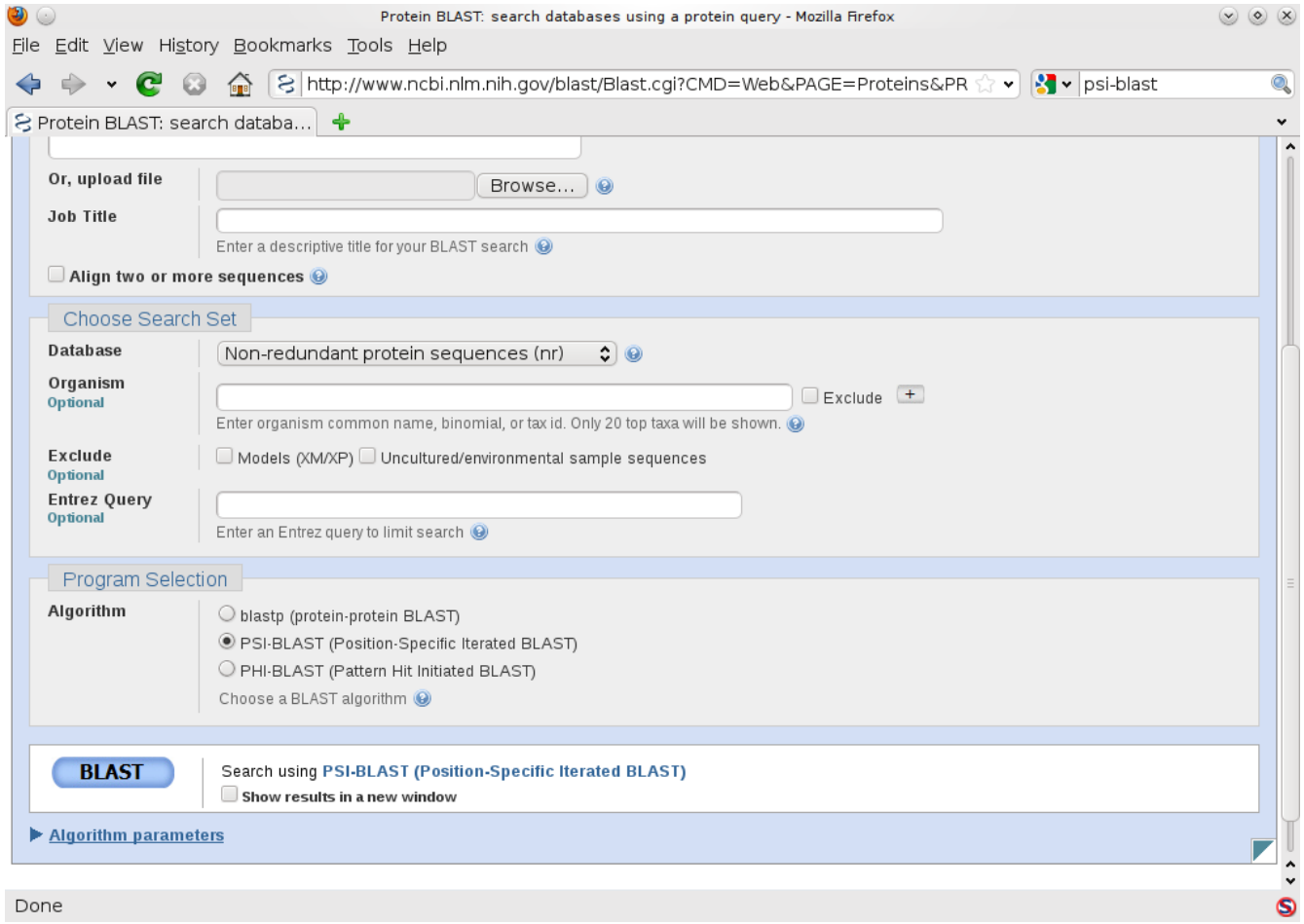


Viewing the alignment and tree in JALVIEW

Related tools

- Multiple Alignment
  - T-Coffee
  - MUSCLE
  - COBALT
- Tree building
  - MrBayes (Bayesian MCMC)
  - PhyML (maximum likelihood)
- Work benches
  - MESQUITE
  - UGENE

Searching with PSI-BLAST



Homework

- Play with CLUSTALX, JALVIEW, and PSI-BLAST
- Read PLoS Comp. Biol. 4:e1000069