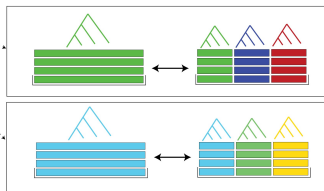
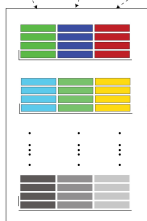


chromosome a



chromosome b



## B) Validate Supergenes

### i) Likelihood Ratio Tests (LRTs)

Does a "true supergene" model or a "false supergene" model provide a better fit?



Tools:

- Concatenator\* (Leigh et al. 2008)
- LRT (Huelsenbeck and Bull 1996)
- LRT (Waddell et al. 2000)

### ii) Tree Topology Tests (TTTs)

How many loci reject the supergene tree?



Tools:

- SH tests\* (Shimodaira and Hasegawa 1999)
- AU test (Shimodaira 2002)
- adaptations of SH/AU (i.e., Baptiste et al. 2002, Susko et al. 2006)

## A) Construct Supergenes

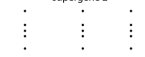
Construct a set of "putative supergenes" to be validated:



"supergene 1"



"supergene 2"

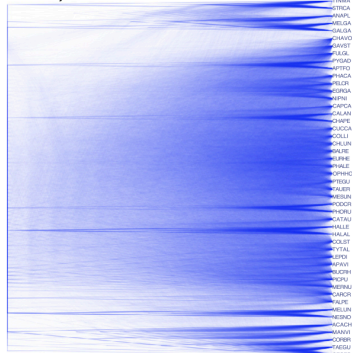


"supergene n"

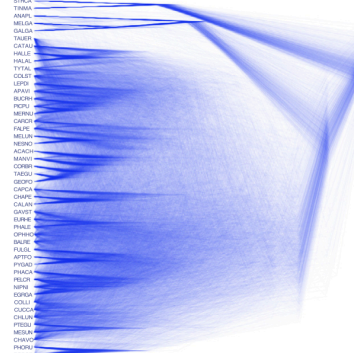
Tools:

- weighted statistical binning\*
- unweighted binning
- random binning
- a priori partitioning

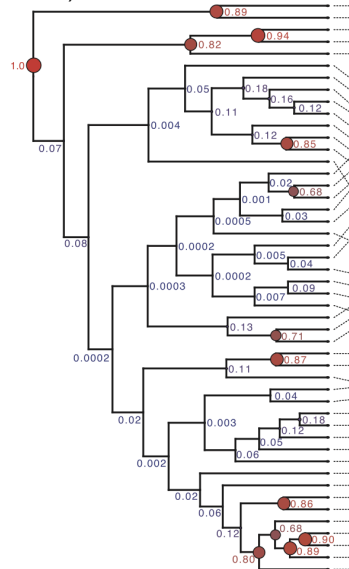
## A) Unbinned Gene Trees



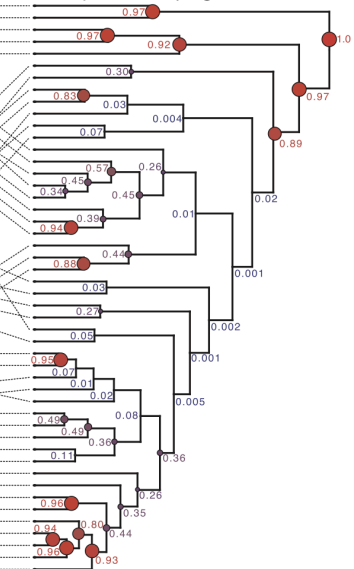
## B) Binned Supergene Trees



## C) Unbinned Gene Trees

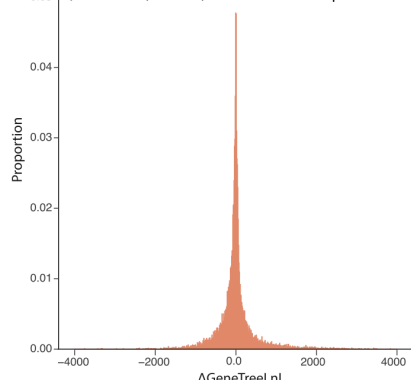


## D) Binned Supergene Trees



## E) Unbinned Gene Trees

8,005 trees (55.41%) favor unbinned species tree



## F) Binned Supergene Trees

1,008 trees (49.85%) favor binned species tree

