A Supergenome is a common coordinate system for all genomes in a multiple alignment. [1]

Based on the work of Fabian Gärtner [1]

- He calculates an order of optimal local alignments that are as co-linear as possible with all the genome sequences

Data
- stored in a Neo4J graph database
- processed with Gremlin which is a graph traversal language

G = (V, E)

EXAMPLE SUPERGENOME
EXAMPLE SUPERGENOME
2 levels of abstraction to visualize the genomes

1. Sequence view

2. Block view

supergenome
- Sugiyama framework is the most popular method for DAG (directed acyclic graph) layouts [1]

- Procedure: Preprocessing and 3 main steps
  1. Cycle removal (Preprocessing)
  2. Layer assignment
  3. Vertex ordering
  4. Other coordinate assignment

▪ Guide sequence is in the middle of the graph
  → ordered in one line from left to right
▪ The other sequences are arranged around
▪ Allow only as few as possible edge-edge crossings and no edge-vertex crossings
Supergenome browser with 2 abstraction levels
Better comparison of multiple sequence alignments
User interaction
  - Choice of guide sequence (supergenome is also possible)
  - Genome selection including order (supergenome) for comparison
  - Navigation between abstraction levels (zoom in & zoom out)
THANK YOU