

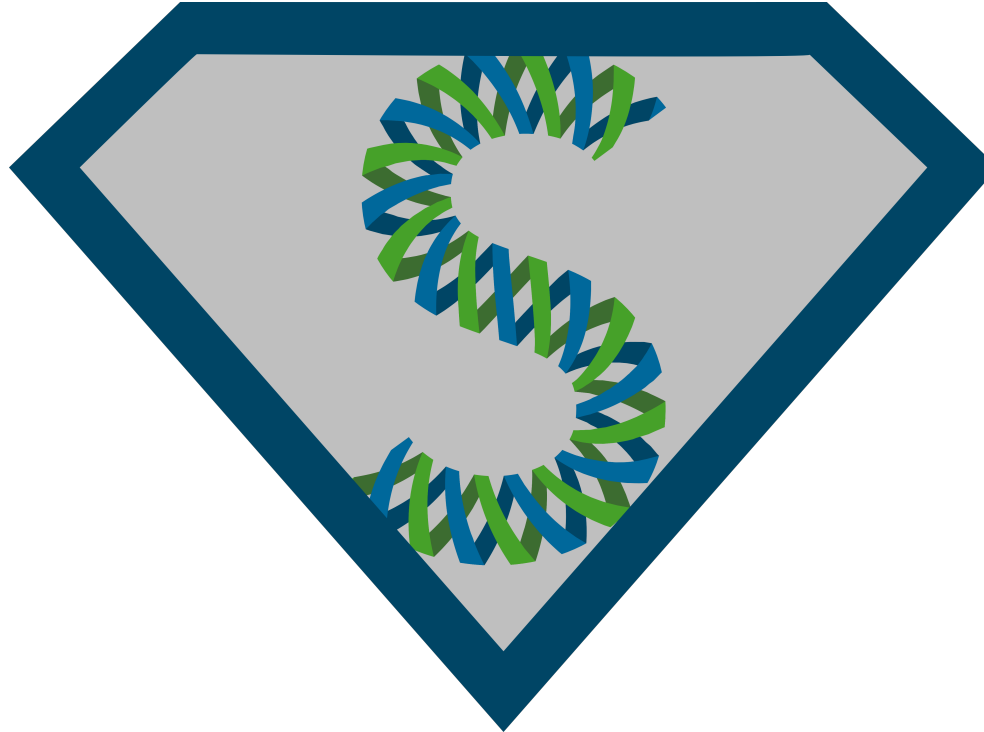


SUPERGENOME BROWSER

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

[1] Herbig, A et al. "GenomeRing: alignment visualization based on SuperGenome coordinates" Bioinformatics (Oxford, England) vol. 28,12 (2012): i7-15.

- 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



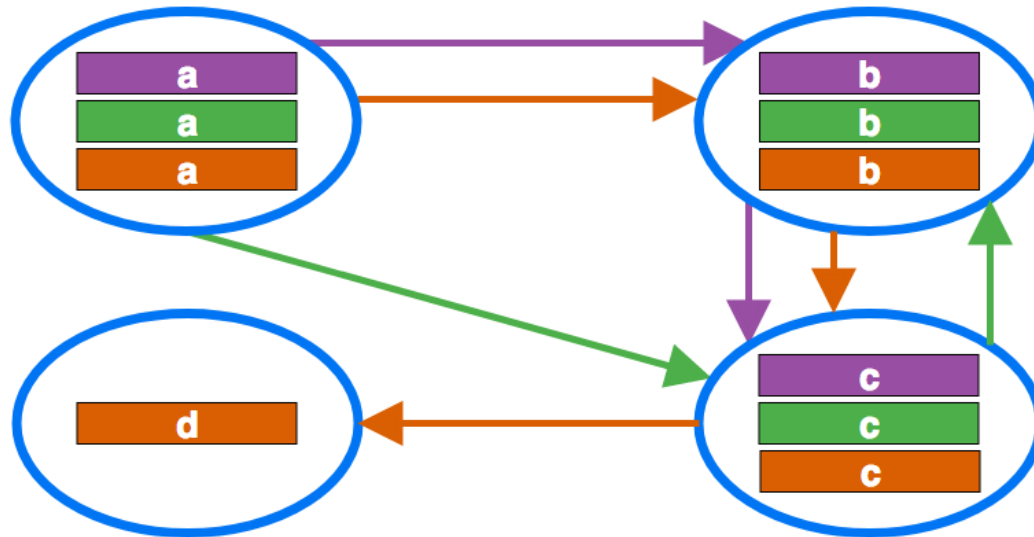
Gremlin
 $G = (V, E)$

[2]

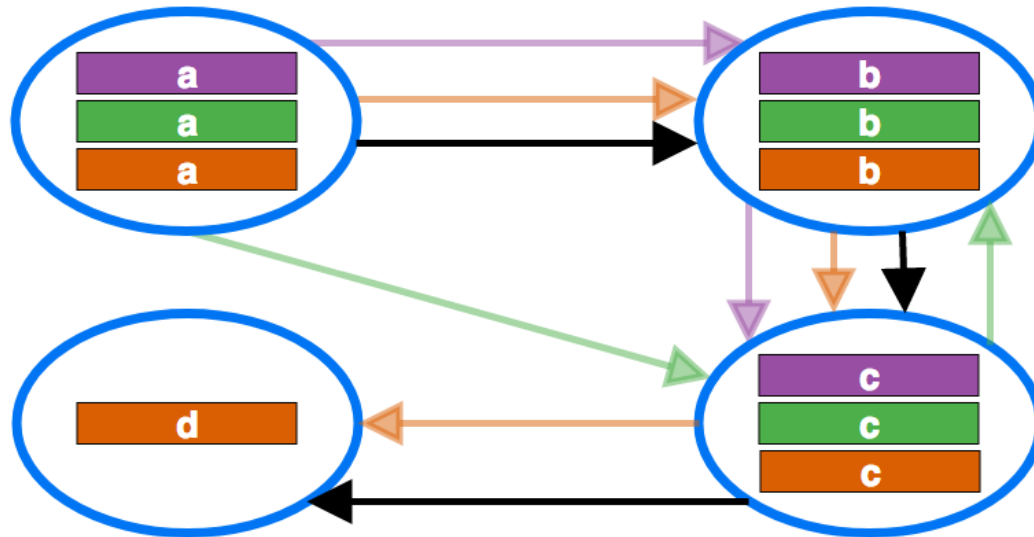
[1] Gärtner, Fabian et al. "Coordinate systems for supergenomes" Algorithms for molecular biology : AMB vol. 13 15. 24 Sep. 2018

[2] <http://tinkerpop.apache.org/docs/current/images/gremlin-logo.png>

EXAMPLE SUPERGENOME



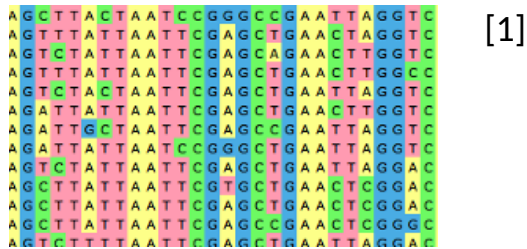
EXAMPLE SUPERGENOME



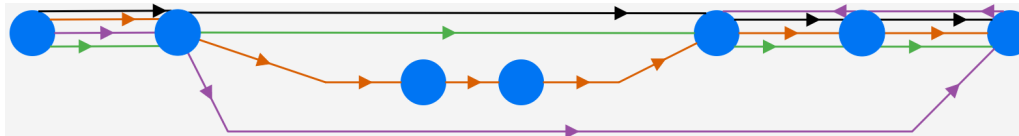


- 2 levels of abstraction to visualize the genomes

1. Sequence view



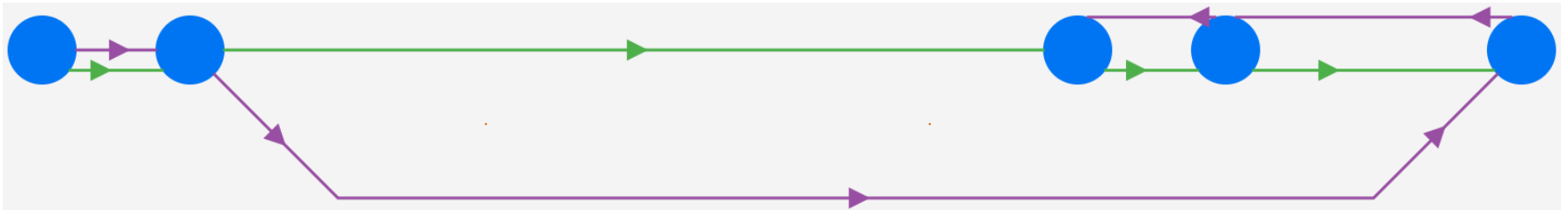
2. Block view



[1] <http://ugene.net/multiple-sequence-alignment-with-muscle/>

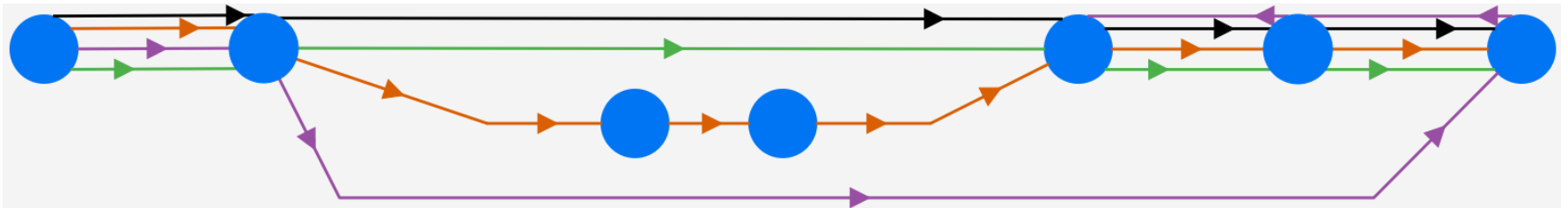






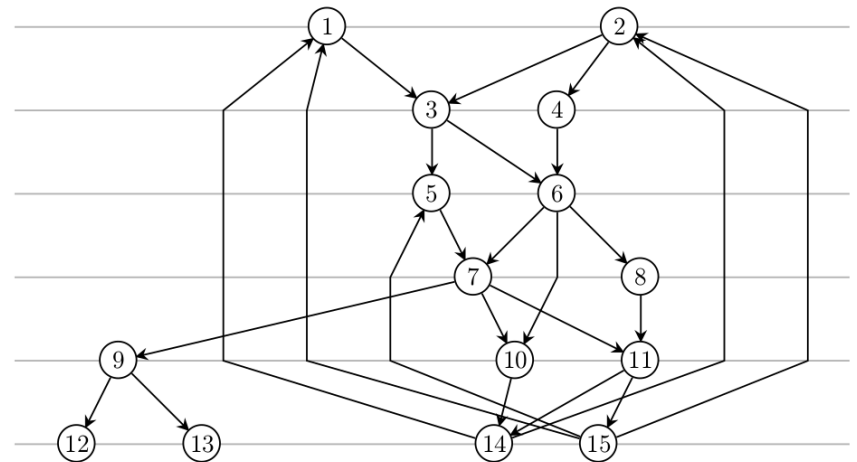


supergenome





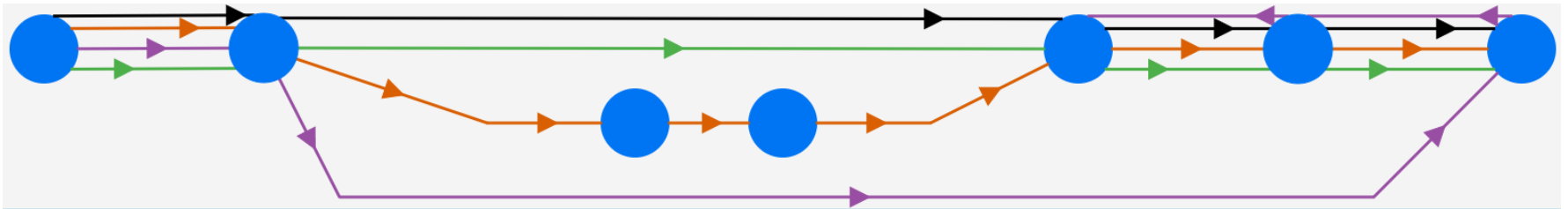
- Sugiyama framework is the most popular method for DAG (directed acyclic graph) layouts [1]
- Procedure: Preprocessing and 3 main steps
 1. Cycle removal (Preprocessing)
 2. Layer assignment
 3. Vertex ordering
 4. Other coordinate assignment



[1] Tamassia, Roberto, editor. Handbook of Graph Drawing and Visualization. Taylor & Francis Group, 2014.



- 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

