

# Project Sibelia

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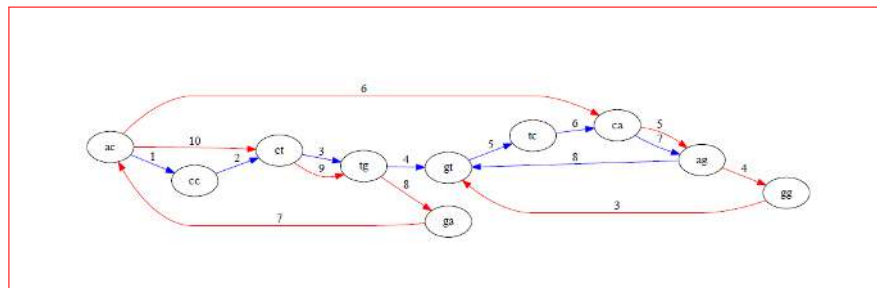
## Brief description

- Sibelia — software to finding synteny blocks
- Synteny blocks — conservative sites of genomes
- Now using for only bacterial genomes

# Algorithm

- Build colored De Bruijn graph
- Graph not stored explicitly
- Simplify graph: find and remove buldges i.e change sequences and graph
- Synteny blocks correspond to non-branching paths in the simplified graph

# Colored De Bruijn graph



- Colored De Bruijn graph for string acctgtcagt
- Paths (1,2) and (10) form a buldge
- Paths (3) and (9) form a non-branching path

# Goal of project

- Replace the current sequence + graph modification algorithm by pure graph algorithm
- Expected improvements in speed and memory
- Using for big genomes as mammals

# Progress

- Output synteny blocks in SAM-format — already done
- Write code for pure graph algorithm — to do

## Questions

Thank you for your attention! Questions?

