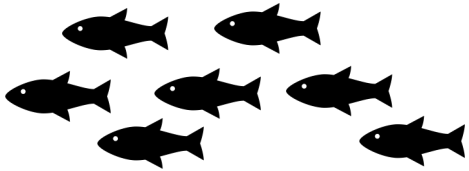
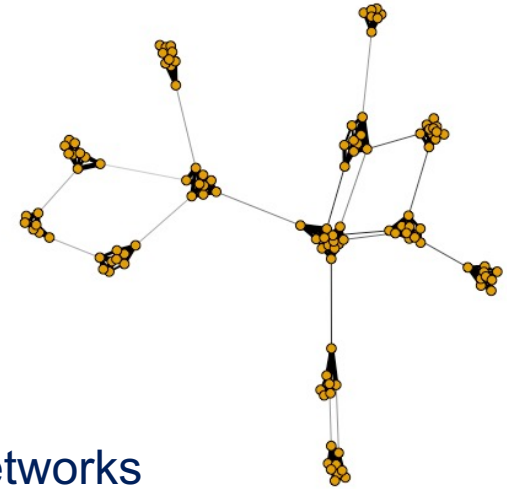
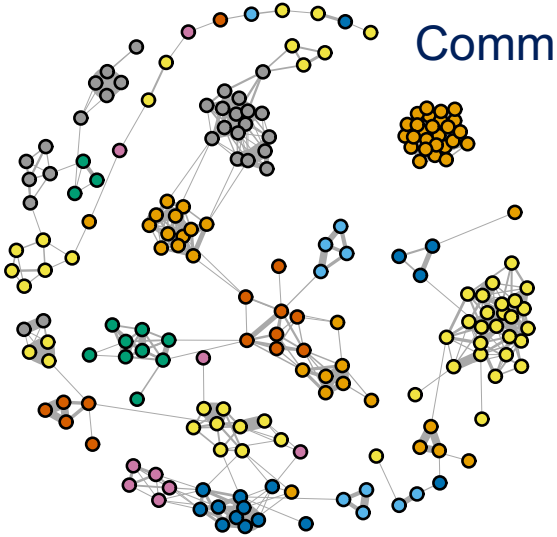
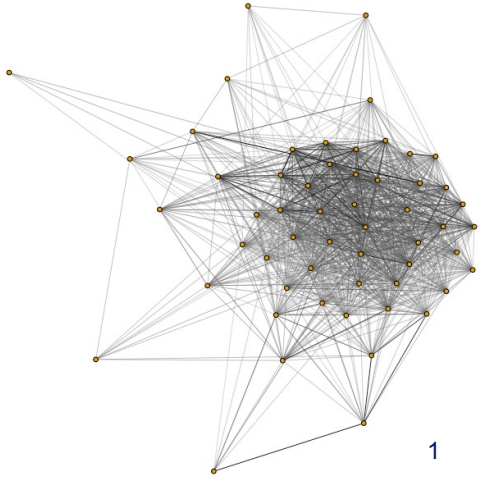




ExoLabel:
Community Detection for Big Biological Networks

Aidan Lakshman, Erik S. Wright





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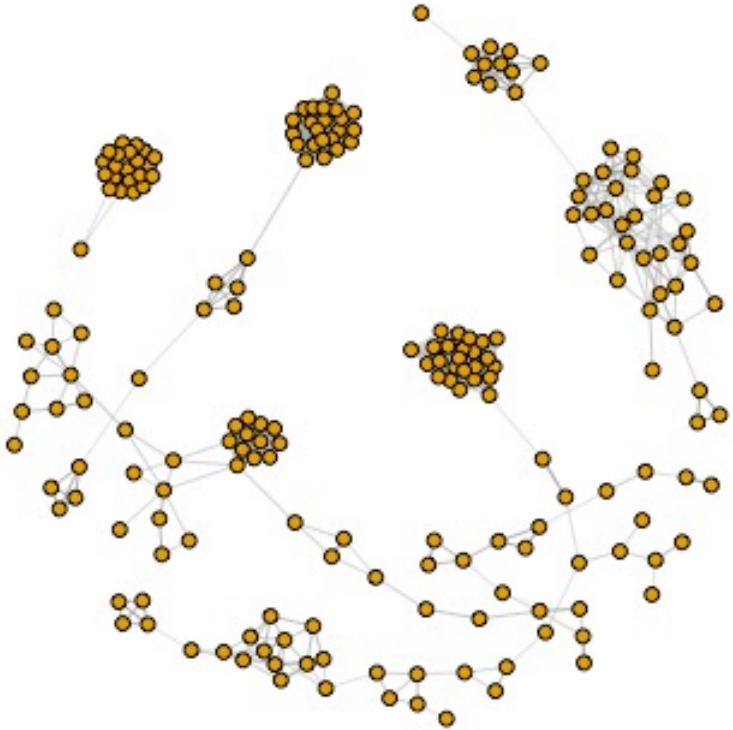

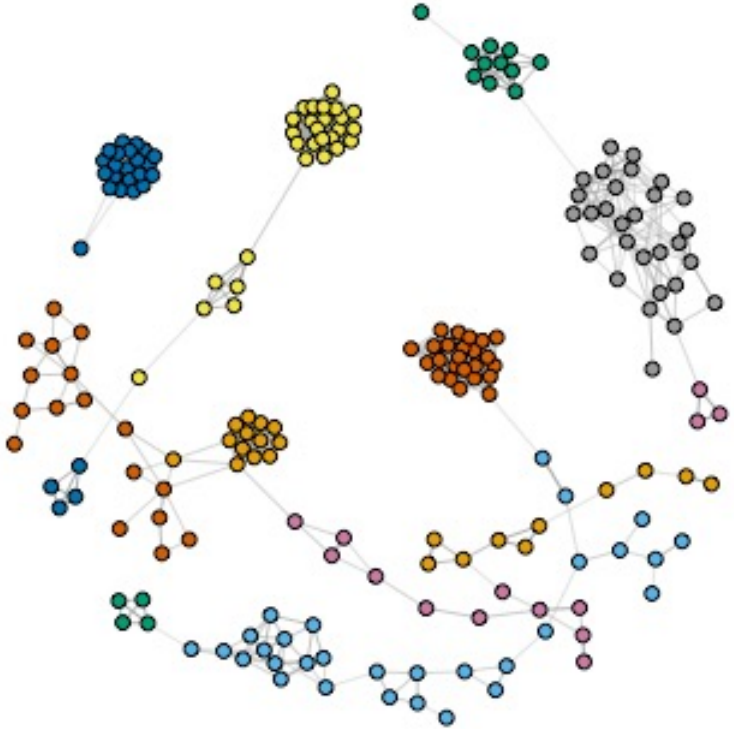

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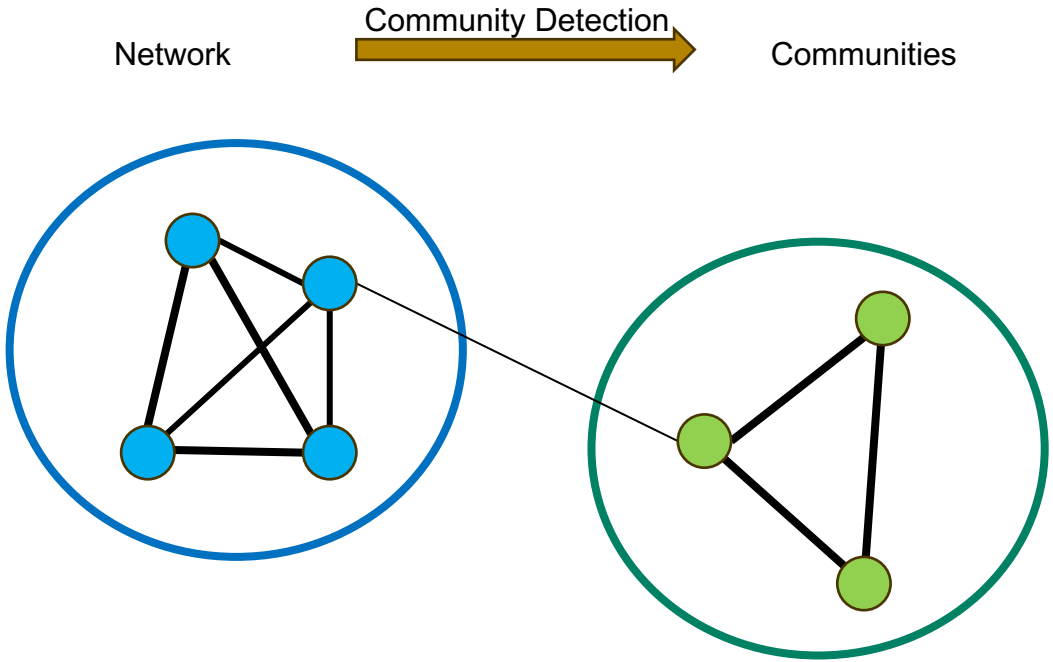
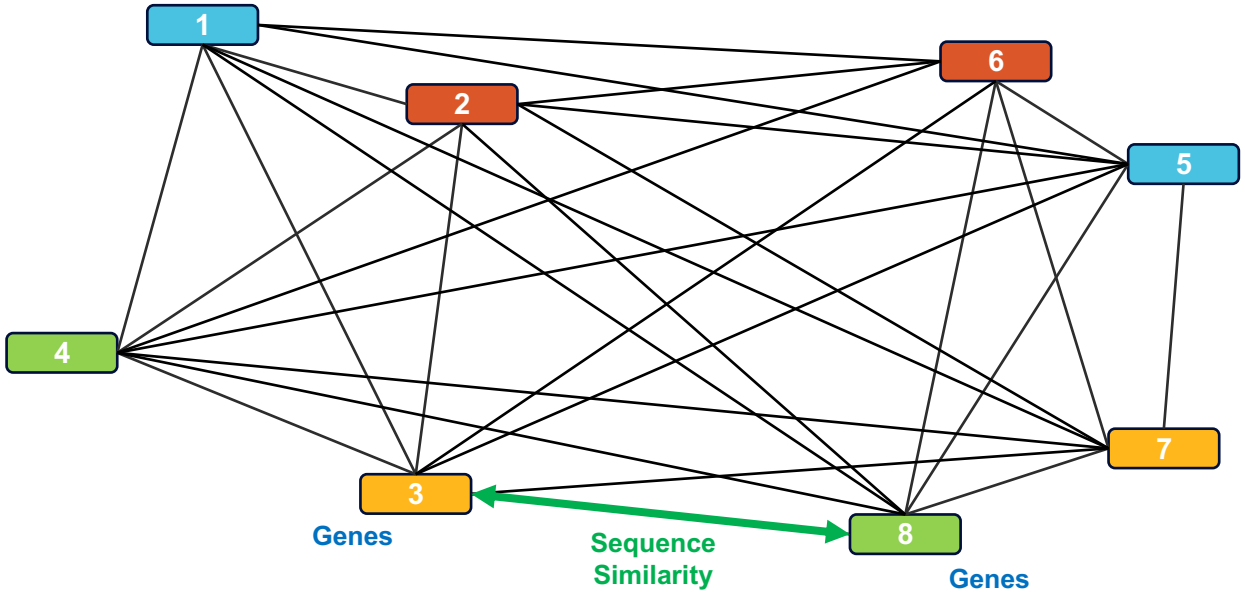

Network
Community Detection
Communities

Comparative genomics depends on detecting community detection in **Sequence Similarity Networks**

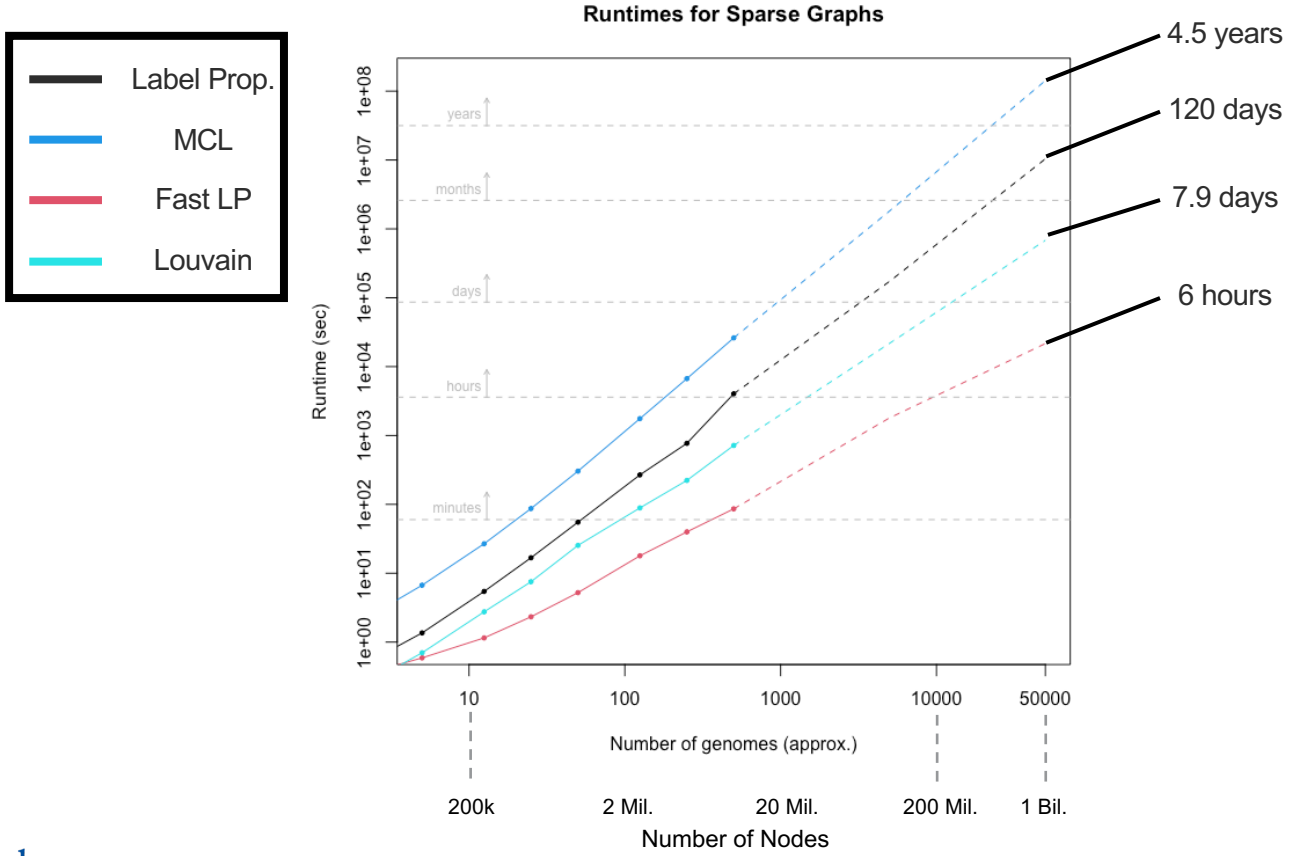


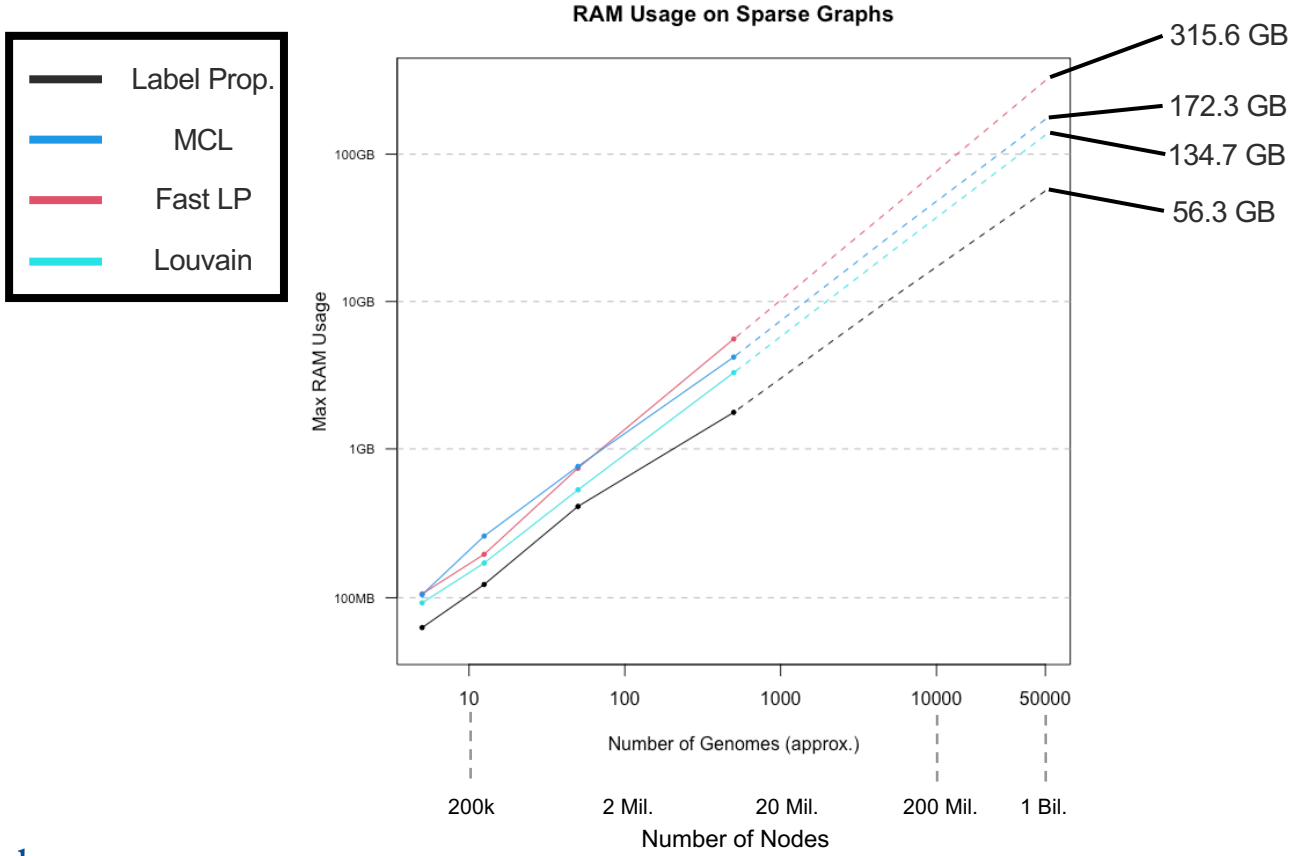
Thousands of genes

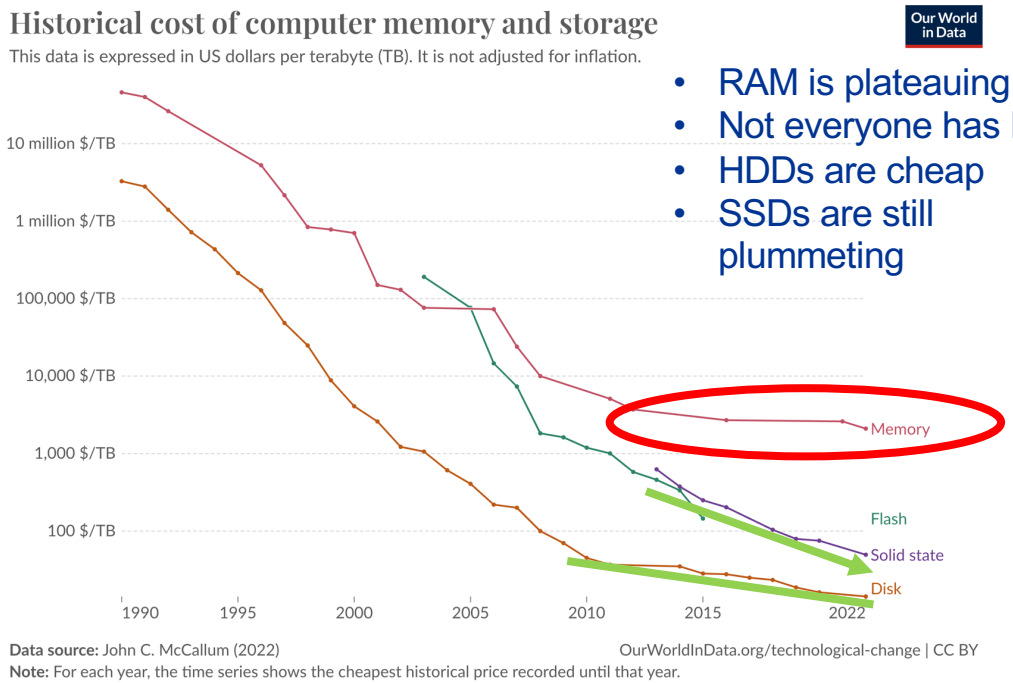
Each additional gene

1 edge per existing genome

Network size is quadratic in number of genomes

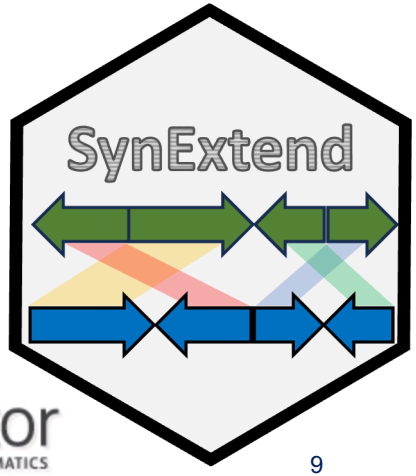

Label Prop.
MCL
Fast LP
Louvain
Runtimes for Sparse Graphs
Runtime (sec)
1e+00
1e+01
1e+02
1e+03
1e+04
1e+05
1e+06
1e+07
1e+08
years
months
days
hours
minutes
4.5 years
120 days
7.9 days
6 hours
10
100
1000
10000
50000
Number of genomes (approx.)
200k
2 Mil.
20 Mil.
200 Mil.
1 Bil.
Number of Nodes


Label Prop.
MCL
Fast LP
Louvain
RAM Usage on Sparse Graphs
315.6 GB
172.3 GB
134.7 GB
56.3 GB
100GB
10GB
1GB
100MB
Max RAM Usage
10
100
1000
10000
50000
Number of Genomes (approx.)
200k
2 Mil.
20 Mil.
200 Mil.
1 Bil.
Number of Nodes



- RAM is plateauing
- Not everyone has HPCs
- HDDs are cheap
- SSDs are still plummeting

ExoLabel



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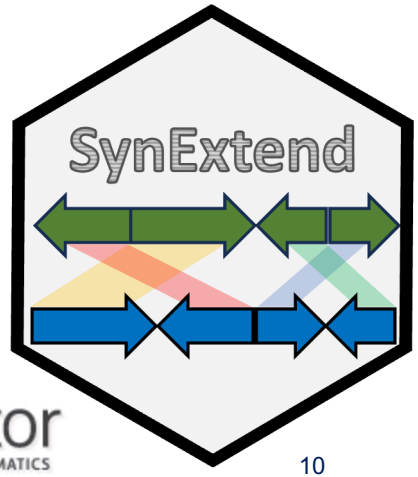
Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

Core algorithm:
Fast Label Propagation

Exo

Data stored out of memory

Label



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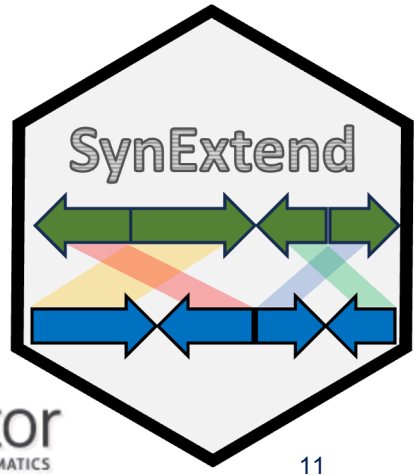
ExoLabel

- Constant memory scaling
- Linear disk scaling
- Log-linear runtime
- Comparable accuracy to other standard methods



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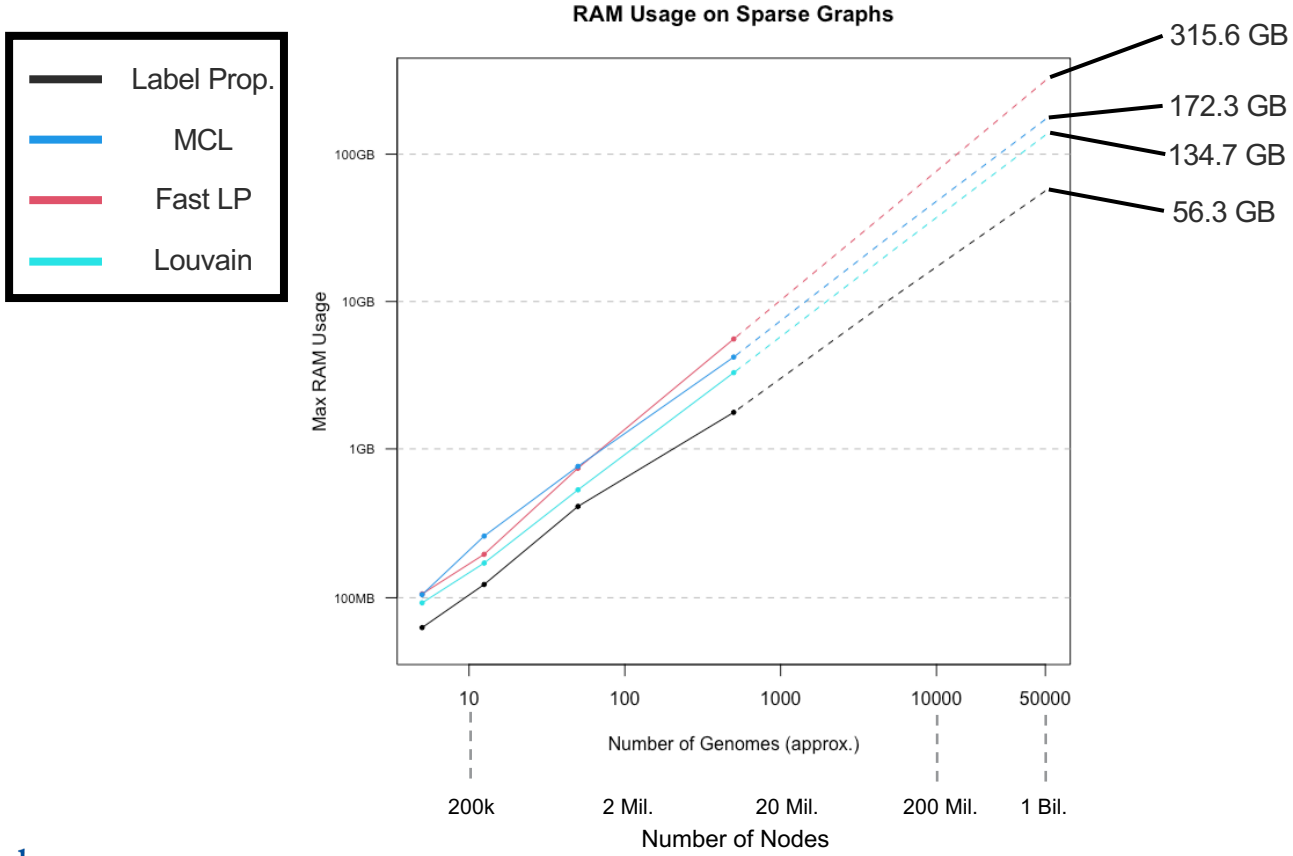
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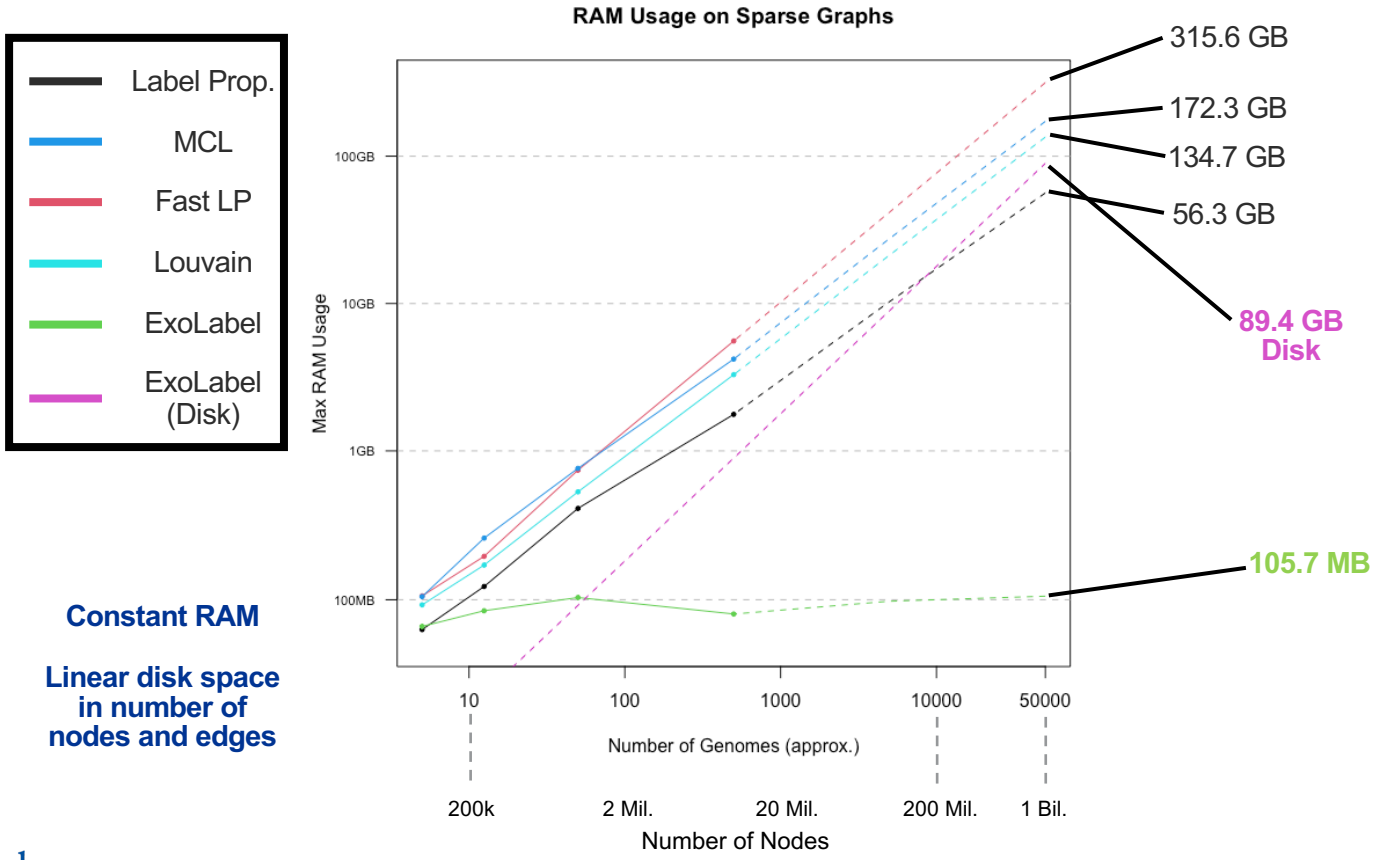

Constant RAM

Linear disk space in number of nodes and edges

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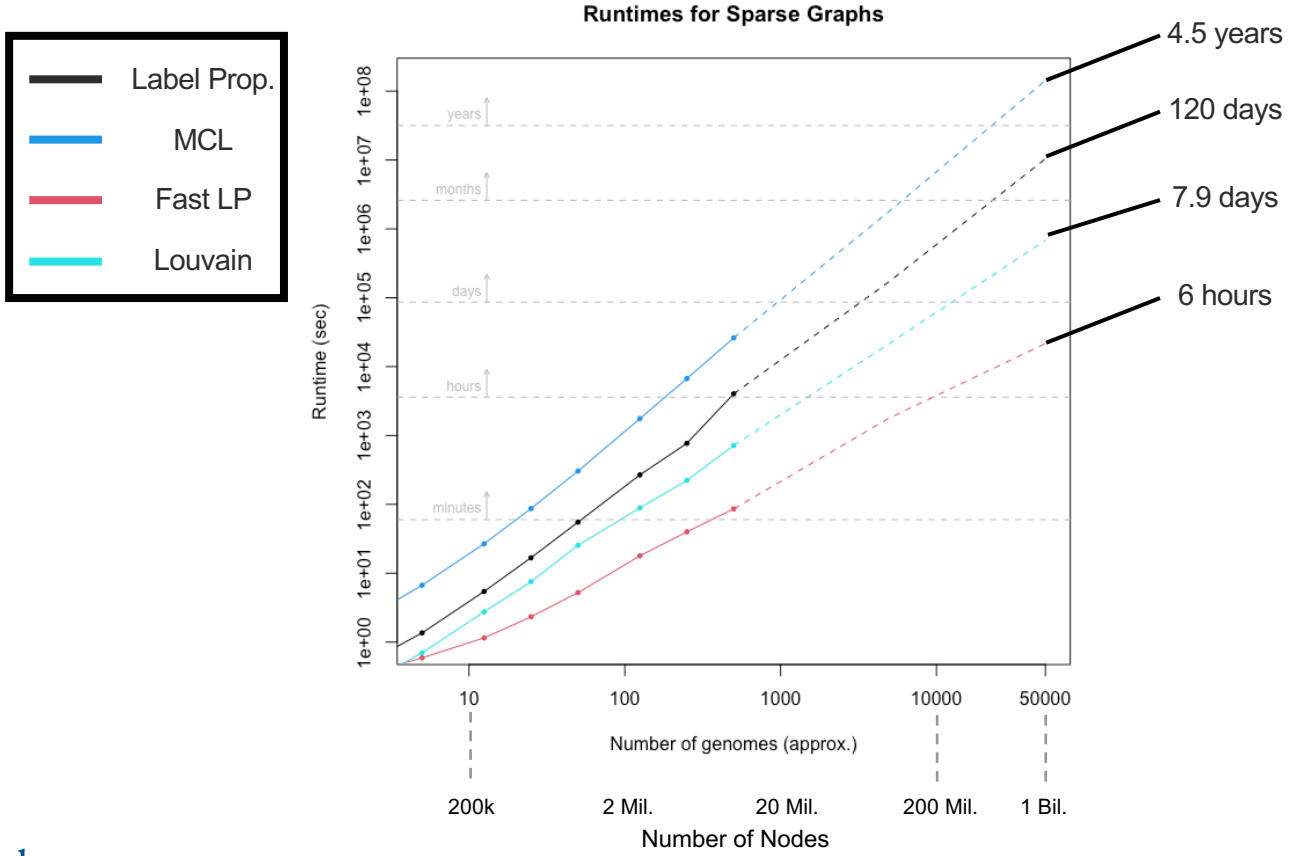
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MCL
Fast LP
Louvain
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4.5 years
120 days
7.9 days
6 hours
Runtime (sec)
1e+00
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1e+02
1e+03
1e+04
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1e+06
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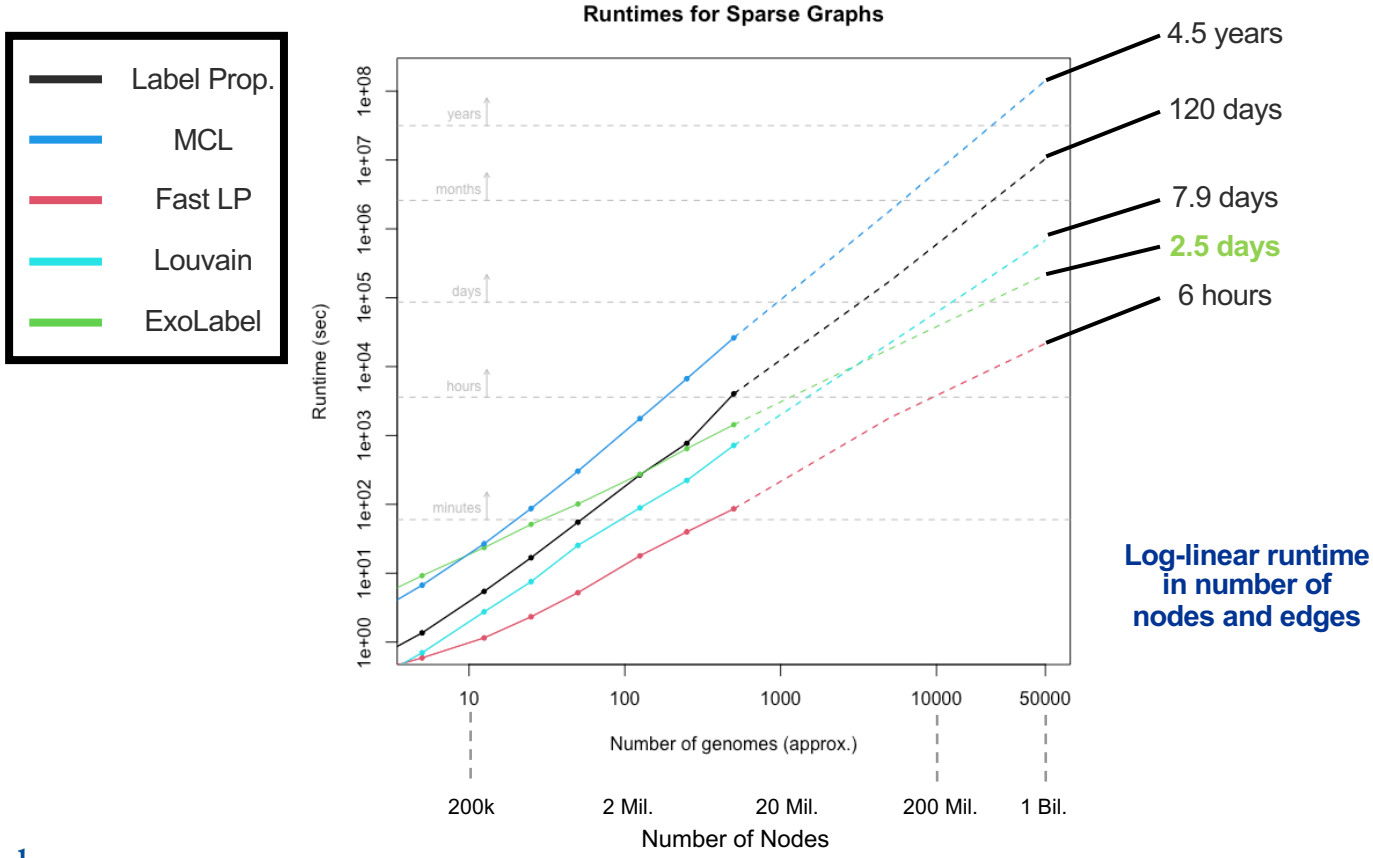

Log-linear runtime in number of nodes and edges

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- Sam Blechman
- Nishant Panicker
- Maria Bond

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AHL27@pitt.edu

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