Pitt DBMI

Community Detection for Big Biological Networks with ExoLabel

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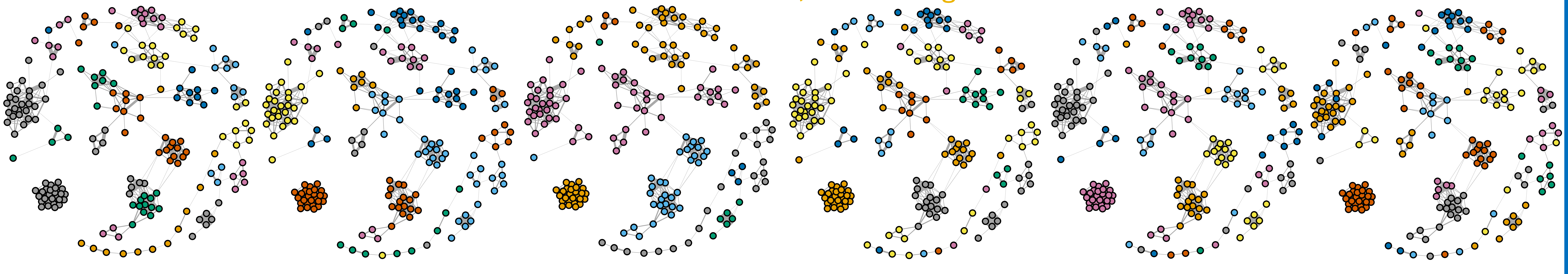
National Library of Medicine



Label Propagation | Fast Label Propagation | Louvain | **ExoLabel** | MCL (I=1.4) | MCL (I=2.0)

Problem

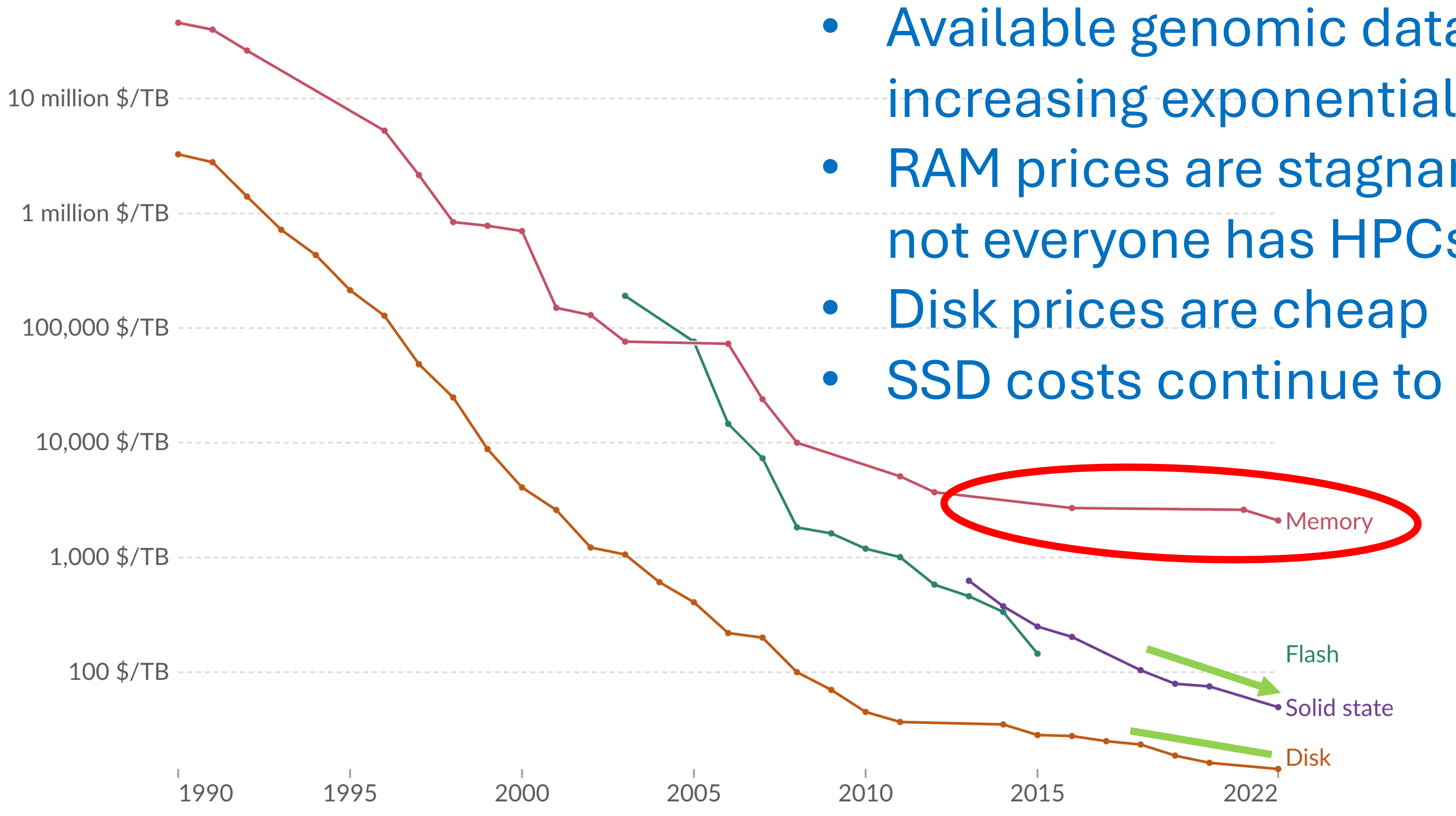
- Comparative genomics depends on **Orthology Detection**
- **Community Detection algorithms** can infer orthology groups from sequence similarity networks
- Current approaches **fail to scale** to modern genomic data

Solution

- We introduce a new algorithm, **ExoLabel**
- **ExoLabel** performs Label Propagation using **disk space to minimize memory consumption**
- **ExoLabel** can identify communities in a network with billions of nodes using **only 100MB of RAM**
- **Exolabel** matches state-of-the-art community detection methods in accuracy and outperforms in runtime & memory

Historical cost of computer memory and storage

This data is expressed in US dollars per terabyte (TB). It is not adjusted for inflation.



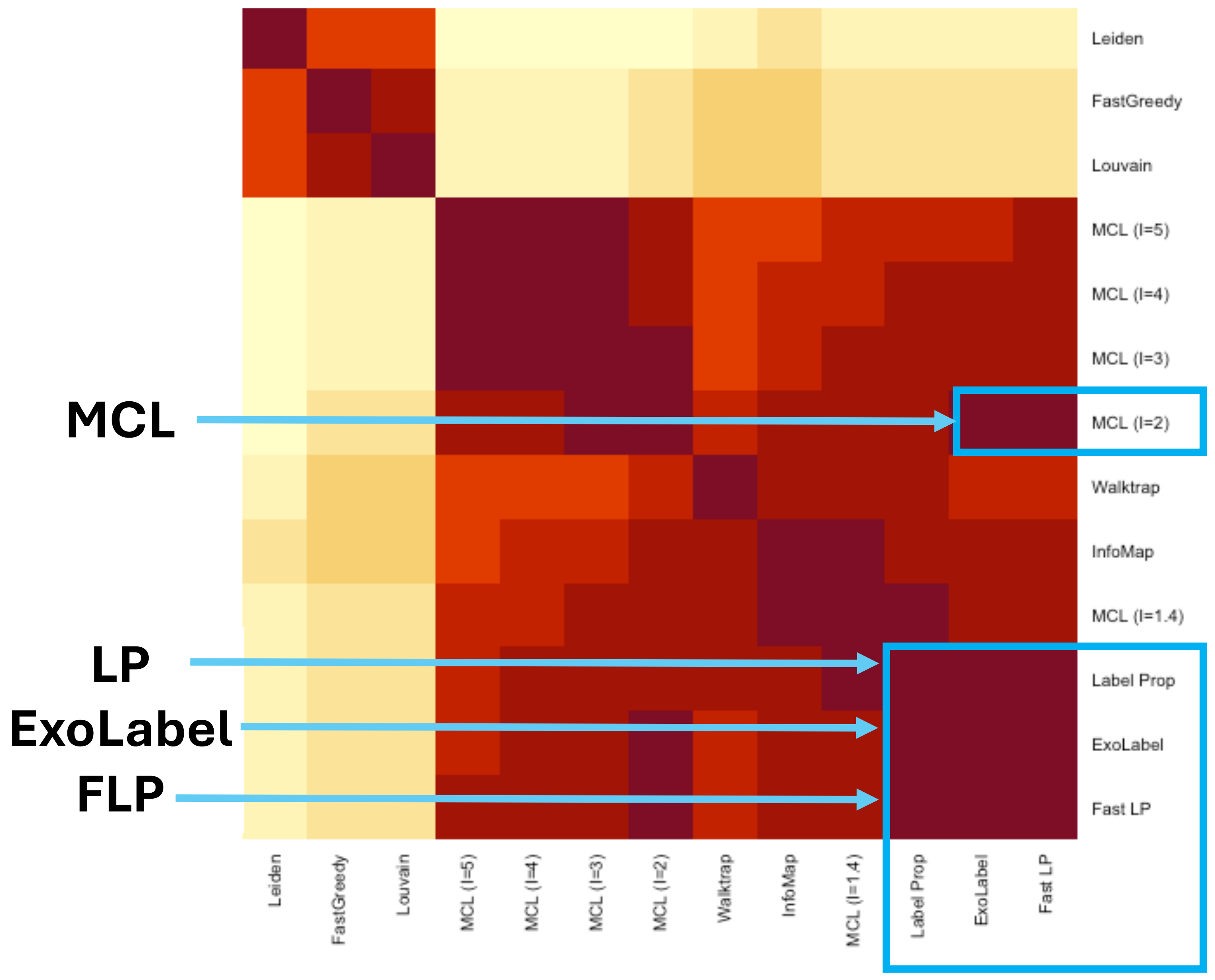
Data source: John C. McCallum (2022) OurWorldInData.org/technological-change | CC BY
Note: For each year, the time series shows the cheapest historical price recorded until that year.

- Available genomic data is increasing exponentially
- RAM prices are stagnant, and not everyone has HPCs
- Disk prices are cheap
- SSD costs continue to plummet

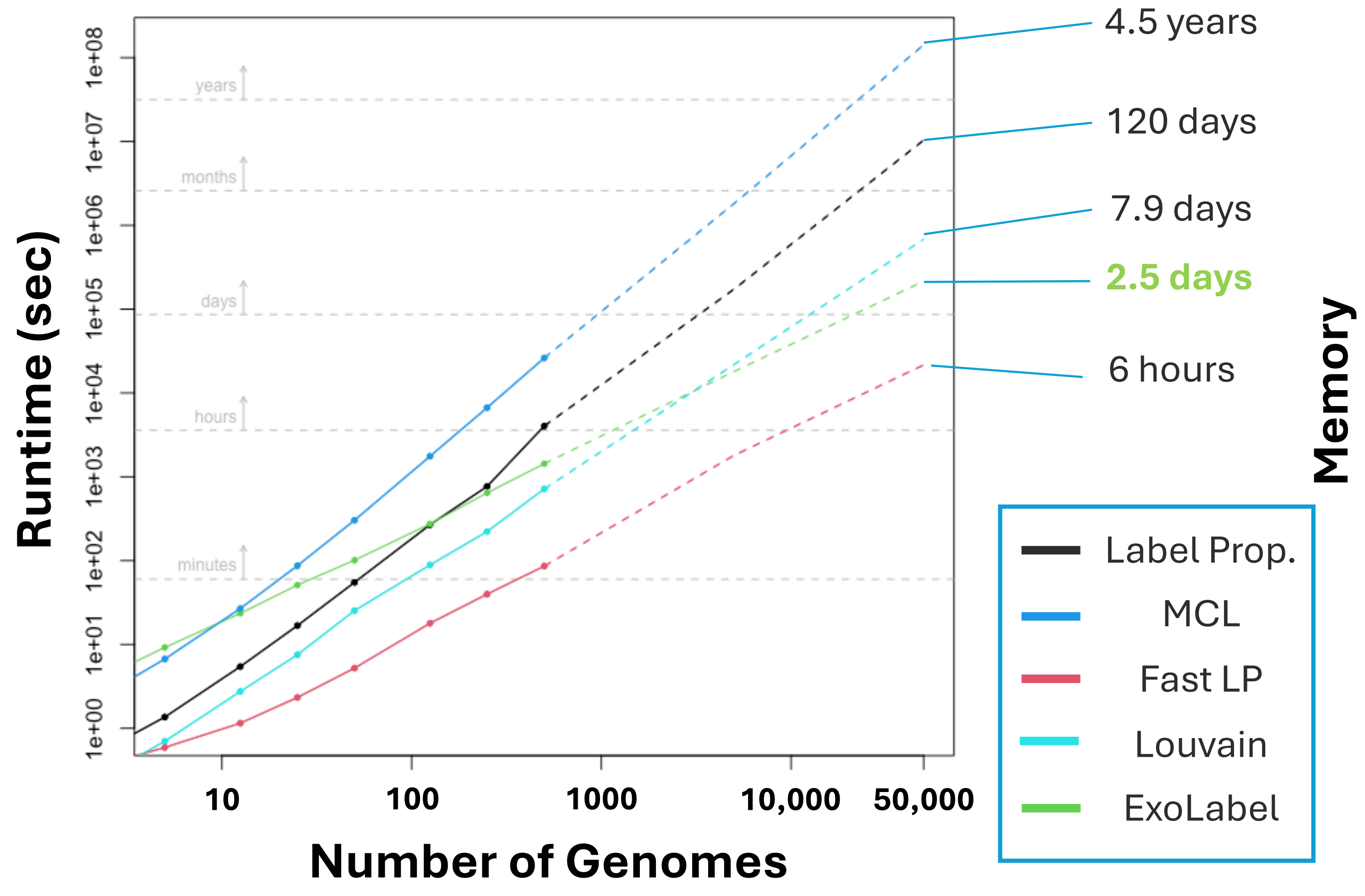
Details

- ExoLabel has log-linear runtime scaling in terms of number of nodes and edges
- Memory scaling is constant
- Disk consumption is linear with respect to number of nodes and edges
- Performance is comparable to low-inflation MCL or Label Propagation

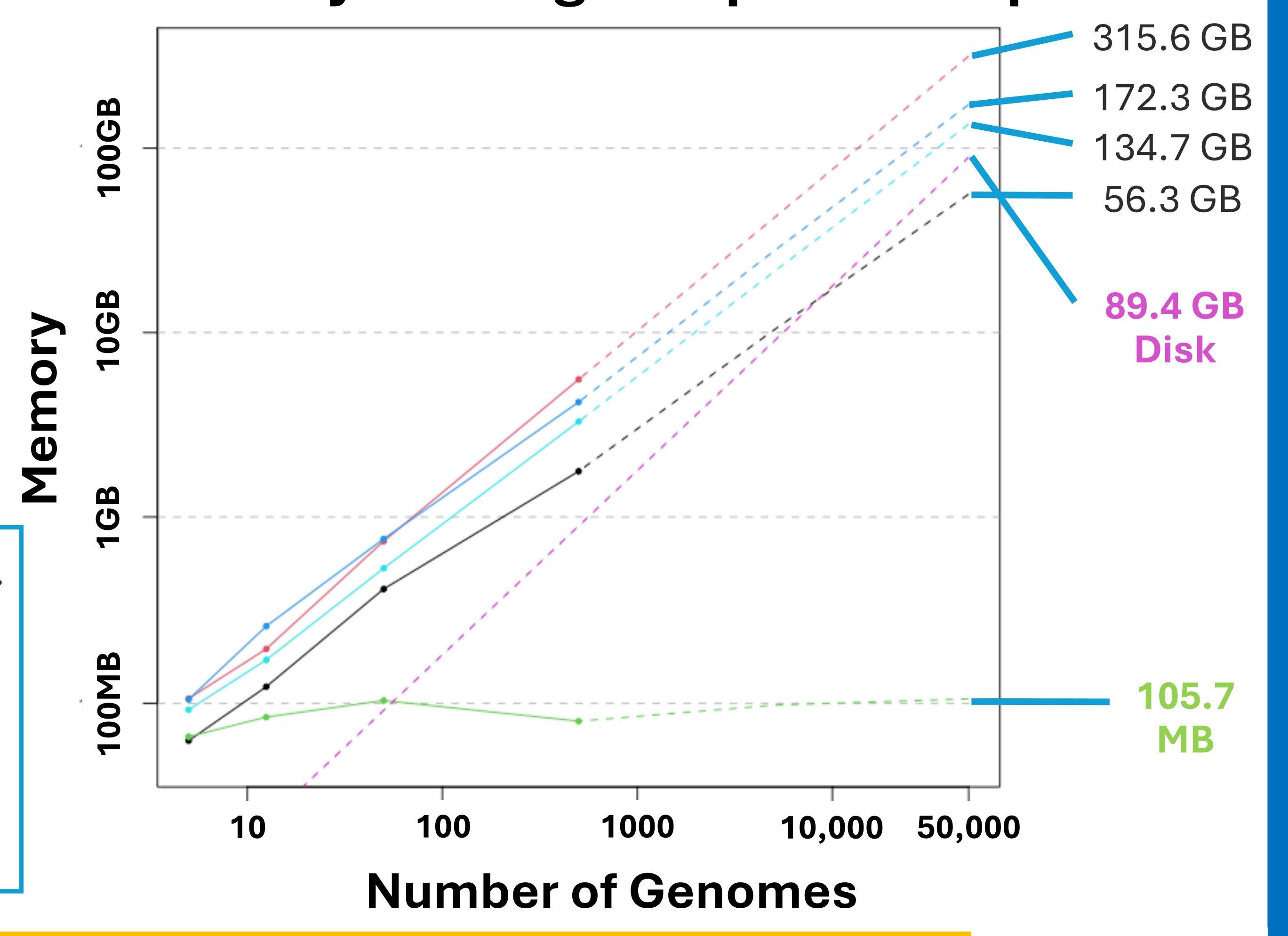
Community Similarity on 50 Prokaryotic Genomes



Runtime Scaling on Sparse Graphs



Memory Scaling on Sparse Graphs



WRIGHT LABORATORY

Our Lab:
www.WrightLabScience.com
www2.DECIPHER.codes

DECIPHER SynExtend

ExoLabel is available in the SynExtend package for R

Contact me!
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