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meta rep

Quantifying similarities between fMRI processing pipelines for efficient multiverse analysis

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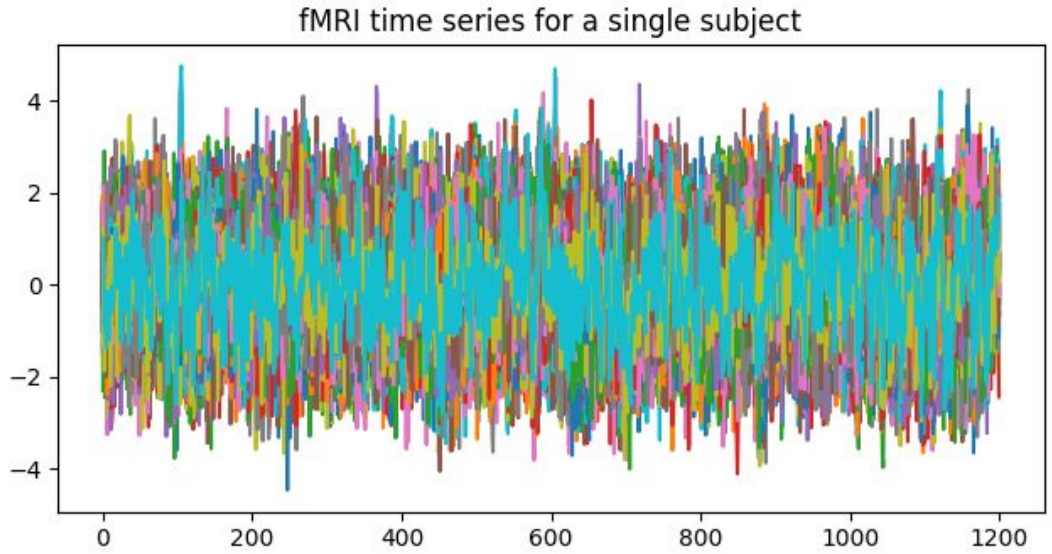
Problem set-up

fMRI data is **noisy** and requires **long preprocessing**/analysis pipelines

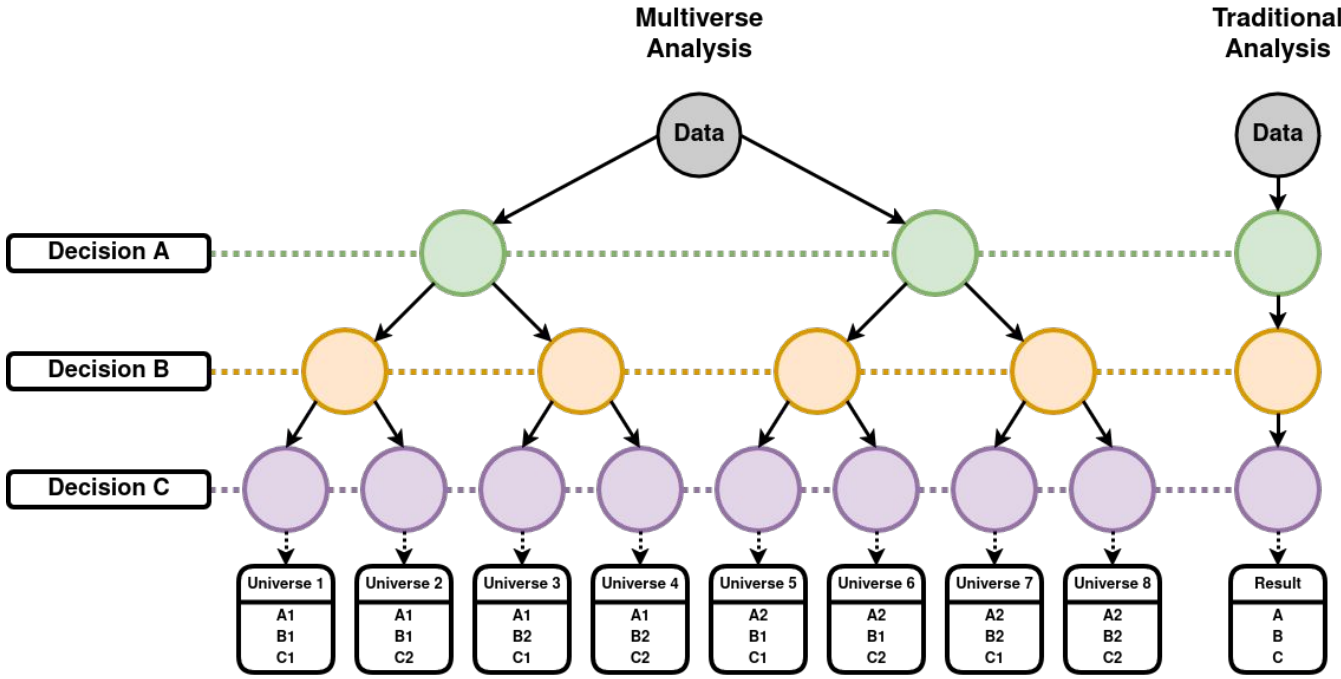
- Researchers are faced with a plethora of arbitrary yet defensible decisions
- Many **researcher degrees of freedom** introduce bias and contribute to the replication crisis



What is multiverse analysis?

Multiverse Analysis: Running multiple (equally defensible) analysis pipelines

- Proposed to help with the issue of flexibility in data processing/analysis
- **Reduces bias** from selective reporting, **improves replicability and robustness**



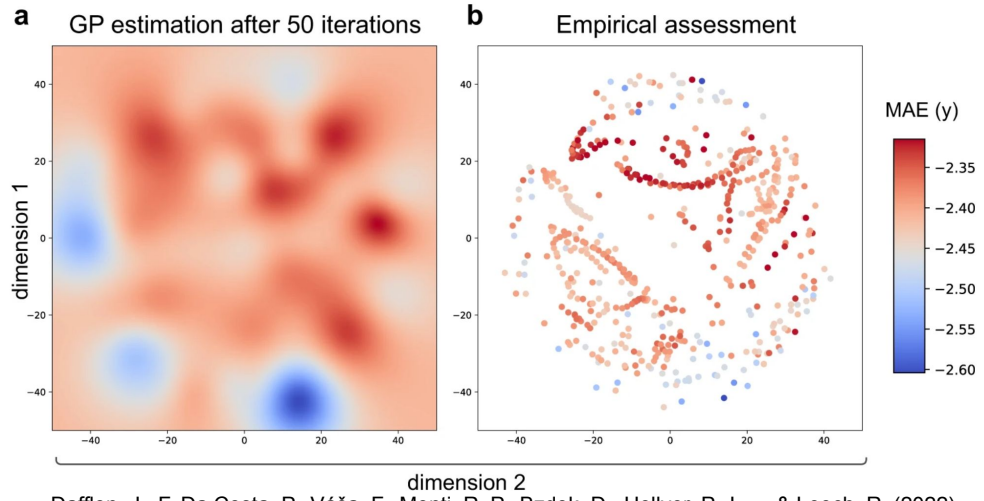
Why do we need multiverse analysis to be more efficient?

- In neuroimaging studies, the **space of decisions is large**
- The size of the multiverse scales with the cartesian product of its decisions

→ It can quickly become computationally infeasible to run an entire multiverse

Why do we need multiverse analysis to be more efficient?

- Dafflon et al. (2022) proposed **subsampling the multiverse**
  - Builds search space from output similarities (e.g., functional connectivity)
  - Uses embedding algorithms to map relationships in a 2D space
  - Proximity in space reflects similar pipeline outputs
- We propose that we can **efficiently subsample** the space of decisions just by the analysis pipelines themselves
  - Embeddings based on pipeline configurations, not output similarity
  - Capture structural differences in the pipeline design

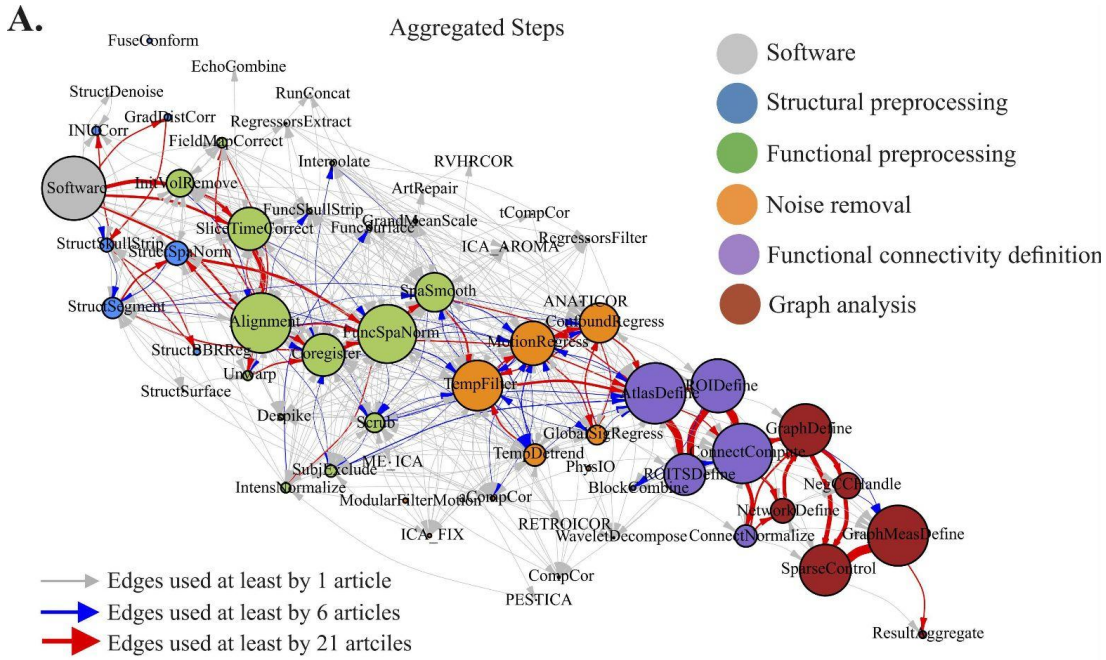


Dafflon, J., F. Da Costa, P., Váša, F., Monti, R. P., Bzdok, D., Hellyer, P. J., ... & Leech, R. (2022). A guided multiverse study of neuroimaging analyses. *Nature Communications*, *13*(1), 3758.

Data: fMRI analysis pipelines

The METEOR Project

- 220 fMRI analysis pipelines derived from literature (Kristanto et al., 2024)
  - 61 distinct data preprocessing and analysis steps

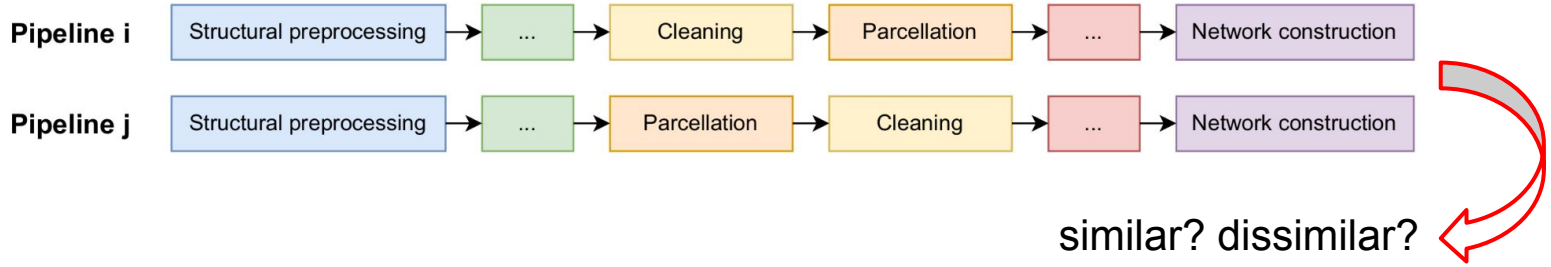


Kristanto, D., Burkhardt, M., Thiel, C., Debener, S., Gießing, C., & Hildebrandt, A. (2024). The multiverse of data preprocessing and analysis in graph-based fMRI: A systematic literature review of analytical choices fed into a decision support tool for informed analysis. *Neuroscience and biobehavioral reviews*, *165*

Similarity of analysis pipelines

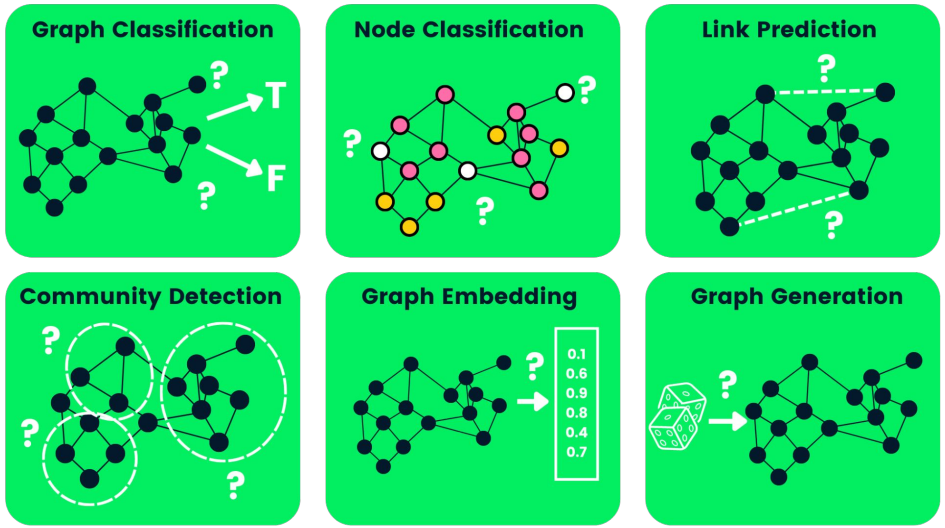
Similarity measures

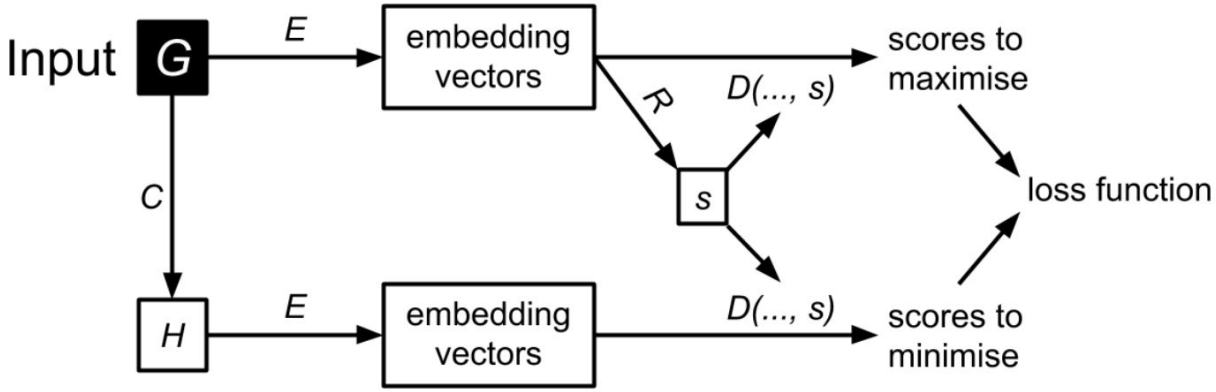
- Classical measures
  - Jaccard index
  - Hamming distance
  - Levenshtein distance
- Graph convolutional network approach
  - Applies Deep Graph Infomax
  - Creates nodal embeddings containing implicit features



Graph convolutional network (GNN) + Deep Graph Infomax (DGI)

- **GNNs**: Learn node/graph embeddings by aggregating neighbor info
- **DGI**: Unsupervised, maximizes info between node and graph embeddings
  - Training: Compares real vs. corrupted graphs to enhance structure
  - Also uses global features (frequency in literature, degree, type, …)
- **Result**: Produces robust embeddings for downstream tasks
  - Embeddings are then used to assess pipeline similarity

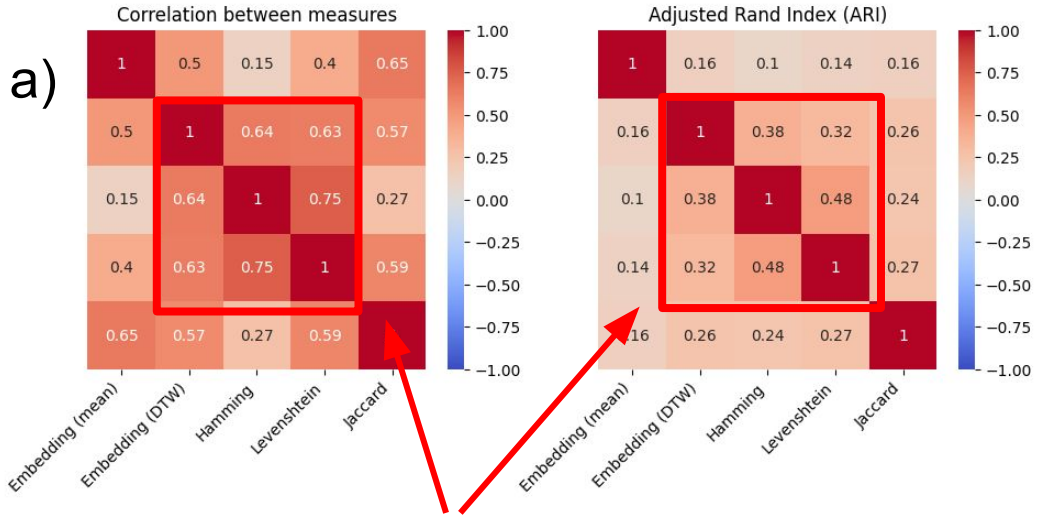




Results

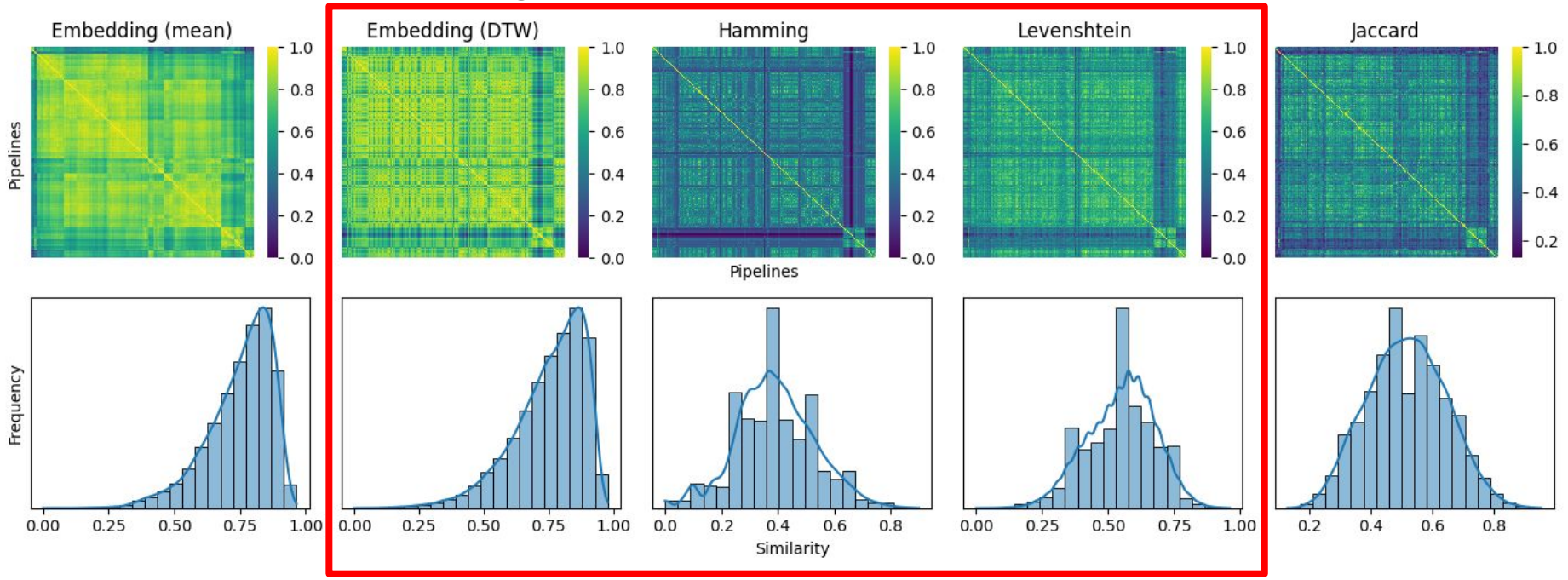
- Reasonable overlap between methods
- Considering order improves ARI (cluster overlap)

a)



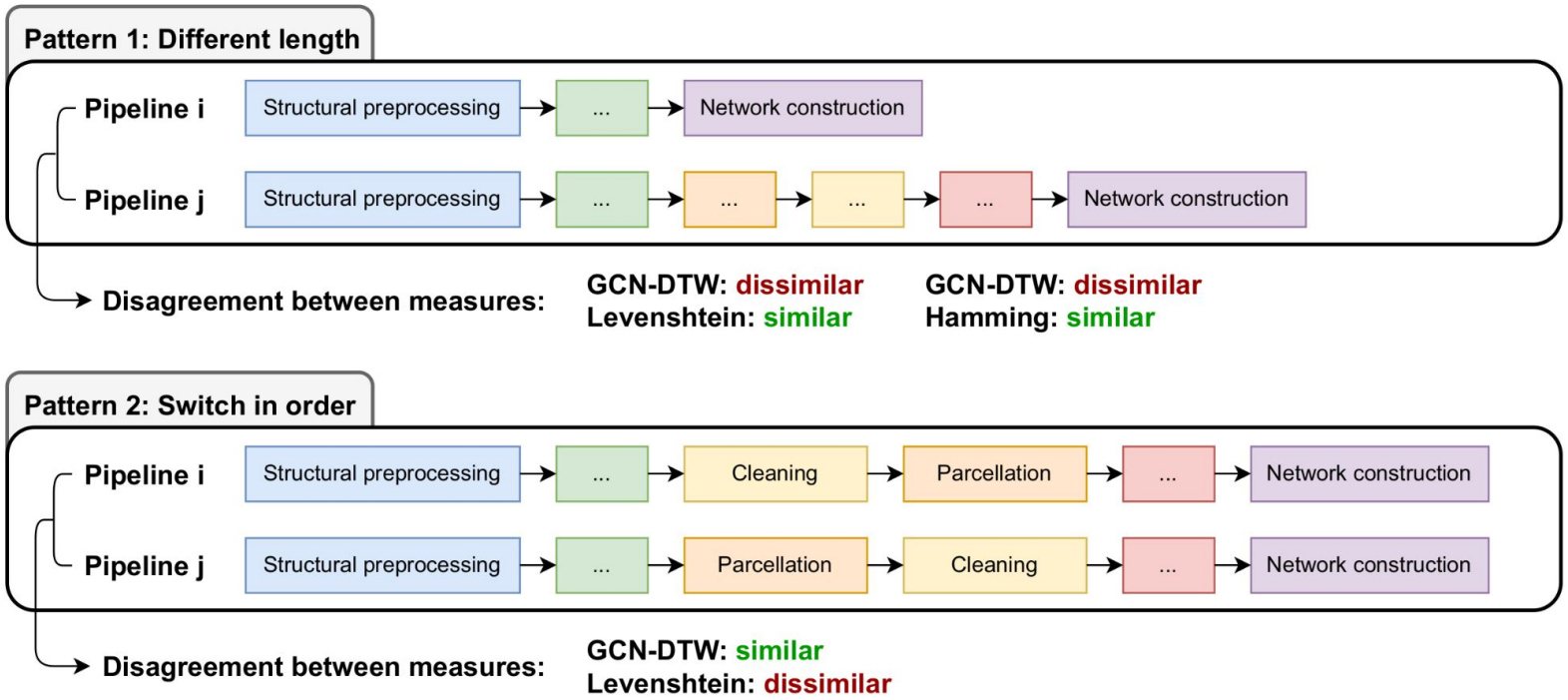
considering order!

b)



Results

- Two distinct patterns:
  - Difference in pipeline length
  - Difference in pipeline ordering



Discussion

Summary

- The GCN approach seems to be promising for capturing relevant information
- Different measures show a general overlap but also distinct behaviours

Advantages

- The GCN approach does not require calculating the entire multiverse
- No need to use (valuable) subjects for creating a search space
- The approach is method-agnostic

Future work

- The performance of the proposed approach needs to be tested on empirical data
- Integrating the GCN approach into efficient multiverse analysis

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Thank you for your attention!

Do you have any further feedback, questions, or ideas? Feel free to reach out! :)

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