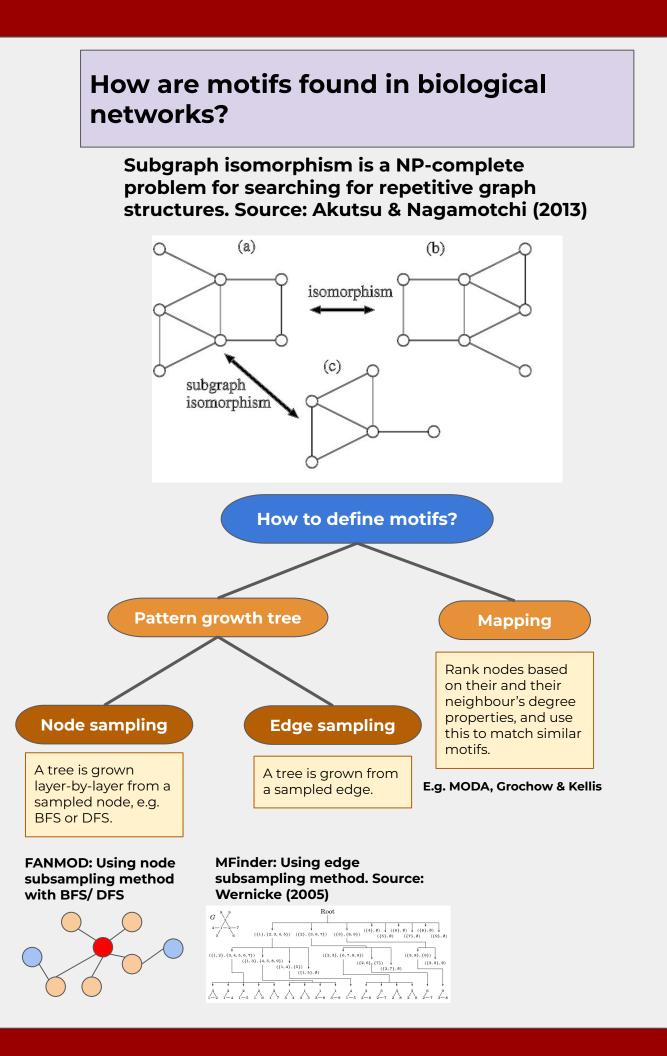
A Python-based pipeline for analyzing Protein-Protein Interaction Networks

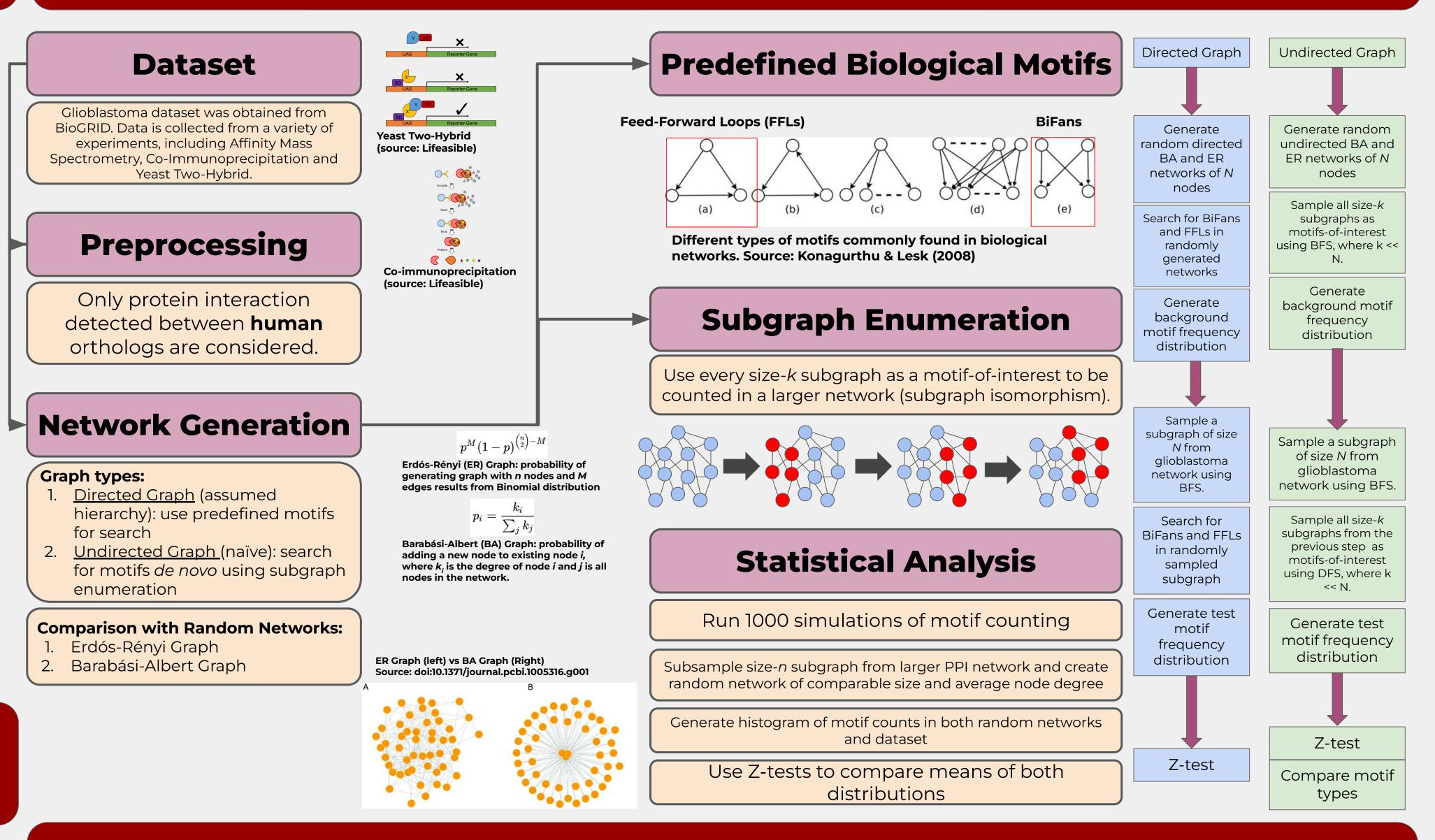
Andrew Ressler, Shamieraah Jamal, Daniel Lee

1. Introduction

What are biological networks? What are motifs in biological networks? **Gene Regulatory Network (GRN). Source:** Huynh-Thu & Sanguinetti (2018) Different types of motifs commonly found in biological networks. Source: Konagurthu & Lesk (2008) Gene regulatory **Cell Signaling Network. Source: Conserved biological systems** Sánchez-Gutiérrez & González-Pérez (2022) of signaling? Are patterns reused to construct more elaborate Are motifs useful in predicting new associations in networks? Find better disease targets? Protein-Protein Interaction (PPI) Network in Glioblastoma (Data from: BioGRID) **Aim: Find statistically** significant, biologically relevant motifs in PPI graphs

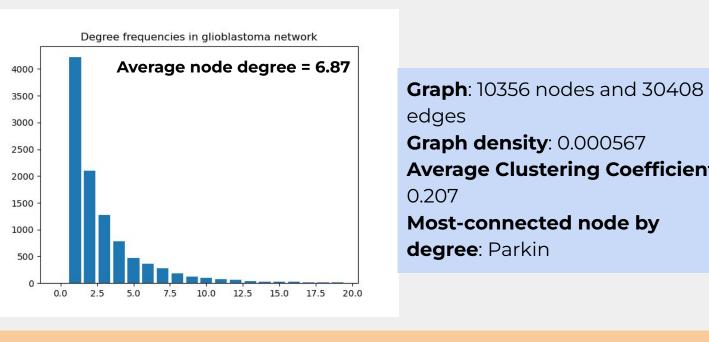


2. Methods



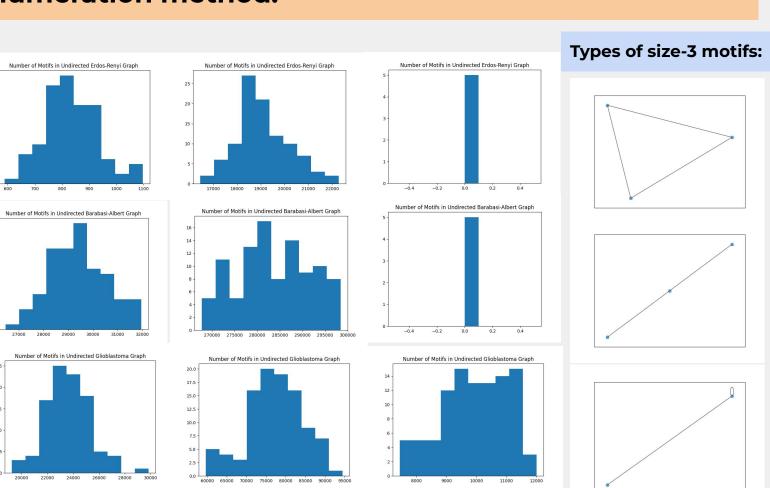
3. Results

1. A description of the glioblastoma dataset

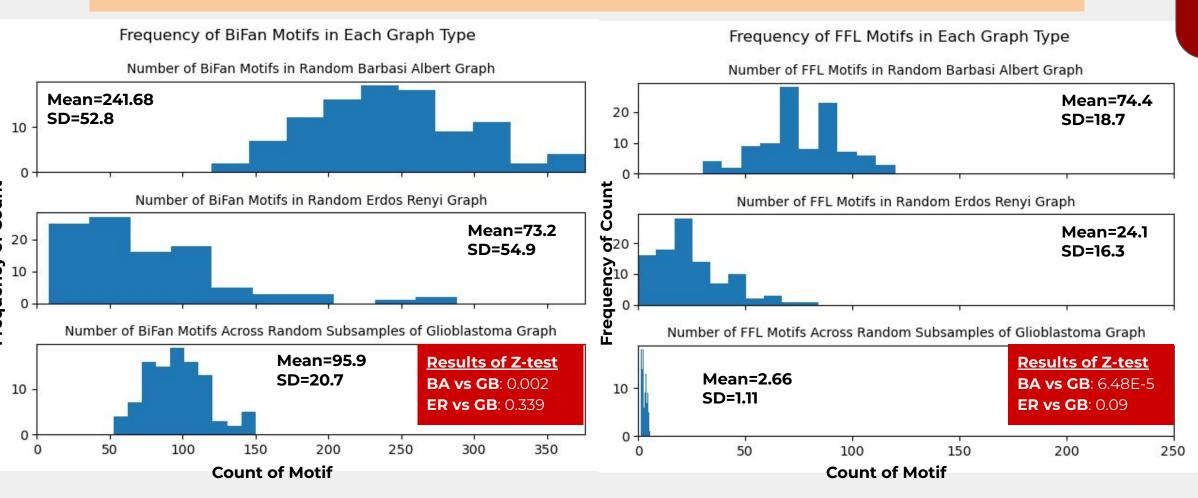


Average Clustering Coefficient:

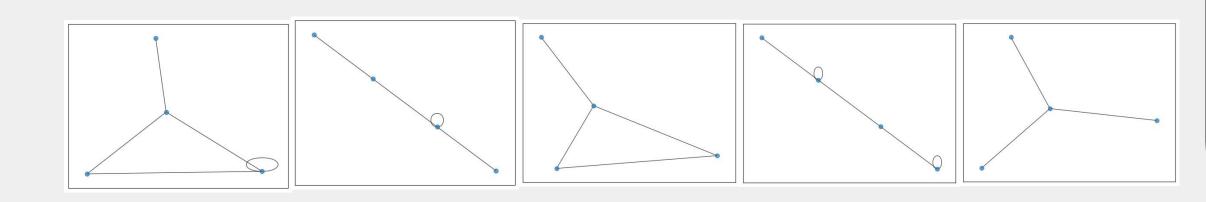
3. Number of size-3 motifs found in subgraph enumeration method.



2. The number of BiFans and FFLs in glioblastoma network is significantly lower than random Barabási-Albert network.



4. Some highly repetitive size-4 motifs found in glioblastoma network.



4. Conclusion

Discussion

- 1. Using predefined motifs is a lot faster.
- 2. PPI network resembles Barabási-Albert Graph in terms of shape of motif distributions → both are scale-free networks following power law.
- 3. BiFan motifs are significantly lower in glioblastoma dataset than BA graph.
- 4. FFL motifs are almost absent from glioblastoma dataset → unique feature of GRNs.

Future Work

- 1. Comparison with normal human PPI dataset from SNAP.
- 2. Try different subgraph-growing strategies such as edge subsampling.
- 3. Create hierarchical subgraphs using cross-reference with cell signaling pathways, to generate a probabilistic graphical model for link prediction.

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5. References