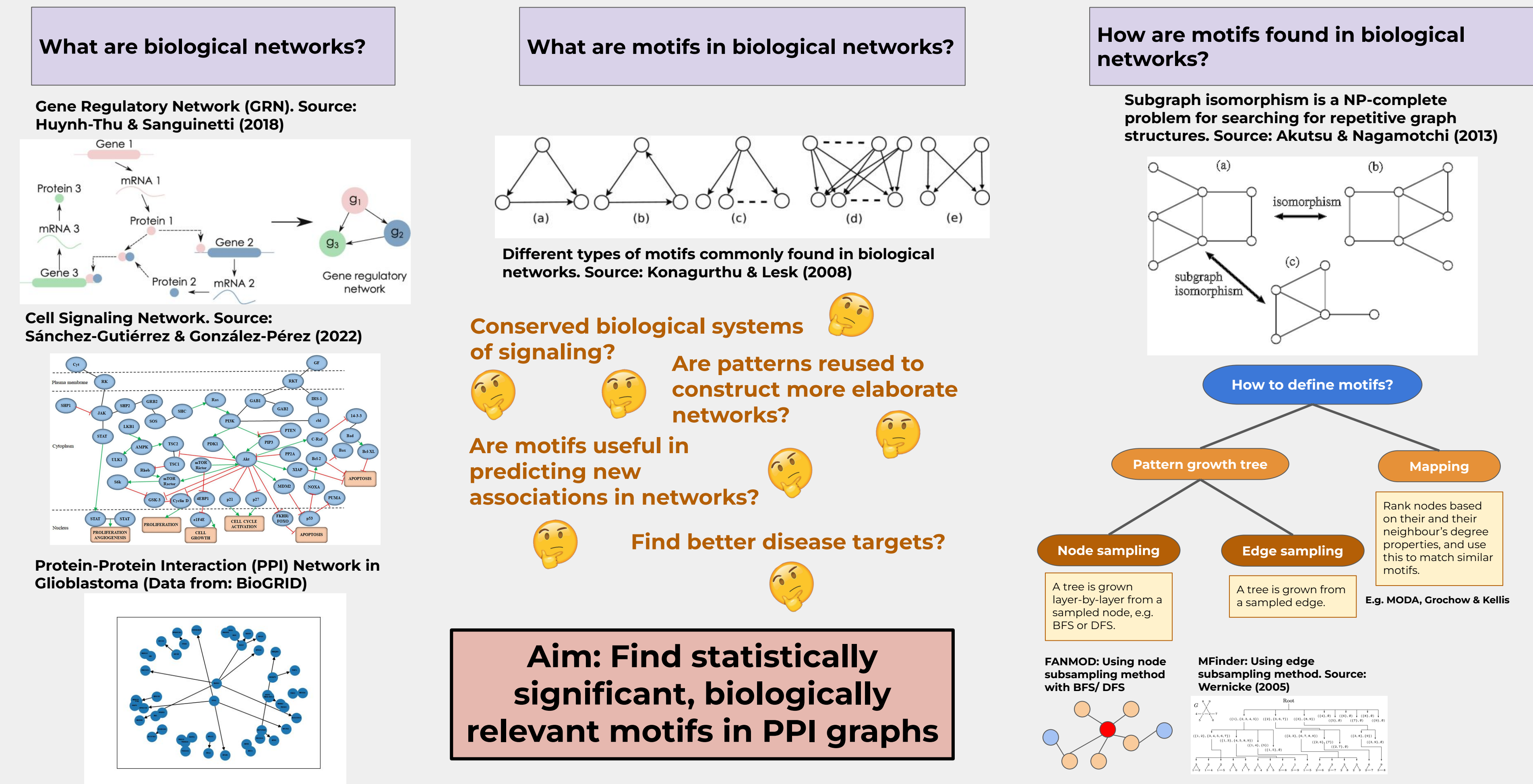


A Python-based pipeline for analyzing Protein-Protein Interaction Networks

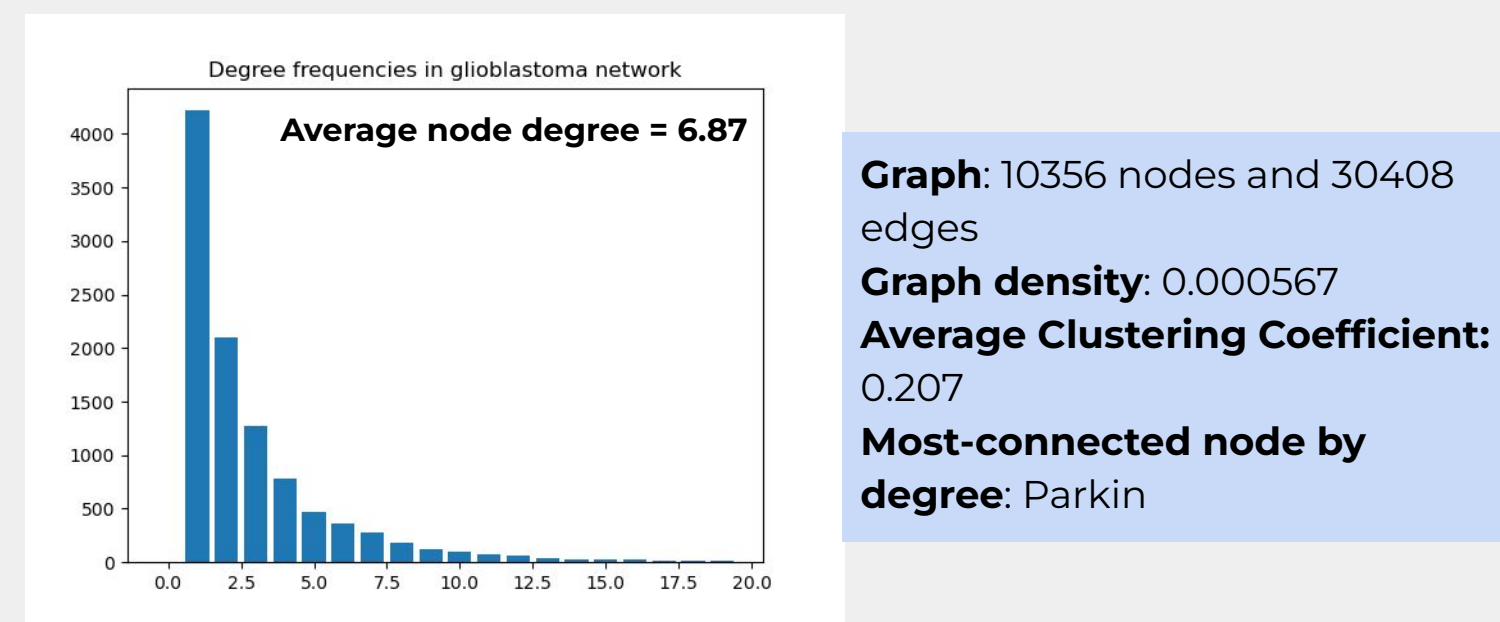
Andrew Ressler, Shamieraah Jamal, Daniel Lee

1. Introduction

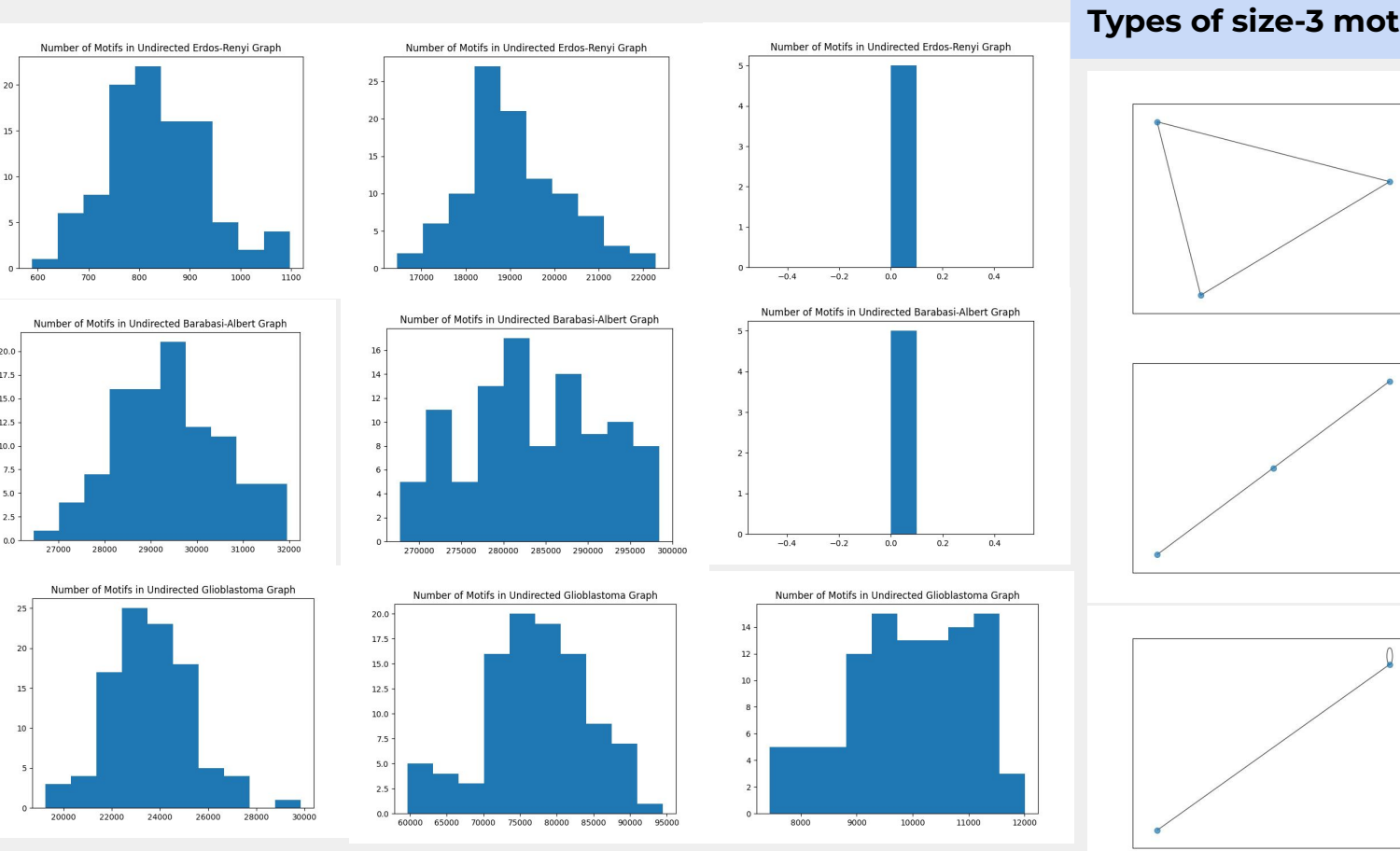


3. Results

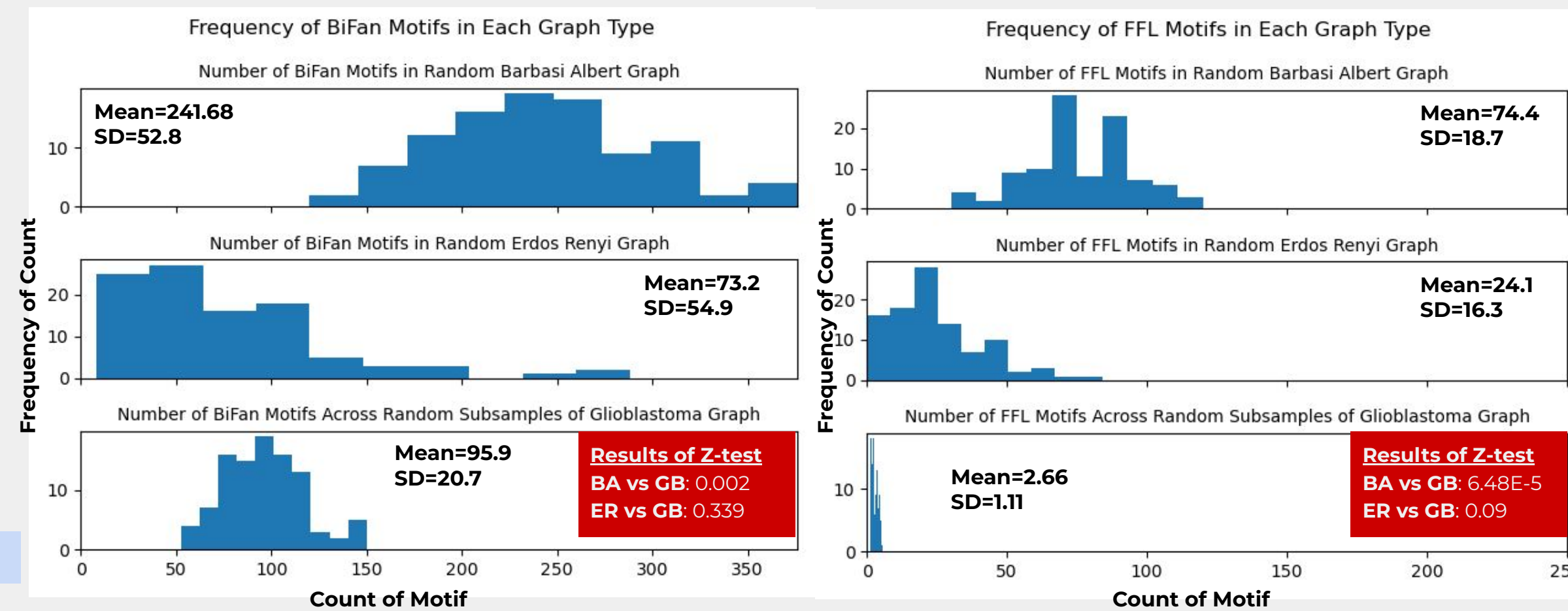
1. A description of the glioblastoma dataset



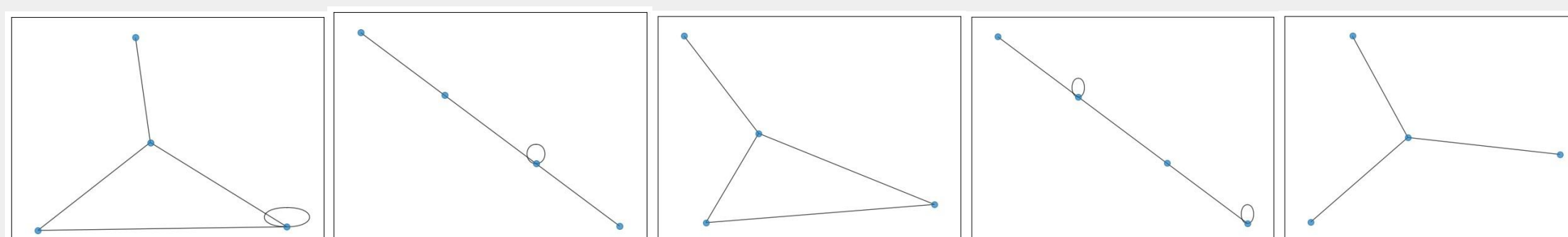
3. Number of size-3 motifs found in subgraph enumeration method.



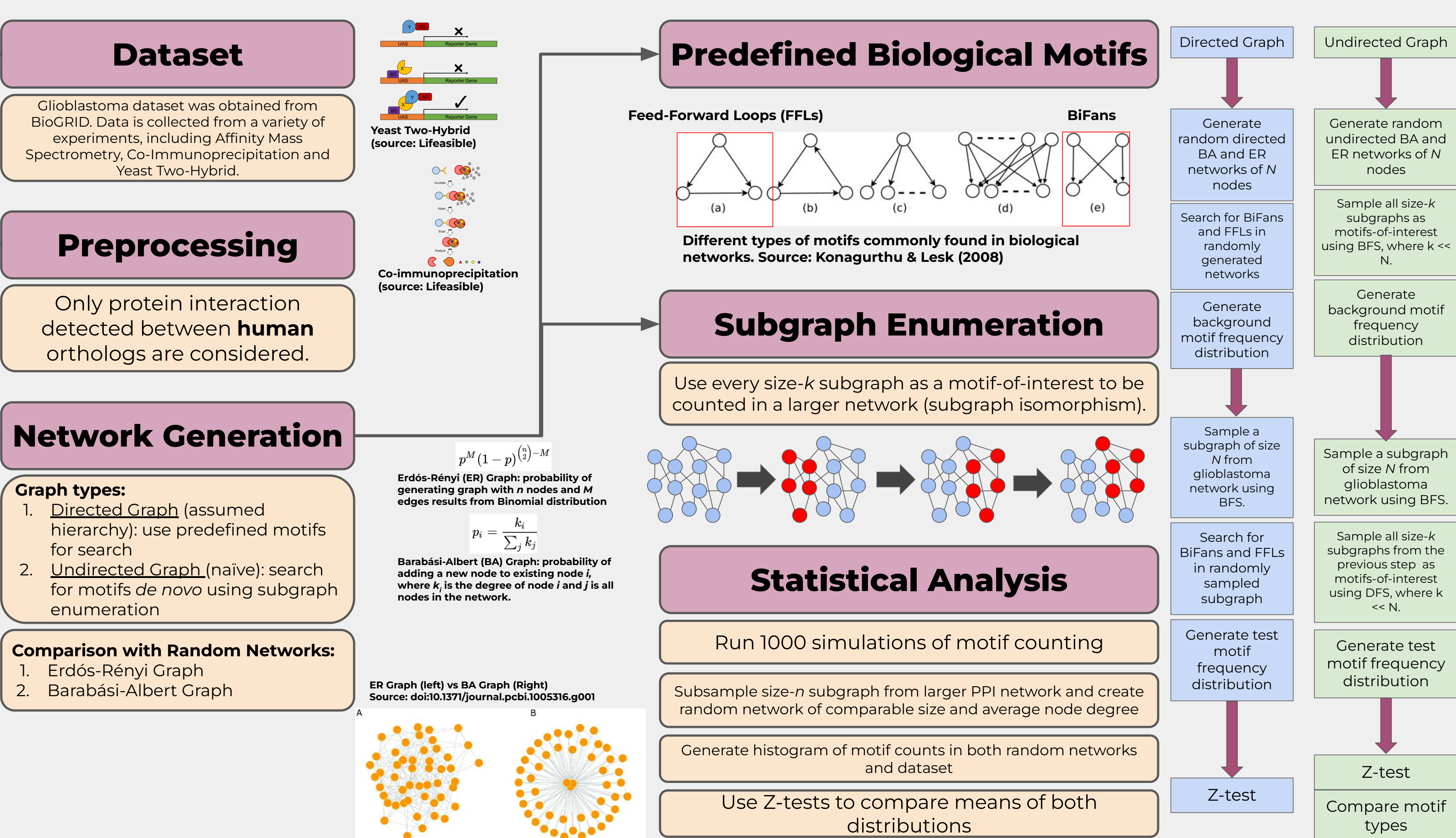
2. The number of BiFans and FFLs in glioblastoma network is significantly lower than random Barabási-Albert network.



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



2. Methods



4. Conclusion

Discussion

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

Future Work

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

5. References

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