# Graph Clustering Algorithms

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Abstract—In this article we provide a brief overview of the few existing graph clustering algorithms that are commonly used in bioinformatics. Then we evaluate their performance and accuracy based on the sample protein-protein interaction network as an input and subgraphs representing potential protein complexes as an output. In particular we use f-measure to evaluate the clustering results by comparing to protein complex data provided. For measuring the accuracy of the algorithms, we compute an f-score for each output cluster by selecting the maximum f-score to a protein complex, and average the f-scores of all output clusters. After evaluation we elaborate our own algorithm that tries to outperform the existing ones.

Index Terms—datamining, graphs, algorithms, bioinformatics

#### I. Introduction

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## II. CONCLUSION

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# APPENDIX A PROOF OF THE FIRST ZONKLAR EQUATION Some text for the appendix.

#### ACKNOWLEDGMENT

The  $\Sigma$  authors would like to thank...

### REFERENCES

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