



GrAPFI: Graph Based Inference for Automatic Protein Function Annotation

Bishnu Sarker, David Ritchie, Sabeur Aridhi

► To cite this version:

Bishnu Sarker, David Ritchie, Sabeur Aridhi. GrAPFI: Graph Based Inference for Automatic Protein Function Annotation. ECCB 2018 - 17th European Conference on Computational Biology, Sep 2018, Athens, Greece. hal-01876907v2

HAL Id: hal-01876907

<https://inria.hal.science/hal-01876907v2>

Submitted on 14 Nov 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

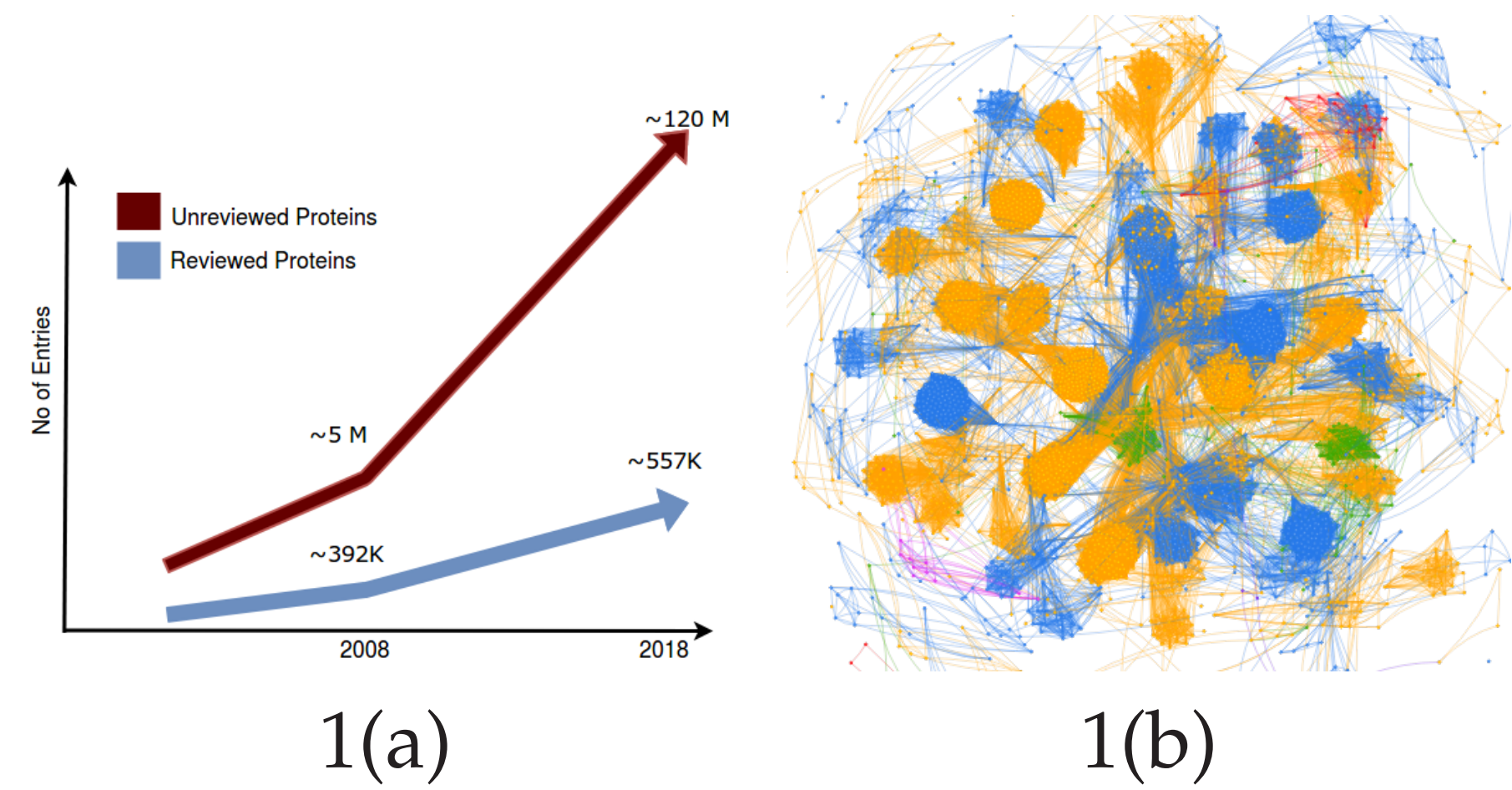
GrAPFI: Graph Based Inference for Automatic Protein Function Annotation

Bishnu Sarker, David W Ritchie and Sabeur Aridhi
University of Lorraine, CNRS, INRIA, LORIA, Vandoeuvre-les-Nancy, France
bishnu.sarker@inria.fr



Scan me

Introduction



The growing number of protein sequences in UniProtKB (Fig-1(a)) makes it increasingly expensive to annotate them manually. Here, we present GrAPFI (Graph based Automatic Protein Function Inference), a tool for the automatic functional annotation of proteins with Enzyme Commission (EC) numbers. The EC System uses a four digit numbering with a hierarchical structure. GrAPFI utilizes the domain composition of the proteins. Our general observation is that protein domains shares functional properties. Fig-1(b). illustrates this for proteins from viruses dataset. The 6 different colors in this figure correspond to the 6 different top level EC classes.

Graph Construction

GrAPFI constructs the protein graph based on domain composition of each protein. Each node of the graph represents a protein, while a link between two nodes means that the proteins exhibit a given minimum level of domain similarity. Each node u is identified by a set of labels $L(u)$ (one or more annotations to propagate), has a set of neighbours $N(u)$, and for every neighbour v it has an associated weight $W_{u,v}$. If u and v have domain composition $D1=(d1,d2,d3,d4)$ and $D2=(d1,d3,d5)$, then,

$$W_{u,v} = \frac{|(d1, d2, d3, d4) \cap (d1, d3, d5)|}{|(d1, d2, d3, d4) \cup (d1, d3, d5)|}$$

$$= \frac{|(d1, d3)|}{|(d1, d2, d3, d4, d5)|}$$

$$= \frac{2}{5} = 0.4.$$

GrAPFI Annotation Workflow

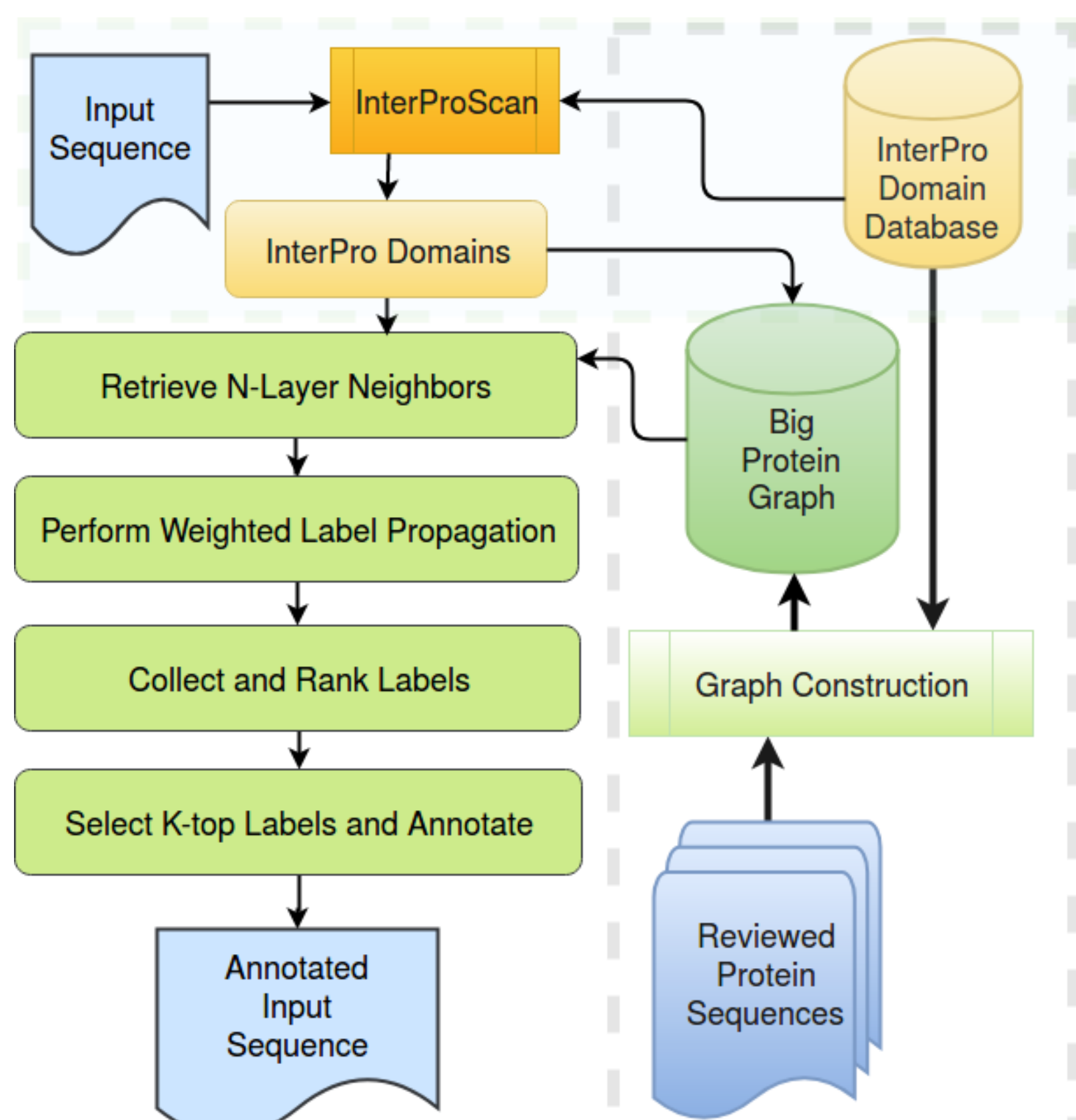


Fig-2: GrAPFI follows the above work-flow to annotate an un-reviewed protein.

Example Function Annotation of 2rk2A Enzyme

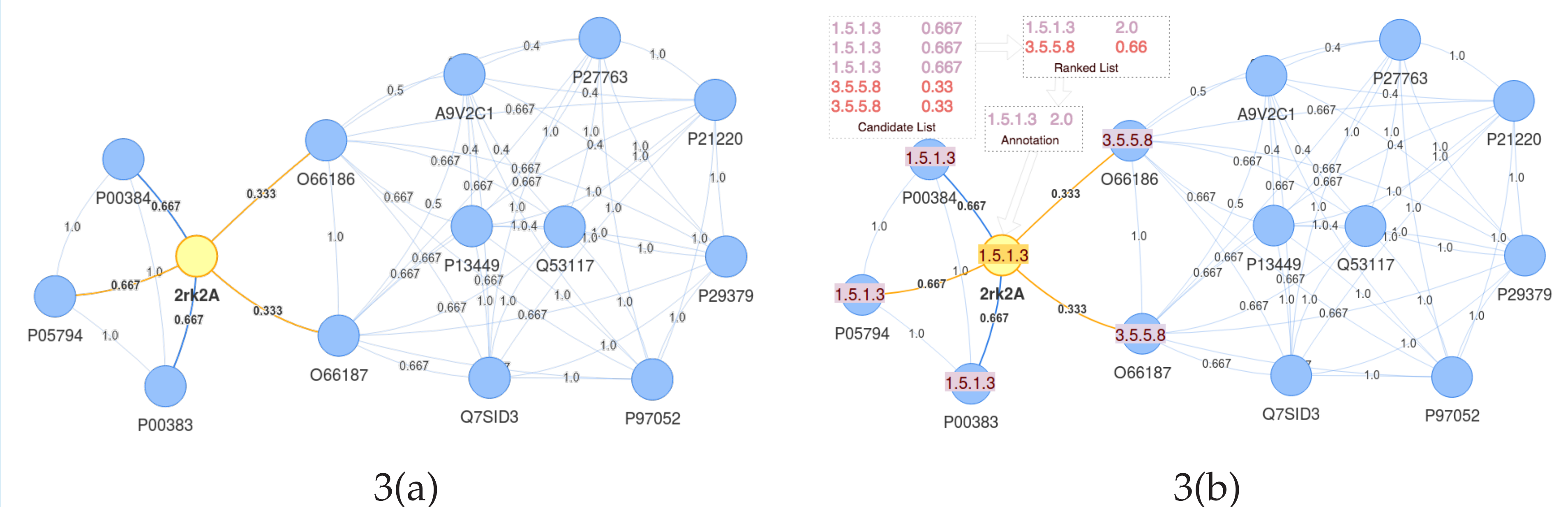
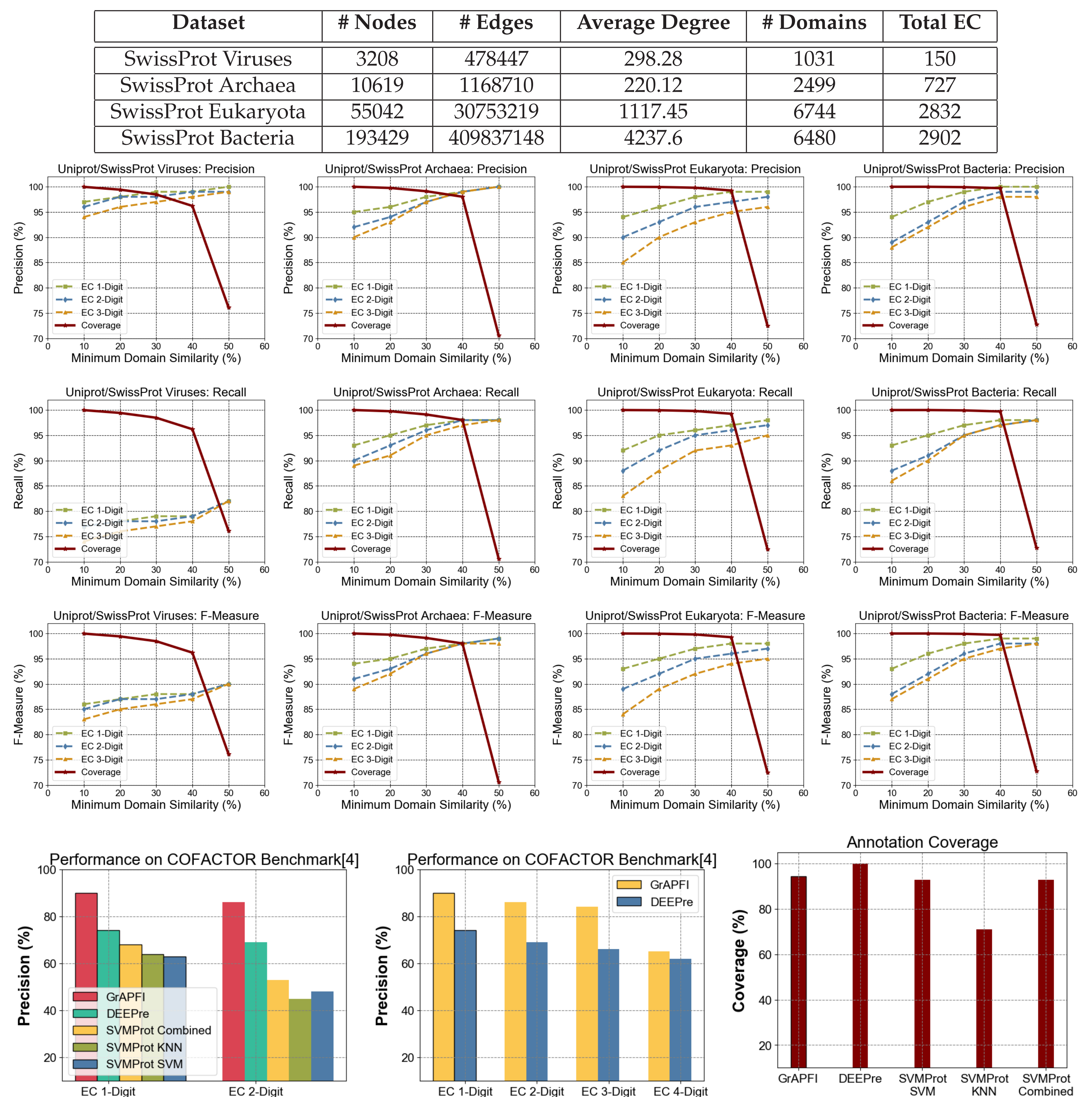


Fig-3(a) shows a query protein (yellow node) connected with its five neighbors. Fig-3(b) shows the result of label propagation applied on the graph in Fig-3(a).

Results



A comparative study is presented based on a benchmark of 318 proteins taken from COFACTOR[4]. After removing proteins that do not have ground truth EC annotation, we had 297 Enzymes to annotate.

Conclusion

GrAPFI is a novel graph based approach for automatic protein functional annotation. It utilizes a domain based graph representation of the UniProtKB/SwissProt protein database. To evaluate the performance, leave one out cross validation is used on the graph built on four species from UniProt/SwissProt namely Viruses, Archaea, Eukaryota and Bacteria. Average precision, $Pr_{avg} = \frac{1}{M} \sum_{p \in P} Pr_p$, recall, $Re_{avg} = \frac{1}{M} \sum_{p \in P} Re_p$ and F-Measure, $F_{Measure} = \frac{2 \times Pr_{avg} \times Re_{avg}}{Pr_{avg} + Re_{avg}}$ are used as performance metrics. Our performance comparison shows GrAPFI outperforms other methods e.g. DEEPre[3], SVMProt[2]. The future work aims at using GrAPFI for protein Annotation with GO terms.

References

1. T. U. Consortium. Uniprot: a hub for protein information. Nucleic Acids Research, 2014.
2. Li, Ying Hong, et al. SVM-prot 2016: A web-server for machine learning prediction of protein functional families from sequence irrespective of similarity, 2016.
3. Li, Yu, et al. DEEPre: sequence-based enzyme EC number prediction by deep learning, 2017.
4. Chengxin Zhang, Peter L. Freddolino, and Yang Zhang. COFACTOR: improved protein function prediction by combining structure, sequence and protein-protein interaction information. Nucleic Acids Research, 2017.

Acknowledgement Bishnu Sarker is funded by an INRIA Cordis-S Doctoral Grant.