Automated HPO-Annotations for newly sequenced proteins by homology inference

K. Nagaraj¹, M. Hanumanthappa¹, O. Tarabai¹, S. Seitz¹

¹ Fakulät für Informatik, Boltzmannstr. 3, 85748 Garching Received on 28.02.2014

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ABSTRACT

Motivation: Rapid genome sequencing and high-throughput technology, automatic function prediction for a novel sequence is an essential matter in bioinformatics. Automatic annotations based on local alignments suffer from several drawbacks (Ori *et al.*, 2006). With our de novo method we try to improve the precision and recall of automatic annotations.

Availability: The webinterface for our created prediction-method is available at https://dataminer.informatik.tu-muenchen.de/ omar.tarabai/.

Contact: name@bio.com

1 INTRODUCTION

There are many proteins in the databases for which the sequence is known, but the function is not. The gap between what we know and what we do not know is growing.

Genomic scale projects have compounded the need for rapid and reliable functional annotation methods. Traditional experimental approaches have become outpaced resulting in an ever-increasing proportion of missing annotations. Computational approaches, including those based on sequence, expression, interaction and tertiary structure, have the potential to impact the growing annotation deficit.

Despite a recent increase in the number and variety of prediction methods, the computational annotation of protein function remains difficult. This stems from a combination of issues such as the inherent limitations of current tools and databases, the difficulty of assessing the predictive power of different methods and more fundamental problems related to the ambiguity of the definition of function itself.

2 APPROACH

3 METHODS

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4 DISCUSSION

5 CONCLUSION

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REFERENCES

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