Automated HPO-Annotations for newly sequenced proteins by homology inference

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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/.

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1 INTRODUCTION

In the databases many proteins are found for which the sequence is known, but the function is still not determined. With the increasing number of sequences, caused for example by genomic scale projects, traditional experimental approaches have become outpaced. This leads to the need for rapid and reliable functional annotation methods (Rodrigues *et al.*, 2007).

Many different approaches have been taken annotate protein function by computational methods, including methods based on sequence, expression, interaction and tertiary structure. Despite this taken effort and the following increase of number and variety of prediction methods, the automatical annotation remains difficult. Reasons for these difficulties can for example be found in the inherent limitations of current tools and databases or the ambiguity of the definition of function itself (Rodrigues *et al.*, 2007).

To overcome this problems and to be able to annotate protein function without relying on tertiary data, this method is created to reliably predict protein function by sequence alone.

2 APPROACH

3 METHODS

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4 DISCUSSION

5 CONCLUSION

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