

# An Efficient Joint Neighborhood Subgraphs Method for Link Prediction

Dinh Tran-Van<sup>1</sup>, Alessandro Sperduti<sup>1</sup>, and Fabrizio Costa<sup>2</sup>

<sup>1</sup> Department of Mathematics, Padova University, Italy

<sup>2</sup> Department of Computer Science, University of Exeter, United Kingdom  
{dinh, sperduti}@math.unipd.it, f.costa@exeter.ac.uk

**Abstract.** The abstract should summarize the contents of the paper and should contain at least 70 and at most 150 words. It should be written using the *abstract* environment.

**Keywords:** We would like to encourage you to list your keywords within the abstract section

## 1 Introduction

## 2 Method

## 3 Experiment

## 4 Results and Discussion

## 5 Conclusion and Future Work

## References

1. Smith, T.F., Waterman, M.S.: Identification of Common Molecular Subsequences. J. Mol. Biol. 147, 195–197 (1981)
2. May, P., Ehrlich, H.C., Steinke, T.: ZIB Structure Prediction Pipeline: Composing a Complex Biological Workflow through Web Services. In: Nagel, W.E., Walter, W.V., Lehner, W. (eds.) Euro-Par 2006. LNCS, vol. 4128, pp. 1148–1158. Springer, Heidelberg (2006)
3. Foster, I., Kesselman, C.: The Grid: Blueprint for a New Computing Infrastructure. Morgan Kaufmann, San Francisco (1999)
4. Czajkowski, K., Fitzgerald, S., Foster, I., Kesselman, C.: Grid Information Services for Distributed Resource Sharing. In: 10th IEEE International Symposium on High Performance Distributed Computing, pp. 181–184. IEEE Press, New York (2001)
5. Foster, I., Kesselman, C., Nick, J., Tuecke, S.: The Physiology of the Grid: an Open Grid Services Architecture for Distributed Systems Integration. Technical report, Global Grid Forum (2002)
6. National Center for Biotechnology Information, <http://www.ncbi.nlm.nih.gov>