A Sample LaTeX Format for the Ninth Workshop on Genome Informatics

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Abstract

This is the abstract of a sample paper for the 8th Workshop on Genome Informatics. The workshop is intended to provide a forum for researchers working in interdisciplinary areas between biological sciences and computer science.

1 Introduction

Here is the introduction text.

The Workshop on Genome Informatics is organized by the Genome Science Research Project funded by a Grant-in-Aid for Scientific Research on Priority Areas from the Ministry of Education, Science, Sports and Culture of Japan.

2 Sample Section

Of course you can create other sections if you want.

2.1 Figures

When you use a figure (Fig. 1) with a special style file, please provide it.

Here are examples of citation [1, 2, 3, 4, 5]. References should be arranged in alphabetical order of authors and cited in the text.

Acknowledgements

The section for acknolwedgements should not be numbered.

References

[1] Bowie, J. U., Lüthy, R. and Eisenberg, D., A method to identify protein sequences that fold into a known three-dimensional structure, *Science*, 253:164–170, 1991.

[2] Kabsch, W. and Sander, C., Dictionary of secondary structure: pattern recognition of hydrogen-bonded and geometric features, *Biopolymers*, 22:2577–2637, 1983.

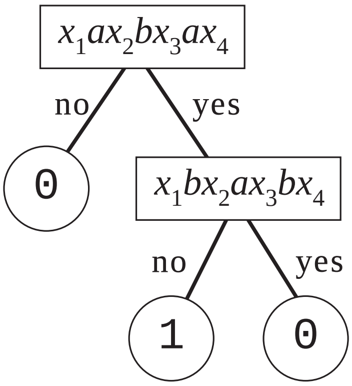

Figure 1: This is a sample figure.

[3] Needleman, S. B. and Wunsch, C. D., A general method applicable to the search for similarities in the amino acid sequences of two proteins, *J. Mol. Biol.*, 48:443–453, 1970.

[4] Smith, T. F. and Waterman, M. S., Identification of common molecular subsequences, *J. Mol. Biol.*, 147:195–197, 1981.

[5] Watson, J. D., Gilman, M., Witkowski, J. and Zoller, M., *Recombinant DNA* (Second Edition), W. H. Freeman and Company, New York, 1992.