A Sample LaTeX Format for the Tenth 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, 3, 2, 4, 5, 6, 7]. References should be arranged in alphabetical order of authors and should be cited in the text.

Acknowledgments

The section for acknolwedgements should not be numbered.

References

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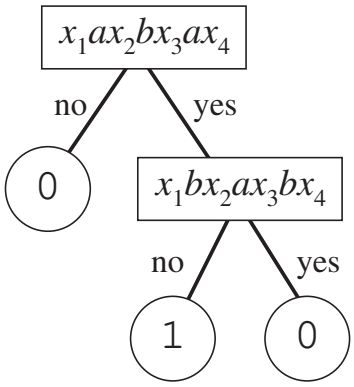

Figure 1: This is a sample figure.

[3] Kobayashi, H. and Imai, H., Improvement of the A* algorithm for multiple sequence alignment, *Genome Informatics 1998*, Universal Academy Press, 120–130, 1998.

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[5] Shibuya, T. and Imai, H., Enumerating suboptimal alignments of multiple biological sequences efficiently, *Proc. Pacific Symposium on Biocomputing 1997*, World Scientifc, 409–420, 1997.

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