

A simple LaTeX template for a general style paper

Charles Darwin

Department of Computer Science, Free University of Berlin, Takustr. 9, 14195 Berlin, Germany
E-mail: charles.darwin@fu-berlin.de

ABSTRACT

The abstract should state what the paper is about and what the main results of the work are. It is usually between 100 and 200 words long. Other people read the abstract to find out if this paper is interesting to them.

1 INTRODUCTION

The introduction gives background information to the topic and usually an overview of the work in the field. In general, it contains many references (Döring *et al.*, 2008; Brudno *et al.*, 2003). Sometimes, you might want to say that Rausch *et al.* published an interesting paper in 2008 or that Needleman and Wunsch (1970) suggested a global alignment algorithm.

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2 METHODS

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2.1 A subsection with a figure

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Here is a reference to fig. 1.

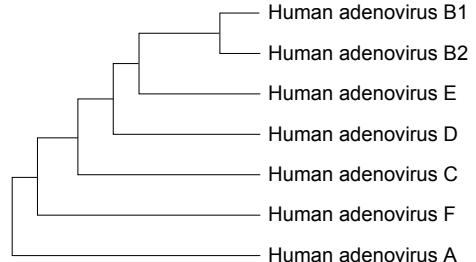


Figure 1. This is a figure caption.

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2.2 Another subsection

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2.2.2 The second sub-sub-section. The previous sub-sub-section was 2.2.1.

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3 RESULTS AND DISCUSSION

The results are in general displayed in figures or tables (e.g. table 1). Results and discussion can also be sepa-

Table 1. This is a table caption

number	percentage		running time	
	case a	case b	case a	case b
1	0.0 %	0.0 %	0.0 s	0.0 s
2	0.0 %	0.0 %	0.0 s	0.0 s
3	0.0 %	0.0 %	0.0 s	0.0 s
4	0.0 %	0.0 %	0.0 s	0.0 s
5	0.0 %	0.0 %	0.0 s	0.0 s

rated into two sections, or the discussion and conclusion may be put together in one section.

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4 CONCLUSION

The conclusion should contain a very brief summary of the results. It discusses alternatives and possible extension, and gives an outlook to what could be done next.

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REFERENCES

- Brudno, M., Do, C. B., Cooper, G. M., Kim, M. F., Davydov, E., Program, N. I. S. C. C. S., Green, E. D., Sidow, A., and Batzoglou, S. (2003). LAGAN and Multi-LAGAN: efficient tools for large-scale multiple alignment of genomic DNA. *Genome Res.*, **13**(4), 721–731.
- Döring, A., Weese, D., Rausch, T., and Reinert, K. (2008). SeqAn an efficient, generic C++ library for sequence analysis. *BMC Bioinformatics*, **9**, 11.
- Needleman, S. B. and Wunsch, C. D. (1970). A general method applicable to the search for similarities in the amino acid sequence of two proteins. *J Mol Biol.*, **48**(3), 443–453.
- Rausch, T., Emde, A.-K., Weese, D., Dring, A., Notredame, C., and Reinert, K. (2008). Segment-based multiple sequence alignment. *Bioinformatics*, **24**(16), i187–i192.