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■ Instructions for *BMC Bioinformatics* authors

Software articles

We encourage authors of software applications, tools or algorithm implementations to publish descriptions of their code using the Software article type.

Availability of software to reviewers and other researchers

The software application/tool described in the manuscript must be available for testing by reviewers in a way that preserves their anonymity. If published, software applications/tools must be freely available to any researcher wishing to use them for non-commercial purposes, without restrictions such as the need for a material transfer agreement. Because weblinks frequently become broken, *BMC Bioinformatics* strongly recommends that all software applications/tools are included with the submitted manuscript as additional files to ensure that the software will continue to be available.

BMC Bioinformatics recommends, but does not require, that the source code of the software should be made available under a suitable open-source license that will entitle other researchers to further develop and extend the software if they wish to do so. Typically, an archive of the source code of the current version of the software should be included with the submitted manuscript as a supplementary file. Since it is likely that the software will continue to be developed following publication, the manuscript should also include a link to the home page for the software project. For open source projects, we recommend that authors host their project with a recognized open-source repository such as bioinformatics.org or sourceforge.net

Should a description of a website be submitted as a Software article or a Database article?

Descriptions of websites and web-based tools should be submitted as Software articles if the intention is that the software that drives the website will be made available to other researchers to extend and use on other websites. On the other hand, if a website's functionality is closely tied to a specific database then the article should instead be submitted as a Database article.

Manuscript sections for Software articles

Manuscripts for Softwares submitted to *BMC Bioinformatics* should be divided into the following sections:

- Title page
- Abstract
- Background
- Implementation
- Results
- Discussion (if applicable)
- Conclusions

- Availability and requirements
- List of abbreviations used (if any)
- Authors' contributions
- Acknowledgements
- References
- Figure legends (if any) - see Figure legends section in main document
- Tables and captions (if any) - see Tables section in main document
- Description of additional data files (if any) - see Additional files section in main document

The **Accession Numbers** of any nucleic acid sequences, protein sequences or atomic coordinates cited in the manuscript should be provided, in square brackets and include the corresponding database name; for example, [EMBL:AB026295, EMBL:AC137000, DDBJ:AE000812, GenBank:U49845, PDB:1BFM, Swiss-Prot:Q96KQ7, PIR:S66116].

The databases for which we can provide direct links are: EMBL Nucleotide Sequence Database (EMBL), DNA Data Bank of Japan (DDBJ), GenBank at the NCBI (GenBank), Protein Data Bank (PDB), Protein Information Resource (PIR) and the Swiss-Prot Protein Database (Swiss-Prot).

Title page

This should list the title of the article. The full names, institutional addresses, and email addresses for all authors must be included on the title page. The corresponding author should also be indicated.

Abstract

This should not exceed 350 words and should be structured into separate sections headed Background, Results, Conclusions. Please do not use abbreviations or references in the abstract.

Background

The background section should be written to be comprehensible to researchers without specialist knowledge in the area concerned. It should clearly described the relevant context and the specific issue which the software described is intended to address.

Implementation

This should include a description of the overall architecture of the software implementation, along with details of any critical issues and how they were addressed.

Results and Discussion

The Results and Discussion may be combined into a single section or presented separately. They may also be broken into subsections with short, informative headings. In any case what should be described is the functionality of the software together with data on how its performance and functionality compare with and improve on functionally similar existing software. There should then be a discussion of the intended use of the software, and the benefits that are envisioned together, if possible, with an outline for the planned future development of new features.

Conclusions

This should state clearly the main conclusions of the article and give a clear explanation of the importance and relevance of the software.

Availability and requirements

Lists the following:

- **Project name:** e.g. My bioinformatics project
- **Project home page:** e.g. http://sourceforge.net/projects/mged
- **Operating system(s):** e.g. Platform independent
- **Programming language:** e.g. Java
- **Other requirements:** e.g. Java 1.3.1 or higher, Tomcat 4.0 or higher
- **License:** e.g. GNU GPL, FreeBSD etc.
- **Any restrictions to use by non-academics:** e.g. licence needed

List of abbreviations

If abbreviations are used in the text either they should be defined in the text where first used, or a list of abbreviations can be provided, which should precede the authors' contributions and acknowledgements.

Authors' contributions

In order to give appropriate credit to each author of a paper, the individual contributions of authors to the manuscript should be specified in this section.

An "author" is generally considered to be someone who has made substantive intellectual contributions to a published study. To qualify as an author one should 1) have made substantial contributions to conception and design, or acquisition of data, or analysis and interpretation of data; 2) have been involved in drafting the manuscript or revising it critically for important intellectual content; and 3) have given final approval of the version to be published. Each author should have participated sufficiently in the work to take public responsibility for appropriate portions of the content. Acquisition of funding, collection of data, or general supervision of the research group, alone, does not justify authorship.

We suggest the following kind of format (please use initials to refer to each author's contribution): AB carried out the molecular genetic studies, participated in the sequence alignment and drafted the manuscript. JY carried out the immunoassays. MT participated in the sequence alignment. ES participated in the design of the study and performed the statistical analysis. FG conceived of the study, and participated in its design and coordination and helped to draft the manuscript. All authors read and approved the final manuscript.

All contributors who do not meet the criteria for authorship should be listed in an acknowledgements section. Examples of those who might be acknowledged include a person who provided purely technical help, writing assistance, or a department chair who provided only general support.

Acknowledgements

Please acknowledge anyone who contributed towards the study by making substantial contributions to conception, design, acquisition of data, or analysis and interpretation of data, or who was involved in drafting the manuscript or revising it critically for important intellectual content, but who does not meet the criteria for authorship. Please also include their source(s) of funding. Please also acknowledge anyone who contributed materials essential for the study.

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Please list the source(s) of funding for the study, for each author, and for the manuscript preparation in the acknowledgements section. Authors must describe the role of the funding body, if any, in study design; in the collection, analysis, and interpretation of data; in the writing of the manuscript; and in the decision to submit the manuscript for publication.

References

All references must be numbered consecutively, in square brackets, in the order in which they are cited in the

text, followed by any in tables or legends. Reference citations should not appear in titles or headings. Each reference must have an individual reference number. Please avoid excessive referencing. If automatic numbering systems are used, the reference numbers must be finalized and the bibliography must be fully formatted before submission.

Only articles and abstracts that have been published or are in press, or are available through public e-print/preprint servers, may be cited; unpublished abstracts, unpublished data and personal communications should not be included in the reference list, but may be included in the text. Notes/footnotes are not allowed. Obtaining permission to quote personal communications and unpublished data from the cited author(s) is the responsibility of the author. Journal abbreviations follow Index Medicus/MEDLINE. Citations in the reference list should contain all named authors, regardless of how many there are.

We encourage authors to use a recent version of EndNote (version 5 and above) or Reference Manager (version 10) when formatting their reference list, as this allows references to be automatically extracted. Authors submitting articles in EndNote 5 or higher or Reference Manager 10 format will save £30 on the £850 (€1250, US$1685) article processing charge. In order to obtain this discount, you should upload the manuscript file containing your EndNote or Reference Manager-formatted bibliography as a .doc file. Please ensure you do not convert to another format (e.g. RTF or PDF). On upload, the discount will be automatically granted and you will receive a confirmation on-screen and by email. You will also be able to preview an HTML version of the extracted references during submission, and we urge authors to check this. EndNote or Reference Manager users should also make sure that any changes made to the reference list are done within their reference management program, rather than by manually editing the formatted bibliography. This is because manually introduced changes will not be picked up in the automatically extracted list.

Further details about EndNote and Reference Manager are available on the BioMed Central site, including information about how to upgrade.

Style files that conform to the BioMed Central style are available for EndNote and Reference Manager. Users of other reference management programs should be able to select other journal styles that output a numeric list styled similarly to the guide below.

Examples of the *BMC Bioinformatics* reference style are shown below. Please take care to follow the reference style precisely; references not in the correct style may be retyped, necessitating tedious proofreading.

Links

Web links and URLs should be included in the reference list. They should be provided in full, including both the title of the site and the URL, in the following format: **The Mouse Tumor Biology Database** [http://tumor.informatics.jax.org/cancer_links.html]

BMC Bioinformatics reference style

Article within a journal

1. Koonin EV, Altschul SF, Bork P: **BRCA1 protein products: functional motifs.** *Nat Genet* 1996, **13:**266-267.

Article within a journal supplement

2. Orengo CA, Bray JE, Hubbard T, LoConte L, Sillitoe I: **Analysis and assessment of ab initio three-dimensional prediction, secondary structure, and contacts prediction.** *Proteins* 1999, **Suppl 3:**149-170.

In press article

3. Kharitonov SA, Barnes PJ: **Clinical aspects of exhaled nitric oxide.** *Eur Respir J*, in press.

Published abstract

4. Zvaifler NJ, Burger JA, Marinova-Mutafchieva L, Taylor P, Maini RN: **Mesenchymal cells, stromal derived factor-1 and rheumatoid arthritis [abstract].** *Arthritis Rheum* 1999, **42:**s250.

Article within conference proceedings

5. Jones X: **Zeolites and synthetic mechanisms.** In *Proceedings of the First National Conference on Porous Sieves: 27-30 June 1996; Baltimore.* Edited by Smith Y. Stoneham: Butterworth-Heinemann; 1996:16-27.

Book chapter, or article within a book

6. Schnepf E: **From prey via endosymbiont to plastids: comparative studies in dinoflagellates.** In *Origins of Plastids. Volume 2.* 2nd edition. Edited by Lewin RA. New York: Chapman and Hall; 1993:53-76.

Whole issue of journal

7. Ponder B, Johnston S, Chodosh L (Eds): **Innovative oncology.** In *Breast Cancer Res* 1998, **10:**1-72.

Whole conference proceedings

8. Smith Y (Ed): *Proceedings of the First National Conference on Porous Sieves: 27-30 June 1996; Baltimore.* Stoneham: Butterworth-Heinemann; 1996.

Complete book

9. Margulis L: *Origin of Eukaryotic Cells.* New Haven: Yale University Press; 1970.

Monograph or book in a series

10. Hunninghake GW, Gadek JE: **The alveolar macrophage.** In *Cultured Human Cells and Tissues.* Edited by Harris TJR. New York: Academic Press; 1995:54-56. [Stoner G (Series Editor): *Methods and Perspectives in Cell Biology,* vol 1.]

Book with institutional author

11. Advisory Committee on Genetic Modification: *Annual Report.* London; 1999.

PhD thesis

12. Kohavi R: **Wrappers for performance enhancement and oblivious decision graphs.** *PhD thesis.* Stanford University, Computer Science Department; 1995.

Link / URL

13. **The Mouse Tumor Biology Database** [http://tumor.informatics.jax.org/cancer_links.html]

back to main instructions for authors