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Submission Guidelines

Software

Criteria

Genome Biology publishes outstanding new software that will be of utility to a wide audience. Applications considered include any aspect of biology or biomedicine studied from a genomic or post-genomic perspective.

Genome Biology classifies original research articles into Research, Method and Software. If your manuscript describes a new method or a research study with biological insights, please see the information about Method and Research manuscripts.

Software articles in *Genome Biology* should describe novel software applications that are likely to be of broad utility and that are shown to be a clear advance over the state-of-the-art existing tools in a side-by-side demonstration using the same dataset. Where possible, the software should be benchmarked using a synthetic dataset (or other dataset where the ground truth is known), and its utility on real data demonstrated. A Software article need not necessarily provide novel biological insights, but these can help to demonstrate the method's utility.

Many of the methods submitted to *Genome Biology* have a significant software component, so would be appropriate either as Method or Software articles. Articles which are more suited to the Software category would include a new implementation of an existing method to give significantly improved performance; a pipeline combining existing methods; a database (although we rarely consider these unless of exceptionally broad utility).

If you wish to make a presubmission enquiry about the suitability of your manuscript, please email the editors who will respond to your enquiry as soon as possible.

Reporting standards

Genome Biology operates a very strict open access, open source and open data policy. All datasets on which the conclusions rely should be either deposited in publicly available repositories (where available and appropriate) or presented in the main manuscript or additional supporting files whenever possible. Please see Springer Nature's information on recommended repositories. Private access links for reviewers should be made available on submission, if possible. If your study involves the use of any third party or previously published data, this data must also be available as a condition of publication.

Authors who need help depositing and curating data may wish to consider uploading their data to Springer Nature's Data Support Services or contacting our Research Data Support Helpdesk. Springer Nature's Data Support Services provide data deposition and curation to help authors follow good practice in sharing and archiving of research data. The services provide secure and private submission of data files, which are curated and managed by the Springer Nature Research Data team for public release, in agreement with the submitting author. These services are provided in partnership with figshare. Checks are carried out as part of a submission screening process to ensure that researchers who should use a specific community-endorsed repository are advised of the best option for sharing and archiving their data. Use of the Data Support Services is optional and does not imply or guarantee that a manuscript will be accepted.

Source code for any in-house scripts that are used in analyses must be either deposited in a public repository or included in the supplementary materials. Source code for tools described in Method or Software articles should be deposited in a public repository, with an OSI-compliant license. The access information and the license should be clearly stated in the manuscript. We also recommend a static deposition of the version described in the manuscript in a repository that assigns DOIs, and for this version to be cited. Please contact our Editorial Office for more information.

Genome Biology follows strict BioMed Central guidelines on ethical approvals needed for both carrying out and publishing research. For details of ethics guidelines, a list of appropriate data and software repositories, and the standards of reporting, please see the BioMed Central Editorial Policies.

Genome Biology advocates complete and transparent reporting of research and requires authors to adhere to the BioMed Central Minimum Standards of Reporting Checklist when reporting their research. On submission, authors will be asked to confirm they have included this information, or give reasons for any instances where it is not made available. Submissions received without these elements may be returned to the authors as incomplete.

It is understood that for some research studies certain aspects of the checklist may not be applicable. The checklist will not be used as a tool for judging the suitability of manuscripts for publication, but is intended as an aid to authors to clearly, completely and transparently let reviewers and readers know what authors did and found.

Preparing your manuscript

The information below details the section headings that you should include in your manuscript and what information should be within each section.

Please note that your manuscript must include a 'Declarations' section including all of the subheadings (please see below for more information).

Title page

The title page should:

- present a title that includes, if appropriate, the study design
- list the full names, institutional addresses and email addresses for all authors
- if a collaboration group should be listed as an author, please list the Group name as an author. If you would like the names of the individual members of the Group to be searchable through their individual PubMed records, please include this information in the "Acknowledgements" section in accordance with the instructions below
- indicate the corresponding author

Abstract

The Abstract should not exceed 100 words. Please minimize the use of abbreviations and do not cite references in the abstract. The abstract should be unstructured.

Keywords

Three to ten keywords representing the main content of the article.

Background

The Background section should explain the background to the study, its aims, a summary of the existing literature and why this study was necessary.

Results

This should include the findings of the study including, if appropriate, results of statistical analysis which must be included either in the text or as tables and figures.

Discussion

For research articles this section should discuss the implications of the findings in context of existing research and highlight limitations of the study. For study protocols and methodology manuscripts this section should include a discussion of any practical or operational issues involved in performing the study and any issues not covered in other sections.

Conclusions

This should state clearly the main conclusions and provide an explanation of the importance and relevance of the study to the field.

Methods (should be included after Conclusions)

The methods section should include:

- the aim, design and setting of the study
- the characteristics of participants or description of materials
- a clear description of all processes, interventions and comparisons. Generic names should generally be used. When proprietary brands are used in research, include the brand names in parentheses
- the type of statistical analysis used, including a power calculation if appropriate
- software tool requirements

List of abbreviations

If abbreviations are used in the text they should be defined in the text at first use, and a list of abbreviations can be provided.

Declarations

All manuscripts must contain the following sections under the heading 'Declarations':

- Ethics approval and consent to participate
- Consent for publication

- Availability of data and material
- Competing interests
- Funding
- Authors' contributions
- Acknowledgements
- Authors' information (optional)

Please see below for details on the information to be included in these sections.

If any of the sections are not relevant to your manuscript, please include the heading and write 'Not applicable' for that section.

Ethics approval and consent to participate

Manuscripts reporting studies involving human participants, human data or human tissue must:

- include a statement on ethics approval and consent (even where the need for approval was waived)
- include the name of the ethics committee that approved the study and the committee's reference number if appropriate

Studies involving animals must include a statement on ethics approval.

See our editorial policies for more information.

If your manuscript does not report on or involve the use of any animal or human data or tissue, please state "Not applicable" in this section.

Consent for publication

If your manuscript contains any individual person's data in any form (including any individual details, images or videos), consent for publication must be obtained from that person, or in the case of children, their parent or legal guardian. All presentations of case reports must have consent for publication.

You can use your institutional consent form or our consent form if you prefer. You should not send the form to us on submission, but we may request to see a copy at any stage (including after publication).

See our editorial policies for more information on consent for publication.

If your manuscript does not contain data from any individual person, please state "Not applicable" in this section.

Availability of data and materials

All manuscripts must include an 'Availability of data and materials' statement. Data availability statements should include information on where data supporting the results reported in the article can be found including, where applicable, hyperlinks to publicly archived datasets analysed or generated during the study. By data we mean the minimal dataset that would be necessary to interpret, replicate and build upon the findings reported in the article. We recognise it is not always possible to share research data publicly, for instance when individual privacy could be compromised, and in such instances data availability should still be stated in the manuscript along with any conditions for access.

Data availability statements can take one of the following forms (or a combination of more than one if required for multiple datasets):

- The datasets generated and/or analysed during the current study are available in the [NAME] repository, [PERSISTENT WEB LINK TO DATASETS]
- The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.
- All data generated or analysed during this study are included in this published article [and its supplementary information files].
- The datasets generated and/or analysed during the current study are not publicly available due [REASON WHY DATA ARE NOT PUBLIC] but are available from the corresponding author on reasonable request.
- Data sharing is not applicable to this article as no datasets were generated or analysed during the current study.
- The data that support the findings of this study are available from [third party name] but restrictions apply to the availability of these data, which were used under license for the current study, and so are not publicly available. Data are however available from the authors upon reasonable request and with permission of [third party name].
- Not applicable. If your manuscript does not contain any data, please state 'Not applicable' in this section.

More examples of template data availability statements, which include examples of openly available and restricted access datasets, are available here.

BioMed Central also requires that authors cite any publicly available data on which the conclusions of the paper rely in the manuscript. Data citations should include a persistent identifier (such as a DOI) and should ideally be included in the reference list. Citations of datasets, when they appear in the reference list, should include the minimum information recommended by DataCite and follow journal style. Dataset identifiers including DOIs should be expressed as full URLs. For example:

Hao Z, AghaKouchak A, Nakhjiri N, Farahmand A. Global integrated drought monitoring and prediction system (GIDMaPS) data sets. figshare. 2014. http://dx.doi.org/10.6084/m9.figshare.853801

With the corresponding text in the Availability of data and materials statement:

The datasets generated during and/or analysed during the current study are available in the [NAME] repository, [PERSISTENT WEB LINK TO DATASETS].[Reference number]

Competing interests

All financial and non-financial competing interests must be declared in this section.

See our editorial policies for a full explanation of competing interests. If you are unsure whether you or any of your co-authors have a competing interest please contact the editorial office.

Please use the authors initials to refer to each authors' competing interests in this section.

If you do not have any competing interests, please state "The authors declare that they have no competing interests" in this section.

Funding

All sources of funding for the research reported should be declared. The role of the funding body in the design of the study and collection, analysis, and interpretation of data and in writing the manuscript should be declared.

Authors' contributions

The individual contributions of authors to the manuscript should be specified in this section. Guidance and criteria for authorship can be found in our editorial policies.

Please use initials to refer to each author's contribution in this section, for example: "FC analyzed and interpreted the patient data regarding the hematological disease and the transplant. RH performed the histological examination of the kidney, and was a major contributor in writing the manuscript. All authors read and approved the final manuscript."

Acknowledgements

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If you do not have anyone to acknowledge, please write "Not applicable" in this section.

Group authorship (for manuscripts involving a collaboration group): if you would like the names of the individual members of a collaboration Group to be searchable through their individual PubMed records, please ensure that the title of the collaboration Group is included on the title page and in the submission system and also include collaborating author names as the last paragraph of the “Acknowledgements” section. Please add authors in the format First Name, Middle initial(s) (optional), Last Name. You can add institution or country information for each author if you wish, but this should be consistent across all authors.

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Endnotes

Endnotes should be designated within the text using a superscript lowercase letter and all notes (along with their corresponding letter) should be included in the Endnotes section. Please format this section in a paragraph rather than a list.

References

Examples of the Vancouver reference style are shown below.

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Web links and URLs: All web links and URLs, including links to the authors' own websites, should be given a reference number and included in the reference list rather than within the text of the manuscript. They should be provided in full, including both the title of the site and the URL, as well as the date the site was accessed, in the following format: The Mouse Tumor Biology Database. http://tumor.informatics.jax.org/mtbwi/index.do. Accessed 20 May 2013. If an author or group of authors can clearly be associated with a web link, such as for weblogs, then they should be included in the reference.

Example reference style:

Article within a journal

Smith JJ. The world of science. Am J Sci. 1999;36:234-5.

Article within a journal (no page numbers)

Rohrmann S, Overvad K, Bueno-de-Mesquita HB, Jakobsen MU, Egeberg R, Tjønneland A, et al. Meat consumption and mortality - results from the European Prospective Investigation into Cancer and Nutrition. BMC Medicine. 2013;11:63.

Article within a journal by DOI

Slifka MK, Whitton JL. Clinical implications of dysregulated cytokine production. Dig J Mol Med. 2000; doi:10.1007/s801090000086.

Article within a journal supplement

Frumin AM, Nussbaum J, Esposito M. Functional asplenia: demonstration of splenic activity by bone marrow scan. Blood 1979;59 Suppl 1:26-32.

Book chapter, or an article within a book

Wyllie AH, Kerr JFR, Currie AR. Cell death: the significance of apoptosis. In: Bourne GH, Danielli JF, Jeon KW, editors. International review of cytology. London: Academic; 1980. p. 251-306.

OnlineFirst chapter in a series (without a volume designation but with a DOI)

Saito Y, Hyuga H. Rate equation approaches to amplification of enantiomeric excess and chiral symmetry breaking. Top Curr Chem. 2007. doi:10.1007/128_2006_108.

Complete book, authored

Blenkinsopp A, Paxton P. Symptoms in the pharmacy: a guide to the management of common illness. 3rd ed. Oxford: Blackwell Science; 1998.

Online document

Doe J. Title of subordinate document. In: The dictionary of substances and their effects. Royal Society of Chemistry. 1999. http://www.rsc.org/dose/title of subordinate document. Accessed 15 Jan 1999.

Online database

Healthwise Knowledgebase. US Pharmacopeia, Rockville. 1998. http://www.healthwise.org. Accessed 21 Sept 1998.

Supplementary material/private homepage

Doe J. Title of supplementary material. 2000. http://www.privatehomepage.com. Accessed 22 Feb 2000.

University site

Doe, J: Title of preprint. http://www.uni-heidelberg.de/mydata.html (1999). Accessed 25 Dec 1999.

FTP site

Doe, J: Trivial HTTP, RFC2169. ftp://ftp.isi.edu/in-notes/rfc2169.txt (1999). Accessed 12 Nov 1999.

Organization site

ISSN International Centre: The ISSN register. http://www.issn.org (2006). Accessed 20 Feb 2007.

Dataset with persistent identifier

Zheng L-Y, Guo X-S, He B, Sun L-J, Peng Y, Dong S-S, et al. Genome data from sweet and grain sorghum (Sorghum bicolor). GigaScience Database. 2011. http://dx.doi.org/10.5524/100012.

Figures, tables and additional files

See General formatting guidelines for information on how to format figures, tables and additional files.

Structuring supplemental information

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Genome Biology recommends formatting your supplemental material in an organized way to make the data included as accessible as possible to readers and reviewers. You may want to consider the following guidelines when organizing your supplemental data.

Table of Contents

A Table of Contents may be used for long supplements and can list the supplemental methods, figures, and text included within the supplement.

Subheadings to Mirror Main Text

The supplement can be structured to mirror the main text. Manuscript subheadings can be used within the supplement so that relevant information is easily found. Please see the published Opinion article by Greenbaum and colleagues for more information.

The following could also be included within supplemental subheadings:

- Additional text/figures that are not part of the main story
- Negative results related to main figures
- Additional background or discussion that is not essential for the main results presented in the paper.
- Workflows relevant to specific figures or experiments (see next section)

Supplemental Figures/Workflows

Supplemental figures and workflows can be included under subheadings that mirror the main text headings. If they are unrelated to a main manuscript heading, a new heading could be used.

Supplemental workflows can include diagrams that outline experimental setup or flow charts for bioinformatics analyses.

Additional discussion can be included with supplemental figures if required.

Supplemental methods/Computer codes/scripts

Supplemental methods should include methods for data not included in the main text or for details such as lists of reagents.

Genome Biology requires computer codes and scripts to be deposited in a publically available repository. In addition, you may wish to include details about codes and scripts within the supplement, within the "Supplemental Methods" section.

Making the Supplement 'Computer-Parse-able' and reproducible

Making your supplement machine readable will make your data easier to find and use.

The following should be included for a computer parse-able supplement:

- Reagents and the companies that produce them should be listed
- Public databases used in the supplement should be signposted
- Software URLs should be included
- Standardized gene names and coordinates for non-coding elements (chromosome number and position) should be used
- Computer parse-able representations of networks should be included

Extended Author Contributions

For large consortium papers, it may be useful to include additional details within the supplement regarding contributions of individuals to specific experiments, which would connect them to specific analyses or reagents used.

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