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Aims

The aim of *Bioinformatics* is to provide an indispensable resource for the experimental practitioner seeking awareness of the disparate sources of data and analytical tools of contemporary biology, biotechnology and medicine based on the molecular level. This includes all areas of genomics, proteomics, metabolomics, interactomics and network biology, imaging, systems biology, chemoinformatics, computational biology and clinical/medical information that have a molecular foundation to the study. Large-scale instrumentation and computerisation is reducing the time needed to be spent in the laboratory. Instead, the time-limiting step is the analysis and interpretation of data. The journal provides topical reviews of new methodologies as they become established.

The Editors, Martin Bishop and Russ Altman, welcome the submission of review papers and case studies for publication. Essential criteria for the publication of papers are that they provide practical guidance to the users of bioinformatics software and databases to supplement available manuals and tutorials, providing a brief conceptual review and overview of the problem addressed, its solution, dynamic range and limitations. We publish reviews of clearly defined subject areas for both experimental biologists and for bioinformatics specialists. Reviews may be broader or more narrowly focussed but must cover a variety of approaches to a very well-specified biological problem or research area. We do not publish work on new methods that have not yet been described elsewhere. Please do not submit manuscripts concerning original research as they will be immediately rejected.

Some areas that members of the Editorial Board have identified as important and presently under represented in the pages of the Journal include the complex fields of epigenetics and the construction of evolutionary models and the elucidation of evolutionary relationships. Methodological approaches of interest include software companion and benchmarking, data cleaning and curation, accuracy of predicted and extracted information, ontologies and text-mining; solutions that allow for the large-scale analysis of biological data in reasonable time (high performance computing solutions and cloud systems), standards, training and change management activities, and the determination of causal relationships from data. There was specific mention of the use of ontologies for semantic-based analysis of molecular data and interaction networks, methods and tools for the automatic or semiautomatic annotation of biological data with terms extracted from ontologies, and methods and tools for enrichment analysis. Articles focusing on illuminating the bottleneck problems in important bioinformatics approaches will be especially helpful to readers. It must be emphasized that these comments are suggestions and are not intended to be prescriptive. As science advances the details of what is important changes and the Editors, Editorial Board and Reviewers will be flexible in these policies.

Types of Submission

Submissions of the following types are accepted for review in the Journal:

- Review articles (2000–7000 words)
- Letters to the Editors (relating to a topic previously published in the journal) (500–1000 words)
- Book reviews (500–1000 words)
- Software and websites reviews (by authors other than the originators) (500–1000 words)
- Case studies in biological research applied to clinical practice (2000–5000 words)
- Protocols for solving a specific problem using different sets of programs (2000–5000 words)
- Opinions articles: topical or controversial area that do not warrant a full review (500–1000 words)
- Supplement available manuals and tutorials, providing a brief conceptual review and overview of the problem addressed, its solution, dynamic range and limitations.