

# Bioinformatics

EDITORIAL NEWS

ISSUE 7 • 2014

## Welcome to the 2014 Bioinformatics Editorial Newsletter

Bioinformatics continues to go from strength to strength thanks to our authors, reviews, board members and editors. We would like to take this opportunity to thank everyone who has supported the journal this year. Submissions have increased again to nearly 2300 in 2014, and we appreciate the support from reviewers to help us process these papers. More authors are choosing to publish their papers under an open access licence, with uptake reaching 27% in 2014.

As always we very much welcome your suggestions for new developments, review or editorial topics, and feedback on any aspect of the journal.

Best regards

The *Bioinformatics* Editor team, [bioinformatics.editorialoffice@oup.com](mailto:bioinformatics.editorialoffice@oup.com)

### Editorial Office and Production Update

	2014
Submissions	2295
Acceptance rate	33%
Time from submission to first decision (average)	37 days
Advance Access online publication time (average)	5 days
Issue publication time (average)	49 days
Optional open access uptake	27%

### Reviews Update

Reviews published this year have covered topics including:

- Toward better understanding of artifacts in variant calling from high-coverage samples (<http://bioinformatics.oxfordjournals.org/content/30/20/2843.abstract>)
- Challenges in RNA virus bioinformatics (<http://bioinformatics.oxfordjournals.org/content/30/13/1793.abstract>)
- Algorithms and tools for protein–protein interaction networks clustering, with a special focus on population-based stochastic methods (<http://bioinformatics.oxfordjournals.org/content/30/10/1343.abstract>)

## Here are the top 10 cited articles published in 2014:

Title	Authors	Issue	Pages	Citations
RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies	Stamatakis, Alexandros	9	1312	87
Trimmomatic: a flexible trimmer for Illumina sequence data	Bolger, Anthony M.; Lohse, Marc; Usadel, Bjoern	15	2114	38
Combining evolutionary information extracted from frequency profiles with sequence-based kernels for protein remote homology detection	Liu, Bin; Zhang, Deyuan; Xu, Ruifeng; et al.	4	472	32
iNuc-PseKNC: a sequence-based predictor for predicting nucleosome positioning in genomes with pseudo k-tuple nucleotide composition	Guo, Shou-Hui; Deng, En-Ze; Xu, Li-Qin; et al.	11	1522	25
Causal analysis approaches in Ingenuity Pathway Analysis	Kraemer, Andreas; Green, Jeff; Pollard, Jack, Jr.; et al.	4	523	25
InterProScan 5: genome-scale protein function classification	Jones, Philip; Binns, David; Chang, Hsin-Yu; et al.	9	1236	19
DIYABC v2.0: a software to make approximate Bayesian computation inferences about population history using single nucleotide polymorphism, DNA sequence and microsatellite data	Cornuet, Jean-Marie; Pudlo, Pierre; Veyssier, Julien; et al.	8	1187	19
featureCounts: an efficient general purpose program for assigning sequence reads to genomic features	Liao, Yang; Smyth, Gordon K.; Shi, Wei	7	923	16
Protter: interactive protein feature visualization and integration with experimental proteomic data	Omasits, Ulrich; Ahrens, Christian H.; Mueller, Sebastian; et al.	6	884	16
Prokka: rapid prokaryotic genome annotation	Seemann, Torsten	14	2068	14

## Conferences

Bioinformatics has been represented at a number of conferences this year, including of course ISMB 2014 in Boston, where the HiTSeq SIG was held as usual. Selected papers from HiTSeq can be found here: <http://bioinformatics.oxfordjournals.org/content/30/24.toc#HITSEQPAPERS>.

## IMPROVER Challenge special issue

Bioinformatics also published selected papers from the sbv IMPROVER Challenge, which can be found here: <http://bioinformatics.oxfordjournals.org/content/31/4>

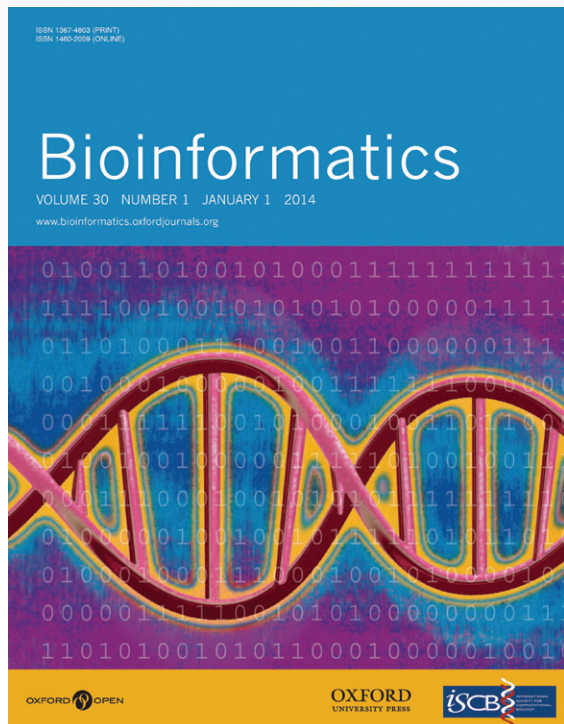
## New Impact Factor

The Bioinformatics impact factor for 2014 was 4.621. The journal is ranked fourth in the Mathematical and Computational Biology category.

4.621

## ISCB articles

Bioinformatics is an official journal of ISCB, and we have collected together the ISCB articles published in the journal over the past year ([http://www.oxfordjournals.org/our\\_journals/bioinformatics/iscb\\_articles.html](http://www.oxfordjournals.org/our_journals/bioinformatics/iscb_articles.html)).



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## How editorial board members can support Bioinformatics

You can help us in a number of ways by:

- ▶ acting as reviewers and identifying colleagues who might review manuscripts for the journal;
- ▶ evaluating manuscripts in difficult cases where we need an extra solid opinion;
- ▶ writing editorials and reviews, or suggesting review topics and authors;
- ▶ contributing advice and ideas on the future development of the journal;
- ▶ helping to raise awareness of the journal.

We also see the Editorial Board as a good source of future Associate Editors, so if you would be interested in taking on such a role, let us know.

