

BIOINFORMATICS

EDITORIAL NEWS

ISSUE 4 | 2011

WELCOME TO THE 2011 BIOINFORMATICS EDITORIAL NEWSLETTER

We would really like to take this opportunity to thank all of the reviewers who have supported the journal this year – around 3000 individuals. Thanks to you we have once again been able to undertake the peer review of around 2000 submissions in 2011.

Once again Bioinformatics sponsored the high-throughput sequencing (HiTSeq) SIG at ISMB/ECCB. This year's award winners were:

- Andrew McPherson 'Comrad: detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data'
- Christian Rödelberger and Peter N. Robinson 'Identity-By-Descent Filtering of Exome Sequence data for Disease-Gene Identification in Autosomal Recessive Disorders'

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

Email us at bioinformatics.editorialoffice@oup.com

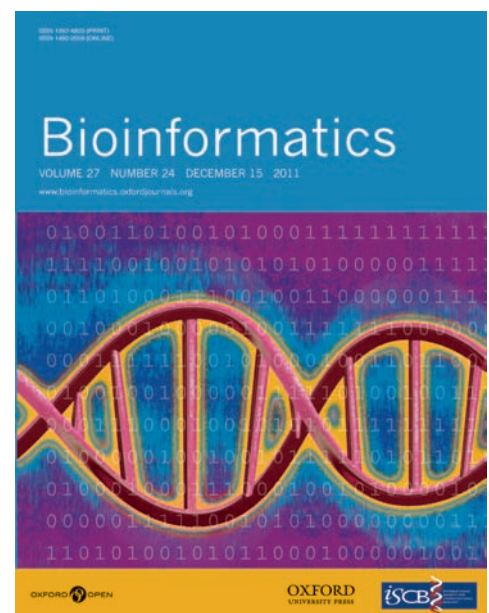
Best regards

Alex Bateman, Alfonso Valencia, and the Bioinformatics Editor team

EDITORIAL OFFICE AND PRODUCTION UPDATE

2011 PROJECTED

Submissions	2000
Acceptance rate	32%
Time from submission to first decision (average)	30 days
Advance Access online publication time (average)	5 days
Issue publication time (average)	53 days
Optional open access uptake	21%



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BIOINFORMATICS

TOP 10 ACCESSED ARTICLES PUBLISHED IN 2011

1	Bioinformatics challenges for personalized medicine	Guy Haskin Fernald, Emidio Capriotti, Roxana Daneshjou, Konrad J. Karczewski, Russ B. Altman	http://bioinformatics.oxfordjournals.org/content/27/13/1741.full
2	On the organization of bioinformatics core services in biology-based research institutes	Olli Kallioniemi, Lodewyk Wessels, and Alfonso Valencia	http://bioinformatics.oxfordjournals.org/content/27/10/1345.full
3	Characterization and improvement of RNA-Seq precision in quantitative transcript expression profiling	Paweł P. Łabaj, Germán G. Leparo, Bryan E. Linggi, Lye Meng Markillie, H. Steven Wiley, and David P. Kreil	http://bioinformatics.oxfordjournals.org/content/27/13/i383.full
4	A pipeline for RNA-seq data processing and quality assessment	Angela Goncalves, Andrew Tikhonov, Alvis Brazma, Misha Kapushesky	http://bioinformatics.oxfordjournals.org/content/27/6/867.full
5	Comparative studies of de novo assembly tools for next-generation sequencing technologies	Yong Lin, Jian Li, Hui Shen, Lei Zhang, Christopher J. Papasian, Hong-Wen Deng	http://bioinformatics.oxfordjournals.org/content/27/15/2031.full
6	GPU-BLAST: using graphics processors to accelerate protein sequence alignment	Panagiotis D. Vouzis, Nikolaos V. Sahinidis	http://bioinformatics.oxfordjournals.org/content/27/2/182.full
7	Identifying cancer driver genes in tumor genome sequencing studies	Ahrim Youn, Richard Simon	http://bioinformatics.oxfordjournals.org/content/27/2/175.full
8	Using bioinformatics to predict the functional impact of SNVs	Melissa S. Cline, Rachel Karchin	http://bioinformatics.oxfordjournals.org/content/27/4/441.full
9	SlideSort: all pairs similarity search for short reads	Kana Shimizu, Koji Tsuda	http://bioinformatics.oxfordjournals.org/content/27/4/464.full
10	PE-Assembler: de novo assembler using short paired-end reads	Pramila Nuwantha Ariyaratne, Wing-Kin Sung	http://bioinformatics.oxfordjournals.org/content/27/2/167.full

EDITORIALS AND REVIEWS UPDATE

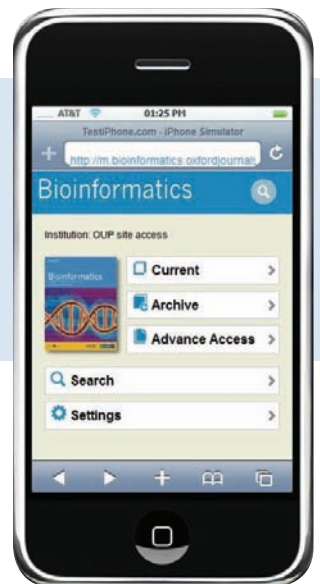
Reviews published this year have covered topics including:

- Using bioinformatics to predict the functional impact of SNVs
<http://bioinformatics.oxfordjournals.org/content/27/4/441.full>
- Proteins without 3D structure: definition, detection and beyond
<http://bioinformatics.oxfordjournals.org/content/27/11/1449.full>
- Bioinformatics challenges for personalized medicine
<http://bioinformatics.oxfordjournals.org/content/27/13/1741.full>
- Computational prediction of eukaryotic phosphorylation sites
<http://bioinformatics.oxfordjournals.org/content/27/21/2927.full>

We have also published Editorials on topics such as the organization of bioinformatics core services in biology-based research institutes (<http://bioinformatics.oxfordjournals.org/content/27/10/1345.full>) and the rise and fall of supervised machine learning techniques (<http://bioinformatics.oxfordjournals.org/content/27/24/3331.full>)

BIOINFORMATICS MOBILE SITE

Bioinformatics now has a mobile-optimized website (<http://m.bioinformatics.oxfordjournals.org/>) which has been developed to provide simpler, more intuitive browsing on mobile devices including iPhone and iPad, Android, Symbian and Windows Mobile smartphones, and Blackberry.



EDITORIAL DEVELOPMENTS

It was recently announced that *Bioinformatics*' impact factor for 2010 is now 4.877 (from 4.926 in 2009). We note that the other top journals in the field also experienced a decrease in impact factor this year.

We were pleased to welcome Mario Albrecht and Janet Kelso to the *Bioinformatics* Associate Editor team at the start of 2011. We thank Dmitrij Frishman and Joaquin Dopazo for their hard work as Associate Editors, and we're delighted that both have agreed to join the Editorial Board now their terms have ended. We are also delighted that Michael Brudno, organiser of the HiTSeq SIG, has joined the Associate Editor team in November. We continue to welcome suggestions for future editorial board members.



JANET KELSO



MARIO ALBRECHT



MICHAEL BRUDNO

BIOINFORMATICS

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Alfonso Valencia, Spain

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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.

