



The Bioconductor channel in F1000Research

Citation

Huber, Wolfgang, Vincent Carey, Sean Davis, Kasper Daniel Hansen, and Martin Morgan. 2015. "The Bioconductor channel in F1000Research." F1000Research 4 (1): 217. doi:10.12688/f1000research.6758.1. <http://dx.doi.org/10.12688/f1000research.6758.1>.

Published Version

doi:10.12688/f1000research.6758.1

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EDITORIAL

The Bioconductor channel in *F1000Research* [version 1; referees: not peer reviewed]

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v1 First published: 10 Jul 2015, 4:217 (doi: [10.12688/f1000research.6758.1](https://doi.org/10.12688/f1000research.6758.1))
Latest published: 10 Jul 2015, 4:217 (doi: [10.12688/f1000research.6758.1](https://doi.org/10.12688/f1000research.6758.1))

Abstract

Bioconductor (bioconductor.org) is a rich source of software and know-how for the integrative analysis of genomic data. The Bioconductor channel in *F1000Research* provides a forum for task-oriented workflows that each cover a solution to a current, important problem in genome-scale data analysis from end to end, invoking resources from several packages by different authors, often combining multiple `omics data types, and demonstrating integrative analysis and modelling techniques.



This article is included in the **Bioconductor** channel.

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How to cite this article: Huber W, Carey V, Davis S *et al.* **The Bioconductor channel in *F1000Research* [version 1; referees: not peer reviewed]** *F1000Research* 2015, 4:217 (doi: [10.12688/f1000research.6758.1](https://doi.org/10.12688/f1000research.6758.1))

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Grant information: W.H. acknowledges support by the European Commission through FP7 project RADIANT.

Competing interests: No competing interests were disclosed.

First published: 10 Jul 2015, 4:217 (doi: [10.12688/f1000research.6758.1](https://doi.org/10.12688/f1000research.6758.1))

Editorial

Bioinformatics is a wonderful field, since so many of the researchers who develop new concepts, methods and tools have embraced the sharing of their research outputs as free, open-source software. This openness has, no doubt, accelerated the breathtaking progress in the field of genomics (and related `omic technologies). Bioconductor (bioconductor.org) has become a place that many developers are choosing to host their software - it gives them a useful infrastructure for development and for providing effective user support¹. It is also a venue where many prospective users go to when they look for a quality solution in genome-scale data analysis, where they will find some of the most advanced tools.

This abundance of tools, however, can be difficult to navigate. Bioconductor comes in two parts: as a collection of individual packages, each developed independently by a research group somewhere on the globe, and often among the experts in their field; and as a layer of infrastructure, with common data structures and core library functionality to glue the packages together and provide, as we call it, 'interoperability'. Many of the individual packages are exquisitely documented by their authors, but there has been less on offer, so far, at the level of cross-package, task-centered workflows. The questions 'What can I do with this particular package?' and 'How do I approach my particular problem?' are subtly different. Users care about the latter. With the Bioconductor channel in *F1000Research*, we aim to provide a place, and the incentives, for

scientists to create and publish such task-oriented workflows. Each workflow will cover a solution to a current, important problem in genome-scale data analysis from end to end; it will invoke resources from several packages from different authors; it will often combine multiple `omics data types and demonstrate integrative analysis and modelling techniques; and it will be by written by scientists who need not be the developers of any of the used packages. We hope that the workflows will make it easier for new and existing users to navigate the offerings of R (<http://www.r-project.org>) and Bioconductor, to adapt workflows to their needs, and to rapidly find solutions for their problems.

Author contributions

W.H., V.J.C., S.D., K.D.H. and M.M. wrote the article.

Competing interests

No competing interests were disclosed.

Grant information

W.H. acknowledges support by the European Commission through FP7 project RADIANT.

Acknowledgments

We thank all contributors to the Bioconductor project.

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