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Collaborative development of software and methods for genomic data analysis

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Bioconductor is an open-source, open-development software project for the analysis and comprehension of high-throughput data in genomics and molecular biology. The project aims to enable interdisciplinary research, collaboration and rapid development of scientific software. Based on the statistical programming language R, Bioconductor comprises over 1000 interoperable packages contributed by a large, diverse community of scientists. Packages cover a range of bioinformatic and statistical applications. They undergo formal initial review and continuous automated testing. I will present an overview of project design and management -both technical and ‘social’- and of our efforts to provide a productive environment developers and a positive user experience.

<http://bioconductor.org>

<http://www.nature.com/nmeth/journal/v12/n2/full/nmeth.3252.html>

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