

Introduction to *R* and *Bioconductor*

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R

R is a language and environment for statistical computing and graphics

R

R is a **language and environment** for statistical computing and graphics

- ▶ Full-featured programming language
- ▶ Interactive and *interpreted* – convenient and forgiving of user errors
- ▶ Coherent, extensively documented

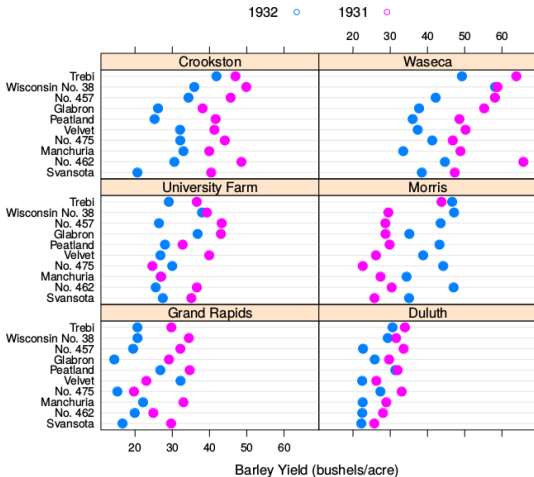
R

R is a language and environment for **statistical computing** and graphics

- ▶ Throughout the language, e.g., `factor` and `NA`
- ▶ Built-in statistical functionality
- ▶ Highly extensible via user-contributed *packages*

R is a language and environment for statistical computing and graphics

- ▶ Explore data
- ▶ Communicate results



R vectors, classes, and functions

- ▶ Vectors

- ▶ logical, integer, numeric, complex, character, raw (byte)
- ▶ factor: discrete levels
- ▶ Missing-ness, NA

- ▶ *data.frame*, *matrix*, and other *objects*

- ▶ Functions

- ▶ Operating on vectors, e.g., `log`, `lm` (fit a linear model)
- ▶ 'Higher order' functions – apply a function to several different vectors, e.g., `lapply(df, log)`

- ▶ Packages

None of this making sense? *R* introduction / refresher tutorial this afternoon

Using R

Documentation

- ▶ `help()`
- ▶ vignettes

Work flows

- ▶ Scripts...
 - ▶ Reproducible
 - ▶ Literate
- ▶ ... mature to *packages*
 - ▶ Coordinate data, analysis, and documentation
 - ▶ Share with others

Bioconductor project goal

Analysis and comprehension of high-throughput genomic data

Bioconductor project goal

Analysis and comprehension of high-throughput genomic data

Statistical analysis

- ▶ Reduce large data to manageable knowledge
- ▶ Cope with technological artifacts
- ▶ Rigorous exploration
- ▶ Designed experiments, e.g., treatment vs. control
- ▶ Leading-edge methods for leading-edge questions

Bioconductor project goal

Analysis and **comprehension** of high-throughput genomic data

- ▶ Understandable
- ▶ Reproducible
- ▶ Effective visualization
- ▶ Biological context, e.g., annotation
- ▶ Training

Bioconductor project goal

Analysis and comprehension of **high-throughput genomic data**

- ▶ Sequencing: RNA-seq, ChIP-seq, variants, copy number...
- ▶ Microarrays: expression, SNP, ...
- ▶ Flow cytometry
- ▶ Proteomics
- ▶ Images
- ▶ ...

What is *Bioconductor*?

Collection of packages in the *R* statistical programming language

- ▶ Developed by the *Bioconductor* core and international contributors
- ▶ Stable 'release' branch, and leading edge 'devel' branch
- ▶ Open source / open development

Used by...

- ▶ Individuals
- ▶ Academic labs & research groups
- ▶ Government agencies
- ▶ Pharma and other companies

How to learn & use *Bioconductor*

1. Install *R* (& *RStudio*?)
2. Identify and install packages
3. Write *R* scripts
 - ▶ Input & ‘massage’ data
 - ▶ Quality assessment
 - ▶ Statistical analysis
 - ▶ Visualization
 - ▶ Annotation
 - ▶ Reports & summaries
4. Share with colleagues, collaborators, and the community

<http://bioconductor.org>

The screenshot shows the Bioconductor website homepage. At the top, there is a search bar and navigation links for Home, Install, Help, Developers, and About. The main content area is divided into several sections:

- Annual Conference:** A section titled "Annual Conference" with a sub-header "Annual Conference". It includes a "Register Now!" link and text about the 2014 conference held in Boston, MA, from July 30 to Aug 1, 2014, at the Dana-Farber Cancer Institute. It also mentions "reduced hotel rates".
- About Bioconductor:** A section titled "About Bioconductor" with a sub-header "About Bioconductor". It describes Bioconductor as providing tools for the analysis and comprehension of high-throughput genomic data, using the R statistical programming language. It notes that it has two releases each year, is open source, and is available as an Amazon Machine Image (AMI).
- Install:** A section titled "Install" with a sub-header "Install". It includes a "Get started with Bioconductor" link and a list of links: "Install Bioconductor", "Custom packages", "Making JAR", "Latest newsletter", "Follow us on Twitter", and "Using R".
- Learn:** A section titled "Learn" with a sub-header "Learn". It includes a "Master Bioconductor tools" link and a list of links: "Recent coverage", "Package vignettes", "Custom work flows", "FAQ", and "Community resources".
- Use:** A section titled "Use" with a sub-header "Use". It includes a "Create bioinformatic solutions with Bioconductor" link and a list of links: "Software, Annotation, and Experiment packages", "Amazon Machine Image", "Latest release announcement", and "Subscribe to the mailing list".
- Develop:** A section titled "Develop" with a sub-header "Develop". It includes a "Contribute to Bioconductor" link and a list of links: "Use 'Devtools'", "Devtools Software, Annotation, and Experiment packages", "Package guidelines", "New package submission", "Advanced programming", "Additional developer resources", and "Build reports".

- ▶ Established work flows, e.g., RNA-seq differential expression with *DESeq2*
- ▶ Flexible bioinformatic analysis, e.g., ...

Project strengths

- ▶ **Extensive**
 - ▶ Respected
 - ▶ Well-used
 - ▶ Accessible
- ▶ 824 software packages, 867 annotation packages, 202 experiment data packages
 - ▶ Sequencing, microarrays, flow cytometry, proteomics, image analysis, ...
 - ▶ All packages with vignettes and help pages
 - ▶ Tutorials, training material, national and international conferences

Project strengths

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“Community repositories that carry out testing are ideal. . . the genetics community is fortunately familiar with the Comprehensive R Archive Network and the principles of stewardship of modular software embodied in the Bioconductor suite. . . The journal has sufficient experience with these resources to endorse their use by authors.” – *Nature Genetics* 46, 1 (2014)

Project strengths

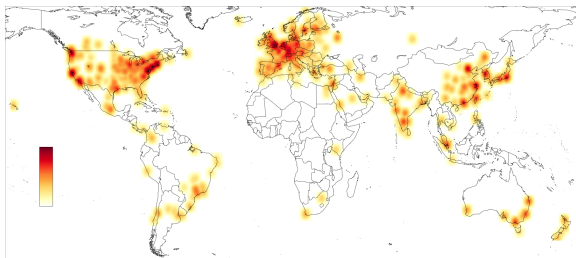
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PubMedCentral full-text citations

		Citations
	<i>Bioconductor</i>	9070
	RNA-seq	
	<i>edgeR</i> Diff. expression	647
	<i>DESeq</i> Diff. expression	648
	Microarray	
	<i>affy</i> Pre-processing	2318
	<i>limma</i> Diff. expression	4503
	<i>GOstats</i> GSEA	436

Project strengths

- ▶ Extensive
- ▶ Respected
- ▶ **Well-used**
- ▶ Accessible



- ▶ 225,000 unique IP addresses downloaded
9.3M packages
- ▶ 397,000 site visitors / year (27% increase)
viewed 2.8M pages
- ▶ ~ 600 mailing list posts from ~ 210
authors per month

Project strengths

- ▶ Extensive
 - ▶ Respected
 - ▶ Well-used
 - ▶ **Accessible**
- <http://bioconductor.org>
- ▶ Package vignettes & help pages
 - ▶ Work flows
 - ▶ Mailing list & 'guest posting' facility
 - ▶ Courses and other training
 - ▶ Annual Conference,
Boston July 30 – Aug 1.

Acknowledgements

- ▶ *Bioconductor* core: Vince Carey, Sean Davis, Kasper Hansen, Wolfgang Huber, Robert Gentleman, Rafael Irizzary, Michael Lawrence, Levi Waldron
- ▶ *Bioconductor* team: Sonali Arora (introductory material, copy number), Marc Carlson (annotation), Nate Hayden (pileup, C++), Valerie Obenchain (variants, ranges), Hervé Pagès (ranges, strings), Paul Shannon (systems biology), Dan Tenenbaum (web, build)
- ▶ The international *Bioconductor* community!
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More: <http://bioconductor.org>