Bioc 2017: Where Software and Biology Connect

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26 July 2017

Welcome!

Special thanks

- Erica Fieck, David Nunes, Pam Jarrett, Meeghan Becker.
- Fast talkers, workshop contributors, scholarship recipients.

Conference home page

- `https://bioconductor.org/bioc2017`
- Includes link to Developer Day schedule, `https://goo.gl/8oRmsp`.

Twitter: #bioc2017

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Today

Informal and flexible

- Want to do something different? Say so!

Schedule `https://goo.gl/8oRmsp`

- Introduction / project overview / group activity
- Lightning talks (two parallel sessions)
- Workshops (bring your laptops!) / Birds-of-a-feather (discussion-oriented)
- Panel discussion

Coffee breaks & box lunches; no evening acivities

Tommorrow: 8:30 am, Jimmy Fund Auditorium

Logistics

Posters

- Please leave at the registration desk, today if possible, Thursday morning at the latest.

Conference Amazon Machine Instances

- Start yours today at `courses.bioconductor.org`
- Username: ...; password: ...
- 'This site can't be reached...' ?? Reload page (AMI is still spinning up)
- 'We're sorry, but something went wrong' ?? Re-submit request for AMI or notify Lori (Amazon ran out of cloud!)

Bioconductor – introduction

Statistical analysis and comprehension of high-throughput genomic data

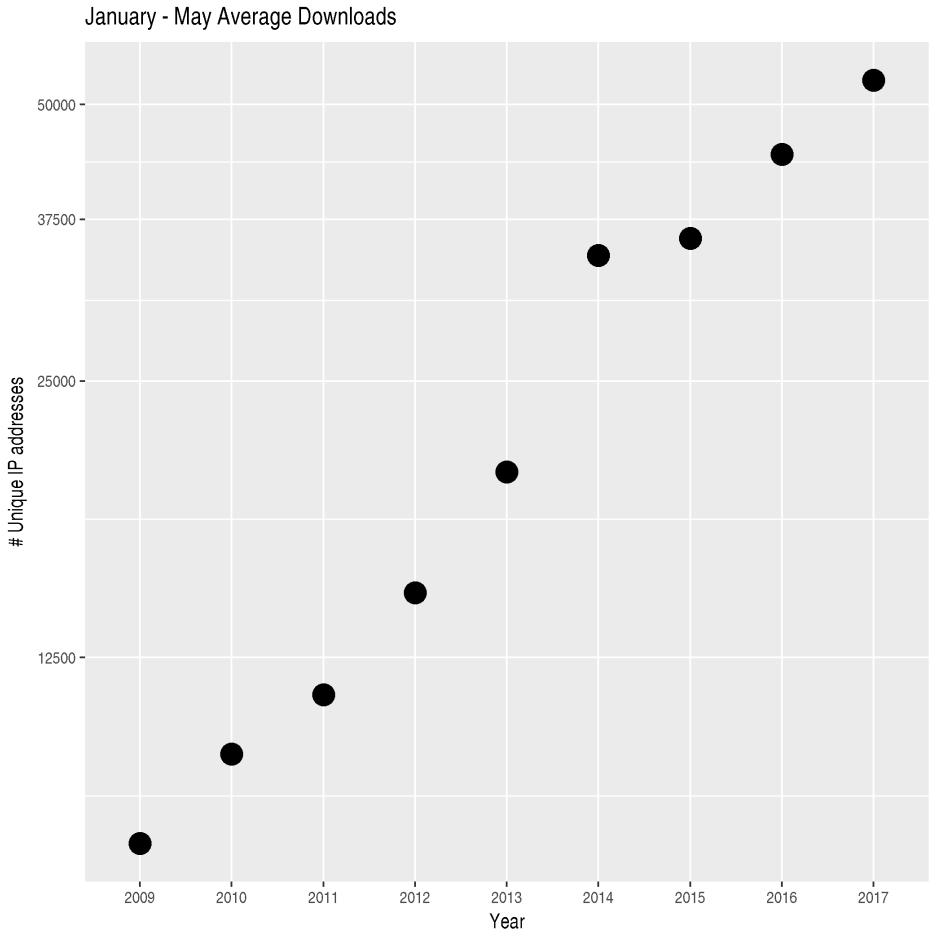
- Started 2001
- 1383 software packages
- $>$ 900 distinct maintainers

Widely used, highly respected

- $>$ 20000 PubMedCentral full-text citations

Supported

- `https://bioconductor.org`
- `https://support.bioconductor.org`

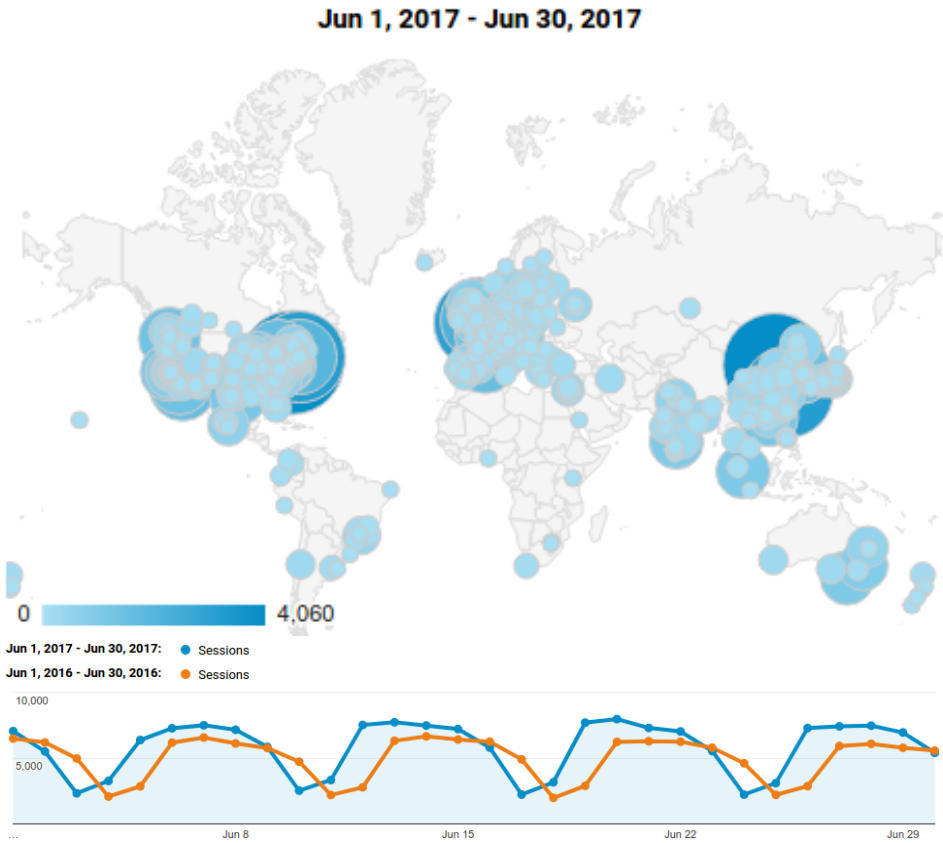


Bioconductor – introduction

- Federally funded through NIH (NHGRI, NCI), EU, ...
- International relevance

Important themes

- Statistical programming
- Leading-edge
- Reproducible
- Integrative
- Documented



Web site visitors

Bioconductor – core team

Valerie Obenchain *VariantAnnotation*, *GenomicFiles*, *GRanges* infrastructure; nightly builds; AWS administration.

Hervé Pagès *GRanges* infrastructure; *Biostrings*, *DelayedArray* & friends; nightly builds.

Marcel Ramos *MultiAssayExperiment* (with Levi Waldron); *SOUNDBoard*.

Lori Shepherd *BiocFileCache*, 'single package builder', docker and AMI solutions.

Nitesh Turaga Transition to git version control.

Daniel van Twisk *Organism.dplyr* / *AnnotationFilter*.

Bioconductor – friends of the core team

Andrzej Olés *BiocStyle*, workflows, build system (chef, git integration).

Mike Smith *biomaRt*, *rhdf5* / *Rhdf5lib*.

Lukas Shiffer Support site markdown!

Organism.dplyr (Yubo Cheng, Daniel van Twisk) – motivation

- *TxDb.**, *org.** annotation package integration not entirely satisfying.
- Databases underly these resources, why not expose in a 'modern' (i.e., *dplyr*) way?

```
library(Organism.dplyr)
src_organism("TxDb.Hsapiens.UCSC.hg38.knownGene")

## src:  sqlite 3.19.3 [/home/mtmorgan/.cache/BiocFileCache/5b
## tbls: id, id_accession, id_go, id_go_all, id_omim_pm,
##   id_protein, id_transcript, ranges_cds, ranges_exon,
##   ranges_gene, ranges_tx
```

- See *Organism.dplyr* and *AnnotationFilter* vignettes for details.

Organism.dplyr – insights

Exposing sql tables is really helpful.

- Easy to see and manipulate data.

A pure *dplyr* approach is too low-level

- Common queries require complicated joins.
- Useful 'verbs' like `select()`, `mapIds()` are and extended on top of *dplyr*.
- Classes like *GRanges* are incredibly useful, even if superficial similarity to a `tibble`.

Ici c'est ne pas une pipe

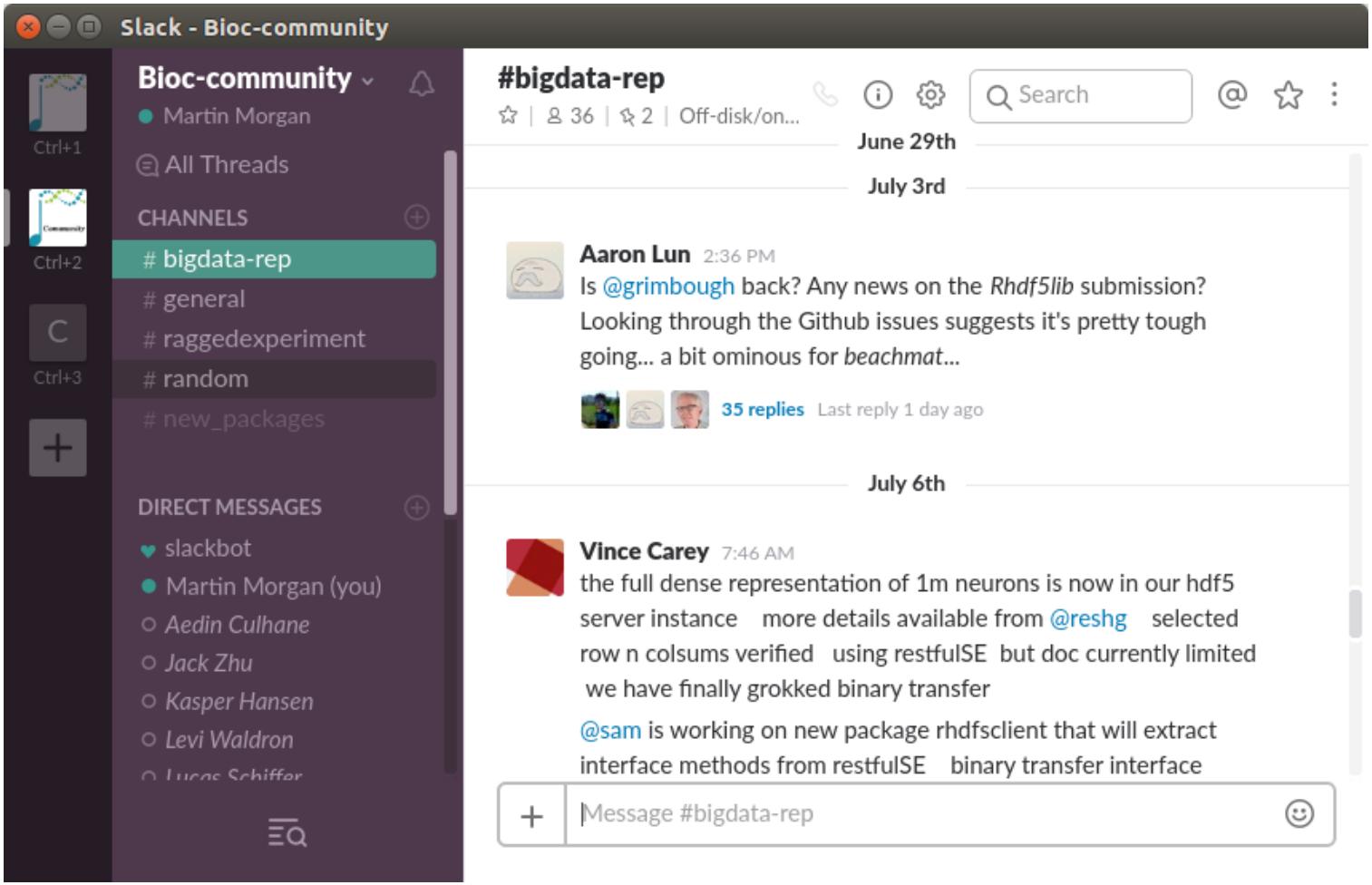
- `tbl(src, "ranges_tx") %>% makeGRangesFromDataFrame()`
- Endomorphisms, consistency, and restricted vocabulary really help users.

TENxGenomics (github only)

- E.g., single-cell RNA-seq, 30,000 genes by 1.3 million samples.
- On-disk representation in hdf5.
- Convenient in-memory 'matrix' abstraction for subsetting, etc.; easy input of manageable subset.
- `https://github.com/mtmorgan/TENxGenomics`

```
> basename(fl)
[1] "1M_neurons_filtered_gene_bc_matrices_h5.h5"
> (tenx <- TENxGenomics(fl))
class: TENxGenomics
h5path: ./1M_neurons_filtered_gene_bc_matrices_h5.h5
dim(): 27998 x 1306127
> tenk <- tenx[, sample(ncol(tenx), 10000)] ## fast
> m <- as.matrix(tenk)                      ## manageable
> se = SummarizedExperiment(list(tenx))     ## rich
```

Slack



Want to join? Look for an invitation on the bioc-devel mailing list next week.

Acknowledgments

Core team (current): Valerie Obenchain, Hervé Pagès, Marcel Ramos, Lori Shepherd, Nitesh Turaga, Daniel van Twisk.

Technical advisory board: Vincent Carey, Kasper Hansen, Wolfgang Huber, Robert Gentleman, Rafael Irizzary, Levi Waldron, Michael Lawrence, Sean Davis, Aedin Culhane

Scientific advisory board: Robert Gentleman (23andMe), Jan Vitek (Northeastern), Vincent Carey (Brigham & Women's), Wolfgang Huber (EBI), Rafael Irizzary (Dana Farber),

Research reported in this presentation was supported by the National Human Genome Research Institute and the National Cancer Institute of the National Institutes of Health under award numbers U41HG004059 and U24CA180996. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.