Bioc 2017: Where Software and Biology Connect

Martin Morgan

Roswell Park Cancer Institute
Buffalo, NY, USA
martin.morgan@roswellpark.org

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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
Sponsors
Today

Informal and flexible

- Want to do something different? Say so!

Schedule [https://goo.gl/8oRmsp](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 activities

Tomorrow: 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://bioconductor.org)
- [https://support.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*.


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?

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

## src: sqlite 3.19.3 [/home/mtmorgan/.cache/BiocFileCache/5b377bf41425_5b377bf41425]
## 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

```r
> 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),

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