The Bioconductor Project for Reproducible Analysis of High Throughput Genomic Data

Martin Morgan (mtmorgan@fredhutch.org)
Fred Hutchinson Cancer Research Center
Seattle, WA, USA

12 January 2015

Outline

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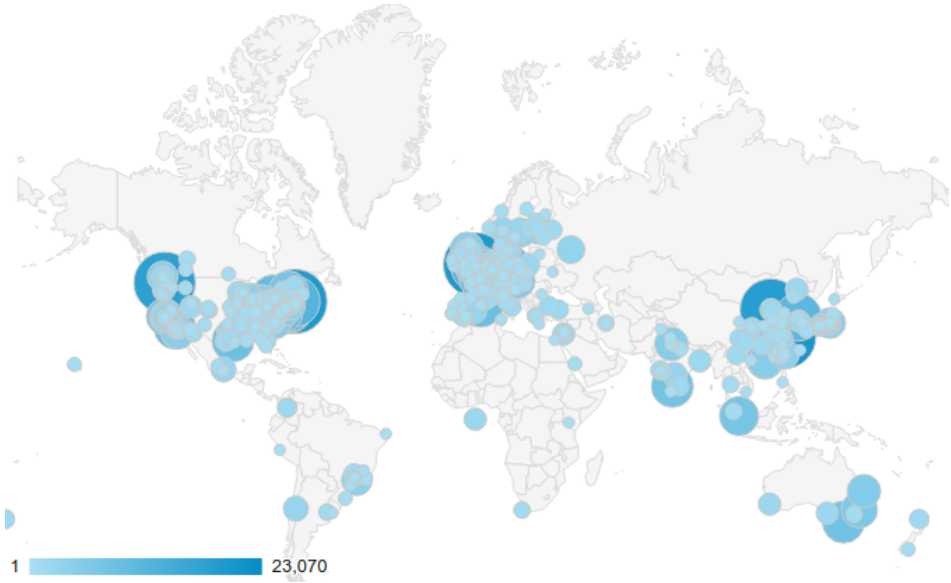
Project status (December, 2014)



2014 Web site visitors, by city

Users

- 320,000 unique IP address package downloads / year
- 1,300 support site contributors / year, 8,200 visitors / month
- 10,500 PubMed Central mentions of 'Bioconductor';
  $\approx$ 22,000 citations to *Bioconductor* packages
- At least 12 of 15 initial TCGA publications

Project status (December, 2014)

Packages & developers

- 935 release packages (vs. 750 last year)
- $>$ 900 bioc-devel subscribers
- 100's of maintainers in N. America, Europe, & world-wide.

Funding

- US NHGRI/NIH U41 (since 2005) – Bioconductor: An Open Computing Resource for Genomics (Morgan, Carey, Irizzary)
- US NSF BIGDATA – Scalable Statistical Computing for Emerging Omics Data Streams (Morgan, Carey, Huber, Taylor)
- US NCI U24: *Bioconductor* for Integrative Analysis for Cancer Genomics (Morgan, Carey, Hansen, Waldron)
- EC – coming soon?!

Recent highlights

Web site

- biocViews curation & use (e.g., docker images)
- Newsletters.
- Indexed course material, recent literature citations, videos (contributions welcome)!

Infrastructure

- `https://support.bioconductor.org`.
- Docker & Amazon machine instances (AMIs, e.g., *StarCluster*)
- *AnnotationHub*: file-based and other annotation resources.
- *BiocParallel*, *GenomicFiles*: processing files $\times$ ranges.
- *BiocStyle*, especially *rmarkdown*-flavored vignettes.
- `findOverlaps`: nested containment list implementation – 3-10 $\times$ faster, up to 1/4th memory use.
- `biocLite()` support for github repositories.

Recent highlights

Contributed pacakges

- !
- !
- !
- !
- !
- . . . !

Recent highlights: *AnnotationHub*

File-based resources, e.g., UCSC *liftOver* files

```
## hg19SNPs <- GRanges(...)
library(AnnotationHub)
hub <- AnnotationHub()
chain <- query(hub, 'hg19ToHg38')[[1]]
hg38SNPs <- liftOver(hg19SNPs, chain)
```

Annotation-style resources, e.g., grasp2

```
library(grasp2db) # Annotation package,
                  # 6 Gb AnnotationHub resource
d <- GRASP2()     # dplyr instance
hispanic <- tbl(d, "count") %>%
    filter(Population=="Hispanic")
semi_join(tbl(d, "variant"), hispanic)
```

Recent highlights: docker

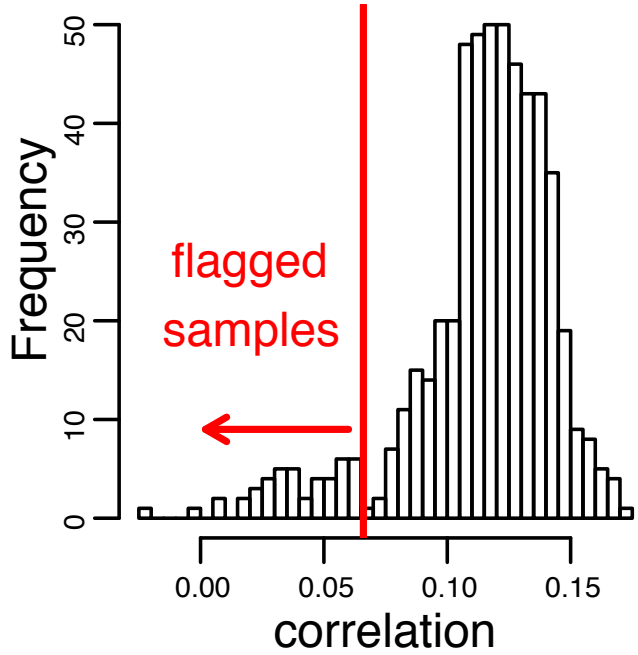
- http://bioconductor.org/help/docker/
- Reproducibility, ease of use, convenience

```
docker run --rm -ti --name
    devel bioconductor/devel_base R
```

Future directions

General

- Integrative analysis.
- 'Populations', e.g., single cells; tumors; many samples.
- Statistically informed actionable insights; visual and interactive.



TCGA ovarian expression / CN correlation; Levi Waldron

Specific

- Allow *SummarizedExperiment* `rowData()` without ranges.
- Update *Rsamtools* via *Rhtslib*
- `mapTo*`: DNA / Protein integration; individual genomes
- *BiocParallel* logging, ease-of-use.
- *methods* performance improvements

Why *Bioconductor*?

A *community* of users and developers.

- Extensive & interoperable
- Statistical (volume, technology, experimental design, population samples)
- Reproducible: long-term, multi-participant science
- Leading edge: embrace novel technologies and analysis
- Accessible: affordable, transparent, usable (e.g., vignettes & man pages)

Huber et al., Orchestrating high-throughput genomic analysis with *Bioconductor*. *Nature Methods*: soon!

Why *Bioconductor*?

More than a software archive.

- Build on relevant software, e.g.,
  - *GenomicRanges* for efficient interoperability; *ExpressionSet* / *SummarizedExperiment* for genetic / phenotypic integration...
  - I/O via *rtracklayer*, *Rsamtools*, *illuminaio*, ...
  - Resource access via *biomaRt*, *GEOquery*, ...
- Commit to long-term support
  - e.g., *affy* in use 10 years after introduction.
  - Comprehensive documentation coupled with traditional scientific publications
  - Engage users via support forum, foster productive collaborations
- Enable transitions
  - User to developer
  - Student to professional

Driving principle: analysis & comprehension of high-throughput genomic data

Future events

- Computational Statistics for Genome Biology (CSAMA), 15-19 June, Brixen / Bressanone, Italy
- *useR!*, 1-3 July, Aalborg, Denmark
- BioC 2015, 20 - 22 July, Seattle, WA USA

Acknowledgments

Core (Seattle): Sonali Arora, Marc Carlson, Nate Hayden, Valerie Obenchain, Hervé Pagès, Paul Shannon, Dan Tenenbaum.

Technical Advisory Board: Vincent Carey, Aedin Culhane, Sean Davis, Robert Gentleman, Kasper Hansen, Wolfgang Huber, Rafael Irizarry, Levi Waldron.

Scientific Advisory Board: Paul Flicek, Simon Tavaré, Simon Urbanek.