

Bioconductor Developer Day

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Orientation

- ▶ Campus map¹
- ▶ Arnold Building
- ▶ Developer Day²

¹<http://www.fhcrc.org/content/dam/public/contact-us/Visit-Us/campusmap.pdf>

²<http://bioconductor.org/developers/developer-day/>

Acknowledgements & Introductions

- ▶ Abby Stimmel
- ▶ *Bioconductor* team: Marc Carlson, Valerie Obenchain, Hervé Pagès, Paul Shannon, Dan Tenenbaum
- ▶ Technical advisory council: Vincent Carey, Wolfgang Huber, Robert Gentleman, Rafael Irizarry, Sean Davis, Kasper Hansen
- ▶ Scientific advisory board: Simon Tavaré, Vivian Bonazzi, Vincent Carey, Wolfgang Huber, Robert Gentleman, Rafael Irizarry, Paul Flicek, Simon Urbanek.
- ▶ NIH / NHGRI U41HG0004059
- ▶ ... and the *Bioconductor* community!

Core team highlights

BiocInstaller

- ▶ useDevel()
- ▶ biocValid()
- ▶ Encouraging updates

```
> R.version.string  
[1] "R version 2.15.3 Patched (2013-03-13 r62579)"  
> source("http://bioconductor.org/biocLite.R")  
Your Bioconductor is out-of-date, upgrade to version  
2.12 by following instructions at  
http://bioconductor.org/install.
```

BiocStyle

- ▶ \LaTeX (and other...) style for consistent, easy-to-use Sweave documents
- ▶ DESCRIPTION file – Suggests: BiocStyle
- ▶ Vignette.Rnw preamble:

```
<<style, eval=TRUE, echo=FALSE, results=tex>>=
BiocStyle::latex()
@
```
- ▶ Example in the package vignette³

³[http://bioconductor.org/packages/devel/bioc/vignettes/
BiocStyle/inst/doc/LatexStyle.pdf](http://bioconductor.org/packages/devel/bioc/vignettes/BiocStyle/inst/doc/LatexStyle.pdf)

BiocParallel

“Modified versions and novel implementation of functions for parallel evaluation, tailored to use with Bioconductor objects.”

```
> library(BiocParallel)  
> registered()  
> bplapply(1:8, function(i) Sys.sleep(1))  
> bpvec(1:32, sqrt, AGGREGATE=list)
```

- ▶ Params: Serial, Multicore, Snow, DoPar, (BatchJobs)
- ▶ register, bpschedule (e.g., recursive=FALSE), (bpstart, bpstop), bpvectorize
- ▶ Example benefit: bplapply subsets rather than coerces to list

Cloud-aided Computation

The AMI

- ▶ Pre-configured, easy to deploy & use

AnnotationHub

- ▶ Genome-scale resources
- ▶ Centralized, readily updated & available

Future scenarios

- ▶ Data proximity, e.g., Ensembl servers in same zone
- ▶ Light-weight computation, e.g.,
 - ▶ Overlap regions-of-interest with each ENCODE track
 - ▶ Re-dispatch *ensemblVEP* annotation tasks