The *Bioconductor* Project: Current Status

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Bioconductor

https://bioconductor.org
https://support.bioconductor.org

Analysis and comprehension of high-throughput genomic data.

- Started 2002
- 1296 *R* packages – developed by 'us' and user-contributed.

Well-used and respected.

- 43k unique IP downloads / month.
- 17,000 PubMedCentral citations.

State of the project

- Packages
- Users
- Web & support sites
- Training & meetings
- Release & devel builders
- Funding
- Governance: (annual) Scientific Advisory Board; (monthly) Technical Advisory Board

Recent developments

- New package reviews
- *ExperimentHub* and *AnnotationHub*
- Large data representation: *HDF5Array*
- (Sneak peak) *Organism.dplyr*

HDF5Array

```
library(HDF5Array)   # available in release & devel
n = 10000; m = 1000; # very large size
h5 = HDF5Array(matrix(rnorm(n * m), n))
h5 + h5              # 'delayed' computation
library(SummarizedExperiment)
SummarizedExperiment(h5) # rich context
```

Sneak peak: *Organism.dplyr*

```
> library(Organism.dplyr) # not yet publicly available
> src = src_ucsc("Homo sapiens")  # any org.* + TxDb.*
using org.Hs.eg.db, TxDb.Hsapiens.UCSC.hg38.knownGene
> src
src:  sqlite 3.8.6 [/home/mtmorgan/organism_dplry.sqlite]
tbls: id, id_accession, id_go, id_go_all, id_omim_pm,
  id_protein, id_transcript, ranges_cds, ranges_exon,
  ranges_gene, ranges_tx
> tbl(src, 'id') %>% filter(symbol == 'BRCA1') %>%
    select(ensembl, symbol, genename)
> exons(src, filter=list(symobl='BRCA1'))      # GRanges
> exons_tbl(src, filter=list(symbol='BRCA1'))  # tibble
```

Programming best practices

- Reuse & interoperability
- Correct, robust, efficient (vectorized) code; *BiocParallel*
- Documentation: classic or *roxygen2*
- Testing: *RUnit* or *testthat*
- Classic, tidy, and semantically rich data

Correct, robust, efficient...

```
f = function(n) {
  x = integer(0)
  for (i in 1:n)
      x = c(x, i)
  x
}
microbenchmark(f(1000),
  f(10000), f(100000))

f1 = function(n) {
  x = integer(n)
  for (i in 1:n)
    x[i] = i
  x
}
```

```
f2 = function(n)
  vapply(1:n, c, integer(1))

f3 = function(n)
  seq_len(n)

## correct
identical(f(100), f3(100))

## robust!
f(0); f3(0)

## efficient
system.time(f3(1e9)
```

Classic, tidy, rich: RNA-seq count data

Classic

- Sample x (phenotype + expression) Feature `data.frame`

Tidy

- 'Melt' expression values to two long columns, replicated phenotype columns. End result: long data frame.

Rich, e.g., `SummarizedExperiment`

- Phenotype and expression data manipulated in a coordinated fashion but stored separately.

Classic, tidy, rich: RNA-seq count data

```
df0 <- as.data.frame(list(mean=colMeans(classic[, -(1:22)])))
df1 <- tidy %>% group_by(probeset) %>%
    summarize(mean=mean(exprs))
df2 <- as.data.frame(list(mean=rowMeans(assay(rich))))
ggplot(df1, aes(mean)) + geom_density()
```

Classic, tidy, rich: RNA-seq count data

Vocabulary

- Classic: extensive
- Tidy: restricted endomorphisms
- Rich: extensive, meaningful

Constraints (e.g., probes & samples)

- Tidy: implicit
- Classic, Rich: explicit

Flexibility

- Classic, tidy: general-purpose
- Rich: specialized

Programming contract

- Classic, tidy: limited
- Rich: strict

Lessons learned / best practices

- Considerable value in semantically rich structures
- Current implementations trade-off user and developer convenience
- Endomorphism, simple vocabulary, consistent paradigm aid use

Future challenges

- Git
- Cloud. Possible visions:
  - As now, but 'in the cloud'
  - Integrated with 'third party' compute efforts, e.g., NCI, NIH in the United States

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