Good software: simple, tidy, rich

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Statistical analysis and comprehension of high-throughput genomic data.

Open – public version control

Reproducible research – vignettes, ‘experiment data’ packages, release / devel branches, . . .

Interoperable – package re-use, data structures, . . .

Usable – documentation, support, . . .
colData(se)
se[, se$dex == "trt"]
rowRanges(se)
rowData(se)
subsetByOverlaps(se, roi)

assays(se)
assay(se, n = 2)
assay(subsetByOverlaps(se, roi))
assay(se[, se$dex == "trt"])

metadata(se)
metadata(se)$modelFormula

Samples (Columns)

Features (Rows)

Samples
Simple, tidy, rich: RNA-seq count data

Vocabulary
- Simple: extensive
- Tidy: restricted endomorphisms
- Rich: extensive, meaningful

Constraints (e.g., probes & samples)
- Tidy: implicit
- Simple, Rich: explicit

Flexibility
- Simple, tidy: general-purpose
- Rich: specialized

Programming contract
- Simple, 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

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Acknowledgments
Pretty big data

- 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
```

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Acknowledgments
Opportunities

Programmer analysts

- https://roswellpark.org/careers
- Programmer / Analyst – R software development 4924
- Senior Programmer Analyst – cloud / new-age sys. admin 4932

Bioconductor annual conference

- Boston, July 26 (D-day) – 28.
- https://bioconductor.org/BioC2017
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