Introduction to *R* and *Bioconductor*

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Vectors – logical, integer, numeric, character, ...
  - list() – contains other vectors (recursive)
  - factor(), NA – statistical concepts
  - Can be named – c(Germany=1, Argentina=0)

matrix(), array() – a vector with a ‘dim’ attribute.
data.frame() – like spreadsheets; list of equal length vectors.
  - Homogenous types within a column, heterogenous types across columns.
  - An example of an R class.

Other classes – more complicated arrangement of vectors.
  - Examples: the value returned by lm(); the DNAStringSet class used to hold DNA sequences.
  - plain, ‘accessor’, ‘generic’, and ‘method’ functions

Packages – base, recommended, contributed.
> 1 + 2 # calculator
[1] 3

> x <- rnorm(1000) # vectors, statistical
> y <- x + rnorm(1000, sd=.8) # vectorized calculation
> df <- data.frame(x=x, y=y) # object construction
> fit <- lm(y ~ x, df) # linear model, formula
> class(fit) # discovery

[1] "lm"
> plot(y ~ x, df, cex.lab=2)
> abline(fit, col="red", lwd=2)

> library(ggplot2)
> ggplot(df, aes(x, y)) +
+ geom_point() +
+ stat_smooth(method="lm")
Functions – built-in (e.g., \texttt{rnorm()}); user-defined

Subsetting – logical, numeric, character; \texttt{df[df$x > 0,]};

Iteration – over vector elements, \texttt{lapply()}, \texttt{mapply()}, \texttt{apply()}, \ldots; e.g., \texttt{lapply(df, mean)}
R: help!

▶ \texttt{?data.frame}
▶ \texttt{methods(lm), methods(class=class(fit))}
▶ \texttt{"plot"}
▶ \texttt{help(package="Biostats")}
▶ \texttt{vignette(package="GenomicRanges")}
▶ StackOverflow; R-help mailing list

“Hey, can you help me with this? I tried…”
Bioconductor

Analysis & comprehension of high-throughput genomic data

- > 12 years old; 1024 packages; widely used
- Sequencing (RNAseq, ChIPseq, variants, copy number, ...), microarrays, flow cytometry, proteomics, ...
- http://bioconductor.org,
  https://support.bioconductor.org

Themes

- Interoperable – classes to work with genome-scale data, shared (where possible!) across packages
- Usable – package vignettes, man pages, examples, ...
- Reproducible – ‘release’ and ‘devel’ versions, updated every 6 months
Data: aligned reads, called peaks, SNP locations, CNVs, …
Annotation: gene models, variants, regulatory regions, …
findOverlaps(), nearest(), and many other useful range-based operations.
Bioconductor: **SummarizedExperiment** motivation

Cisplatin-resistant non-small-cell lung cancer gene sets


Baggerly & Coombes 2009 Ann Appl Stat 3: 1309-1334

Coordinated, programmatic manipulation of feature, sample, and assay data
Bioconductor: *SummarizedExperiment*

Regions of interest × samples
- `assay()` – matrix, e.g., counts of reads overlapping regions of interest.
- `rowData()` – regions of interest as GRanges or GRangesList
- `colData()` – DataFrame describing samples.

```r
> assay(se)[, se$Treatment == "Control"]  # Control counts
```
**Bioconductor**: a fun demo of *GRanges* interoperability

*GenomicFeatures* And ‘annotation’ packages to represent gene models as *GRanges*.

*GenomicAlignments* To input aligned reads as *GRanges*.

*Gviz* For visualization.

*shiny* For interactivity.
**Bioconductor: Resources**

http://bioconductor.org

- Packages – biocViews, landing pages (e.g., *AnnotationHub*)
- Course & conference material; work flows; publications
- Developer resources

https://support.bioconductor.org

- Question & answer forum for users; usually fast, expert, friendly responses
- Contributed tutorials, news

Citations

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