Introduction to \textit{R} and \textit{Bioconductor}

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> 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"

> head(methods(class="lm"), 3)
[1] "add1.lm"  "alias.lm"  "anova.lm"
R: Statistical Computing Environment

> 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")
R: Statistical Computing Environment

- Vectors – logical, integer, numeric, character, ...
  - `list()` – contains other vectors (recursive)
  - `factor()`, NA – statistical concepts
  - Can be named – c(Portugal=1, France=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.
  - function, ‘generic’, and ‘method’

- Packages – base, recommended, contributed.
R: programming concepts

- Functions – built-in (e.g., `rnorm()`); user-defined
- Subsetting – logical, numeric, character; `df[df$x > 0,]`
- Iteration – over vector elements, `lapply()`, `mapply()`, `apply()`, ...; e.g., `lapply(df, mean)`
R: help!

- ?data.frame, ?"plot<tab>"
- methods(class=class(fit)), methods(anova)
- help(package="Biostrings")
- 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

- 15 years old; 1211 packages; widely used
- Sequencing (RNAseq, ChIPseq, variants, copy number, ...), microarrays, flow cytometry, proteomics, ...
- [http://bioconductor.org](http://bioconductor.org), [https://support.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
Bioconductor: GenomicRanges

```r
> gr = exons(TxDb.Hsapiens.UCSC.hg19.knownGene); gr
GRanges with 289969 ranges and 1 metadata column:

<table>
<thead>
<tr>
<th>seqnames</th>
<th>ranges</th>
<th>strand</th>
<th>exon_id</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;Rle&gt;</td>
<td>&lt;IRanges&gt; &lt;Rle&gt;</td>
<td></td>
<td>&lt;integer&gt;</td>
</tr>
<tr>
<td>[1]</td>
<td>chr1 [11874, 12227]</td>
<td>+</td>
<td>1</td>
</tr>
<tr>
<td>[2]</td>
<td>chr1 [12595, 12721]</td>
<td>+</td>
<td>2</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>[289967]</td>
<td>chrY [59358329, 59359508]</td>
<td>-</td>
<td>277748</td>
</tr>
<tr>
<td>[289968]</td>
<td>chrY [59360007, 59360115]</td>
<td>-</td>
<td>277749</td>
</tr>
<tr>
<td>[289969]</td>
<td>chrY [59360501, 59360854]</td>
<td>-</td>
<td>277750</td>
</tr>
</tbody>
</table>

seqinfo: 93 sequences (1 circular) from hg19 genome
```

- 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

Hsu et al. 2007 J Clin Oncol 25: 4350-4357 (retracted)

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.

> se[, se$Treatment == "Control"] # Control samples only
**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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