

BRM5012 R practical: Bioconductor

Flavours of R

Base R

What comes standard with R.

Tidyverse

```
install.packages("tidyverse")
```

Bioconductor

```
# Setup
source("https://bioconductor.org/biocLite.R")
biocLite()
# Install a specific package
biocLite("limma")
```

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R has 4 decades of history.

Tidyverse is a set of modern packages.

Tidyverse is easy to pick up, has made R much more widely accessible. Key concepts are tidy data and pipelines.

Bioconductor is a separate package repository from CRAN (the usual package repository).

Bioconductor packages are for dealing with biological data efficiently.

Bioconductor is not tidy. Expect to have to work a little harder to make use of these.

What Bioconductor is for

Differential expression analysis from microarray or RNA-seq

- ▶ limma, edgeR, DESeq2, ...
- ▶ Further packages to normalize, impute, batch correct, check quality, ...

Visualization

- ▶ ComplexHeatmap, Gviz, ggbio, ...

Peaks, regions, motifs in genome (eg ChIP-seq)

- ▶ GenomicRanges, GenomicFeatures, ...

Single-cell sequencing

Statistical methods for $p \gg n$ data

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Too many uses to count, ask a different person and get a different list.

50% of bioinformatics is read this file format, wrangle, write other file format.

Often used in combination with command-line software (eg read aligner).

More types

Up to now we have been using vectors and data frames (specifically Tidyverse “tibbles”).

To use Bioconductor, several further types are important.

- ▶ `matrix`
- ▶ `DNASTring`, `DNASTringSet`, `AAString`
- ▶ `GRanges`
- ▶ Others: `SeqInfo`, `TxDb`, `EnsDb`, `OrgDb`, `SummarizedExperiment`,
...

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`matrix` is another tabular data type from base R. Conceptually, each cell is an observation, rather than each row as in a tidy data frame.

The rest are Bioconductor types. Note the use of CamelCase, this is typical in Bioconductor. Tidyverse separates words with underscores, and base R uses dots!

Bioconductor has evolved over time to cope with more complex data.

Getting reference data

Analysis usually occurs in the context of:

- ▶ a genome assembly: DNA sequences of chromosomes
- ▶ gene annotations: ranges of positions in chromosome and strand

More on this later in the week!

In Bioconductor:

- ▶ AnnotationHub package gives access to reference data from various sources
 - ▶ access specific versions, good for reproducibility
- ▶ rtracklayer package to load files

Others

- ▶ biomaRt to access BioMart servers
- ▶ Data packages

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Documentation

Most packages have “vignettes” explaining normal usage.

Information about types available with, eg:

```
? "GRanges-class"
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Aim for this session is to cover fundamentals of Bioconductor, so you can look up the package you need for your particular task and understand how to use it.