# Introduction to *R* and *Bioconductor*

Martin Morgan[1]

June 23 – 28, 2013

[1] mtmorgan@fhcrc.org

# Overview

*R*

1. Vectors, data frames, arrays
2. Statistical concepts
3. Functions
4. Packages
5. From script to collaboration
6. HELP!

*Bioconductor*

1. A short history
2. Sequence analysis
3. Classes, generics and methods
4. HELP!

# Vectors, data frames, arrays

```
> x <- c(1, 2, 3, 4, 5)
> x
[1] 1 2 3 4 5
> log(x)
[1] 0.0000000 0.6931472 1.0986123 1.3862944 1.6094379
> x[c(3, 2)]
[1] 3 2
> x[3:2]
[1] 3 2
> x[c(TRUE, FALSE)]
[1] 1 3 5
```

# Vectors, data frames, arrays

```
> df <- data.frame(
+     age = c(17, 23, 32, 37),
+     sex = c("Male", "Female", "Female", "Male"))
> df
  age    sex
1  17   Male
2  23 Female
3  32 Female
4  37   Male
> df[df$age < 30 & df$sex == "Male", ]
  age  sex
1  17 Male
```

# Vectors, data frames, arrays

```
> m <- matrix(1:8, 2, 4)
> m
     [,1] [,2] [,3] [,4]
[1,]    1    3    5    7
[2,]    2    4    6    8
> log(m)
          [,1]     [,2]     [,3]     [,4]
[1,] 0.0000000 1.098612 1.609438 1.945910
[2,] 0.6931472 1.386294 1.791759 2.079442
> rowSums(m)
[1] 16 20
```

# Statistical concepts

```
> df$sex

[1] Male   Female Female Male
Levels: Female Male

> df$height <- c(180, 172, NA, 177)
> df

  age    sex height
1  17   Male    180
2  23 Female    172
3  32 Female     NA
4  37   Male    177
```

# Functions

`dir`, `read.table` (and friends), `scan` List files, input data.

`c`, `factor`, `data.frame`, `matrix` Create objects.

`summary`, `table`, `xtabs` Summarize, cross-tabulate variables.

`t.test`, `aov`, `lm`, `anova`, `chisq.test` Compare groups.

`dist`, `hclust` Cluster data.

`plot` Visualize data.

`lapply`, `sapply`, `mapply`, `aggregate` Apply a function to each element of a list or vector.

`ls`, `str` List objects and their structure.

`library`, `search` Attach to or describe the library search path.

# Packages

| | |
|---|---|
| Base | *base*, *stats*, *graphics*, ... |
| Recommended | *lattice*, ... |
| Contributed | *data.table*, *XML*, *biglm*, ... |

- Install a contributed package

```
> source("http://bioconductor.org/biocLite.R")
> biocLite("data.table")
```

- Use during a session

```
> library(lattice)
```

# From script to collaboration

Increasingly complicated tasks

1. Commands entered at the prompt
2. Scripts and functions saved in `.R` files
3. `.R` files and documentation ordered in packages

```
% dir MyPackage
data/ NAMESPACE DESCRIPTION man/ R/ vignettes/
```

4. Packages shared with colleagues

Net result: sophisticated, highly reproducible research

# HELP!

```
> help.start()
> ?t.test
> vignette("datatable-faq")
```

- Books and training resources
- *R* web site and mailing list[2]
- StackOverflow[3]

[2] http://r-project.org
[3] http://stackoverflow.com/questions/tagged/r

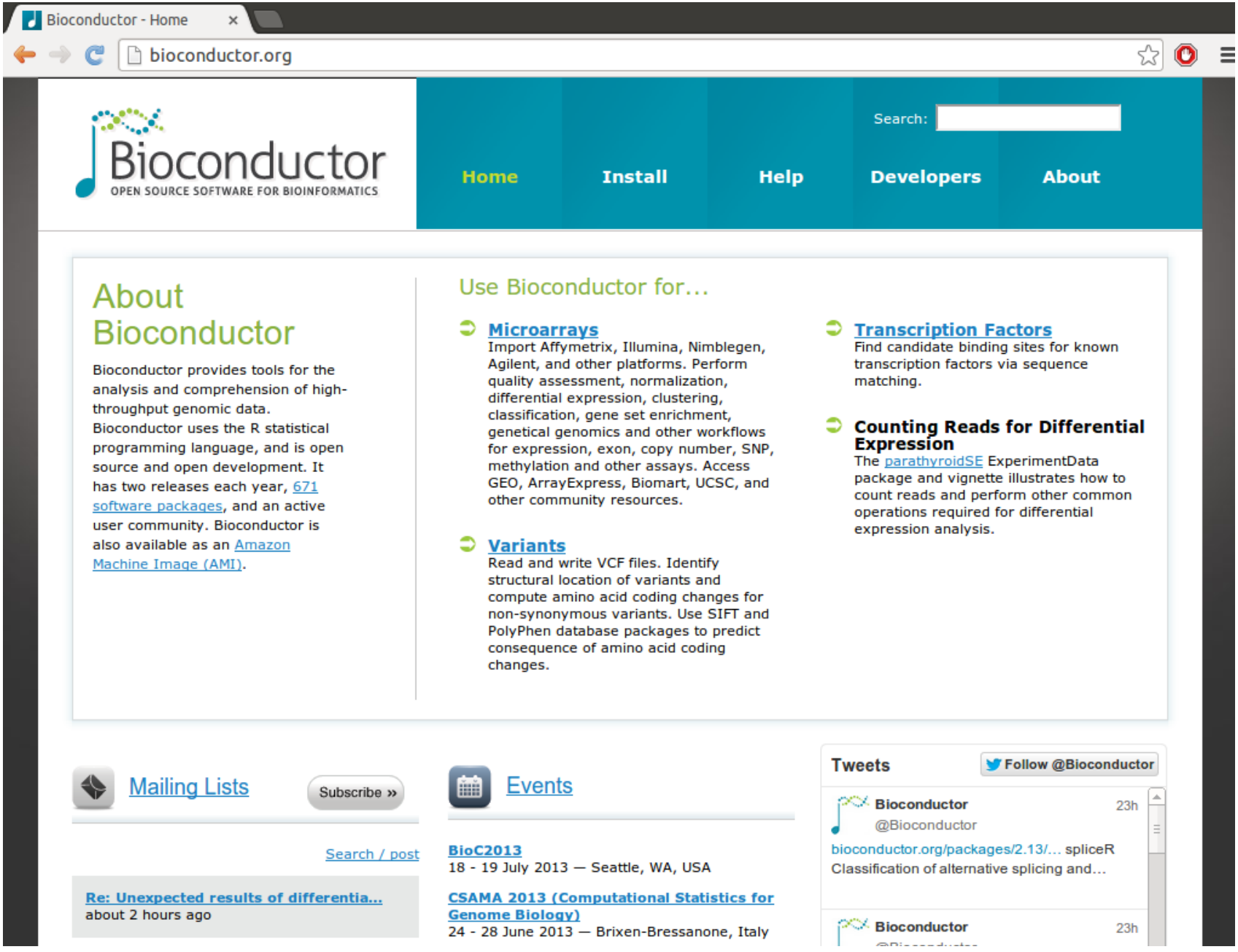
# *Bioconductor*: A short history

Then

- Founded 2001
- Analysis and *comprehension* of high throughput genomic data
- Initial focus: microarrays
- Reproducibility, statistical analysis, computation

Now

- $>$ 670 software packages
- World-wide contributions
- Sequence analysis, microarrays, systems biology, flow cytometry, ...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Variants
Read and write VCF files. Identify structural location of variants and compute amino acid coding changes for non-synonymous variants. Use SIFT and PolyPhen database packages to predict consequence of amino acid coding changes.
Transcription Factors
Find candidate binding sites for known transcription factors via sequence matching.
Counting Reads for Differential Expression
The parathyroidSE ExperimentData package and vignette illustrates how to count reads and perform other common operations required for differential expression analysis.
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bioconductor.org/packages/2.13/... spliceR
Classification of alternative splicing and...
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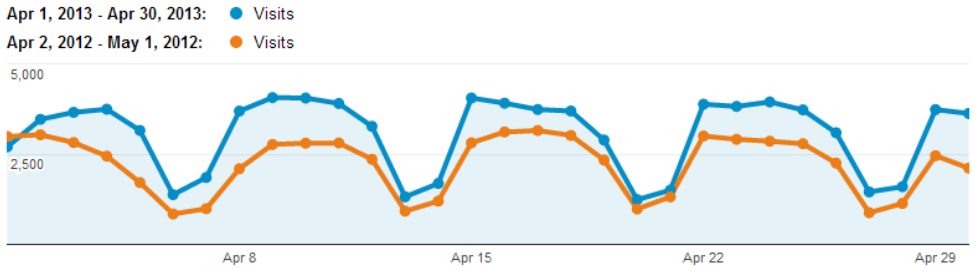
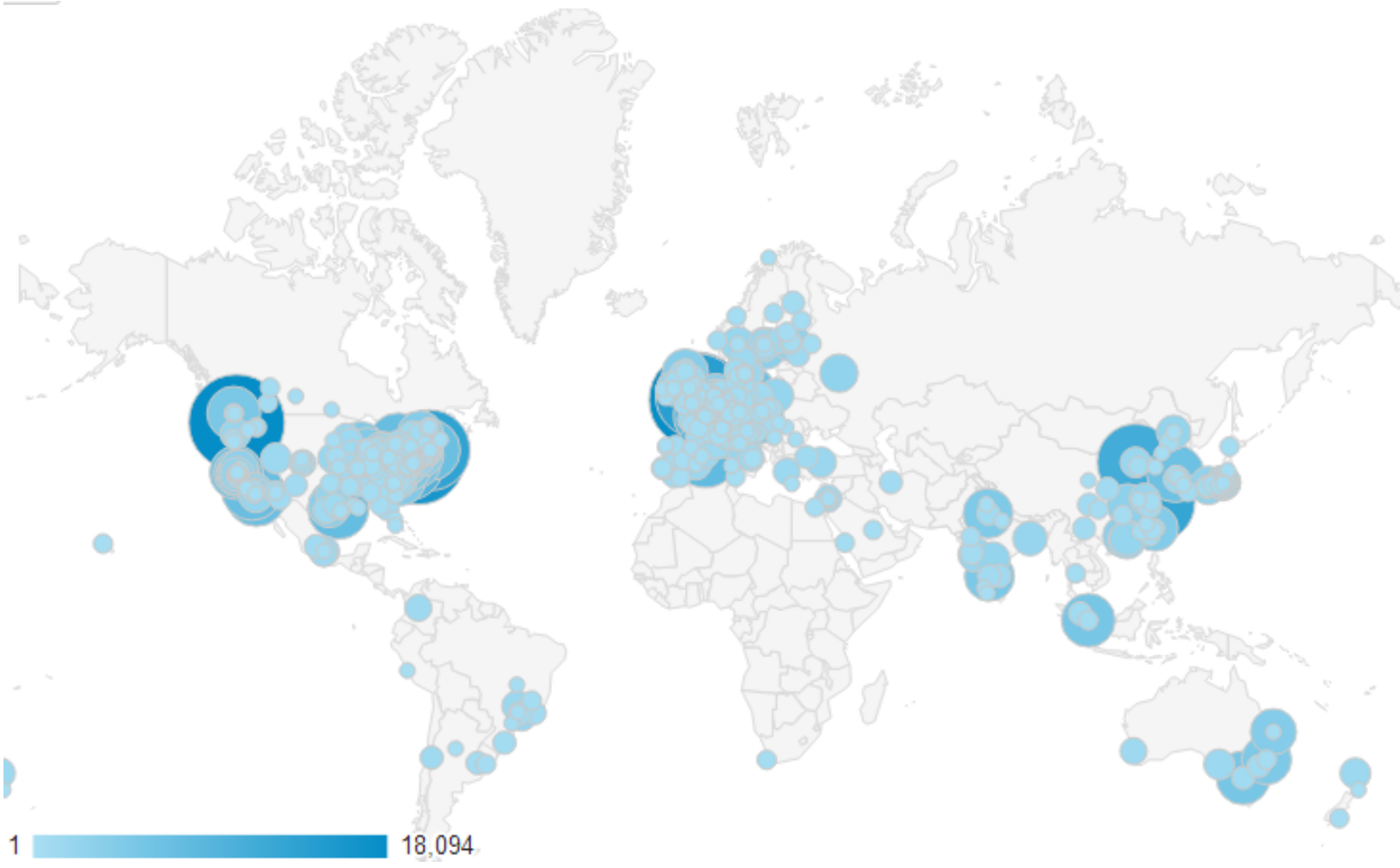
# *Bioconductor*: A short history



# Sequence Analysis (many packages!)

| | |
|---|---|
| I/O | *ShortRead* (FASTQ), *Rsamtools* (BAM), *rtracklayer* (GFF, WIG, BED), *VariantAnnotation* (VCF), ... |
| Representation | *IRanges*, *GenomicRanges*, *GenomicFeatures*, *Biostrings*, *BSgenome*, ... |
| Annotation | *GenomicFeatures*, *biomaRt*, *AnnotationHub*, .... |
| Alignment | *gmapR*, *Rsubread*, *Biostrings*, ... |
| Visualization | *ggbio*, *Gviz*, ... |
| RNA-seq | *DESeq*, *edgeR*, *DEXSeq*, *cummeRbund*, ... |
| ChIP-seq | *DiffBind*, *ChIPpeakAnno*, ... |
| Variants | *VariantAnnotation*, *VariantTools*, ... |
| Motifs | *MotifDb*, *seqLogo*, ... |
| Work flows | *QuasR*, ... |
| ... | ... |

# Classes, generics and methods

```
> library(ShortRead)
> fq <-
+   readFastq("~/BigData/fastq/SRR031724_1_subset.fastq")
> fq            # 'S4' class

class: ShortReadQ
length: 1000000 reads; width: 37 cycles

> sread(fq)   # 'generic' and 'method'; another S4 class

  A DNAStringSet instance of length 1000000
           width seq
       [1]    37 GTTTTGTCCAAGTTCTGGTAGCTGAATCCTGGGGCGC
       [2]    37 GTTGTCGCATTCCTTACTCTCATTCGGGAATTCTGTT
       [3]    37 GAATTTTTTGAGAGCGAAATGATAGCCGATGCCCTGA
       ...   ... ...
 [1000000]    37 GAAGTCGGTACCCTCGAACAGAGAGTCGATCTCAATG
```

# HELP!

- Use tab completion to find help on *generics* and *methods*

```
> ?sread
> ?"reverseComplement<tab>"  # tab key for completions!
> ?"reverseComplement,DNAStringSet-method"
```

- Discover available functions and their definition.

```
> showMethods("reverseComplement")
> showMethods(class="DNAStringSet", where=search())
> selectMethod("reverseComplement", "DNAStringSet")
```

# Acknowledgements

*Bioconductor* core

- Vince Carey
- Wolfgang Huber
- Robert Gentleman
- Rafael Irizzary
- Sean Davis
- Kasper Hansen

*Bioconductor* team

- Marc Carlson (annotation)
- Valerie Obenchain (variants, ranges)
- Hervé Pagès (ranges, strings)
- Paul Shannon (systems biology)
- Dan Tenenbaum (web, build)

And the *Bioconductor* community!