

# Brief Intro to R for Flow Packages Users

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Introduction

Atomic Vectors

Matrix

data.frame

Lists

Functions

The `flowFrame` and `flowSet` Classes

# Outline

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# Packages

## Repository

R distributes software via *packages*.

- ▶ *CRAN* – primarily for statistics research and data analysis.
- ▶ *Bioconductor* – focus on analysis of high-throughput biological data.

## Starting R

Finding packages; installing packages; and attaching packages.

```
> ## attaching packages  
> library(flowCore)
```

# Installing Packages

## Install Bioconductor packages (and their dependencies)

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

## Install from the flowTrack package

```
> pkg <- "myDir/flowTrack_1.0.0.tar.gz"  
> install.packages(pkg, repos=NULL, type="source")
```

# Getting Help in R

- ▶ `help.start` and HTML help button in the Windows GUI
- ▶ `help` and `?`: `help('data.frame')`
- ▶ `help.search`, `apropos`
- ▶ `browseVignettes`
- ▶ `RSiteSearch`
- ▶ R Mailing lists

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## Atomic Vectors

Vector: one-dimensional array of items of the same type.

```
> # numeric  
> L <- c(1.2, 4.3, 2.3, 4)  
> W <- c(13.8, 22.4, 18, 18.9)  
> # most of functions are vectorized  
> length(L)
```

```
[1] 4
```

```
> area <- L * W  
> area
```

```
[1] 16.56 96.32 41.40 75.60
```

Other basic data types:

```
> s <- "a string" # character  
> t <- TRUE # logical  
> i <- 1L # integer  
> i <- 1+1i # complex
```



# Functions for Creating Vectors

## Functions

- ▶ `c` - concatenate
- ▶ `:` - integer sequences
- ▶ `rep` - repetitive patterns

```
> 1:10
```

```
[1] 1 2 3 4 5 6 7 8 9 10
```

```
> rep(1:2, 3)
```

```
[1] 1 2 1 2 1 2
```

## Exercise

1. Read the help page for `seq`
2. Use `seq` to generate a sequence of even integers between one to ten.

# Subsetting Vectors

## Naming

```
> ## name the elements of a vector
> v <- c(a=1.1, b=2, c=100, d=50, e=60)
> v
```

a	b	c	d	e
1.1	2.0	100.0	50.0	60.0

## Subsetting with positive indices

```
> v[c(1,3,4)]
```

a	c	d
1.1	100.0	50.0

## Subsetting with negative indices

```
> v[-c(1:3)] # exclude elements
```

d e

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# Matrix

`matrix` - two-dimensional vector, all elements share a common type.

```
> x <- matrix(1:25, ncol=5, dimnames=list(letters[1:5],  
+                                         LETTERS[1:5]))
```

```
> x
```

	A	B	C	D	E
a	1	6	11	16	21
b	2	7	12	17	22
c	3	8	13	18	23
d	4	9	14	19	24
e	5	10	15	20	25

```
> x[, 2]
```

a	b	c	d	e
6	7	8	9	10

# Matrix

## Exercise

1. Remove the second row and the fourth column from  $x$
2. Subset  $x$  to keep the 'D' column.

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# data.frame

- ▶ A special R structure.
- ▶ Analogous to a table where each row represents a sample and each column an attribute of a sample.

## data.frame

```
> df <- data.frame(type=c("case", "case",  
+                       "control", "control"), time=rexp(4))
```

```
> df
```

	type	time
1	case	0.77739394
2	case	1.95270944
3	control	0.91402175
4	control	0.02171282

```
> df$time
```

```
[1] 0.77739394 1.95270944 0.91402175  
[4] 0.02171282
```

```
> names(df)
```

```
[1] "type" "time"
```



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## Lists

*Recursive* data structure – a list can contain other lists and other types of data structures.

```
> lst <- list(a=1:4, b=c("X", "Y"),  
+           uspaper=list(length=11, width=8.5))
```

```
> lst
```

```
$a
```

```
[1] 1 2 3 4
```

```
$b
```

```
[1] "X" "Y"
```

```
$uspaper
```

```
$uspaper$length
```

```
[1] 11
```

```
$uspaper$width
```

```
[1] 8.5
```

## Subsetting Lists

- ▶ `[[` – extracting a single element from a list

```
> lst[[1]]
```

```
[1] 1 2 3 4
```

- ▶ `[` – extracting a sub-list of the list

```
> lst[1]
```

```
$a
```

```
[1] 1 2 3 4
```

- ▶ `$` – accessing list elements by name.

```
> lst[["b"]]
```

```
[1] "X" "Y"
```

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# Functions

```
> say <- function(name, greeting="hello")
+ {
+   paste(greeting, name)
+ }
> say("world")

[1] "hello world"
```

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# The flowFrame and flowSet Classes

- ▶ `flowFrame` - a class representing the data contained in a FCS file.
  1. raw measurement
  2. keywords in the FCS files
  3. annotation for parameters (stains, sample names, range)
- ▶ `flowSet` - a collection of `flowFrame`.

## The flowFrame and flowSet Classes

```
> library(flowCore)
> data(GvHD)
> class(GvHD)
[1] "flowSet"
attr(,"package")
[1] "flowCore"
> GvHD
```

A flowSet with 35 experiments.

```
An object of class "AnnotatedDataFrame"
 rowNames: s5a01, s5a02, ..., s10a07 (35 total)
 varLabels and varMetadata description:
  Patient: Patient code
  Visit: Visit number
  ...: ...
 name: NA
 (5 total)
```



# flowFrame

## Subsetting

```
> f[, "FSC-H"]
```

```
flowFrame object 's5a01'
```

```
with 3420 cells and 1 observables:
```

	name	desc	range	minRange
\$P1	FSC-H	FSC-Height	1024	0

	maxRange
\$P1	1023

```
119 keywords are stored in the 'description' slot
```

## Extracting raw data

```
> head(exprs(f))
```

## Some Methods for `flowFrame`

- ▶ `exprs`
- ▶ `colnames`, `featureNames` - names
- ▶ `keyword`, `identifier` - FCS keywords  
> `keyword(f, "FILENAME")`  
`$FILENAME`  
`[1] "s5a01"`
- ▶ `parameters` - parameter annotation
- ▶ `range` - dynamic range
- ▶ `plot`, `xyplot` - visualization (`flowViz`)
- ▶ `spillover` - spillover matrix
- ▶ `transform`, `filter`, `Subset` and etc. - actions

## Some Methods for `flowFrame`

### `xyplot`

```
> library(flowViz)
> xyplot(`FSC-H` ~ `SSC-H`, f)
```

- ▶ accessing `flowViz::xyplot`.
- ▶ formula: ``FSC-H` ~ `SSC-H``. Variables `FSC-H` (Y axis of the plot) and `SSC-H` (X axis of the plot) are the primary variables; separated `~`.
- ▶ data: a `flowFrame`.

# Some Methods for `flowSet`

## Working with `flowSet`

- ▶ `[`, `[[`, `$` - subsetting
- ▶ `sampleNames`, `colnames` - names
- ▶ `phenoData`, `pData` - metadata
- ▶ `fsApply` - apply family, `flowSet`-specific iterator

## Actions items

compensation, transformation, normalization, filtering and gating

# Some Methods for `flowSet`

## Examples

```
> head(pData(phenoData(GvHD)))
```

	Patient	Visit	Days	Grade	name
s5a01	5	1	-6	3	s5a01
s5a02	5	2	0	3	s5a02
s5a03	5	3	6	3	s5a03
s5a04	5	4	12	3	s5a04
s5a05	5	5	19	3	s5a05
s5a06	5	6	26	3	s5a06

```
> ## loop over a flowset to get the range for the
```

```
> ## first three flowFrames
```

```
> fsApply(GvHD[1:3], range)
```

## Selected Reference

- ▶ *Software for Data Analysis: Programming with R* by John Chambers.
- ▶ *R Programming for Bioinformatics* by Robert Gentleman.
- ▶ *Multivariate Data Visualization with R* by Deepayan Sarker.