A short R refresher

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Genetic data analysis with R
PR∼Statistics, Millport Field Station
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Installing R

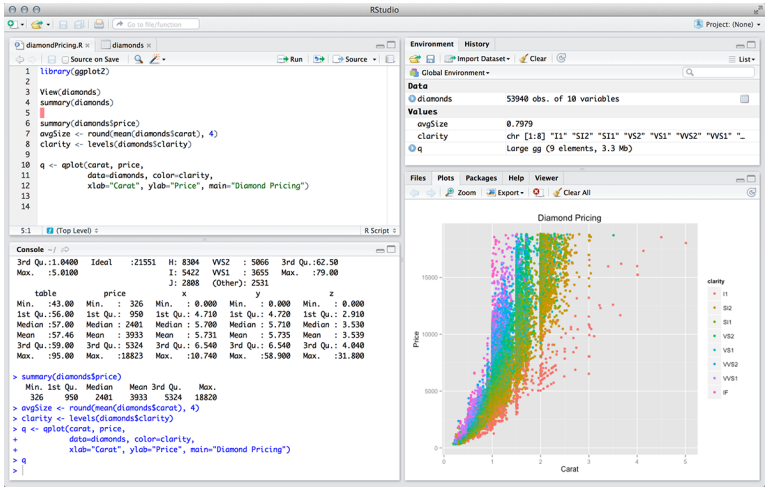
Get latest version from: `https://www.r-project.org/`

We are using 3.3.1. To check your version:

```
> R.version.string

[1] "R version 3.3.1 (2016-06-21)"
```

Using R



Editor / GUI:

- Rstudio: `https://www.rstudio.com/`
- Emacs: `http://www.gnu.org/software/emacs/`
- Tinn-R: `https://sourceforge.net/projects/tinn-r/`
- ...

Installing development versions of packages

1. on Window$, install *Rtools*: `https://cran.r-project.org/bin/windows/Rtools/`
2. install the package *devtools*
3. install packages using `install_github`

For instance:

```
> devtools::install_github("thibautjombart/adegenet")
```

will install the current devel version of *adegenet*

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will install the current devel version of *adegenet*

When you know the name of the beast

What does `t.test` do? How does it work?

```
> ?t.test
```

```
t.test                  package:stats                  R Documentation

Student's t-Test

Description:

     Performs one and two sample t-tests on vectors of data.

Usage:

     t.test(x, ...)

     ## Default S3 method:
     t.test(x, y = NULL,
            alternative = c("two.sided", "less", "greater"),
...
```

When the beast is anonymous

You do not know the function's name, only some keywords; for instance:

```
> ??"Hardy Weinberg"
```

Package	Topic	Title
adegenet	HWE.test.genind	Hardy-Weinberg Equilibrium test for multilocus data
pegas	hw.test	Test of Hardy-Weinberg Equilibrium

```
> help.search("Hardy Weinberg")
```

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Other searching options

- `RSiteSearch()`: looks through manuals and ML archives
- `example()`: runs the example in the manual page (unless `dontrun`'ed)
- `apropos()`: when part of the name is known

```
> apropos("hw")

[1] "HWE.test.genind" "hw.test"
```

What does the beast eat?

What arguments does it accept? How do I specify them?

To list the arguments of a function:

```
> library(pegas)
> args(hw.test)

function (x, B = 1000, ...)
NULL
```

But even better (!):

```
> ?hw.test
```

In case of trouble

1. read the documentation
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If this is not enough, ask someone.

Where can you ask questions?

- general questions: R-help
  `http://stat.ethz.ch/mailman/listinfo/r-help`
- phylogenetics: R-sig-phylo
  `https://stat.ethz.ch/mailman/listinfo/r-sig-phylo`
- genetics: R-sig-phylo
  `https://stat.ethz.ch/mailman/listinfo/r-sig-genetics`
- *adegenet*: the adegenet forum
  `http://lists.r-forge.r-project.org/mailman/listinfo/adegenet-forum`

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Asking questions on Github

Using github's **issue** system

- every github project has an 'issue' system for discussions
- mainly used for: questions, bug reports, feature requests, contributions
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- for adegenet, go to:
  `https://github.com/thibautjombart/adegenet/issues`
- or just type in R: `adegenetIssues()`

Logicals operators 1/2

Basic logical operators

```
> a <- 1:10; a

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

> a < 5

 [1]  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE

> a > 5

 [1] FALSE FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE

> a <= 5

 [1]  TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE

> a == 5

 [1] FALSE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE FALSE

> a != 5

 [1]  TRUE  TRUE  TRUE  TRUE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE
```

Using logicals 2/2

Logicals operators recycle their arguments

The shortest argument is repeated to match the length of the longer one.

```
> a <- 1:10
> b <- c(1,10)
> a == b

 [1]  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE
```

Same happens with arithmetic operators:

```
> a + b

 [1]  2 12  4 14  6 16  8 18 10 20
```

Logicals as numbers

In short: TRUE=1, FALSE=0.

```
> a <- c(TRUE, FALSE, TRUE)
> sum(a)

[1] 2

> mean(a)

[1] 0.6666667

> !a

[1] FALSE  TRUE FALSE

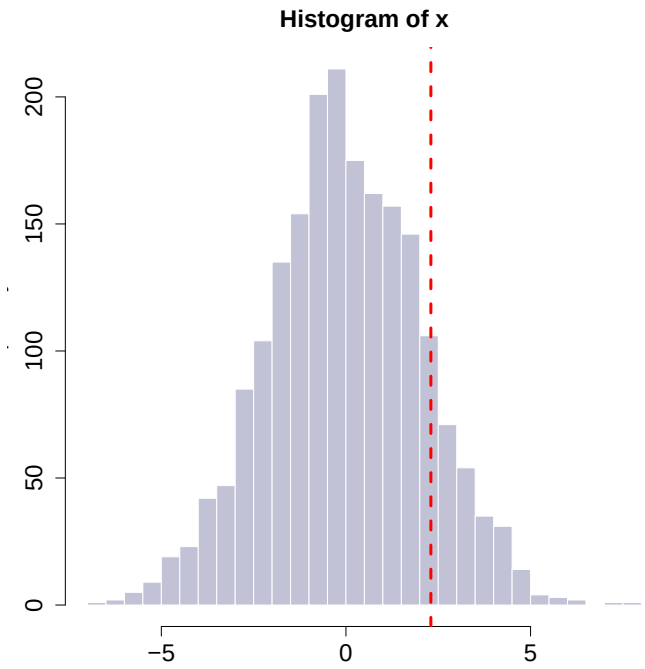
> sum(!a)

[1] 1
```

Logicals as numbers: example

What is the p-value of $X = 2.3$ given the empirical distribution 'x'?

```
> x <- rnorm(1000, sd=2)
> hist(x, nclass=30, col="#c2c2d6",
+      border="white")
> abline(v = 2.3, lty=2, col="red")
```




```
> mean(x >= 2.3)

[1] 0.1295

> pnorm(2.3, 0, 2, lower.tail=FALSE)

[1] 0.1250719
```

Matching values

`which`: indices of `TRUE`s in a logical vector:

```
> which(c(TRUE, FALSE, FALSE, TRUE, FALSE))

[1] 1 4
```

`%in%`: which x is in y:

```
> c(1,5,11) %in% 0:10

[1]  TRUE  TRUE FALSE
```

`match`: positions of x matched in y:

```
> match(c(1,5,11), 0:10)

[1]  2  6 NA
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Subsetting using indices

```
> x <- letters[1:10]
> x

 [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j"

> x[c(1,3,4)]

[1] "a" "c" "d"

> x[-c(1,3,4)]

[1] "b" "e" "f" "g" "h" "i" "j"
```

Subsetting using logicals

```
> set.seed(1)
> x <- sample(1:10)
> x

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

> x > 5

 [1] FALSE FALSE FALSE  TRUE FALSE  TRUE  TRUE  TRUE  TRUE FALSE

> x[x > 5]

[1]  7  8  9  6 10
```

Subsetting using names

```
> names(x) <- letters[1:10]
> x

 a  b  c  d  e  f  g  h  i  j
 3  4  5  7  2  8  9  6 10  1

> x[c("a", "g", "a", "b", "c")]

a g a b c
3 9 3 4 5
```

Application: subsetting a genind object

```
> data(microbov)
> microbov


/// GENIND OBJECT /////////

 // 704 individuals; 30 loci; 373 alleles; size: 1.1 Mb

 // Basic content
   @tab:  704 x 373 matrix of allele counts
   @loc.n.all: number of alleles per locus (range: 5-22)
   @loc.fac: locus factor for the 373 columns of @tab
   @all.names: list of allele names for each locus
   @ploidy: ploidy of each individual  (range: 2-2)
   @type:  codom
   @call: genind(tab = truenames(microbov)$tab, pop = truenames(microbov)$pop)

 // Optional content
   @pop: population of each individual (group size range: 30-61)
   @other: a list containing: coun  breed  spe
```

Application: subsetting a genind object

Keep only Salers and Zebu, and loci with $\geq$ 10 alleles:

```
> ind.to.keep <- pop(microbov) %in% c("Salers","Zebu")
> loc.to.keep <- nAll(microbov) >= 10
> x <- microbov[i=ind.to.keep, loc=loc.to.keep]
> x


/// GENIND OBJECT /////////

 // 100 individuals; 22 loci; 310 alleles; size: 178.3 Kb

 // Basic content
   @tab:  100 x 310 matrix of allele counts
   @loc.n.all: number of alleles per locus (range: 10-22)
   @loc.fac: locus factor for the 310 columns of @tab
   @all.names: list of allele names for each locus
   @ploidy: ploidy of each individual  (range: 2-2)
   @type:  codom
   @call: .local(x = x, i = i, j = j, loc = ..1, drop = drop)

 // Optional content
   @pop: population of each individual (group size range: 50-50)
   @other: a list containing: coun  breed  spe
```

Is this 'refresher' over yet??

There's more!

- looping: `for`, `apply`, `lapply`, `sapply`, ...
- regular expressions: `grep`, `sub`, `gsub`, ...
- classes and methods: S3, S4, R6, ...
- integration of foreign languages: `.C`, `.Call`, *Rcpp*, ...
- advanced graphics: *ggplot2*, *ggvis*, JS plugins, ...

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If you're seeing this, you need a break.