R

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Basic Types

- Atomic vectors: logical, integer, double, complex, character, raw

- lists, environments, functions, S4 classes

Vectors

```
c(1, 2, 3)
1:3
vector(mode="double", length = 5)
character(3)
c(5, 4) * 2
```

Assignment

```
v <- 1:10
x = c(a=6, b=5, c=4)

f(thisIs = notAssignment)
f(not <- recommended)
```

Integer Subsetting

```
> x <- 1:6
> x[6]
[1] 6


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


> x[c(-1, -3, -5)]
[1] 2 4 6
```

Logical Subsetting

```
> x > 3
[1] FALSE FALSE FALSE  TRUE  TRUE TRUE
> x[x > 3]
[1] 4 5 6
```

Subsetting by Name

```
> names(x) <- letters[1:length(x)]
> x
a b c d e f
1 2 3 4 5 6
> x[c("f", "a", "c", "e")]
f a c e
6 1 3 5
```

Vectorized

```
> pkgs = installed.packages()[, "Package"]
> tab = table(unlist(strsplit(pkgs, "")))
> tab[c("b", "B")]
```

Vectorized

```
> pkgs = installed.packages()[, "Package"]
> tab = table(unlist(strsplit(pkgs, "")))
> tab[c("b", "B")]


 b  B
26  9
```

Functions

```
> f <- function(x) 2 * x
> f(2)
[1] 4
> f(1:4)
[1] 2 4 6 8
```

Functions

```
> diag
function (x = 1, nrow, ncol)
{
        if (is.matrix(x)) {
        if (nargs() > 1L)
            stop("'nrow' or 'ncol' cannot be specified when 'x' is a matrix")
        if ((m <- min(dim(x))) == 0L)
            return(vector(typeof(x), 0L))
        y <- c(x)[1L + 0L:(m - 1L) * (dim(x)[1L] + 1L)]
        nms <- dimnames(x)
```

Lists

```
> f <- function(x) 2 * x
> v <- list(a = 1:2, b = "hi",
            c = list(TRUE, f))

> v
$a [1] 1 2
$b [1] "hi"
$c
 $c[[1]] [1] TRUE
 $c[[2]] function (x) 2 * x
```

Lists

```
> f <- function(x) 2 * x
> v <- list(a = 1:2, b = "hi",
            c = list(TRUE, f))

> v[["b"]]  ## or v[[2]] or v$b
[1] "hi"

> v[1:2]
$a [1] 1 2
$b [1] "hi"
```

data.frame

```
> data.frame(nchar = sapply(t, nchar),
             text=t, row.names=NULL)
  nchar    text
1     1       a
2     5   named
3     4    list
4     2      of
5     7 vectors
6     4    with
7     5   equal
8     6  length
```

data.frame

```
> df[1:2, ]
  nchar   text
1     1      a
2     5  named

> df[2, 1]
[1] 5
```

data.frame

```
df[["nchar"]] # or df$nchar
[1] 1 5 4 2 7 4 5 6


> names(df)
[1] "nchar" "text"


> dim(df)
[1] 8 2
```

replacement

```
> df[2, 1] <- 10
> df[1:2, ]
  nchar  text
1     1      a
2    10 named
```

replacement

```
df[1, 1] <- 20

s[[3]] <- "hi"

            s[[2]] <- NULL

v[8] <- 100

      names(y) <- c("a", "b")
```

Packages

```
> contrib <- contrib.url(biocinstallRepos())
> zz <- available.packages(contrib)
> nrow(zz)
```

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Packages

```
> biocLite("somePackage")
> library("somePackage")
> search()
> sessionInfo()
```

end