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INTRODUCTION

#) THE R ENVIRONMENT

R is an integrated suite of software facilities for data manipulation, calculation and graphical display. Among other things it has

- an effective data handling and storage facility
- a suite of operators for calculations on arrays, in particular matrices,
- a large, coherent, integrated collection of intermediate tools for data analysis,
- graphical facilities for data analysis and display either directly at the computer or on hard-copy, and
- a well developed, simple and effective programming language (called 'S') which includes conditionals, loops, under defined recursive functions and input and output facilities

* R is very much a vehicle for newly developing methods of interactive data analysis.

```
> a = 1
```

```
> b = 2
```

```
> c = a + b
```

```
> c
```

```
[1] 3
```

```
> cos(pi/2)
```

```
[1] 6.123032e-17
```

```
> tan(pi/2)
```

```
[1] 1.633124e+16
```

```
> sin(pi/2)
```

```
[1] 1
```

```
> patientid=c(1,2,3,4)
> age=c(25,34,28,32)
> diabetes=c("Type1","Type2","Type3","Type4")
> status=c("Poor","Improved","Excellent","Poor")
> patientData=data.frame(patientid,age,diabetes,status)
patientData
  patientid age diabetes status
1         1  25    Type1    Poor
2         2  34    Type2  Improved
3         3  28    Type3  Excellent
4         4  32    Type4    Poor

> patientData[1:2]
  patientid age
1         1  25
2         2  34
3         3  28
4         4  32

> patientData[diabetes=="diabetes", "status"]
  diabetes status
1    Type1    Poor
2    Type2  Improved
3    Type3  Excellent
4    Type4    Poor

> patientData$age
[1] 25 34 28 32
```

[illegible]

```

3      5 18
4      6 32
> patientdata[c("diabetes", "status")]
diabetes status
1 Type1 Poor
2 Type2 Improved
3 Type1 Excellent
4 Type1 Poor
> patientdata$age
[1] 28 34 28 32
> nlist(Batch=3, label="Lung Cancer Patients", subtype=c("A", "B", "C"))
> n
Batch
[1] 3
Label
[1] "Lung Cancer Patients"
Subtype
[1] "A" "B" "C"
> is.list(x)
[1] TRUE

```

```

> n[[1]]
[1] 3
> n[[2]]
[1] "Lung Cancer Patients"
> n[[3]]
[1] "A" "B" "C"
> n$subtype
[1] "A" "B" "C"
> n[["subtype"]]
[1] "A" "B" "C"
> length(x)
[1] 3

> p=list(operator="Mkg", location="New York")
> nlist(count=100.24, operator="x")
> final_list=c(x, y, z)
> final_list
Batch
[1] 3
Label
[1] "Lung Cancer Patients"
Subtype
[1] "A" "B" "C"
Operator
[1] "Mkg"
Location
[1] "New York"
Count
[1] 100.24

```

```

> a[[1]]
[1] 3
> a[[2]]
[1] "Lung Cancer Patients"
> a[[3]]
[1] "a" "b" "c"
> subtypes
[1] "a" "b" "c"
> a[!subtypes]
[1] "a" "b" "c"
> length(a)
[1] 3

> y[!is.na(ispdate=="Mary", isdate=="New York")]
> y[is.na(ispdate=="Mary", isdate=="New York")]
> y[is.na(ispdate=="Mary", isdate=="New York")]
> y[is.na(ispdate=="Mary", isdate=="New York")]
Batch
[1] 3

label
[1] "Lung Cancer Patients"

subtype
[1] "a" "b" "c"

superior
[1] "Mary"

isolation
[1] "New York"

isotop
[1] 1000.24

isotope
[1] "yes"

```

```

Batch
[1] "a" "b" "c"

superior
[1] "Mary"

isolation
[1] "New York"

isotop
[1] 1000.24

isotope
[1] "yes"

> a[!is.na(ispdate=="Mary", isdate=="New York")]
> y[is.na(ispdate=="Mary", isdate=="New York")]
> y[is.na(ispdate=="Mary", isdate=="New York")]
> y[is.na(ispdate=="Mary", isdate=="New York")]
Batch
[1] 3
[1] "Lung Cancer Patients"
[1] "Lung Cancer Patients"
[1] "Lung Cancer Patients"

```

```

Batch
[1] 3
label "Lung Cancer Patients"
subtype Character,3
> expdata.frame(samples=c("a","b","c"), values=c(2.43, 5.32, -1.23))
> backupdata <-
+ data.frame(patients=c("a","b","c"), marked=c("yes","yes","no"))
> y=as.matrix(x)
> y
[1,]
Batch
[1] 3
label "Lung Cancer Patients"
subtype Character,3
> expdata.frame(samples=c("a","b","c"), values=c(2.43, 5.32, -1.23))
> backupdata.frame(patients=c("a","b","c"), marked=c("yes","yes","no"))
> a=merge(exp, backup, by.x="samples", by.y="patients")
> a
samples values marked
1 a 2.43 yes
2 b 5.32 yes
3 c -1.23 no
>

```