

# Getting Started with R

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## Always First Command

```
> library(NCStats)
```

## Basic Vectors

```
> ( profs <- c("Derek","Young","Jodi") )
```

```
[1] "Derek" "Young" "Jodi"
```

```
> ( nums <- c(4,2,6,4,3) )
```

```
[1] 4 2 6 4 3
```

```
> ( heads <- c(TRUE, TRUE, FALSE, FALSE) )
```

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

```
> ls()
```

```
[1] "f"          "fnm"        "gt5"        "heads"      "iris"       "need2render"  
[7] "nums"       "profs"      "set"        "setver"     "setver1"    "ver_and_gt5"  
[13] "ver_or_gt5"
```

```
> nums[3]
```

```
[1] 6
```

```
> profs[2]
```

```
[1] "Young"
```

```
> heads[1]
```

```
[1] TRUE
```

## Basic Data Frames

```
> setwd("C:/aaaWork/Web/GitHub/NCMTH107/modules/Getting_Started_R")
> iris <- read.csv("Iris.csv")
> str(iris)
```

```
'data.frame': 150 obs. of 5 variables:
 $ seplen : int  50 46 46 51 55 48 52 49 44 50 ...
 $ sepwid : int  33 34 36 33 35 31 34 36 32 35 ...
 $ petlen : int  14 14 10 17 13 16 14 14 13 16 ...
 $ petwid : int   2 3 2 5 2 2 2 1 2 6 ...
 $ species: Factor w/ 3 levels "setosa","versicolor",...: 1 1 1 1 1 1 1 1 1 1 ...
```

```
> headtail(iris)      # NOT the entire data.frame
```

```
      seplen sepwid petlen petwid  species
1         50     33     14      2   setosa
2         46     34     14      3   setosa
3         46     36     10      2   setosa
148        57     25     50     20 virginica
149        58     28     51     24 virginica
150        63     33     60     25 virginica
```

```
> ls()
```

```
[1] "f"           "fnm"         "gt5"         "heads"       "iris"        "need2render"
[7] "nums"        "profs"       "set"         "setver"     "setver1"    "ver_and_gt5"
[13] "ver_or_gt5"
```

## Working With Data Frames

```
> iris[2,]
```

```
      seplen sepwid petlen petwid species
2         46     34     14      3   setosa
```

```
> iris$seplen
```

```
[1] 50 46 46 51 55 48 52 49 44 50 44 47 48 51 48 50 50 43 58 51 49 51 50 46 57 50 54 52
[29] 55 49 54 50 44 47 46 51 50 49 54 54 51 48 48 45 57 51 54 51 52 53 65 62 59 61 60 56
[57] 57 63 70 64 61 55 54 58 55 50 67 56 58 60 57 57 49 56 57 66 52 60 50 55 58 62 59 60
[85] 67 63 56 63 61 64 51 57 61 56 69 55 55 66 68 67 64 67 63 69 65 65 58 68 62 77 67 76
[113] 49 67 59 63 64 79 67 77 63 72 61 61 64 62 77 63 58 72 71 64 60 63 77 60 69 74 56 73
[141] 67 65 69 72 65 64 68 57 58 63
```

```
> iris$seplen[3]
```

```
[1] 46
```

```
> iris[3,2]
```

```
[1] 36
```

```
> iris[c(1,3,5),]
```

	seplen	sepwid	petlen	petwid	species
1	50	33	14	2	setosa
3	46	36	10	2	setosa
5	55	35	13	2	setosa

## Filtering Data Frames

```
> set <- filterD(iris,species=="setosa")
> str(set)
```

```
'data.frame':  50 obs. of  5 variables:
 $ seplen : int  50 46 46 51 55 48 52 49 44 50 ...
 $ sepwid : int  33 34 36 33 35 31 34 36 32 35 ...
 $ petlen : int  14 14 10 17 13 16 14 14 13 16 ...
 $ petwid : int   2 3 2 5 2 2 2 1 2 6 ...
 $ species: Factor w/ 1 level "setosa": 1 1 1 1 1 1 1 1 1 1 ...
```

```
> gt5 <- filterD(iris,seplen>5)
> headtail(gt5)
```

	seplen	sepwid	petlen	petwid	species
1	50	33	14	2	setosa
2	46	34	14	3	setosa
3	46	36	10	2	setosa
148	57	25	50	20	virginica
149	58	28	51	24	virginica
150	63	33	60	25	virginica

```
> setver1 <- filterD(iris,species!="virginica")
> str(setver1)
```

```
'data.frame':  100 obs. of  5 variables:
 $ seplen : int  50 46 46 51 55 48 52 49 44 50 ...
 $ sepwid : int  33 34 36 33 35 31 34 36 32 35 ...
 $ petlen : int  14 14 10 17 13 16 14 14 13 16 ...
 $ petwid : int   2 3 2 5 2 2 2 1 2 6 ...
 $ species: Factor w/ 2 levels "setosa","versicolor": 1 1 1 1 1 1 1 1 1 1 ...
```

```
> setver <- filterD(iris,species %in% c("setosa","versicolor"))
> str(setver)
```

```
'data.frame': 100 obs. of 5 variables:
 $ seplen : int 50 46 46 51 55 48 52 49 44 50 ...
 $ sepwid : int 33 34 36 33 35 31 34 36 32 35 ...
 $ petlen : int 14 14 10 17 13 16 14 14 13 16 ...
 $ petwid : int 2 3 2 5 2 2 2 1 2 6 ...
 $ species: Factor w/ 2 levels "setosa","versicolor": 1 1 1 1 1 1 1 1 1 1 ...
```

```
> ver_and_gt5 <- filterD(iris,species=="versicolor",seplen>5)
> headtail(ver_and_gt5)
```

	seplen	sepwid	petlen	petwid	species
1	65	28	46	15	versicolor
2	62	22	45	15	versicolor
3	59	32	48	18	versicolor
48	66	30	44	14	versicolor
49	68	28	48	14	versicolor
50	67	30	50	17	versicolor

```
> ver_or_gt5 <- filterD(iris,species=="versicolor" | seplen>5)
> headtail(ver_or_gt5)
```

	seplen	sepwid	petlen	petwid	species
1	50	33	14	2	setosa
2	46	34	14	3	setosa
3	46	36	10	2	setosa
148	57	25	50	20	virginica
149	58	28	51	24	virginica
150	63	33	60	25	virginica

```
> ls()
```

[1]	"f"	"fnm"	"gt5"	"heads"	"iris"	"need2render"
[7]	"nums"	"profs"	"set"	"setver"	"setver1"	"ver_and_gt5"
[13]	"ver_or_gt5"					