

Getting Started with R

R Handout

Derek H. Ogle

Always First Command

```
> library(NCStats)
```

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 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

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