

## Lecture 13 - R Software

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## Viewing Objects within Objects

In matrix and data frame objects the items are all the same length (resulting in the rectangular object), but in a list object the items can be different lengths.

### Looking inside complicated data objects

```
> fw
  abund flow
1     9    2
2    25    3
3    15    5
4     2    9
5    14   14
6    25   24
```

If you type the name of one of these (abund or flow) you will get an error:

```
> abund
Error: object 'abund' not found
```

if you append \$ and then put the name of the required column, we have:

```
> fw $ abund
[1] 9 25 15 2 14 25
```

We can use the square brackets as before to select out parts of the item:

```
> fw $ abund[1:4]
[1] 9 25 15 2
```

Suppose, we are given with the matrix of the form

```
> bird
```

	Garden	Hedgerow	Parkland	Pasture	Woodland
Blackbird	47	10	40	2	2
Chaffinch	19	3	5	0	2
Great Tit	50	0	10	7	0

If you try this with a matrix, however, you get a quite different result:

```
> bird$Garden
Error in bird$Garden : $ operator is invalid for atomic vectors
```

This is because a matrix is essentially a single data item that has been displayed in rows and columns. Therefore, the command will be

```
> bird[, 'Garden']
```

Blackbird	Chaffinch	Great Tit
47	19	50

For the columns, the command will be

```
> bird['Chaffinch',]
```

Garden	Hedgerow	Parkland	Pasture	Woodland
19	3	5	0	2

### [Quick looks at complicated data objects](#)

Suppose, the data be given in matrix form as:

```
>mf
```

	Length	Speed	Algae	NO3	BOD
1	20	12	40	2.25	200
2	21	14	45	2.15	180
3	22	12	45	1.75	135
4	23	16	80	1.95	120
5	21	20	75	1.95	110
6	20	21	65	2.75	120
⋮	⋮	⋮	⋮	⋮	⋮
25	22	15	75	1.75	95

## head(), tail(), summary()

If we wish to select the first few lines of a data object, we use the `head()` command.

```
> head(mf, n = 5)
```

	Length	Speed	Algae	NO3	BOD
1	20	12	40	2.25	200
2	21	14	45	2.15	180
3	22	12	45	1.75	135
4	23	16	80	1.95	120
5	21	20	75	1.95	110

Remark: By default the `head()` command, shows the first six rows.

We can also display the bottom of the data using the `tail()` command:

```
> tail(mf, n = 5)
```

	Length	Speed	Algae	NO3	BOD
21	16	22	35	2.55	200
22	25	9	85	2.85	55
23	24	11	80	2.95	87
24	23	16	80	2.85	97
25	22	15	75	1.75	95

Suppose, the data be given as:

```
> bird
```

	Garden	Hedgerow	Parkland	Pasture	Woodland
Blackbird	47	10	40	2	2
Chaffinch	19	3	5	0	2
Great Tit	50	0	10	7	0
House Sparrow	46	16	8	4	0
Robin	9	3	0	0	2
Song Thrush	4	0	6	0	0

There is another way to get information about an object, you can use the [summary\(\)](#) command.

```
> summary(bird.m)
```

Garden	Hedgerow	Parkland	Pasture	Woodland
Min. : 4.00	Min. : 0.000	Min. : 0.00	Min. :0.000	Min. :0
Median :32.50	Median : 3.000	Median : 7.00	Median :1.000	Median :1
Mean :29.17	Mean : 5.333	Mean :11.50	Mean :2.167	Mean :1
Max. :50.00	Max. :16.000	Max. :40.00	Max. :7.000	Max. :2