```
> library(ISwR)
> data(thuesen)
> dim(thuesen)
[1] 24  2
> thuesen
   blood.glucose short.velocity
1          15.3           1.76
2          10.8           1.34
3           8.1           1.27
4          19.5           1.47
5           7.2           1.27
6           5.3           1.49
7           9.3           1.31
8          11.1           1.09
9           7.5           1.18
10         12.2           1.22
11          6.7           1.25
12          5.2           1.19
13         19.0           1.95
14         15.1           1.28
15          6.7           1.52
16          8.6            NA
17          4.2           1.12
18         10.3           1.37
19         12.5           1.19
20         16.1           1.05
21         13.3           1.32
22          4.9           1.03
23          8.8           1.12
24          9.5           1.70
> attach(thuesen)
> lm(short.velocity~blood.glucose)

Call:
lm(formula = short.velocity ~ blood.glucose)

Coefficients:
  (Intercept)  blood.glucose
      1.09781        0.02196

> summary(lm(short.velocity~blood.glucose))

Call:
lm(formula = short.velocity ~ blood.glucose)

Residuals:
    Min      1Q   Median      3Q     Max
```

-0.40141 -0.14760 -0.02202 0.03001 0.43490

Coefficients:
            Estimate Std. Error t value Pr(>ltl)
(Intercept)   1.09781   0.11748   9.345 6.26e-09 ***
blood.glucose 0.02196   0.01045   2.101   0.0479 *

Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.2167 on 21 degrees of freedom
  (1 observation deleted due to missingness)
Multiple R-squared: 0.1737,   Adjusted R-squared: 0.1343
F-statistic: 4.414 on 1 and 21 DF, p-value: 0.0479

```
> plot(blood.glucose,short.velocity)
> thuesen
   blood.glucose short.velocity
1       15.3         1.76
2       10.8         1.34
3        8.1         1.27
4       19.5         1.47
5        7.2         1.27
6        5.3         1.49
7        9.3         1.31
8       11.1         1.09
9        7.5         1.18
10      12.2         1.22
11       6.7         1.25
12       5.2         1.19
13      19.0         1.95
14      15.1         1.28
15       6.7         1.52
16       8.6          NA
17       4.2         1.12
18      10.3         1.37
19      12.5         1.19
20      16.1         1.05
21      13.3         1.32
22       4.9         1.03
23       8.8         1.12
24       9.5         1.70
> plot(blood.glucose,short.velocity)
> abline(lm(short.velocity~blood.glucose))
> abline(lm(short.velocity~blood.glucose))
Error in int_abline(a = a, b = b, h = h, v = v, untf = untf, ...) :
  plot.new has not been called yet
```

```
> plot(blood.glucose,short.velocity)
> abline(lm(short.velocity~blood.glucose))
> lm.velo<-lm(short.velocity~blood.glucose)
> lm.velo

Call:
lm(formula = short.velocity ~ blood.glucose)

Coefficients:
 (Intercept)  blood.glucose
    1.09781        0.02196

> fitted(lm.velo)
      1        2        3        4        5        6        7
1.433841 1.335010 1.275711 1.526084 1.255945 1.214216 1.302066
      8        9       10       11       12       13       14
1.341599 1.262534 1.365758 1.244964 1.212020 1.515103 1.429449
     15       17       18       19       20       21       22
1.244964 1.190057 1.324029 1.372346 1.451411 1.389916 1.205431
     23       24
1.291085 1.306459
> resid(lm.velo)
          1           2           3           4           5
 0.326158532  0.004989882 -0.005711308 -0.056084062  0.014054962
          6           7           8           9          10
 0.275783754  0.007933665 -0.251598875 -0.082533795 -0.145757649
         11          12          13          14          15
 0.005036223 -0.022019994  0.434897199 -0.149448964  0.275036223
         17          18          19          20          21
-0.070057471  0.045971143 -0.182346406 -0.401411486 -0.069916424
         22          23          24
-0.175431237 -0.171085074  0.393541161
> thuesen
   blood.glucose short.velocity
1         15.3          1.76
2         10.8          1.34
3          8.1          1.27
4         19.5          1.47
5          7.2          1.27
6          5.3          1.49
7          9.3          1.31
8         11.1          1.09
9          7.5          1.18
10        12.2          1.22
11         6.7          1.25
12         5.2          1.19
13        19.0          1.95
```

```
14       15.1        1.28
15        6.7        1.52
16        8.6         NA
17        4.2        1.12
18       10.3        1.37
19       12.5        1.19
20       16.1        1.05
21       13.3        1.32
22        4.9        1.03
23        8.8        1.12
24        9.5        1.70
> 1.76-1.433841
[1] 0.326159
>  1.09781+ 0.02196*15.3
[1] 1.433798
> 1.09781+ 0.02196*10.8
[1] 1.334978
> plot(blood.glucose,short.velocity); abline(lm.velo)
> plot(blood.glucose,short.velocity)
> lines(blood.glucose,fitted(lm.velo))
Error in xy.coords(x, y) : 'x' and 'y' lengths differ
> length(blood.glucose)
[1] 24
> length(fitted(lm.velo))
[1] 23
> plot(blood.glucose,short.velocity)
> lines(blood.glucose[!is.na(short.velocity)],fitted(lm.velo))
> length(blood.glucose[!is.na(short.velocity)])
[1] 23
> thuesen
   blood.glucose short.velocity
1        15.3        1.76
2        10.8        1.34
3         8.1        1.27
4        19.5        1.47
5         7.2        1.27
6         5.3        1.49
7         9.3        1.31
8        11.1        1.09
9         7.5        1.18
10       12.2        1.22
11        6.7        1.25
12        5.2        1.19
13       19.0        1.95
14       15.1        1.28
15        6.7        1.52
16        8.6         NA
```

```
17      4.2     1.12
18      10.3    1.37
19      12.5    1.19
20      16.1    1.05
21      13.3    1.32
22      4.9     1.03
23      8.8     1.12
24      9.5     1.70
> thuesen[3,1]
[1] 8.1
> thuesen[3,1]=NA
> thuesen
  blood.glucose short.velocity
1       15.3    1.76
2       10.8    1.34
3       NA      1.27
4       19.5    1.47
5       7.2     1.27
6       5.3     1.49
7       9.3     1.31
8       11.1    1.09
9       7.5     1.18
10      12.2    1.22
11      6.7     1.25
12      5.2     1.19
13      19.0    1.95
14      15.1    1.28
15      6.7     1.52
16      8.6     NA
17      4.2     1.12
18      10.3    1.37
19      12.5    1.19
20      16.1    1.05
21      13.3    1.32
22      4.9     1.03
23      8.8     1.12
24      9.5     1.70
> lm.velo<-lm(short.velocity~blood.glucose)
> lm.velo

Call:
lm(formula = short.velocity ~ blood.glucose)

Coefficients:
    (Intercept)  blood.glucose10.8  blood.glucose11.1
        1.370             -0.030            -0.280
blood.glucose12.2  blood.glucose12.5  blood.glucose13.3
```

```
          -0.150              -0.180              -0.050
blood.glucose15.1  blood.glucose15.3  blood.glucose16.1
          -0.090               0.390              -0.320
 blood.glucose19  blood.glucose19.5   blood.glucose4.2
           0.580               0.100              -0.250
 blood.glucose4.9   blood.glucose5.2   blood.glucose5.3
          -0.340              -0.180               0.120
 blood.glucose6.7   blood.glucose7.2   blood.glucose7.5
           0.015              -0.100              -0.190
 blood.glucose8.8   blood.glucose9.3   blood.glucose9.5
          -0.250              -0.060               0.330
  blood.glucoseNA
          -0.100

> fitted(lm.velo)
    1     2     3     4     5     6     7     8     9    10    11
1.760 1.340 1.270 1.470 1.270 1.490 1.310 1.090 1.180 1.220 1.385
   12    13    14    15    17    18    19    20    21    22    23
1.190 1.950 1.280 1.385 1.120 1.370 1.190 1.050 1.320 1.030 1.120
   24
1.700
> plot(blood.glucose,short.velocity)
Warning message:
In xy.coords(x, y, xlabel, ylabel, log) : NAs introduced by coercion
> attach(thuesen)
The following objects are masked from a:

    blood.glucose, short.velocity

The following objects are masked from thuesen (pos = 4):

    blood.glucose, short.velocity

> plot(blood.glucose,short.velocity)
> lines(blood.glucose[!is.na(short.velocity)],fitted(lm.velo))
> plot(blood.glucose,short.velocity)
> lines(blood.glucose[!is.na(short.velocity) & !is.na(blood.glucose)],fitted(lm.velo))
Error in xy.coords(x, y) : 'x' and 'y' lengths differ
> lm.velo<-lm(thuesen$short.velocity~thusen$blood.glucose)
Error in eval(predvars, data, env) : object 'thusen' not found
> lm.velo<-lm(thuesen$short.velocity~thuesen$blood.glucose)
> lm.velo

Call:
lm(formula = thuesen$short.velocity ~ thuesen$blood.glucose)

Coefficients:
```

```
          (Intercept)  thuesen$blood.glucose
             1.09841              0.02193

> plot(blood.glucose,short.velocity)
> lines(blood.glucose[!is.na(short.velocity)],fitted(lm.velo))
Error in xy.coords(x, y) : 'x' and 'y' lengths differ
> length(blood.glucose[!is.na(short.velocity)])
[1] 23
> length(fitted(lm.velo))
[1] 22
> plot(blood.glucose,short.velocity)
> lines(blood.glucose[!is.na(short.velocity) & !is.na(blood.glucose)],fitted(lm.velo))
> length(blood.glucose[!is.na(short.velocity) & !is.na(blood.glucose)])
[1] 22
> length(fitted(lm.velo))
[1] 22
> thuesen
   blood.glucose short.velocity
1        15.3          1.76
2        10.8          1.34
3          NA          1.27
4        19.5          1.47
5         7.2          1.27
6         5.3          1.49
7         9.3          1.31
8        11.1          1.09
9         7.5          1.18
10       12.2          1.22
11        6.7          1.25
12        5.2          1.19
13       19.0          1.95
14       15.1          1.28
15        6.7          1.52
16        8.6            NA
17        4.2          1.12
18       10.3          1.37
19       12.5          1.19
20       16.1          1.05
21       13.3          1.32
22        4.9          1.03
23        8.8          1.12
24        9.5          1.70
> data(thuesen)
> thuesen
   blood.glucose short.velocity
1        15.3          1.76
2        10.8          1.34
```

```
3        8.1        1.27
4       19.5        1.47
5        7.2        1.27
6        5.3        1.49
7        9.3        1.31
8       11.1        1.09
9        7.5        1.18
10      12.2        1.22
11       6.7        1.25
12       5.2        1.19
13      19.0        1.95
14      15.1        1.28
15       6.7        1.52
16       8.6         NA
17       4.2        1.12
18      10.3        1.37
19      12.5        1.19
20      16.1        1.05
21      13.3        1.32
22       4.9        1.03
23       8.8        1.12
24       9.5        1.70
> attach(thuesen)
The following objects are masked from thuesen (pos = 3):

    blood.glucose, short.velocity

The following objects are masked from a:

    blood.glucose, short.velocity

The following objects are masked from thuesen (pos = 5):

    blood.glucose, short.velocity

> options(na.action=na.exclude)
> lm.velo<-lm(short.velocity~blood.glucose)
> fitted(lm.velo)
      1        2        3        4        5        6        7
1.433841 1.335010 1.275711 1.526084 1.255945 1.214216 1.302066
      8        9       10       11       12       13       14
1.341599 1.262534 1.365758 1.244964 1.212020 1.515103 1.429449
     15       16       17       18       19       20       21
1.244964       NA 1.190057 1.324029 1.372346 1.451411 1.389916
     22       23       24
1.205431 1.291085 1.306459
> plot(blood.glucose,short.velocity)
```

```
> lines(blood.glucose,fitted(lm.velo))
>
> plot(blood.glucose,short.velocity)
> abline(lm.velo)
> segments(blood.glucose,fitted(lm.velo),blood.glucose,short.velocity)
> arrows(blood.glucose,fitted(lm.velo),blood.glucose,short.velocity)
> ?arrows
starting httpd help server ... done
> arrows(blood.glucose,fitted(lm.velo),blood.glucose,short.velocity, angle = 30)
> arrows(blood.glucose,fitted(lm.velo),blood.glucose,short.velocity, angle = 90)
> plot(fitted(lm.velo),resid(lm.velo)) ;qqnorm(resid(lm.velo))
> logret<- read.table("~/Desktop/d_logret_6stocks.txt", header=T)
>  names(logret)
[1] "Date"     "Pfizer"   "Intel"     "Citigroup" "AmerExp"
[6] "Exxon"     "GenMotor"
> attach(logret)
> head(logret)
     Date     Pfizer     Intel   Citigroup     AmerExp
1 1-Aug-00 -0.001438612  0.04998126  0.04427510  0.017410003
2 1-Sep-00  0.017489274 -0.25561927 -0.03353650  0.012656982
3 2-Oct-00 -0.017046116  0.03454674 -0.01164558 -0.004897625
4 1-Nov-00  0.012012934 -0.07255067 -0.02267479 -0.038275870
5 1-Dec-00  0.016278701 -0.10249787  0.01070831  0.000000000
6 2-Jan-01 -0.008063083  0.09022312  0.03990062 -0.066129678
       Exxon    GenMotor
1  0.010224894  0.09329402
2  0.037989020 -0.03220924
3  0.000330555 -0.01960217
4 -0.003650020 -0.09489160
5 -0.005252049  0.01246125
6 -0.014169243  0.02297158
> lm(Pfizer~Intel)

Call:
lm(formula = Pfizer ~ Intel)

Coefficients:
(Intercept)       Intel
  -0.003903     0.023078

> summary(lm(Pfizer~Intel))

Call:
lm(formula = Pfizer ~ Intel)

Residuals:
    Min       1Q   Median      3Q      Max
```

-0.055920 -0.013845 0.000851 0.017246 0.045693

Coefficients:
          Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.003903   0.002913 -1.340   0.185
Intel   0.023078   0.043112   0.535   0.594

Residual standard error: 0.02321 on 62 degrees of freedom
Multiple R-squared: 0.0046,   Adjusted R-squared: -0.01145
F-statistic: 0.2865 on 1 and 62 DF, p-value: 0.5944

```
> dim(logret)
[1] 64  7
> fit1<-lm(Pfizer~Intel)
> fit1$coeff
(Intercept)      Intel
-0.00390318  0.02307791
> plot(Intel, Pfizer)
> abline(lm(Pfizer~Intel))
> lm(Pfizer~-1+Intel)
```

Call:
lm(formula = Pfizer ~ -1 + Intel)

Coefficients:
  Intel
0.02819

```
> summary(lm(Pfizer~-1+Intel))
```

Call:
lm(formula = Pfizer ~ -1 + Intel)

Residuals:
     Min   1Q   Median   3Q   Max
-0.059716 -0.017863 -0.003199 0.013654 0.041790

Coefficients:
     Estimate Std. Error t value Pr(>|t|)
Intel 0.02819   0.04321   0.652   0.516

Residual standard error: 0.02336 on 63 degrees of freedom
Multiple R-squared: 0.006712,   Adjusted R-squared: -0.009054
F-statistic: 0.4257 on 1 and 63 DF, p-value: 0.5165

```
> fitted(fit1)
          1         2         3         4
```

```
-0.0027497170 -0.0098023371 -0.0031059136 -0.0055774973
       5             6             7             8
-0.0062686160 -0.0018210192 -0.0064923877 -0.0047271105
       9            10            11            12
-0.0022878538 -0.0052477127 -0.0031038796 -0.0037146614
      13            14            15            16
-0.0045385026 -0.0070402547 -0.0021212967 -0.0009819628
      17            18            19            20
-0.0042821637 -0.0028213677 -0.0059497454 -0.0032712130
      21            22            23            24
-0.0045135463 -0.0042470549 -0.0080473355 -0.0036202090
      25            26            27            28
-0.0050925670 -0.0057292852 -0.0017022410 -0.0020107797
      29            30            31            32
-0.0068456348 -0.0038440493 -0.0029181916 -0.0044837431
      33            34            35            36
-0.0026787417 -0.0026536331 -0.0039080966 -0.0021070376
      37            38            39            40
-0.0025084798 -0.0042859774 -0.0020956820 -0.0037217564
      41            42            43            44
-0.0043582645 -0.0043933007 -0.0043342526 -0.0046129133
      45            46            47            48
-0.0044586338 -0.0028463996 -0.0042444389 -0.0051438634
      49            50            51            52
-0.0052474851 -0.0044988550 -0.0028588657 -0.0038303210
      53            54            55            56
-0.0034637745 -0.0043153992 -0.0031999337 -0.0042246509
      57            58            59            60
-0.0037819547 -0.0024999688 -0.0042572917 -0.0034819521
      61            62            63            64
-0.0044139479 -0.0043265083 -0.0043836219 -0.0025482778
> resid(fit1)
        1             2             3             4
 0.0013111050  0.0272916111 -0.0139402024  0.0175904313
        5             6             7             8
 0.0225473170 -0.0062420638  0.0060694077 -0.0361791835
        9            10            11            12
 0.0264780818  0.0022689257 -0.0266775094  0.0162190934
       13            14            15            16
-0.0261246974  0.0268557347  0.0211850277  0.0165258578
       17            18            19            20
-0.0318636273  0.0221780547 -0.0001004526 -0.0099167620
       21            22            23            24
-0.0341268797 -0.0157651711  0.0130369555 -0.0305389430
       25            26            27            28
 0.0165446340 -0.0510936318  0.0410847420  0.0003900007
       29            30            31            32
```

```
-0.0066475122  0.0029294243 -0.0047795374  0.0234781331
        33            34           35           36
-0.0030081733  0.0083405481  0.0456925796 -0.0080028214
        37            38           39           40
-0.0427578312  0.0108328714  0.0192801070  0.0319773724
        41            42           43           44
 0.0265121525  0.0201413757  0.0064494286 -0.0146753167
        45            46           47           48
 0.0130664378 -0.0002174194 -0.0088913861 -0.0253478596
        49            50           51           52
 0.0171237381 -0.0238331950 -0.0213420733 -0.0115263230
        53            54           55           56
-0.0106209155 -0.0422010728  0.0431754497  0.0038865469
        57            58           59           60
 0.0184150057  0.0171305578 -0.0008315333 -0.0138138029
        61            62           63           64
-0.0096267851 -0.0043561977 -0.0559197441  0.0049599148
>  plot(Intel, Pfizer)
> lines(Intel, fitted(fit1))
> a<-3
> a
[1] 3
> (a<-3)
[1] 3
> fit1<-lm(Pfizer~Intel)
> fit1

Call:
lm(formula = Pfizer ~ Intel)

Coefficients:
(Intercept)       Intel
  -0.003903     0.023078

> (fit1<-lm(Pfizer~Intel))

Call:
lm(formula = Pfizer ~ Intel)

Coefficients:
(Intercept)       Intel
  -0.003903     0.023078

> getwd()
[1] "/Users/minshu"
> attach(thuesen)
The following objects are masked from thuesen (pos = 4):
```

blood.glucose, short.velocity

The following objects are masked from thuesen (pos = 5):

    blood.glucose, short.velocity

The following objects are masked from a:

    blood.glucose, short.velocity

The following objects are masked from thuesen (pos = 7):

    blood.glucose, short.velocity

```
> thuesen
   blood.glucose short.velocity
1        15.3         1.76
2        10.8         1.34
3         8.1         1.27
4        19.5         1.47
5         7.2         1.27
6         5.3         1.49
7         9.3         1.31
8        11.1         1.09
9         7.5         1.18
10       12.2         1.22
11        6.7         1.25
12        5.2         1.19
13       19.0         1.95
14       15.1         1.28
15        6.7         1.52
16        8.6          NA
17        4.2         1.12
18       10.3         1.37
19       12.5         1.19
20       16.1         1.05
21       13.3         1.32
22        4.9         1.03
23        8.8         1.12
24        9.5         1.70
> cor(blood.glucose,short.velocity)
[1] NA
> cor(blood.glucose,short.velocity,use="complete.obs")
[1] 0.4167546
> cor(thuesen,use="complete.obs")
              blood.glucose short.velocity
```

```
blood.glucose     1.0000000     0.4167546
short.velocity    0.4167546     1.0000000
> cor(blood.glucose[1:15],short.velocity[1:15])
[1] 0.5408959
> cor(blood.glucose,short.velocity,use="complete.obs")
[1] 0.4167546
> cor.test(blood.glucose,short.velocity)

        Pearson's product-moment correlation

data:  blood.glucose and short.velocity
t = 2.101, df = 21, p-value = 0.0479
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.005496682 0.707429479
sample estimates:
     cor
0.4167546

> cor(Intel, Pfizer)
[1] 0.06782663
> summary(fit1)

Call:
lm(formula = Pfizer ~ Intel)

Residuals:
     Min      1Q   Median      3Q      Max
-0.055920 -0.013845  0.000851  0.017246  0.045693

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.003903   0.002913  -1.340    0.185
Intel        0.023078   0.043112   0.535    0.594

Residual standard error: 0.02321 on 62 degrees of freedom
Multiple R-squared:  0.0046,      Adjusted R-squared:  -0.01145
F-statistic: 0.2865 on 1 and 62 DF,  p-value: 0.5944

>
> cor.test(Intel, Pfizer)
```