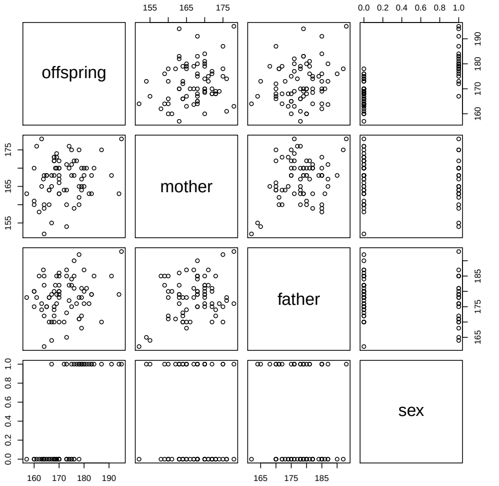
Solution of assignment 2, ST2304



Problem 1

The regression coeffiecient is the slope of the regression line, which is the difference in mean height between females and males.

```
> summary(regsex)

Call:
lm(formula = offspring ~ sex)

Residuals:
     Min       1Q   Median       3Q      Max
-13.4000  -3.5191  -0.1383   2.1234  14.6000

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 167.8766     0.7882 212.983  < 2e-16 ***
sex          12.5234     1.3376   9.362 5.75e-14 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 5.404 on 70 degrees of freedom
Multiple R-squared: 0.556,Adjusted R-squared: 0.5496
F-statistic: 87.65 on 1 and 70 DF,  p-value: 5.749e-14
```

Sex has an significant effect on height, as the P-value ($5.75 \cdot 10^{-14}$) is small. The estimate of the regression coefficient (12.5234) is therefore significantly different from zero. Here we can reject the null hypothesis (β=0), and say that sex has a significant effect on height.

A t-test based on the assumption that the two variances (in female and male heigths) as are equal and estimated by the pooled variance, can be done using the optional argument `var.equal=TRUE`

```
> t.test(offspring[sex==0],offspring[sex==1],var.equal=TRUE)

Two Sample t-test
```

```
data:  offspring[sex == 0] and offspring[sex == 1]
t = -9.3623, df = 70, p-value = 5.749e-14
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -15.191256  -9.855553
sample estimates:
mean of x mean of y
 167.8766  180.4000
```

The conclusion of the test is that we reject the null hypothesis of equal means of the heights in the two sexes ($H_0 : \mu_{\text{female}} - \mu_{\text{male}} = 0$) as the P-value is small ($5.749 \cdot 10^{-14}$). We see that the difference between the means given in the t-test (180.4-167.88) is equal to the estimate for the slope in the regression (12.52). Also, the p-values in the t-test and the regression are exactly the same (which makes sense) as the two tests are equivalent.

```
> regherit<-lm(offspring~sex+midparent)
> summary(regherit)

Call:
lm(formula = offspring ~ sex + midparent)

Residuals:
    Min      1Q  Median      3Q     Max
-9.3030 -2.5560  0.2545  2.5900 13.9421

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  58.1637    19.3822   3.001  0.00374 **
sex          13.5562     1.1280  12.018  < 2e-16 ***
midparent     0.6336     0.1119   5.664 3.14e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.497 on 69 degrees of freedom
Multiple R-squared: 0.6969,Adjusted R-squared: 0.6881
F-statistic: 79.32 on 2 and 69 DF,  p-value: < 2.2e-16
```

The heritability of heigth is here found to be 63%, this seems to be about the same found in the literature for stature of humans ($h^2 = 0.65$) (Russel, 2005). We have estimated the so called narrow sense heritability which is the proportion of the total phenotypic variance which can be attributed to so called additive genetic effects. Part of the remaining variance may also include genetic effects due to dominance and epistatis.

$$\text{heigth} = \alpha + \beta_{\text{midp}}\text{midp} + \beta_{\text{sex}}\text{sex} + \epsilon \tag{1}$$

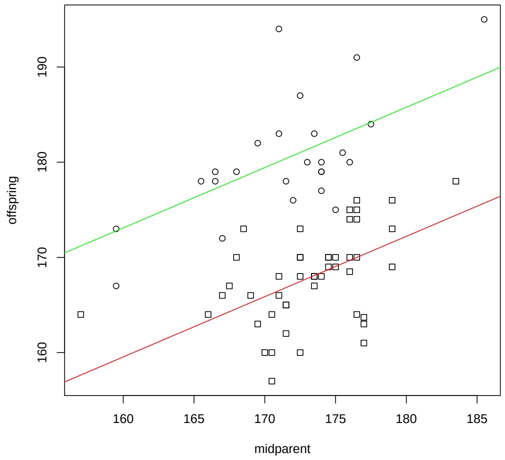
α is intercept, the regression coefficients, (β_{midp} and β_{sex}), represent the effect of the explanatory variables `sex` and `midp` on `height`.

The estimated expected response as function of midparental value for each sex is found by substituting the parameter estimates into (1) and setting `sex` equal to 0 and 1, respectively. This yields the equations

$$\begin{aligned} \text{heigth} &= 58.16 + 0.63 \cdot \text{midp} + 13.55 \cdot 0 \qquad (2) \\ &= 58.16 + 0.63 \cdot \text{midp} \qquad (3) \end{aligned}$$

and

$$\text{heigth} = 58.16 + 0.63 \cdot \text{midp} + 13.55 \cdot 1 \quad (4)$$
$$= 71.71 + 0.63 \cdot \text{midp} \quad (5)$$



Including the midparent value in the regression, increased the estimated sex difference in heigth from 12.52 to 13.56, in addition the standard error decreased from 1.34 to 1.13 (midparent explain more of the height).

```
> regherit<-lm(offspring~midparent)
> summary(regherit)

Call:
lm(formula = offspring ~ midparent)

Residuals:
    Min      1Q  Median      3Q     Max 
-14.349  -4.889  -1.809   6.203  22.443 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)   
(Intercept) 100.3828    33.2833   3.016  0.00357 **
midparent     0.4162     0.1928   2.159  0.03425 * 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1 

Residual standard error: 7.852 on 70 degrees of freedom
Multiple R-squared: 0.06245,Adjusted R-squared: 0.04906 
F-statistic: 4.663 on 1 and 70 DF,  p-value: 0.03425 
```

Removing the sexas a explanatory variable in the regression changes the estimate of heritability to 0.4162.

These changes in the parameter estimates occurs because there is a correlations between the explanatory variables which makes the design unbalanced.

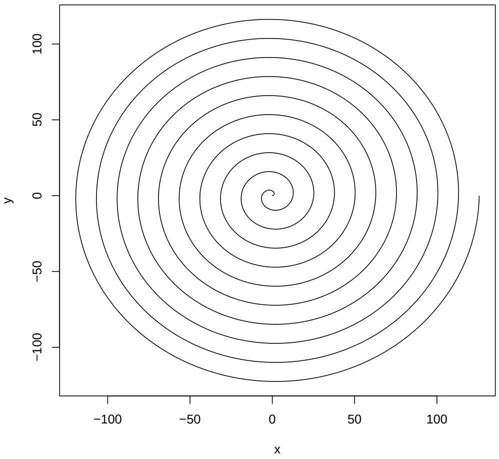
R-code

```
heights <- read.table("http://www.math.ntnu.no/~jarlet/statmod/heights.dat")
attach(heights)
#Make scatter plots of all variable combinations
pairs(heights)

#Estimate the difference in height between the sexes
regsex<-lm(offsring~sex)
summary(regsex)

# two-sample t-test of difference between the sexes
t.test(offspring[sex==0],offspring[sex==1],var.equal=TRUE)

# or
midparent<-(mother+father)/2

# add midparental as a second explanatory variable
regherit<-lm(offspring~sex+midparent)
summary(regherit)


 #scatter plot of the heights of the students versus their midparental values
 plot(midparent,offspring,pch=sex)

#lines representing the estimated expected response as function of midparental value for
abline(58.1637,0.6336,col="red")
abline(58.1637+ 13.5562,0.6336,col="green")

#removing \sex as a parameter in the regression
regherit<-lm(offspring~midparent)
summary(regherit)
```

Problem 2 Setting the proportionality constant $a = 2$, a plot of the parametric curve repesented by the functions

$$x(t) = 2t\cos(t) \tag{6}$$
$$y(t) = 2t\sin(t) \tag{7}$$

is shown below.



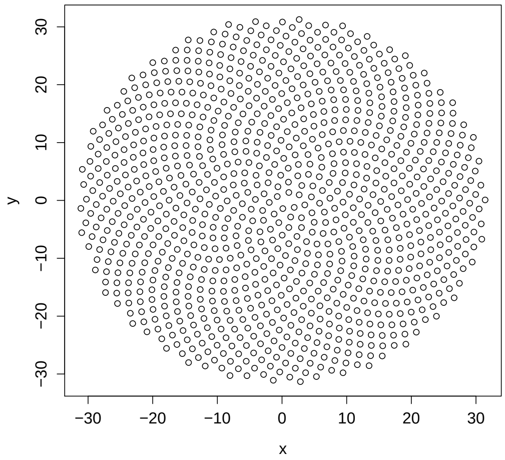
For the sunflower problem, $\theta(i)$ is the anglular direction from the centre of seed number i, $\theta(i) = \pi(3-\sqrt{5})i$ and $r(i) = a\sqrt{i}$ is the distance from the centre of seed number i.

Transforming from these polar coordinates to ordinary cartesian coordinates, we get

$$x(i) = a\sqrt{i}\cos(\pi(3-\sqrt{5})i) \tag{8}$$

$$y(i) = a\sqrt{i}\sin(\pi(3-\sqrt{5})i) \tag{9}$$

If we choose a=4 and makes a sequence with n = 1000 number of seeds, i=1,...,n and compute the corresponding x and y-values we get



An animation showing the growth process is available at `http://www.math.ntnu.no/~jarlet/biomat/solsikke.gif`

R code

```
#make a sequence of t values
t<-seq(0,10*2*pi,by=0.01)
# make the x and y functions
x=2*t*cos(t)
y=2*t*sin(t)

#plot the vectors x,y
plot(x,y,type="l")

#plot the sunflower
a <- 4
i <- seq(1:1000)
theta <-pi*(3-sqrt(5))*i
r <- a*sqrt(i)
x <- r*sin(theta)
y <- r*cos(theta)
plot(x,y)
```