```
setwd("C:/R")

load("fdata.RData")

attach(final)

model01 <- glm(disorder ~ som1 + som2 + som3 + som4 + som5, data=final, family="binomial")

model01$coef

exp(model01$coed)

model02 <- glm(disorder ~ som6+som7+som8+som9, data=final, family="binomial")

model02$coef

exp(model02$coef)

model03 <- glm(diroder ~ som10+som11+som12+som13+som14, data=final, family="binomial")

model03$coef

exp(model03$coef)

summary(model01)

summary(model02)

summary(model03)

detach(final)
```

SUmmary Model01

Deviance Residuals:

 Min 1Q Median 3Q Max

-3.3107 -0.2463 0.0000 0.0957 3.0752

Coefficients:

 Estimate Std. Error z value Pr(>|z|)

(Intercept) -4.7196 0.5726 -8.242 < 2e-16 ***

som1 0.5215 0.2351 2.218 0.02656 *

som2 1.2390 0.2970 4.172 3.02e-05 ***

som3 0.5441 0.1171 4.648 3.35e-06 ***

som4 0.5320 0.1468 3.624 0.00029 ***

som5 2.4536 0.4228 5.804 6.48e-09 ***

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

Null deviance: 447.70 on 322 degrees of freedom

Residual deviance: 123.75 on 317 degrees of freedom

 AIC: 135.75

Number of Fisher Scoring iterations: 8

Summary model02

Deviance Residuals:

 Min 1Q Median 3Q Max

-2.34372 -0.62207 0.00045 0.49654 1.86426

Coefficients:

 Estimate Std. Error z value Pr(>|z|)

(Intercept) -1.5442 0.2009 -7.685 1.53e-14 ***

som6 1.9406 0.4662 4.163 3.15e-05 ***

som7 1.0921 0.2536 4.307 1.66e-05 ***

som8 1.1669 0.4176 2.794 0.0052 **

som9 1.1918 0.1925 6.190 6.03e-10 ***

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

 Null deviance: 447.70 on 322 degrees of freedom

Residual deviance: 270.32 on 318 degrees of freedom

 AIC: 280.32

Number of Fisher Scoring iterations: 7

Summary model03

Deviance Residuals:

 Min 1Q Median 3Q Max

-1.84363 -0.26365 0.00067 0.05370 3.09428

Coefficients:

 Estimate Std. Error z value Pr(>|z|)

(Intercept) -4.7789 0.6066 -7.878 3.32e-15 ***

som10 1.0075 0.3260 3.090 0.0020 **

som11 0.7396 0.3913 1.890 0.0587 .

som12 0.5288 0.3161 1.673 0.0944 .

som13 1.4370 0.2148 6.689 2.24e-11 ***

som14 1.0204 0.4125 2.474 0.0134 *

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

 Null deviance: 447.70 on 322 degrees of freedom

Residual deviance: 110.32 on 317 degrees of freedom

 AIC: 122.32

Number of Fisher Scoring iterations: 8

1. Build a first logistic model using only SOM1, SOM2, SOM3, SOM4 and SOM5. What are the important features in this model? What is the interpretation of the SOM1 coefficient?

    The important features of this model are somatic markers 2 to 5.
    The SOM1 coefficient is not important because it has a relatively higher p-value.

2. Build a second model using only SOM6, SOM7, SOM8, SOM9. What are the most important features in this model?

    The most important features in this model somatic markers 6, 7, and 9.

3. Build a third model using only SOM10, SOM11, SOM12, SOM13, SOM14. What are the most important features in this model?

    Somatic markers 10, 13, and 14 are important in this model (marked by *). Somatic markers 11 and 12 are on the edge of being considered important features (marked by .).

4. Compare the three models. Which one is better at predicting the likelihood of the disorder?

    Model03 is the best for predicting the likelihood of the disorder because it has relatively low residual deviance and AIC scores.