

Code

```
# Prepare the model and get a summary for som1-5
```

```
model1 <- glm(disorder~som1 + som2 + som3 + som4 + som5, data = final, family  
= "binomial")
```

```
model1$coef
```

```
exp(model1$coef)
```

```
summary(model1)
```

```
# Prepare the model and get a summary for som6-9
```

```
model2 <- glm(disorder~som6 + som7 + som8 + som9, data = final, family =  
"binomial")
```

```
model2$coef
```

```
exp(model2$coef)
```

```
summary(model2)
```

```
# Prepare the model and get a summary for som10-14
```

```
model3 <- glm(disorder~som10 + som11 + som12 + som13 + som14, data = final,  
family = "binomial")
```

```
model3$coef
```

```
exp(model3$coef)
```

```
summary(model3)
```

Results

Call:

```
glm(formula = disorder ~ som1 + som2 + som3 + som4 + som5, family =  
"binomial",  
     data = final)
```

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

(Dispersion parameter for binomial family taken to be 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

Call:

```
glm(formula = disorder ~ som6 + som7 + som8 + som9, family = "binomial",  
     data = final)
```

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

(Dispersion parameter for binomial family taken to be 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

Call:

```
glm(formula = disorder ~ som10 + som11 + som12 + som13 + som14,  
     family = "binomial", data = final)
```

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

(Dispersion parameter for binomial family taken to be 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

Interpretation

1. The important features in this model are SOM2-5 as demonstrated by their '***' markings and their small p-values. SOM1 is not important for analyzing the disorder as shown by the high p-value.
2. All of the somatic markers 6-9 are important in this model. Only marker 8, with a slightly higher p-value and a marking '**' is of lesser, but still significant, importance.
3. In this model, we see that the order of importance of the markers is 13, 10, 14 and lastly 11 and 12. Marker 13 has a '***' marking, 10 is '**', 14 is '*' and 11/12 are ''.
4. In terms of which model is better for predicting the likelihood of the disorder, model 3 is the best, followed closely by model 1 and model 2 in a distant 3rd. The best way to see which is