Litorela

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# Litorela report

## Effect of soil type on germination of Litorela uniflora

### Model:

* succ = number of germinated seeds
* fail = succ - sum (all seeds)
* treat = soil type

#put together some model  
mod <- glm(cbind(succ, fail) ~ treat, data=data,family=binomial)  
mod

##   
## Call: glm(formula = cbind(succ, fail) ~ treat, family = binomial, data = data)  
##   
## Coefficients:  
## (Intercept) treatcontrol treatmud treatpeat   
## -1.9924 1.9524 0.8398 -0.9520   
## treatsand treatsand\_clay treatsand\_mud treatsand\_peat   
## -0.3212 -1.1856 0.1771 -1.4837   
## treattopsoil   
## -18.1260   
##   
## Degrees of Freedom: 89 Total (i.e. Null); 81 Residual  
## Null Deviance: 249.9   
## Residual Deviance: 107 AIC: 233.1

summary(mod)

##   
## Call:  
## glm(formula = cbind(succ, fail) ~ treat, family = binomial, data = data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.6543 -0.9036 -0.1997 0.5192 2.7690   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -1.9924 0.3077 -6.475 9.50e-11 \*\*\*  
## treatcontrol 1.9524 0.3670 5.319 1.04e-07 \*\*\*  
## treatmud 0.8398 0.3867 2.172 0.0299 \*   
## treatpeat -0.9520 0.5525 -1.723 0.0849 .   
## treatsand -0.3212 0.4656 -0.690 0.4903   
## treatsand\_clay -1.1856 0.5959 -1.990 0.0466 \*   
## treatsand\_mud 0.1771 0.4216 0.420 0.6744   
## treatsand\_peat -1.4837 0.6621 -2.241 0.0250 \*   
## treattopsoil -18.1260 1417.4364 -0.013 0.9898   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 249.93 on 89 degrees of freedom  
## Residual deviance: 107.05 on 81 degrees of freedom  
## AIC: 233.08  
##   
## Number of Fisher Scoring iterations: 17

anova(mod, test="Ch")

## Analysis of Deviance Table  
##   
## Model: binomial, link: logit  
##   
## Response: cbind(succ, fail)  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev Pr(>Chi)   
## NULL 89 249.93   
## treat 8 142.88 81 107.05 < 2.2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

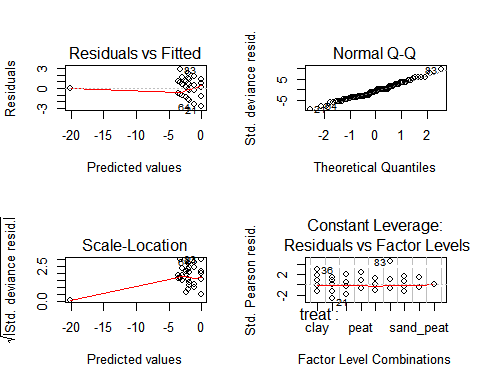
### Results

Vliv pudniho typu je vyznamny.

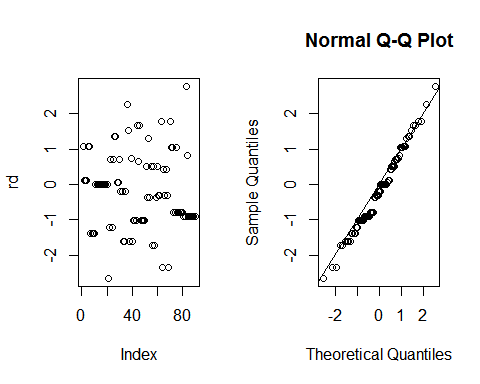
### Residuals

Residua se chovaji pomerne normalne, takze model fituje data dobre.

#see what is going on with residuals  
par(mfrow=c(2,2))  
plot(mod)



par(mfrow=c(1,2))  
rd=residuals(mod)  
plot(rd)  
qqnorm(residuals(mod, type="deviance"))  
abline(a=0,b=1)



### Germination probability (%)

#back-transformation of coeficients for each treatment to mean survival probability  
plogis (mod$coefficients[1]) #intercept (clay)

## (Intercept)   
## 0.12

plogis (mod$coefficients[1]+mod$coefficients[2]) #control

## (Intercept)   
## 0.49

plogis (mod$coefficients[1]+mod$coefficients[3]) #mud

## (Intercept)   
## 0.24

plogis (mod$coefficients[1]+mod$coefficients[4]) #peat

## (Intercept)   
## 0.05

plogis (mod$coefficients[1]+mod$coefficients[5]) #sand

## (Intercept)   
## 0.09

plogis (mod$coefficients[1]+mod$coefficients[6]) #sand\_clay

## (Intercept)   
## 0.04

plogis (mod$coefficients[1]+mod$coefficients[7]) #sand\_mud

## (Intercept)   
## 0.14

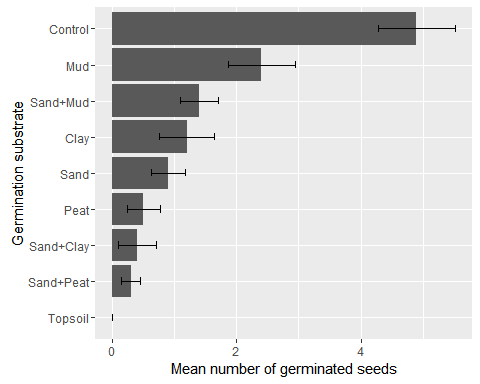
plogis (mod$coefficients[1]+mod$coefficients[8]) #sand\_peat

## (Intercept)   
## 0.03

plogis (mod$coefficients[1]+mod$coefficients[9]) #topsoil

## (Intercept)   
## 1.831042e-09

### Bar plot:



## THE END

## Effect of place of origin on germination of Litorela uniflora

### Model:

* succ = number of germinated seeds
* fail = succ - sum (all seeds)
* loc = place of origin

### Results

Vliv lokality ma vyznamny vliv na klicivost semen L. uniflora.

mod <- glm(cbind(succ, fail) ~ loc, data=data,family=binomial)  
mod

##   
## Call: glm(formula = cbind(succ, fail) ~ loc, family = binomial, data = data)  
##   
## Coefficients:  
## (Intercept) lockr locla locmr locno   
## -3.5973 1.4721 1.1550 -0.7068 -17.3653   
## locos locry locst   
## 1.7255 1.3237 0.4193   
##   
## Degrees of Freedom: 21 Total (i.e. Null); 14 Residual  
## Null Deviance: 33.57   
## Residual Deviance: 14.82 AIC: 71.65

summary(mod)

##   
## Call:  
## glm(formula = cbind(succ, fail) ~ loc, family = binomial, data = data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.0418 -0.7269 -0.0001 0.3858 1.3132   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.5973 0.7167 -5.019 5.19e-07 \*\*\*  
## lockr 1.4721 0.8085 1.821 0.0686 .   
## locla 1.1550 0.8336 1.386 0.1659   
## locmr -0.7068 1.2358 -0.572 0.5674   
## locno -17.3653 4323.6575 -0.004 0.9968   
## locos 1.7255 0.7931 2.176 0.0296 \*   
## locry 1.3237 0.8193 1.616 0.1062   
## locst 0.4193 0.9279 0.452 0.6514   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 33.571 on 21 degrees of freedom  
## Residual deviance: 14.816 on 14 degrees of freedom  
## AIC: 71.651  
##   
## Number of Fisher Scoring iterations: 17

anova(mod, test="Ch")

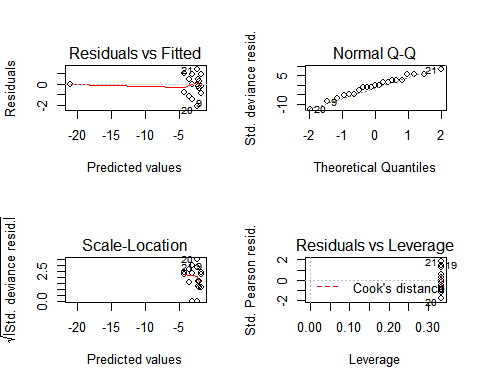
## Analysis of Deviance Table  
##   
## Model: binomial, link: logit  
##   
## Response: cbind(succ, fail)  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev Pr(>Chi)   
## NULL 21 33.571   
## loc 7 18.755 14 14.816 0.00899 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### Residuals

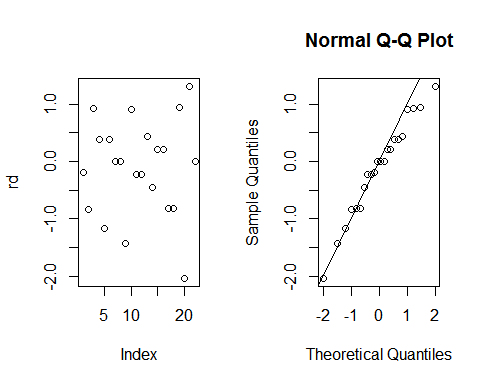
Residua se chovaji pomerne normalne, takze model fituje data dobre.

par(mfrow=c(2,2))  
plot(mod)

## Warning: not plotting observations with leverage one:  
## 7  
  
## Warning: not plotting observations with leverage one:  
## 7



par(mfrow=c(1,2))  
rd=residuals(mod)  
plot(rd)  
qqnorm(residuals(mod, type="deviance"))  
abline(a=0,b=1)



### Germination probability (%)

Bohuzel netusim co ktery kod znamena, takze je to tam takto. Pripadalo mi to lepsi nez lok1-lokx.

#plogis - "ka", "kr", "la", "mr", "no", "os", "ry", "st"  
plogis (mod$coefficients[1]) #intercept (ka)

## (Intercept)   
## 0.02666667

plogis (mod$coefficients[1]+mod$coefficients[2]) #kr

## (Intercept)   
## 0.1066667

plogis (mod$coefficients[1]+mod$coefficients[3]) #la

## (Intercept)   
## 0.08

plogis (mod$coefficients[1]+mod$coefficients[4]) #mr

## (Intercept)   
## 0.01333333

plogis (mod$coefficients[1]+mod$coefficients[5]) #no

## (Intercept)   
## 7.871599e-10

plogis (mod$coefficients[1]+mod$coefficients[6]) #os

## (Intercept)   
## 0.1333333

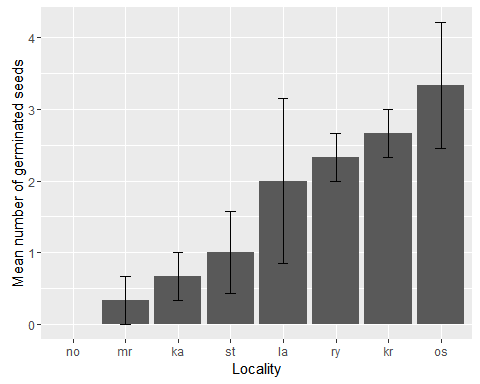
plogis (mod$coefficients[1]+mod$coefficients[7]) #ry

## (Intercept)   
## 0.09333333

plogis (mod$coefficients[1]+mod$coefficients[8]) #st

## (Intercept)   
## 0.04

### Bar plot



### THE END

## Germination under a layer of soil (climabox)

### Model:

* succ = number of germinated seeds
* fail = succ - sum (all seeds)
* depth = soil layer depth

### Results

Vliv faktoru hloubka je vyznamny.

#put together some model  
mod <- glm(cbind(succ, fail) ~ depth, data=substr,family=binomial)  
mod

##   
## Call: glm(formula = cbind(succ, fail) ~ depth, family = binomial, data = substr)  
##   
## Coefficients:  
## (Intercept) depth   
## -1.696 -1.019   
##   
## Degrees of Freedom: 11 Total (i.e. Null); 10 Residual  
## Null Deviance: 38.3   
## Residual Deviance: 15.95 AIC: 33.88

summary(mod)

##   
## Call:  
## glm(formula = cbind(succ, fail) ~ depth, family = binomial, data = substr)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.84721 -0.77249 -0.44611 0.09039 1.71574   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -1.6965 0.2984 -5.685 1.31e-08 \*\*\*  
## depth -1.0189 0.3300 -3.088 0.00202 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 38.304 on 11 degrees of freedom  
## Residual deviance: 15.950 on 10 degrees of freedom  
## AIC: 33.88  
##   
## Number of Fisher Scoring iterations: 6

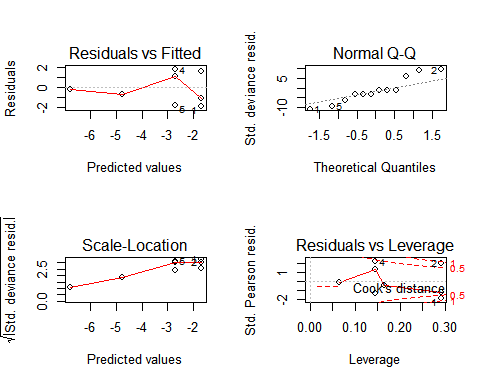
anova(mod, test="Ch")

## Analysis of Deviance Table  
##   
## Model: binomial, link: logit  
##   
## Response: cbind(succ, fail)  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev Pr(>Chi)   
## NULL 11 38.304   
## depth 1 22.354 10 15.950 2.268e-06 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

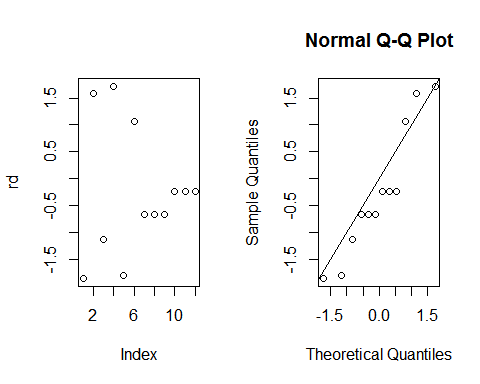
### Residuals

Residua se chovaji pomerne normalne, takze model fituje data dobre.

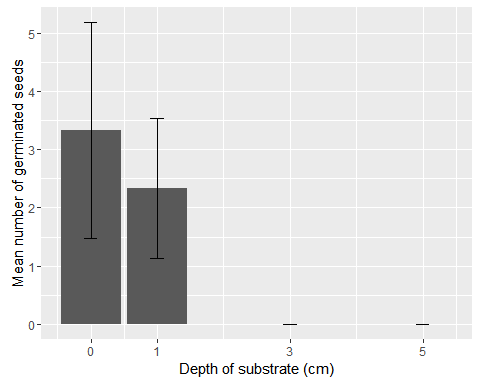
#see what is going on with residuals  
par(mfrow=c(2,2))  
plot(mod)



par(mfrow=c(1,2))  
rd=residuals(mod)  
plot(rd)  
qqnorm(residuals(mod, type="deviance"))  
abline(a=0,b=1)



### Barplot



### THE END

## Germination under a layer of soil (glasshouse)

### Model:

* y = number of germinated seeds / number of fails
* treat = soil layer depth

## [1] 12

### Results

Vliv faktoru hloubka je vyznamny.

#put together some model  
m1=glm(y~treat, family=binomial)  
m1

##   
## Call: glm(formula = y ~ treat, family = binomial)  
##   
## Coefficients:  
## (Intercept) treat   
## 0.3516 -1.3576   
##   
## Degrees of Freedom: 11 Total (i.e. Null); 10 Residual  
## Null Deviance: 118.4   
## Residual Deviance: 9.667 AIC: 35.38

anova(m1, test="Ch")

## Analysis of Deviance Table  
##   
## Model: binomial, link: logit  
##   
## Response: y  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev Pr(>Chi)   
## NULL 11 118.404   
## treat 1 108.74 10 9.667 < 2.2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

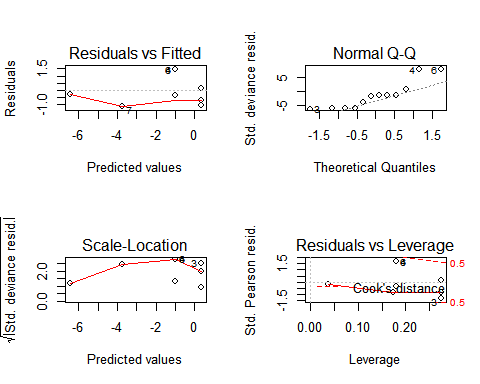
summary(m1)

##   
## Call:  
## glm(formula = y ~ treat, family = binomial)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.0936 -1.0812 -0.3000 -0.1792 1.4325   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 0.3516 0.2127 1.653 0.0983 .   
## treat -1.3576 0.2173 -6.248 4.15e-10 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 118.4043 on 11 degrees of freedom  
## Residual deviance: 9.6671 on 10 degrees of freedom  
## AIC: 35.382  
##   
## Number of Fisher Scoring iterations: 5

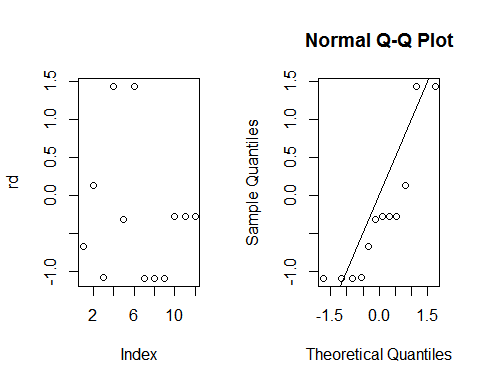
### Residuals

Residua se chovaji divne. Asi schazi nejaky vysvetlujici faktor.

#see what is going on with residuals  
par(mfrow=c(2,2))  
plot(m1)



rd=residuals(m1,type = c("deviance"))  
par(mfrow=c(1,2))  
rd=residuals(m1)  
plot(rd)  
qqnorm(residuals(m1, type="deviance"))  
abline(a=0,b=1)



### Barplot

