Overdisp

Oct 29

28/10/2020

```r
ftable(xtabs(cbind(survive,total) ~ location + period, data = troutegg))
```

```
##                  survive total
## location period
## 1        4            89    94
##          7            94    98
##          8            77    86
##          11          141   155
## 2        4           106   108
##          7            91   106
##          8            87    96
##          11          104   122
## 3        4           119   123
##          7           100   130
##          8            88   119
##          11           91   125
## 4        4           104   104
##          7            80    97
##          8            67    99
##          11          111   132
## 5        4            49    93
##          7            11   113
##          8            18    88
##          11            0   138
```

```r
bmod <- glm(cbind(survive,total-survive) ~
              location + period,
            family = binomial,
            data = troutegg)

summary(bmod)
```

```
##
## Call:
## glm(formula = cbind(survive, total - survive) ~ location + period,
##     family = binomial, data = troutegg)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.8305  -0.3650  -0.0303   0.6191   3.2434
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)   4.6358     0.2813  16.479  < 2e-16 ***
## location2    -0.4168     0.2461  -1.694   0.0903 .
## location3    -1.2421     0.2194  -5.660 1.51e-08 ***
## location4    -0.9509     0.2288  -4.157 3.23e-05 ***
## location5    -4.6138     0.2502 -18.439  < 2e-16 ***
## period7      -2.1702     0.2384  -9.103  < 2e-16 ***
## period8      -2.3256     0.2429  -9.573  < 2e-16 ***
## period11     -2.4500     0.2341 -10.466  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1021.469  on 19  degrees of freedom
## Residual deviance:   64.495  on 12  degrees of freedom
## AIC: 157.03
##
## Number of Fisher Scoring iterations: 5
```

```r
# plot(bmod)

bmod2 <- glm(cbind(survive,total-survive) ~
               location + period,
             family = quasibinomial,
             data = troutegg)

summary(bmod2)
```

```
##
## Call:
## glm(formula = cbind(survive, total - survive) ~ location + period,
##     family = quasibinomial, data = troutegg)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.8305  -0.3650  -0.0303   0.6191   3.2434
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   4.6358     0.6495   7.138 1.18e-05 ***
## location2    -0.4168     0.5682  -0.734 0.477315
## location3    -1.2421     0.5066  -2.452 0.030501 *
## location4    -0.9509     0.5281  -1.800 0.096970 .
## location5    -4.6138     0.5777  -7.987 3.82e-06 ***
## period7      -2.1702     0.5504  -3.943 0.001953 **
## period8      -2.3256     0.5609  -4.146 0.001356 **
## period11     -2.4500     0.5405  -4.533 0.000686 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 5.330358)
##
##     Null deviance: 1021.469  on 19  degrees of freedom
## Residual deviance:   64.495  on 12  degrees of freedom
## AIC: NA
```

```
##
## Number of Fisher Scoring iterations: 5
```