Fitting Various Models in R

```
In [1]: library(data.table)
        library(MASS)
        library(VGAM)

        ichs.data <- data.table(read.table('ichs.txt'))
        head(ichs.data)
```

```
Loading required package: stats4
Loading required package: splines
```

id	gender	height	cosv	sinv	xero	baseage	age	infect
121013	0	-3	-1	0	0	31	31	0
121013	0	-3	0	-1	0	31	34	0
121013	0	-2	1	0	0	31	37	0
121013	0	-2	0	1	0	31	40	0
121013	0	-2	-1	0	0	31	43	1
121013	0	-3	0	-1	0	31	46	0

```
In [2]: bernoulli.model <- glm(infect ~ 1, data=ichs.data, family = quasibinomial)
        summary(bernoulli.model)
```

```
Call:
glm(formula = infect ~ 1, family = quasibinomial, data = ichs.data)

Deviance Residuals:
    Min       1Q    Median       3Q      Max
-0.4322  -0.4322   -0.4322  -0.4322   2.1987

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -2.3239     0.1013  -22.93   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 1.000834)

    Null deviance: 721.45  on 1199  degrees of freedom
Residual deviance: 721.45  on 1199  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```

```
In [3]:  binomial.model <- glm(
            cbind(infect, n - infect) ~ 1, family = quasibinomial,
            data=ichs.data[,list(n=length(infect), infect=sum(infect)),by=.(id)])
         summary(binomial.model)
```

Call:
glm(formula = cbind(infect, n - infect) ~ 1, family = quasibinomial,
    data = ichs.data[, list(n = length(infect), infect = sum(infect)),
        by = .(id)])

Deviance Residuals:
    Min   1Q   Median   3Q   Max
 -1.0587 -1.0587 -0.7486   0.6014   4.3975

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -2.3239   0.1175 -19.77   <2e-16 ***

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

(Dispersion parameter for quasibinomial family taken to be 1.346287)

    Null deviance: 312.47 on 274 degrees of freedom
Residual deviance: 312.47 on 274 degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5

```
beta.binomial.model <- vglm(
    cbind(infect, n - infect) ~ 1, family = betabinomial,
    data=ichs.data[,list(n=length(infect), infect=sum(infect)),by=.(id)])
summary(beta.binomial.model)
```

Warning message in checkwz(wz, M, trace = trace, wzepsilon = control$wzepsilon):
"22 diagonal elements of the working weights variable 'wz' have been replaced by
1.819e-12"Warning message in checkwz(wz, M = M, trace = trace, wzepsilon = contro
l$wzepsilon):
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1.819e-12"Warning message in checkwz(wz, M = M, trace = trace, wzepsilon = contro
l$wzepsilon):
"22 diagonal elements of the working weights variable 'wz' have been replaced by
1.819e-12"

Call:
vglm(formula = cbind(infect, n - infect) ~ 1, family = betabinomial,
    data = ichs.data[, list(n = length(infect), infect = sum(infect)),
        by = .(id)])

Pearson residuals:
               Min   1Q Median   3Q   Max
logit(mu)   -0.7131 -7.131e-01 -0.5279 0.8009 4.098
logit(rho) -1.2916 2.847e-11 0.1347 0.2801 11.956

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept):1 -2.3117   0.1159 -19.95 < 2e-16 ***
(Intercept):2 -2.4126   0.4188   -5.76 8.4e-09 ***

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

Number of linear predictors: 2

Names of linear predictors: logit(mu), logit(rho)

Log-likelihood: -221.2778 on 548 degrees of freedom

Number of iterations: 3

Warning: Hauck-Donner effect detected in the following estimate(s):
'(Intercept):2'

```
In [5]: binomial.model <- glm(
            cbind(infect, n - infect) ~ 1 + baseage, family = quasibinomial,
            data=ichs.data[,list(n=length(infect), infect=sum(infect), baseage=mean(baseag
        e)),by=.(id)])
        summary(binomial.model)
```

```
Call:
glm(formula = cbind(infect, n - infect) ~ 1 + baseage, family = quasibinomial,
    data = ichs.data[, list(n = length(infect), infect = sum(infect),
        baseage = mean(baseage)), by = .(id)])

Deviance Residuals:
    Min       1Q    Median       3Q       Max
-1.4390  -0.8773  -0.5940   0.3292    4.1245

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -2.549413   0.135822 -18.770  < 2e-16 ***
baseage     -0.027499   0.006375  -4.314 2.25e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 1.196207)

    Null deviance: 312.47  on 274  degrees of freedom
Residual deviance: 287.74  on 273  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```

```
In [6]: beta.binomial.model <- vglm(
            cbind(infect, n - infect) ~ 1 + baseage, family = betabinomial,
            data=ichs.data[,list(n=length(infect), infect=sum(infect), baseage=mean(baseag
        e)),by=.(id)])
        summary(beta.binomial.model)
```

Warning message in checkwz(wz, M, trace = trace, wzepsilon = control$wzepsilon):
"22 diagonal elements of the working weights variable 'wz' have been replaced by
1.819e-12"Warning message in checkwz(wz, M = M, trace = trace, wzepsilon = contro
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l$wzepsilon):
"22 diagonal elements of the working weights variable 'wz' have been replaced by
1.819e-12"Warning message in matrix.power(wz, M = M, power = 0.5, fast = TRUE):
"Some weight matrices have negative eigenvalues. They will be assigned NAs"Warnin
g message in matrix.power(wz, M = M, power = 0.5, fast = TRUE):
"Some weight matrices have negative eigenvalues. They will be assigned NAs"

Call:
vglm(formula = cbind(infect, n - infect) ~ 1 + baseage, family = betabinomial,
    data = ichs.data[, list(n = length(infect), infect = sum(infect),
        baseage = mean(baseage)), by = .(id)])

Coefficients:
               Estimate Std. Error z value Pr(>|z|)
(Intercept):1 -2.520914   0.135098 -18.660 < 2e-16 ***
(Intercept):2 -2.707920   0.507098 -5.340 9.29e-08 ***
baseage   -0.026456   0.006302 -4.198 2.69e-05 ***

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

Number of linear predictors: 2

Names of linear predictors: logit(mu), logit(rho)

Log-likelihood: -211.5263 on 547 degrees of freedom

Number of iterations: 6

Warning: Hauck-Donner effect detected in the following estimate(s):
'(Intercept):1', '(Intercept):2'