Experimental Phonetics Reading Group (2014 Dec. 20)

Running Regression in R (I) R tutorial #2

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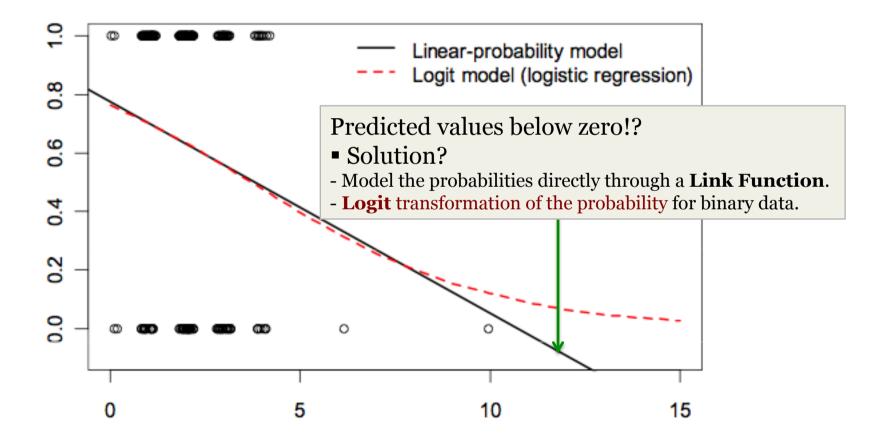
Logistic Regression: glm ()

Analyzing Linguistic Data (Baayen)

Dichotomous response

- Data sets with *binary (dichotomous)* dependent variables :
 - o correct, incorrect
 - o "s", "∫"
 - 1. (Linear) Probability model

Dichotomous response



Dichotomous response

- Data sets with *binary (dichotomous)* dependent variables :
 - o correct, incorrect
 - o "s", "∫"
 - 1. (Linear) Probability model
 - 2. Generalized linear model (GLM)
 - **Logit** or probit regression models.

Odds, Odds-ratio, Logit

• *Odds* is the relative chance of an event (the ratio of two probabilities).

odds = probability of an event =
$$\pi$$

1 - probability of an event 1- π

- *Odds-ratio* is the ratio of two odds.
- *Log-odds (Logit)* is the natural logarithm of the odds.
- The log-odds is modeled as a linear function in *logistic regression*.

Logistic Regression

• *Logistic regression* (logit model) models the logit (log-odds) as a linear function of the independent variables:

$$logit(\pi_i) = log(\underline{\pi_i}) = \beta_0 + \beta_1 \chi_{1i}$$

1- π_i

✓ Logistic regression coefficients refer to the log-odds.
 ✓ Those logistic regression coefficients are exponentiated to be interpretable.

Data in R



Reading objects from files (.cvs)

http://homepages.wmich.edu/~hillenbr/voweldata.html

> dat = read.csv(file.choose(), header= T) # "reg_dat_logi.csv"

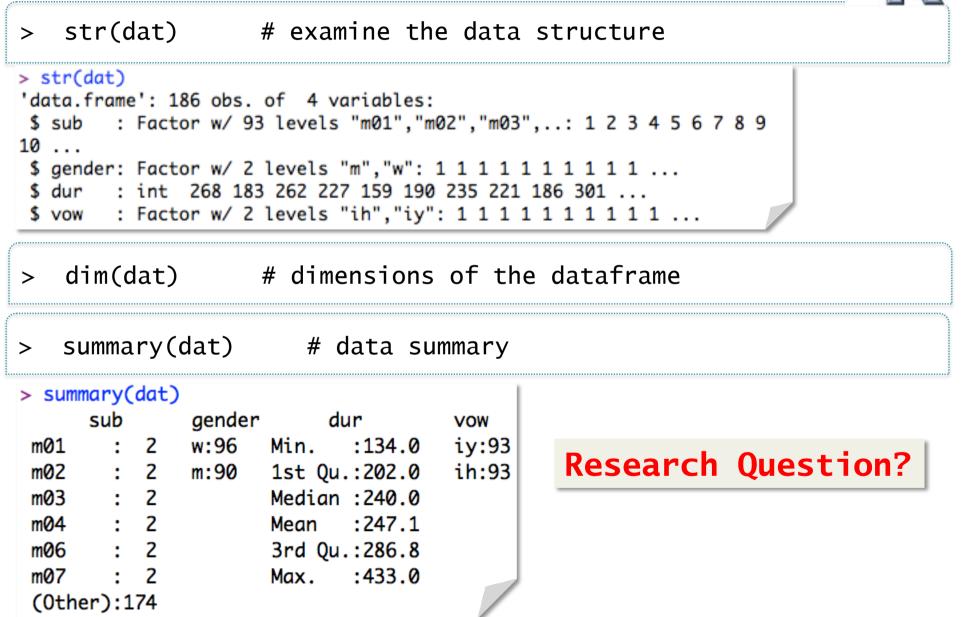
> head(dat) # first 6 rows > tail(dat) # last 6 rows > dat[15:20,] # 15th~ 20th rows of the data

> dat[15:20,]

	sub	gender	dur	VOW
15	m18	m	179	ih
16	m19	m	194	ih
17	m20	m	221	ih
18	m21	m	145	ih
19	m22	m	220	ih
20	m23	m	207	ih

Data in R: Reading objects from files (.cvs)

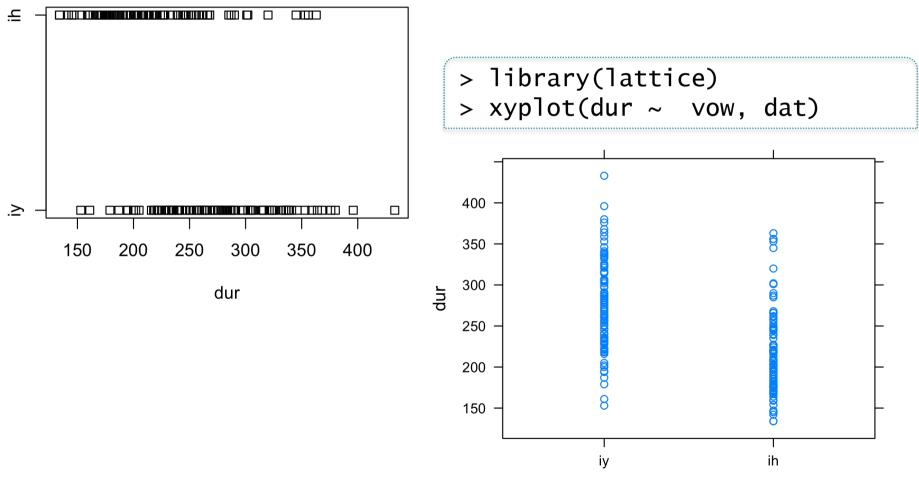




Visual Inspection: plot()



> stripchart(dur ~ vow, dat)



Logistic Regression: glm()



Dichotomous dependent variable: "1" or "0"

- > dat\$dv[dat\$vow == "ih"] = 0
- > dat\$dv[dat\$vow == "iy"] = 1
- > dat\$dv[dat\$vow == "ih"] = 0
- > dat\$dv[dat\$vow == "iy"] = 1
- > dat\$dv = as.factor(dat\$dv)
- > is.numeric(dat\$dv)
- [1] FALSE
- > is.factor(dat\$dv)

[1] TRUE

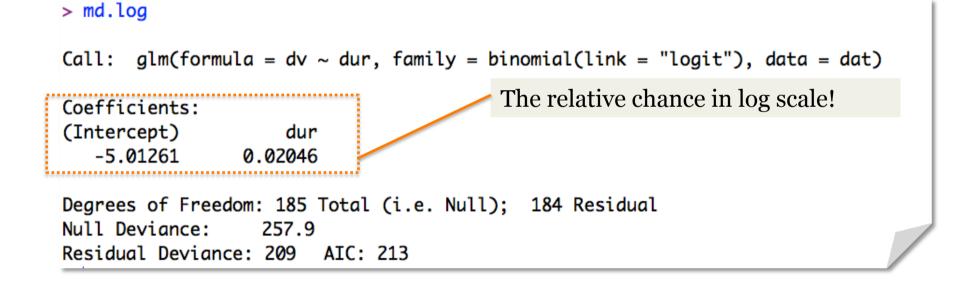
Reference level of the dependent variable: "iy" (vs. "ih")

> dat\$vow = relevel(as.factor(dat\$vow), ref = "iy")



Formula: Generalized Linear Model

> md.log = glm(dv ~ dur, data = dat, binomial(link = "logit"))





> summary(md.log)

```
> summary(md.log)
Call:
glm(formula = dv \sim dur, family = binomial(link = "logit"), data = dat)
                                           The relative chance of being "iy" in log scale:
Deviance Residuals:
   Min
             10 Median
                                      Max > exp()
                              3Q
-2.2362 -0.8828 -0.1189 0.9573 2.0119
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -5.012615 0.858001 -5.842 5.15e-09 ***
                       0.003473
                                 5.891 3.85e-09 ***
dur
            0.020461
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 257.85 on 185 degrees of freedom
Residual deviance: 209.03 on 184 degrees of freedom
AIC: 213.03
Number of Fisher Scoring iterations: 4
```



- > summary(md.log)
- > exp(coef(md.log)) # coefficients on odds-scale

<pre>> exp(coef(md.log))</pre>	
(Intercept) dur	
0.006653483 1.020671766	

• **Intercept**: With o ms. the relative chance (odds) of being "iy" is 0.006.

• **Slope**: With one ms. increase of duration, the relative chance (odds) for "iy" increases by 2%.

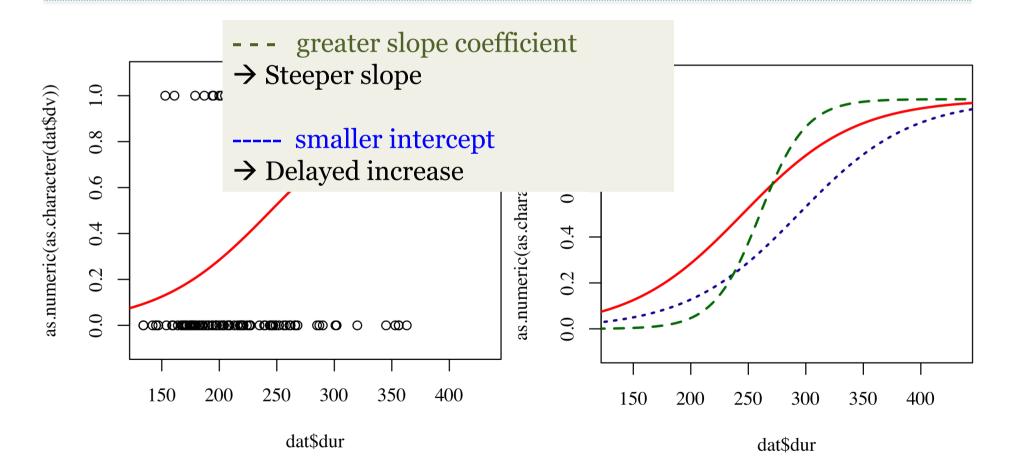
• ex: the token with 200ms duration has a relative chance of 0.0067 \times 1. 02²⁰⁰ of getting "iy".

Linear regression: logit plot



> plot(dat\$dur, as.numeric(as.character(dat\$dv)), ylim = c(-0.1,1.1))

> lines(100:450, predict(md.log, data.frame(dur = 100:450), type = 'response'), lwd = 2, col = 'red', lty = 1)





<pre>> summary(md.log)</pre>					
·		• Null deviance : the deviance estimated from a model with only an intercept.			
	<pre>> summary(md.log)</pre>				
	Call: glm(formula = dv ~	• Residual deviance : the deviance estimated from a model with only an intercept and independent variables. i.e., generalization of the residual sum of squares for a linear model.			
	Deviance Residuals Min 1Q -2.2362 -0.8828	 The smaller the deviance, the better the fit (the better the model's predictive power) 			
	Coefficients: Estim (Intercept) -5.012 dur 0.020	 The difference between Null and Residual deviances follows a chi-square distribution. 			
	Signif. codes: 0	• anova()			
	(Dispersion parameter for binomial family taken to be 1)				
Null deviance: 257.85 on 185 degrees of freedom Residual deviance: 209.03 on 184 degrees of freedom AIC: 213.03					
	Number of Fisher Scoring iterations: 4				



Null deviance: 257.85 on 185 degrees of freedom Residual deviance: 209.03 on 184 degrees of freedom

> 1 - pchisq(257.85 - 209.03, 185 - 184)
> anova(md.log, test = "Chisq") # deviance test, likelihood-ratio test

> (anova(md.log, test = "Chisq")) • If the difference in the null and fitted residual Analysis of Deviance Table deviance is rather large, the model has significant predictive power. Model: binomial, link: logit • A very small p-value shows that we have a model with explanatory value. Response: dv Terms added sequentially (first to last) Df Deviance Resid. Df Resid. Dev Pr(>Chi) NULL 185 257.85 48.821 184 209.03 2.805e-12 *** dur



> summary(md.log)

	 Akaike Information Criterion: An index of fit that adds a penalty term to the deviance which takes the number of parameters into account. The smaller, the better model. 			
-2.2362 -0.8828 -0.1189 0.9573 2.0119				
Coefficients: Estimate Std. Error z value Pr(> z) (Intercept) -5.012615 0.858001 -5.842 5.15e-09 *** dur 0.020461 0.003473 5.891 3.85e-09 *** Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1				
(Dispersion parameter for binomial family taken to be 1)				
Null deviance: 257.85 on 185 degrees of freedom Residual deviance: 209.03 on 184 degrees of freedom AIC: 213.03				
Number of Fisher Scoring iterations: 4				

Logistic Regression: glm () interaction term

Data in R



Reading objects from files (.cvs)

> dat = read.csv(file.choose(), header= T) # "reg_dat_logi.csv"
> summary(dat)

> summary(dat)

	sub		gender	dı	ır	VOW
m01	:	2	w:96	Min.	:134.0	iy:93
m02	:	2	m:90	1st Qu.	:202.0	ih:93
m03	:	2		Median	:240.0	
m04	:	2		Mean	:247.1	
m06	:	2		3rd Qu.	:286.8	
m07	:	2		Max.	:433.0	
(Oth	er):1	74				

Data in R

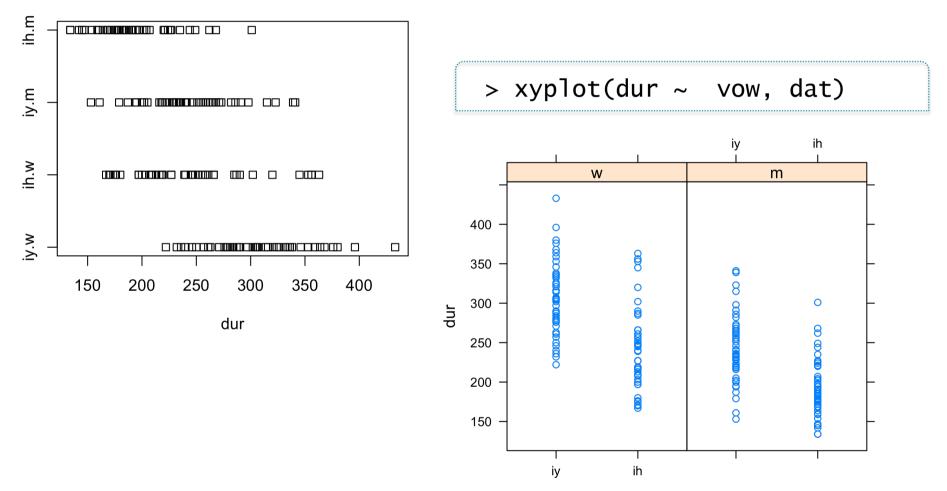


```
> tapply(dat$dur, dat$vow, mean)
> tapply(dat$dur, list(vow = dat$vow, gender = dat$gender), mean)
```

Visual Inspection: plot()



> stripchart(dur ~ vow, dat)



VOW

Logistic Regression: glm()



Dichotomous variable: "1" or "0"

- > dat\$dv[dat\$vow == "ih"] = 0
- > dat\$dv[dat\$vow == "iy"] = 1
- > dat\$dv[dat\$vow == "ih"] = 0
- > dat\$dv[dat\$vow == "iy"] = 1
- > dat\$dv = as.factor(dat\$dv)
- > is.numeric(dat\$dv)

[1] FALSE

> is.factor(dat\$dv)

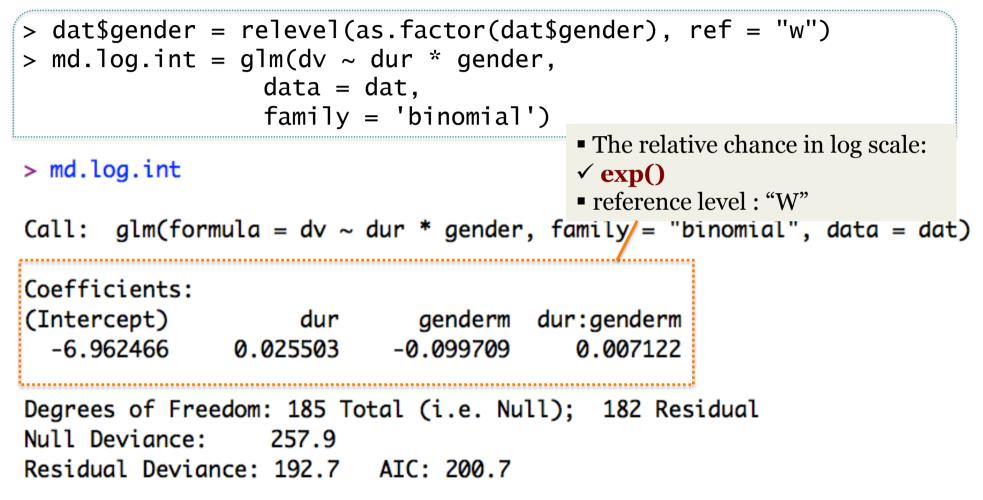
[1] TRUE

Reference level of the dependent variable: "iy" (vs. "ih")

> dat\$vow = relevel(as.factor(dat\$vow), ref = "iy")



Formula: Generalized Linear Model (interaction)





```
> summary(md.log.int)
Call:
qlm(formula = dv \sim dur * gender, family = "binomial", data = dat)
Deviance Residuals:
    Min
               10
                    Median
                                  3Q
                                           Max
-2.37459 -0.79081 -0.08848 0.86138
                                       2,09255
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -6.962466 1.488865 -4.676 2.92e-06 ***
            0.025503 0.005403 4.720 2.36e-06 ***
dur
                                          0.964
aenderm
           -0.099709 2.188005 -0.046
dur:genderm 0.007122 0.009136 0.780
                                          0.436
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 257.85 on 185 degrees of freedom
Residual deviance: 192.75 on 182 degrees of freedom
AIC: 200.75
Number of Fisher Scoring iterations: 4
```





<pre>> coef(md.log.int)</pre>					
(Intercept)	dur	genderm	dur:genderm		
-6.962466270	0.025502649	-0.099708607	0.007121983		
<pre>> exp(coef(md.log.int))</pre>					
(Intercept)	dur	genderm	dur:genderm		
0.0009467587	1.0258306236	0.9051011196	1.0071474048		

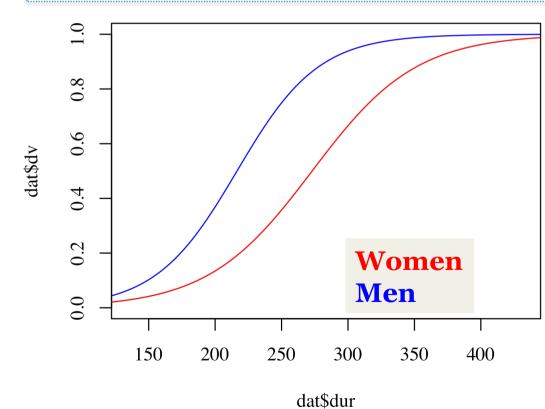
• **Intercept (women)**: With 0 ms. the relative chance (odds) of being "iy" produced by women is 0.0009.

• **Slope (women)**: With one ms. increase of duration, the relative chance (odds) for "iy" produced by women increases by 2.5%.

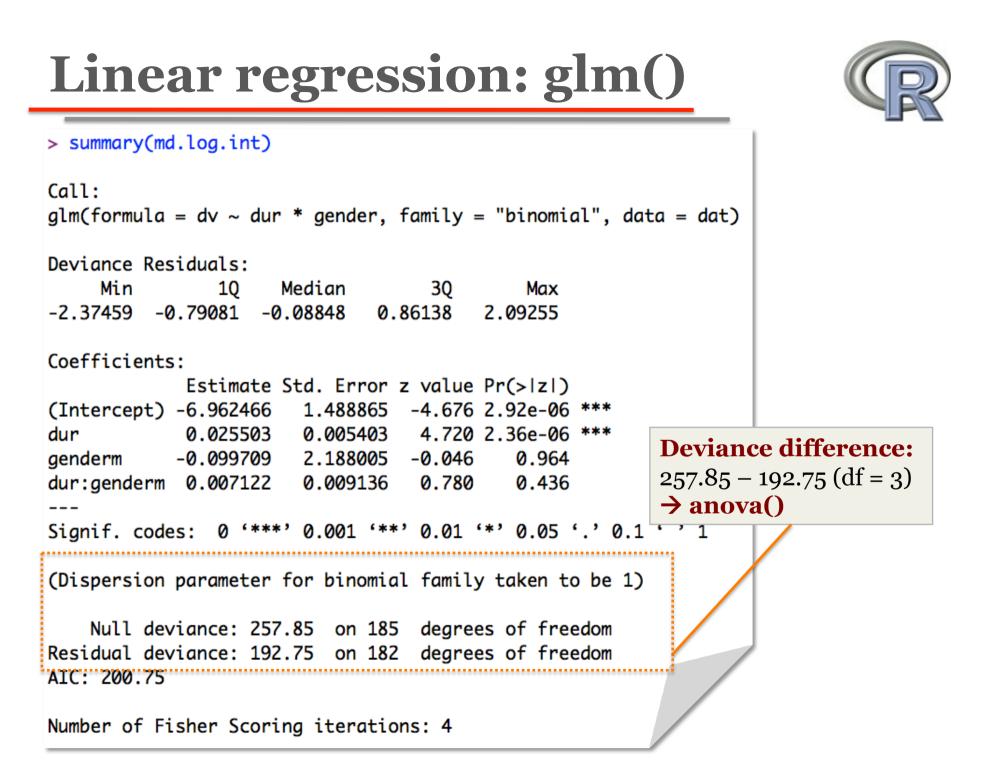
Intercept (men): With 0 ms. the relative chance (odds) of being "iy" produced by men is 0.0008569124 (0.0009467587 * 0.9051011196).
Slope (men): With one ms. increase of duration, the relative chance (odds) for "iy" produced by men increases by 3.3% (1.0258306236 * 1.0071474048)



> plot(dat\$dur, dat\$dv, ylim = c(0,1), type = "n")
> lines(100:450, predict(md.log.int, data.frame(dur = 100:450, gender
= "w"), type = 'response'), lwd = 1, col = 'red', lty = 1)
> lines(100:450, predict(md.log.int, data.frame(dur = 100:450, gender
= "m"), type = 'response'), lwd = 1, col = 'blue', lty = 1)



	women	men
slope	0.025503	0.032624632
intercept	-6.962466	-7.062174877





Null deviance: 257.85 on 185 degrees of freedom Residual deviance: 192.75 on 182 degrees of freedom

> 1 - pchisq(257.85 - 192.75, 185 - 182)

```
> 1 - pchisq(257.85-192.75, 185-182)
[1] 4.773959e-14
```

 Large difference between null and fitted residual deviance & a very small p-value

 \rightarrow the model has significant predictive power.

• Note that the model has a meaningful difference when duration factor, gender factor and interaction factor were added.



```
> md.log.int.0 = glm(dv ~ 1, data = dat, family = 'binomial')
> md.log.int.1 = glm(dv ~ dur , data = dat, family = 'binomial')
> md.log.int.2 = glm(dv ~ dur + gender, data = dat, family = 'binomial')
> md.log.int = glm(dv ~ dur + gender + dur:gender, data = dat, family = 'binomial')
```

```
Analysis of Deviance Table

    Addition of duration factor

Model 1: dv ~ 1

    Addition of gender factor

    Addition of gender and duration interaction

Model 2: dv \sim dur
Model 3: dv \sim dur + gender
Model 4: dv \sim dur + gender + dur:gender
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
        185
                257.85
1
2
        184
                209.03 1 48.821 2.805e-12
3
        183 193.37 1 15.662 7.572e-05
        182 192.75 1 0.621 0.4307
4
```



> summary(md.log)

	 Akaike Information Criterion: An index of fit that adds a penalty term to the deviance which takes the number of parameters into account. The smaller, the better model. 		
-2.2362 -0.8828 -0.1189 0.9573 2.0119 Coefficients: Estimate Std. Error z value Pr(> z) (Intercept) -5.012615 0.858001 -5.842 5.15e-09 ***			
dur 0.020461 0.003473 5.891 3.8 Signif. codes: 0 '***' 0.001 '**' 0.01 '*' (Dispersion parameter for binomial family ta	0.05'.'0.1''1		
Null deviance: 257.85 on 185 degrees o Residual deviance: 209.03 on 184 degrees o AIC: 213.03 Number of Fisher Scoring iterations: 4			