

# empirical logits

*Chris Parrish*

*January 11, 2016*

empirical logits

reference:

- Cannon, et al., Stat2, chapter 09, example 9.9

Migraines.

Import the data.

```
migraines <- c(39, 61, 22, 78)
dim(migraines) <- c(2, 2)
dimnames(migraines) <- list("pain-free"=c("yes", "no"),
                             treatment=c("TMS", "placebo"))
migraines
```

```
##           treatment
## pain-free TMS placebo
##      yes  39      22
##      no   61      78
```

```
addmargins(migraines)
```

```
##           treatment
## pain-free TMS placebo Sum
##      yes  39      22  61
##      no   61      78 139
##      Sum 100     100 200
```

```
migraines.table <- round(rbind(odds=c(39 / 61, 22 / 78),
                               log.odds=c(log(39 / 61), log(22 / 78))), 3)
colnames(migraines.table) <- c("TMS", "placebo")
migraines.table
```

```
##           TMS placebo
## odds      0.639   0.282
## log.odds -0.447  -1.266
```

```
slope <- log(39 / 61) - log(22 / 78)
slope  # slope = log(OR) = log(odds.TMS / odds.placebo)
```

```
## [1] 0.8183542
```

glm.

```
migraines.data <- cbind(migraines[1, ], migraines[2, ])
treatment <- 1:0
migraines.glm <- glm(migraines.data ~ treatment, family=binomial)
options(show.signif.stars=FALSE)
summary(migraines.glm)
```

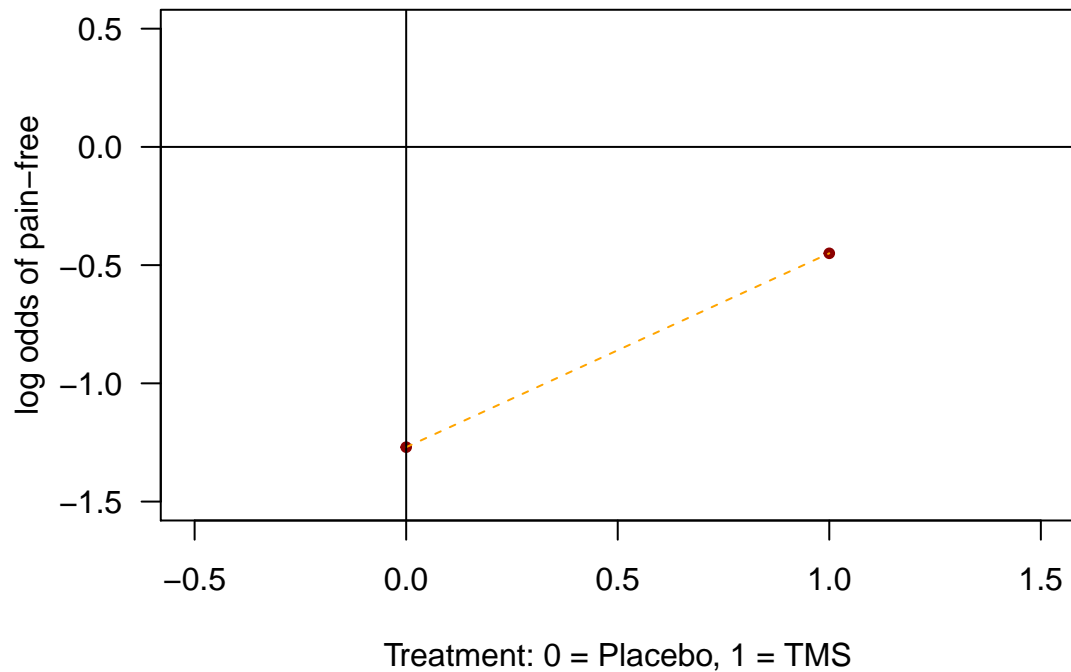
```
##
## Call:
## glm(formula = migraines.data ~ treatment, family = binomial)
##
## Deviance Residuals:
## [1]  0  0
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.2657      0.2414  -5.243 1.58e-07
## treatment    0.8184      0.3167   2.584 0.00977
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 6.8854e+00 on 1 degrees of freedom
## Residual deviance: 3.7970e-14 on 0 degrees of freedom
## AIC: 13.701
##
## Number of Fisher Scoring iterations: 3
```

```
beta1 <- coef(migraines.glm)[2]
beta1 # beta1 = slope
```

```
## treatment
## 0.8183542
```

Illustration.

```
plot(x=c(0, 1), y=c(-1.27, -0.45),
     pch=20, las=1, col="darkred",
     xlim=c(-0.5, 1.5), ylim=c(-1.5, 0.5),
     xlab="Treatment: 0 = Placebo, 1 = TMS",
     ylab="log odds of pain-free")
segments(0, -1.27, 1, -0.45,
         col="orange", lty="dashed")
abline(h=0)
abline(v=0)
```



Marriage

Import the data.

```
marriage <- c(176, 134, 148, 142)
dim(marriage) <- c(2, 2)
dimnames(marriage) <- list("mother married"=c("yes", "no"),
                           child=c("boy", "girl"))
marriage
```

```
##           child
## mother married boy girl
##           yes 176 148
##           no  134 142
```

```
addmargins(marriage)
```

```
##           child
## mother married boy girl Sum
##           yes 176 148 324
##           no  134 142 276
##           Sum 310 290 600
```

```
marriage.table <- round(rbind(odds=c(148 / 142, 176 / 134),
                             log.odds=c(log(148 / 142), log(176 / 134))), 3)
colnames(marriage.table) <- c("girl", "boy")
marriage.table
```

```
##           girl  boy
## odds       1.042 1.313
## log.odds   0.041 0.273
```

```
slope <- log(148 / 142) - log(176 / 134)
slope # slope = log(OR) = log(odds.girl / odds.boy)
```

```
## [1] -0.231259
```

glm.

```
marriage.data <- cbind(marriage[2, ], marriage[1, ])
treatment <- 1:0
marriage.glm <- glm(marriage.data ~ treatment, family=binomial)
summary(marriage.glm)
```

```
##
## Call:
## glm(formula = marriage.data ~ treatment, family = binomial)
##
## Deviance Residuals:
## [1]  0  0
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.04139   0.11747  -0.352   0.725
## treatment   -0.23126   0.16414  -1.409   0.159
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 1.9879e+00 on 1 degrees of freedom
## Residual deviance: 4.8406e-14 on 0 degrees of freedom
## AIC: 16.294
##
## Number of Fisher Scoring iterations: 2
```

```
beta1 <- coef(marriage.glm)[2]
beta1 # beta1 = slope
```

```
## treatment
## -0.231259
```

Illustration.

```
plot(x=c(0, 1), y=c(log(176 / 134), log(148 / 142)),
     pch=20, las=1, col="darkred",
     xlim=c(-0.5, 1.5), ylim=c(-1.5, 0.5),
     xlab="Treatment: 0 = Boy, 1 = Girl",
     ylab="log odds of marriage")
segments(0, log(176 / 134), 1, log(148 / 142),
         col="orange", lty="dashed")
abline(h=0)
abline(v=0)
```

