

multiple_possibilities_GLMM

Christoph Voelter

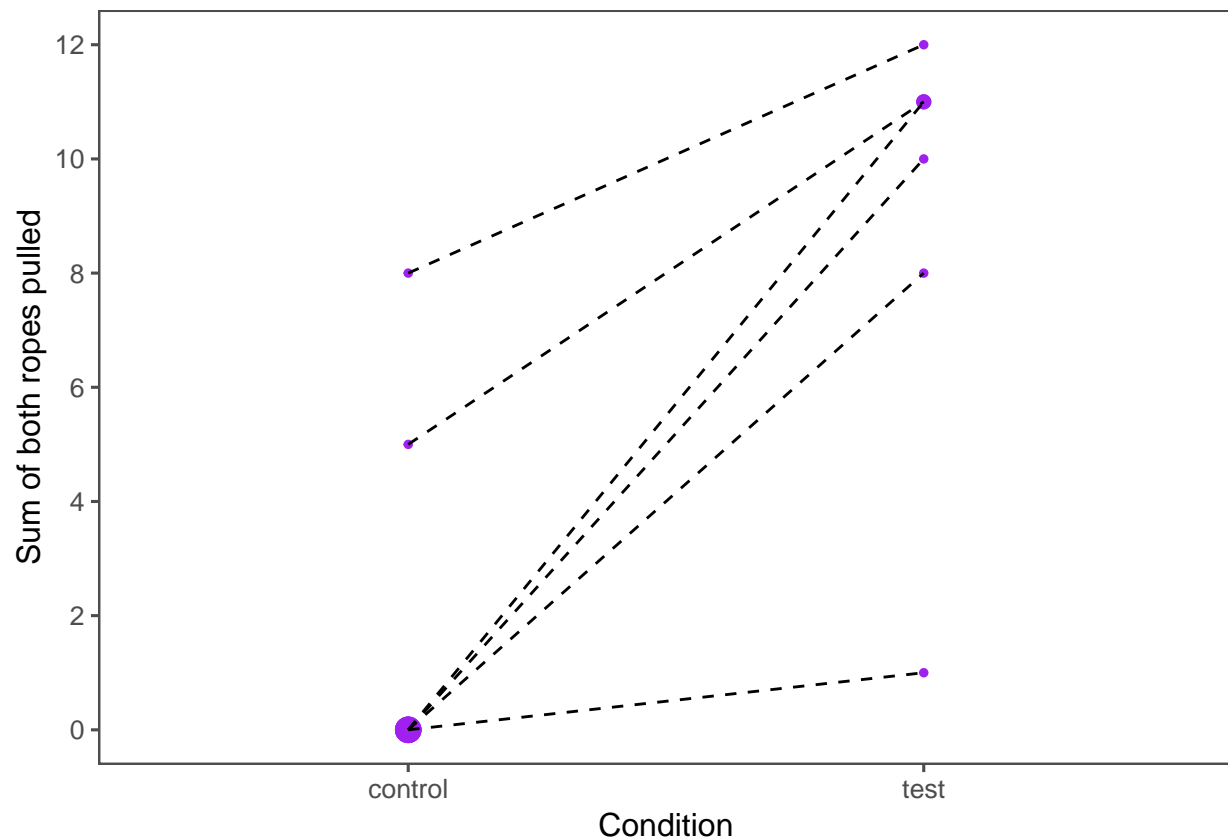
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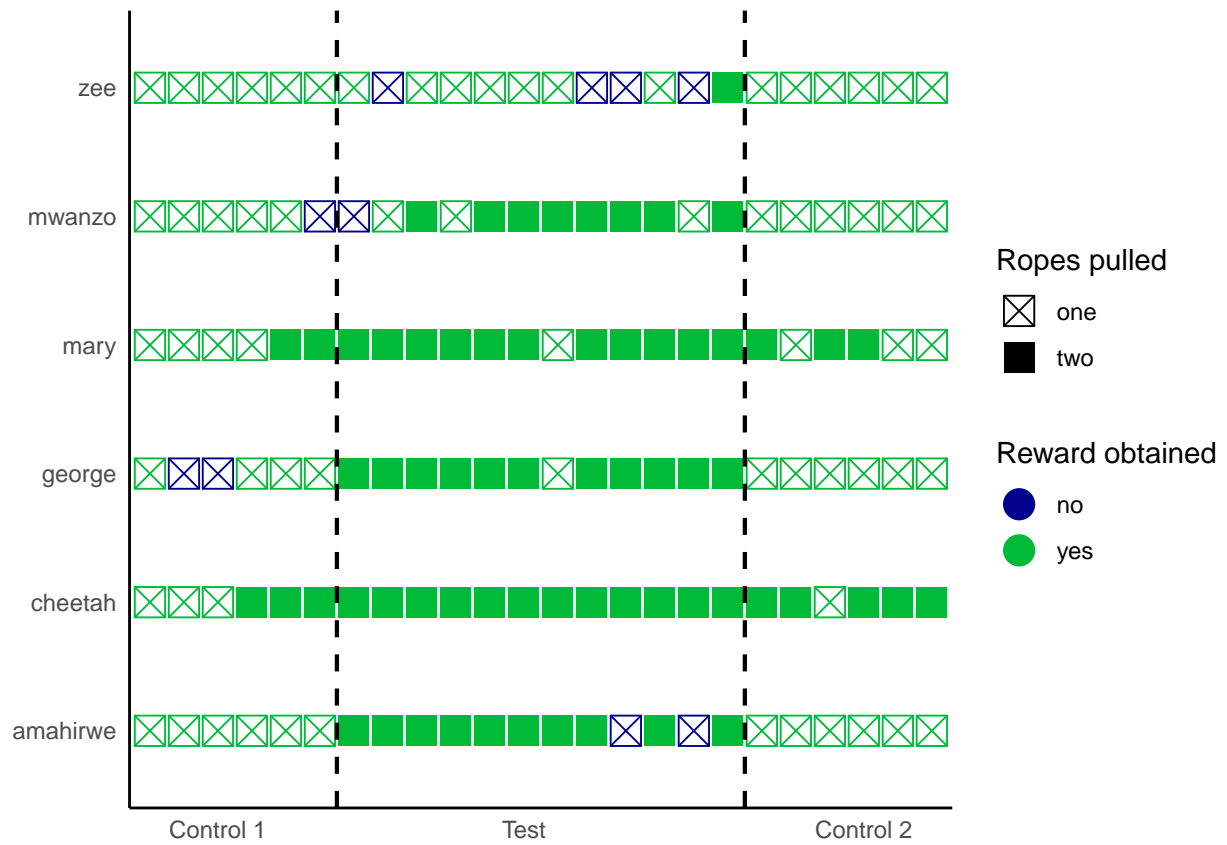
```
capFirst <- function(s) {  
  paste(toupper(substring(s, 1, 1)), substring(s, 2), sep = "")  
}  
  
all.data$chimp <- capFirst(all.data$chimp)  
str(all.data)
```

Summary

Both the paired-samples t-test and a mixed model show a significant effect for condition. There was no significant interaction between session and condition.

Plotting data





Paired-sample t-test

```
contr_data <- plot_individual %>%
  filter(condition == "control")

exp_data <- plot_individual %>%
  filter(condition == "test")

t.test(exp_data$correct_resp, contr_data$correct_resp, paired = TRUE, alternative = "two.sided")

##
## Paired t-test
##
## data: exp_data$correct_resp and contr_data$correct_resp
## t = 4.3234, df = 5, p-value = 0.007546
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  2.702818 10.630515
## sample estimates:
## mean of the differences
##                6.666667
```

GLMM

GLMM 01 with session * condition interaction

```
# centering variables for modeling
model.data <- all.data %>%
  mutate(z.trial = scale(trial, scale = T, center = T),
         z.session = scale(session, scale=T, center=T),
         condition = relevel(condition, ref = "control"))

## code to run the model
mm.1 <- glmer(both_ropes ~ condition*z.session + z.trial +
  (1+ z.session*condition+z.trial|chimp)
  , data = model.data
  , family = binomial
  , control=glmerControl(optimizer="bobyqa",optCtrl=list(maxfun=2e5))
)

## singular fit
```

Confidence intervals

Confidence intervals for the binomial models were derived using the function bootMer of the R package lme4, using 1,000 parametric bootstraps and bootstrapping over the random effects.

```
boot.res=boot.glmm(model.res=mm.1, excl.warnings=T,nboots=1000, para=T)
saveRDS(boot.res, "multpos_model.rds")

##
##          orig   X2.5. X97.5.
## (Intercept) -4.779 -10.744 -1.214
## conditiontest 10.899  5.243 17.994
## z.session    -0.213 -2.789  2.923
## z.trial       0.775  0.048  2.168
```

```
## conditiontest:z.session -4.545 -9.715 1.872
```

Null model

```
mm.1.null <- glmer(both_ropes ~ 1 +
  (1+ z.session*condition+z.trial|chimp)
  , data = model.data
  , family = binomial
  , control=glmerControl(optimizer="bobyqa",optCtrl=list(maxfun=2e5))
)
```

```
## singular fit
```

Full-null model comparison

```
anova(mm.1, mm.1.null, test="Chisq")
```

```
## Data: model.data
## Models:
## mm.1.null: both_ropes ~ 1 + (1 + z.session * condition + z.trial | chimp)
## mm.1: both_ropes ~ condition * z.session + z.trial + (1 + z.session *
## mm.1: condition + z.trial | chimp)
##          Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## mm.1.null 16 133.21 180.72 -50.602 101.205
## mm.1      20 128.07 187.46 -44.033 88.066 13.139      4 0.01062 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model output

- Coefficients

```
round(summary(mm.1)$coefficients, 3)
```

```
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -4.779      2.995  -1.596   0.111
## conditiontest      10.899      4.761   2.289   0.022
## z.session         -0.213      1.499  -0.142   0.887
## z.trial            0.775      0.349   2.218   0.027
## conditiontest:z.session -4.545      5.436  -0.836   0.403
```

- Individual predictors: likelihood ratio tests

Drop1: P values for the individual effects were based on likelihood ratio tests comparing the full with respective reduced models (Barr et al., 2013; R function drop1 with argument 'test' set to "Chisq").

```
xdrop1=drop1(mm.1, test="Chisq")
```

```
## singular fit
## singular fit
```

```
round(xdrop1,3)
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## both_ropes ~ condition * z.session + z.trial + (1 + z.session *
## condition + z.trial | chimp)
```

```
##          Df      AIC      LRT Pr(Chi)
```

```
## <none>                128.07
## z.trial                1 130.40 4.333 0.037 *
## condition:z.session   1 126.71 0.648 0.421
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

GLMM02 without the interaction

```
mm.2 <- glmer(both_ropes ~ condition+z.session + z.trial +
              (1+ z.session+condition+z.trial|chimp)
              , data = model.data
              , family = binomial
              , control=glmerControl(optimizer="bobyqa",optCtrl=list(maxfun=2e5))
              )
```

singular fit

Confidence intervals

Confidence intervals for the binomial models were derived using the function bootMer of the R package lme4, using 1,000 parametric bootstraps and bootstrapping over the random effects.

```
boot.res2=boot.glmm(model.res=mm.2, excl.warnings=T,nboots=1000, para=T)
saveRDS(boot.res2, "multpos_model2.rds")
```

```
##              orig   X2.5. X97.5.
## (Intercept) -4.625 -12.637 -0.866
## conditiontest 6.360   3.678 14.699
## z.session     0.122  -0.845  1.181
## z.trial       0.693   0.050  1.908
```

Null model

```
mm.2.null <- glmer(both_ropes ~ 1 +
                  (1+ z.session+condition+z.trial|chimp)
                  , data = model.data
                  , family = binomial
                  , control=glmerControl(optimizer="bobyqa",optCtrl=list(maxfun=2e5))
                  )
```

singular fit

Full-null model comparison

```
anova(mm.2, mm.2.null, test="Chisq")
```

```
## Data: model.data
## Models:
## mm.2.null: both_ropes ~ 1 + (1 + z.session + condition + z.trial | chimp)
## mm.2: both_ropes ~ condition + z.session + z.trial + (1 + z.session +
## mm.2: condition + z.trial | chimp)
##              Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## mm.2.null    11 127.25 159.92 -52.624  105.249
## mm.2          14 124.28 165.85 -48.137   96.275 8.9742    3 0.02964 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model output

- Coefficients

```
round(summary(mm.2)$coefficients, 3)
```

```
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -4.625      2.836  -1.631   0.103
## conditiontest   6.360      2.438   2.608   0.009
## z.session       0.122      0.406   0.301   0.764
## z.trial         0.693      0.338   2.048   0.041
```

- Individual predictors: likelihood ratio tests

Drop1: P values for the individual effects were based on likelihood ratio tests comparing the full with respective reduced models (Barr et al., 2013; R function drop1 with argument 'test' set to "Chisq").

```
xdrop1=drop1(mm.2, test="Chisq")
```

```
## singular fit
## singular fit
## singular fit
```

```
round(xdrop1,3)
```

```
## Single term deletions
##
## Model:
## both_ropes ~ condition + z.session + z.trial + (1 + z.session +
##      condition + z.trial | chimp)
##           Df    AIC    LRT Pr(Chi)
## <none>      124.28
## condition   1 130.90 8.629   0.003 **
## z.session   1 122.36 0.086   0.769
## z.trial     1 125.93 3.656   0.056 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

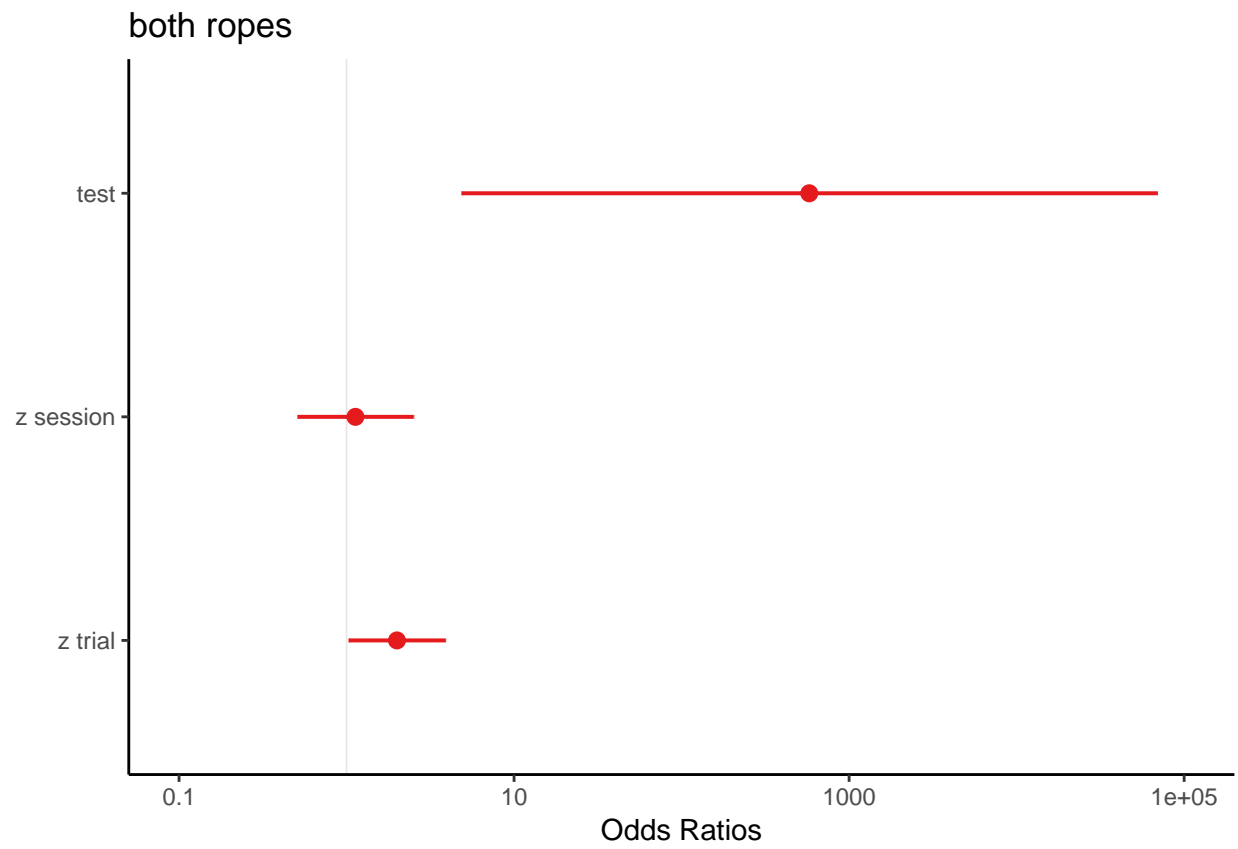
check for collinearity in the previous model.

```
## condition    z.trial z.session
## 1.042645    1.040646  1.002028
```

-> no collinearity

Model output

```
plot_model(mm.2, type='est')
```



```
plot_model(mm.2, type='re')
```

Random effects

