multiple_possibilities_GLMM

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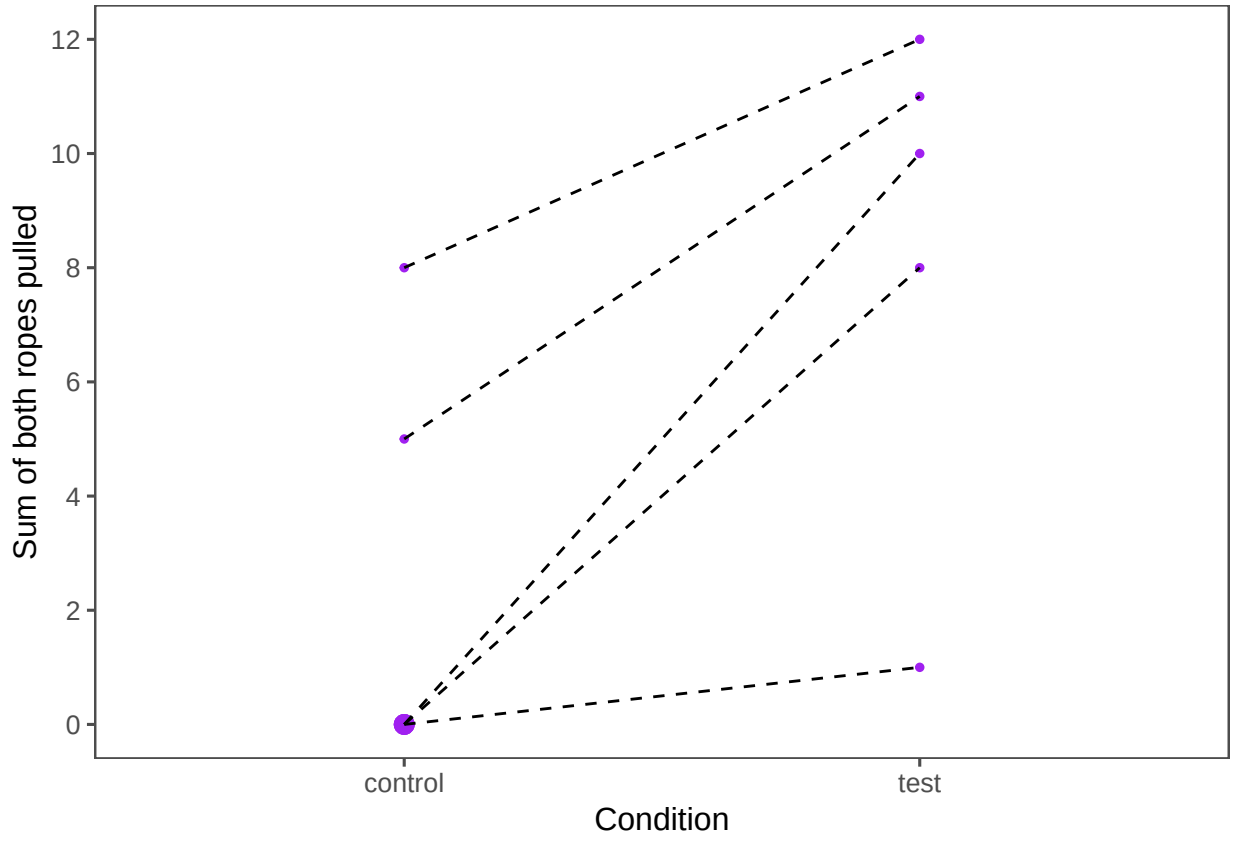
Plotting data

```
plot_individual <- all.data %>%
  group_by(condition, chimp) %>%
  summarize(correct_resp = sum(both_ropes))

plot_ind2 <- plot_individual %>% add_count(correct_resp)
ggplot(
  data=plot_ind2, aes(condition, correct_resp, group = chimp)) +
  geom_point(size = plot_ind2$n, colour = "purple") +
  geom_line(lty=2)+
  #ylim(0,12)+
  labs(x="Condition",y="Sum of both ropes pulled")+
  theme_few()+
  scale_y_continuous(breaks=seq(0,12,2))
```



Summary

Both the paired-samples t-test and a mixed model show a significant effect for condition. Obviously, there is a lot of uncertainty regarding the strength of the effect of condition given the small sample size.

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 = 3.7131, df = 4, p-value = 0.0206
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   1.463054 10.136946
## sample estimates:
## mean of the differences
##                     5.8
```

GLMM

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

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

## save model output
saveRDS(mm.1, "multpos_model.rds")
```

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=F)
saveRDS(mm.1, "multpos_model.rds")
round(boot.res,3)
```

```
##                 orig   X2.5. X97.5.
## (Intercept)   -3.593 -13.102  0.108
## conditiontest  5.091   3.012 14.756
## z.trial        0.596  -0.024  1.678
```

Null model

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

Full-null model comparison

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

```
## Data: model.data
## Models:
## mm.1.null: both_ropes ~ 1 + (1 + condition + z.trial | chimp)
## mm.1: both_ropes ~ condition + z.trial + (1 + condition + z.trial |
## mm.1:     chimp)
##           Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## mm.1.null  7 113.52 133.04 -49.762   99.523
## mm.1       9 106.29 131.38 -44.147   88.293 11.23      2   0.003642 **
## ---
## 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)     -3.593      2.438  -1.474    0.141
## conditiontest    5.091      1.872   2.720    0.007
## z.trial          0.596      0.324   1.838    0.066
```

- 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")
round(xdrop1,3)
```

```
## Single term deletions
##
## Model:
## both_ropes ~ condition + z.trial + (1 + condition + z.trial |
```

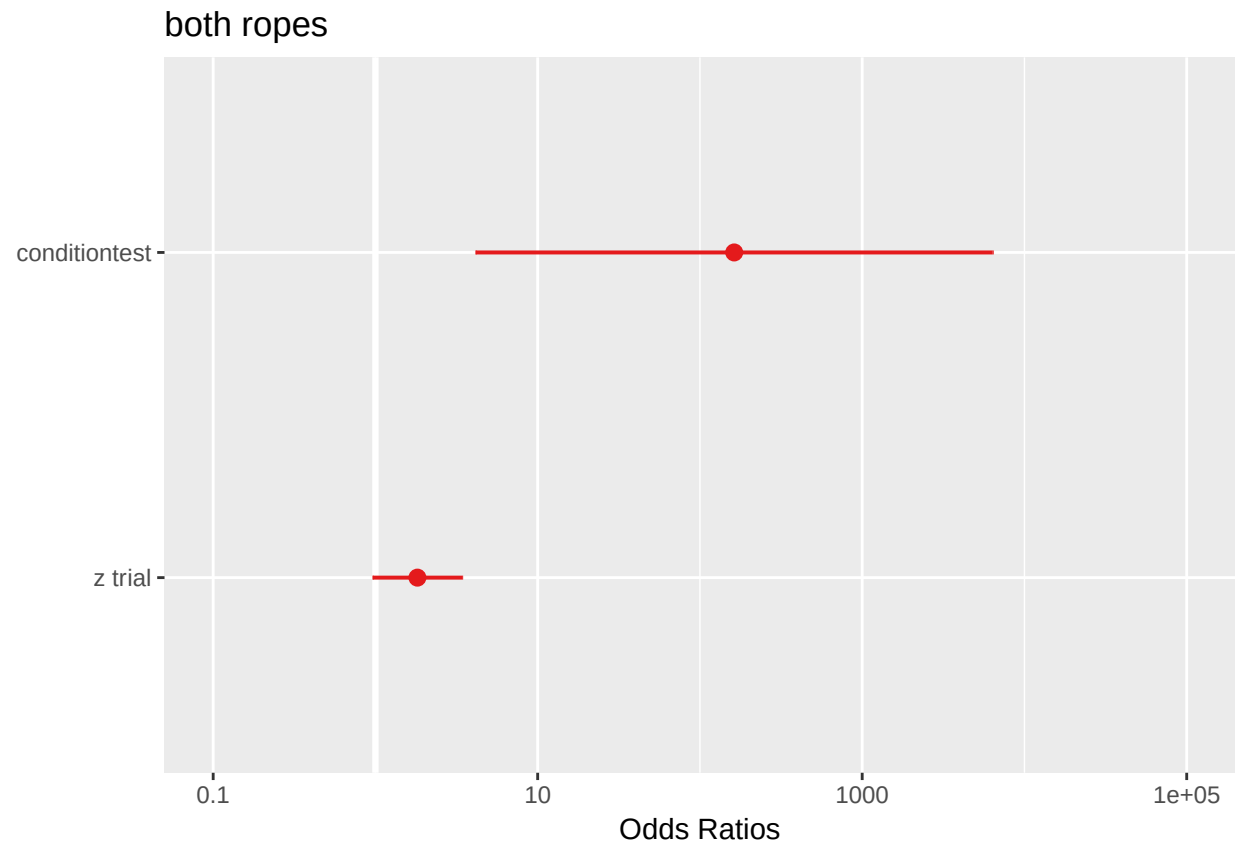
```
##     chimp)
##           Df    AIC   LRT Pr(Chi)
## <none>       106.29
## condition  1 110.97 6.678   0.010 **
## z.trial    1 107.23 2.938   0.087 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

check for colinearity in the previous model.

-> no collinearity

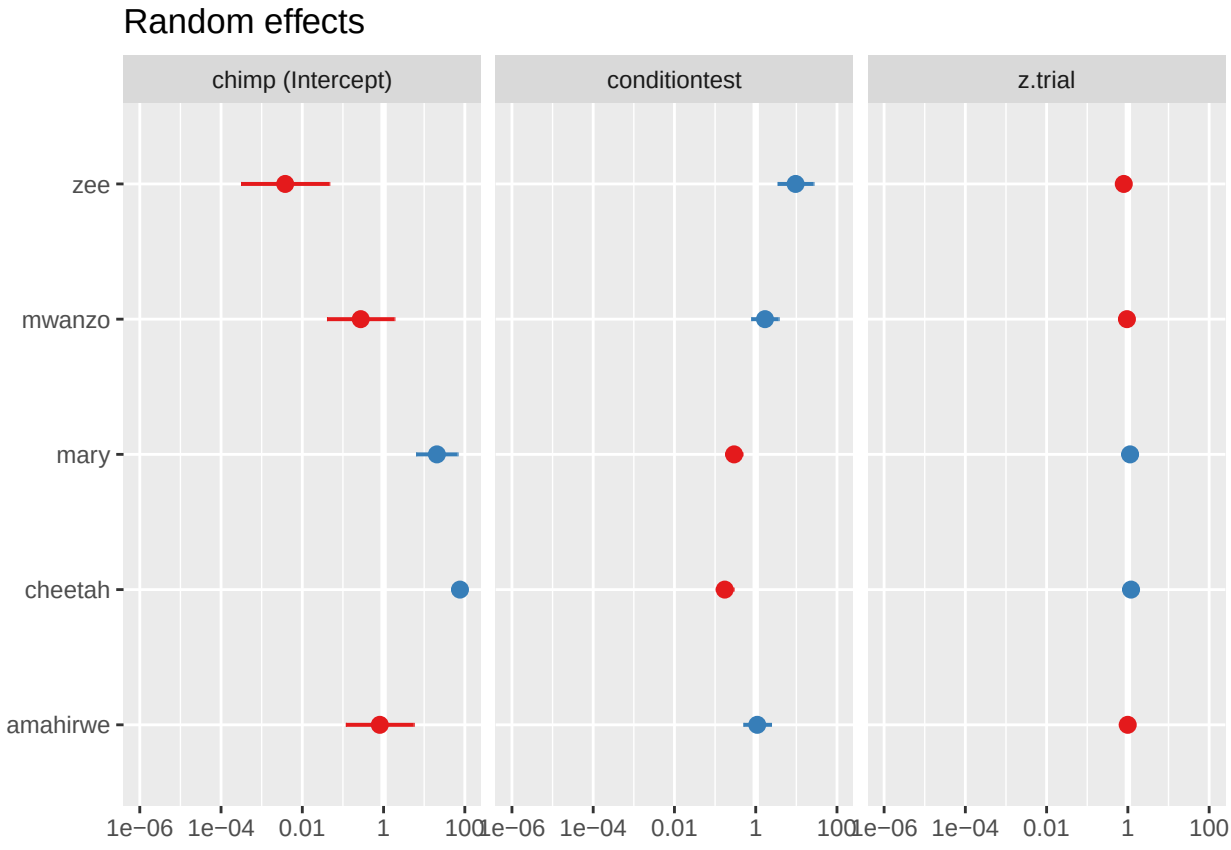
```
### Model plotting

plot_model(mm.1, type='est')
```




```
plot_model(mm.1, type='re')
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```


Random effects
chimp (Intercept)
conditiontest
z.trial
zee
mwanzo
mary
cheetah
amahirwe
1e−06
1e−04
0.01
1
100