

Familiarity Facilitates Feature-based Face Processing Models for Accuracy

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Contents

Setup	1
Model on Target Present Trials	2
Model on Target Absent Trials	4

Setup

In this document we'll analyze the accuracy creating Logit Mixed-Effect Models separately for Target Present and Target Absent trials.

```
# return version information
version

##
## platform      x86_64-apple-darwin13.4.0
## arch          x86_64
## os            darwin13.4.0
## system        x86_64, darwin13.4.0
## status
## major         3
## minor         2.3
## year          2015
## month         12
## day           10
## svn rev       69752
## language      R
## version.string R version 3.2.3 (2015-12-10)
## nickname      Wooden Christmas-Tree

packages <- c('lme4',
              'car',
              'dplyr')

for (package in packages) {
  require(package, character.only=T)
  cat(paste(package, packageVersion(package), '\n'))
}

## lme4 1.1.11
## car 2.1.1
## dplyr 0.4.3
```

```

data <- read.csv('data.csv')
# set order of levels for plotting
data$orientation <- factor(data$orientation,
                           levels=c('Upright', 'Inverted'))
data$target_presence <- factor(data$target_presence,
                              levels=c('Target Present', 'Target Absent'))

# set set_size as a factor
data$set_size <- as.factor(data$set_size)

```

Set up zero-sum contrasts for factors.

```

contrasts(data$set_size) <- contr.poly(3)
contrasts(data$orientation) <- c(-1, 1)
contrasts(data$familiarity) <- c(-1,1)
contrasts(data$target_sex) <- c(-1,1)

```

Model on Target Present Trials

```

# get target present trials
data_tp <- data %>%
  filter(target_presence == 'Target Present')

```

Try to fit a very general model using the bobyqa optimizer (Nelder_Mead is another option but might not converge sometimes).

```

m1 <- glmer(correct ~ set_size*familiarity*orientation + target_sex +
            (1 + target_sex | subid) +
            (1 + target_sex | stimuli_combination),
            family=binomial,
            data=data_tp,
            control=glmerControl(optimizer="bobyqa"))

```

Now we start reducing the random effect structure. First removing the random slope for stimuli_combination.

```

m2 <- glmer(correct ~ set_size*familiarity*orientation + target_sex +
            (1 + target_sex | subid) +
            (1 | stimuli_combination),
            family=binomial,
            data=data_tp,
            control=glmerControl(optimizer="bobyqa"))

anova(m1, m2)

```

```

## Data: data_tp
## Models:
## m2: correct ~ set_size * familiarity * orientation + target_sex +
## m2:      (1 + target_sex | subid) + (1 | stimuli_combination)
## m1: correct ~ set_size * familiarity * orientation + target_sex +

```

```
## m1:      (1 + target_sex | subid) + (1 + target_sex | stimuli_combination)
##      Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## m2 17 4311.2 4432.2 -2138.6  4277.2
## m1 19 4314.7 4450.0 -2138.4  4276.7 0.4265      2      0.808
```

The two models are not statistically different, thus we keep reducing m2 by entirely removing the random effect for `stimuli_combination`.

```
m3 <- glmer(correct ~ set_size*familiarity*orientation + target_sex +
             (1 + target_sex | subid),
             family=binomial,
             data=data_tp,
             control=glmerControl(optimizer="bobyqa"))

anova(m2, m3)
```

```
## Data: data_tp
## Models:
## m3: correct ~ set_size * familiarity * orientation + target_sex +
## m3:      (1 + target_sex | subid)
## m2: correct ~ set_size * familiarity * orientation + target_sex +
## m2:      (1 + target_sex | subid) + (1 | stimuli_combination)
##      Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## m3 16 4309.2 4423.1 -2138.6  4277.2
## m2 17 4311.2 4432.2 -2138.6  4277.2 9e-04      1      0.976
```

The random effect for `stimuli_combination` doesn't seem to be necessary. We thus try to reduce model m3 further by removing the random slope for `subid`.

```
m4 <- glmer(correct ~ set_size*familiarity*orientation + target_sex +
             (1 | subid),
             family=binomial,
             data=data_tp,
             control=glmerControl(optimizer="bobyqa"))

anova(m3, m4)
```

```
## Data: data_tp
## Models:
## m4: correct ~ set_size * familiarity * orientation + target_sex +
## m4:      (1 | subid)
## m3: correct ~ set_size * familiarity * orientation + target_sex +
## m3:      (1 + target_sex | subid)
##      Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## m4 14 4308.6 4408.2 -2140.3  4280.6
## m3 16 4309.2 4423.1 -2138.6  4277.2 3.4123      2      0.1816
```

We thus keep model m4 as our final model. Now we'll test significance of the factors using Type 3 Analysis of Deviance with Wald's χ^2 test.

```
Anova(m4, type=3)
```

```
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: correct
##
##               Chisq Df Pr(>Chisq)
## (Intercept)    648.8183  1 < 2.2e-16 ***
## set_size       75.0142  2 < 2.2e-16 ***
## familiarity     0.2208  1  0.63843
## orientation    19.3724  1  1.075e-05 ***
## target_sex     18.7299  1  1.506e-05 ***
## set_size:familiarity  0.2258  2  0.89324
## set_size:orientation  4.7812  2  0.09157 .
## familiarity:orientation  0.4209  1  0.51651
## set_size:familiarity:orientation  3.2441  2  0.19749
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model on Target Absent Trials

We'll repeat the same process for Target Absent trials.

```
# get target absent trials
data_ta <- data %>%
  filter(target_presence == 'Target Absent')
```

Fit a very general model.

```
m1 <- glmer(correct ~ set_size*familiarity*orientation + target_sex +
  (1 + target_sex | subid) +
  (1 + target_sex | stimuli_combination),
  family=binomial,
  data=data_ta,
  control=glmerControl(optimizer="bobyqa"))
```

Remove the random slope for stimuli_combination.

```
m2 <- glmer(correct ~ set_size*familiarity*orientation + target_sex +
  (1 + target_sex | subid) +
  (1 | stimuli_combination),
  family=binomial,
  data=data_ta,
  control=glmerControl(optimizer="bobyqa"))

anova(m1, m2)
```

```
## Data: data_ta
## Models:
## m2: correct ~ set_size * familiarity * orientation + target_sex +
## m2:      (1 + target_sex | subid) + (1 | stimuli_combination)
```

```
## m1: correct ~ set_size * familiarity * orientation + target_sex +
## m1:      (1 + target_sex | subid) + (1 + target_sex | stimuli_combination)
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m2 17 2281.6 2402.6 -1123.8 2247.6
## m1 19 2285.5 2420.7 -1123.7 2247.5 0.1085      2      0.9472
```

The two models are not statistically different, thus we keep reducing m2 by entirely removing the random effect for stimuli_combination.

```
m3 <- glmer(correct ~ set_size*familiarity*orientation + target_sex +
             (1 + target_sex | subid),
             family=binomial,
             data=data_ta,
             control=glmerControl(optimizer="bobyqa"))

anova(m2, m3)
```

```
## Data: data_ta
## Models:
## m3: correct ~ set_size * familiarity * orientation + target_sex +
## m3:      (1 + target_sex | subid)
## m2: correct ~ set_size * familiarity * orientation + target_sex +
## m2:      (1 + target_sex | subid) + (1 | stimuli_combination)
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m3 16 2279.6 2393.5 -1123.8 2247.6
## m2 17 2281.6 2402.6 -1123.8 2247.6      0      1      0.9994
```

The random effect for stimuli_combination doesn't seem to be necessary. We thus try to reduce model m3 further by removing the random slope for subid.

```
m4 <- glmer(correct ~ set_size*familiarity*orientation + target_sex +
             (1 | subid),
             family=binomial,
             data=data_ta,
             control=glmerControl(optimizer="bobyqa"))

anova(m3, m4)
```

```
## Data: data_ta
## Models:
## m4: correct ~ set_size * familiarity * orientation + target_sex +
## m4:      (1 | subid)
## m3: correct ~ set_size * familiarity * orientation + target_sex +
## m3:      (1 + target_sex | subid)
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m4 14 2299.9 2399.6 -1136.0 2271.9
## m3 16 2279.6 2393.5 -1123.8 2247.6 24.34      2 5.185e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

For Target Absent trials the random slope for subid significantly improves the fit of the model. Thus, we keep m3 as our final model. We'll test significance of the factors using Type 3 Analysis of Deviance with Wald's χ^2 test.

```
Anova(m3, type=3)
```

```
## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: correct
##
##           Chisq Df Pr(>Chisq)
## (Intercept)    636.5013  1 < 2.2e-16 ***
## set_size       25.5386  2  2.847e-06 ***
## familiarity     6.7503  1  0.009373 **
## orientation    16.5406  1  4.762e-05 ***
## target_sex      3.5718  1  0.058767 .
## set_size:familiarity 0.0397  2  0.980336
## set_size:orientation 1.4752  2  0.478264
## familiarity:orientation 0.0034  1  0.953688
## set_size:familiarity:orientation 0.7234  2  0.696477
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```