Familiarity Facilitates Feature-based Face Processing Models for Accuracy

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Contents

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/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.

```r
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
```