

Statistical analysis guide for

Error patterns of native and non-native listeners' perception of speech in noise

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Compile the datasets

Before beginning the analyses, if you haven't already done so, compile the E-prime output files into the merged .txt files (`merge_full.txt` and `merge_subset.txt`) that will be used in the analyses. If you already have these files (and they represented the complete dataset), no need to run it again.

Make sure to update the first line of code in `data_compiler_20181009.R` to reflect the path to the output files on your own computer before you run it: `path = "~/Documents/Projects/EAB/outputs_with_block/"`

Import needed libraries

The following libraries are required to perform the analyses that appear below. If you don't already have these libraries (and their dependencies) installed, run `install.packages('name_of_library')` for each package, using the name of the missing library to download and install it. Then run the `library` command to load it.

```
library(lme4)
library(lmerTest)
library(plyr)
library(effsize)
```

Import and clean up the data

When the merged dataset file has been prepared, import it into R.

```
mydata <- read.csv('merge_full.txt')
```

To perform the analyses with a subset of the data, encompassing only the first eight appearances of each mask type for each subject (to balance the number of trials per mask type encountered in the experiment), simply run this line instead: `mydata <- read.csv('merge_subset.txt')`

Several small formatting changes need to be made in order to prepare this file for analysis:

- Label `native` participants (native English speakers) as those participants with `Subject_ID #` less than 2000
- Label `nonnative` participants (non-native English speakers) with `Subject_ID #` greater than or equal to 2000
- Re-level the conditions to treat `SSN` as the reference or baseline condition

```
mydata$group[mydata$subject_id<2000] <- 'native'
mydata$group[mydata$subject_id>=2000] <- 'nonnative'
mydata$condition <- relevel(mydata$condition, 'SSN')
```

Further, several small steps (not enumerated here) to extract each error type and re-combine the datasets are outlined contained in the Markdown source used to generate this file: `Supplemental-Statistical_analyses_in_R.Rmd`. The source file is provided in this repository and can be viewed and/or executed in R.

Estimate the models

Model of DNH (Did Not Hear) errors

```
dnh_model <- glmer(DNH~(1|subject_id)+group*condition,mydata,family='binomial')
summary(dnh_model)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: DNH ~ (1 | subject_id) + group * condition
## Data: mydata
##
##      AIC      BIC   logLik deviance df.resid
## 1856.3 1906.0 -919.1 1838.3 1847
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.0674 -0.6187 -0.1860  0.6170  8.5531
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## subject_id (Intercept) 0.7956  0.8919
## Number of obs: 1856, groups: subject_id, 29
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -3.6979    0.3760  -9.834 < 2e-16 ***
## groupnonnative     2.6360    0.4629   5.694 1.24e-08 ***
## condition1T        2.4950    0.3340   7.470 8.04e-14 ***
## condition2Talker   2.9864    0.3331   8.966 < 2e-16 ***
## condition8Talker   3.6402    0.3634  10.017 < 2e-16 ***
## groupnonnative:condition1T -1.1363    0.3853  -2.950 0.00318 **
## groupnonnative:condition2Talker -1.9113    0.3836  -4.982 6.28e-07 ***
## groupnonnative:condition8Talker -0.9493    0.4622  -2.054 0.04000 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) grpnnn cndt1T cndt2T cndt8T grp:1T grp:2T
## groupnonntv -0.810
## condition1T -0.687  0.556
## condtn2Tlkr -0.704  0.570  0.778
## condtn8Tlkr -0.659  0.533  0.725  0.745
## grpnnntv:1T  0.593 -0.574 -0.865 -0.672 -0.625
## grpnnntv:2T  0.609 -0.587 -0.674 -0.866 -0.644  0.696
## grpnnntv:8T  0.514 -0.497 -0.566 -0.581 -0.781  0.588  0.600
anova(dnh_model)

## Analysis of Variance Table
##              Df  Sum Sq Mean Sq F value
## group          1   6.180   6.180  6.1803
## condition      3 188.876  62.959 62.9588
```

```
## group:condition 3 26.457 8.819 8.8189
```

Omnibus Model with Error Type

```
omni_model <- lmer(error_rate~(1|subject_id)+group*condition*error_type,mydata_errors[mydata_errors$error_type!="dnh", ]  
summary(omni_model)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
## lmerModLmerTest]  
## Formula: error_rate ~ (1 | subject_id) + group * condition * error_type  
## Data: mydata_errors[mydata_errors$error_type != "dnh", ]  
##  
## REML criterion at convergence: -852.4  
##  
## Scaled residuals:  
##      Min       1Q   Median       3Q      Max   
## -2.4477 -0.5854 -0.2308  0.4923  6.2414   
##  
## Random effects:  
##      Groups      Name      Variance Std.Dev.   
## subject_id (Intercept) 0.004687 0.06846   
## Residual                0.038793 0.19696   
## Number of obs: 2426, groups: subject_id, 29  
##  
## Fixed effects:  
##  
##              Estimate Std. Error   
## (Intercept)      7.076e-02  2.061e-02   
## groupponnative    1.151e-01  3.035e-02   
## condition1T       5.397e-02  1.840e-02   
## condition2Talker  1.378e-01  1.914e-02   
## condition8Talker  1.749e-01  2.704e-02   
## error_typemorph   1.635e-02  1.500e-02   
## groupponnative:condition1T 6.107e-03  3.028e-02   
## groupponnative:condition2Talker 9.832e-03  2.975e-02   
## groupponnative:condition8Talker 8.779e-02  5.254e-02   
## groupponnative:error_typemorph 6.654e-03  2.336e-02   
## condition1T:error_typemorph -6.183e-02  2.575e-02   
## condition2Talker:error_typemorph -8.690e-02  2.681e-02   
## condition8Talker:error_typemorph -2.587e-02  3.816e-02   
## groupponnative:condition1T:error_typemorph 4.291e-03  4.223e-02   
## groupponnative:condition2Talker:error_typemorph -3.786e-02  4.170e-02   
## groupponnative:condition8Talker:error_typemorph -1.876e-01  7.397e-02   
##  
##              df t value   
## (Intercept)      4.083e+01  3.432   
## groupponnative    4.469e+01  3.791   
## condition1T       2.396e+03  2.934   
## condition2Talker  2.395e+03  7.197   
## condition8Talker  2.385e+03  6.468   
## error_typemorph   2.383e+03  1.090   
## groupponnative:condition1T 2.399e+03  0.202   
## groupponnative:condition2Talker 2.395e+03  0.330   
## groupponnative:condition8Talker 2.388e+03  1.671   
## groupponnative:error_typemorph 2.383e+03  0.285
```

```

## condition1T:error_typemorph          2.383e+03 -2.401
## condition2Talker:error_typemorph     2.383e+03 -3.241
## condition8Talker:error_typemorph     2.383e+03 -0.678
## groupnonnative:condition1T:error_typemorph 2.383e+03  0.102
## groupnonnative:condition2Talker:error_typemorph 2.383e+03 -0.908
## groupnonnative:condition8Talker:error_typemorph 2.383e+03 -2.536
##                                     Pr(>|t|)
## (Intercept)                          0.001383 **
## groupnonnative                         0.000446 ***
## condition1T                            0.003382 **
## condition2Talker                       8.17e-13 ***
## condition8Talker                       1.20e-10 ***
## error_typemorph                       0.275726
## groupnonnative:condition1T             0.840158
## groupnonnative:condition2Talker       0.741053
## groupnonnative:condition8Talker       0.094886 .
## groupnonnative:error_typemorph        0.775762
## condition1T:error_typemorph           0.016433 *
## condition2Talker:error_typemorph      0.001209 **
## condition8Talker:error_typemorph      0.497862
## groupnonnative:condition1T:error_typemorph 0.919089
## groupnonnative:condition2Talker:error_typemorph 0.363938
## groupnonnative:condition8Talker:error_typemorph 0.011268 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)           if you need it

anova(omni_model)

## Type III Analysis of Variance Table with Satterthwaite's method
##
##           Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## group           0.6777  0.67765     1    31.93 17.4684 0.0002117
## condition       4.8013  1.60042     3 2397.00 41.2553 < 2.2e-16
## error_type      0.8372  0.83716     1 2383.25 21.5801 3.578e-06
## group:condition 0.0201  0.00670     3 2397.00  0.1726 0.9149620
## group:error_type 0.1858  0.18582     1 2383.25  4.7900 0.0287216
## condition:error_type 1.2591  0.41970     3 2383.25 10.8189 4.648e-07
## group:condition:error_type 0.2780  0.09266     3 2383.25  2.3885 0.0670818
##
## group           ***
## condition       ***
## error_type      ***
## group:condition
## group:error_type *
## condition:error_type ***
## group:condition:error_type .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Word-Level Analysis

```
contentword <- lmer(error_rate~(1|subject_id)+group*condition,worddat)
summary(contentword)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: error_rate ~ (1 | subject_id) + group * condition
## Data: worddat
##
## REML criterion at convergence: -110.9
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -2.1560 -0.6103 -0.2349 0.4203 5.5168
##
## Random effects:
## Groups Name Variance Std.Dev.
## subject_id (Intercept) 0.007311 0.0855
## Residual 0.049561 0.2226
## Number of obs: 1213, groups: subject_id, 29
##
## Fixed effects:
## Estimate Std. Error df t value
## (Intercept) 7.095e-02 2.512e-02 3.299e+01 2.824
## groupnonnative 1.157e-01 3.689e-02 3.571e+01 3.135
## condition1T 5.489e-02 2.097e-02 1.195e+03 2.618
## condition2Talker 1.398e-01 2.181e-02 1.194e+03 6.410
## condition8Talker 1.757e-01 3.062e-02 1.181e+03 5.740
## groupnonnative:condition1T 2.934e-03 3.461e-02 1.198e+03 0.085
## groupnonnative:condition2Talker 5.879e-03 3.388e-02 1.194e+03 0.174
## groupnonnative:condition8Talker 8.174e-02 5.962e-02 1.185e+03 1.371
## Pr(>|t|)
## (Intercept) 0.00798 **
## groupnonnative 0.00343 **
## condition1T 0.00896 **
## condition2Talker 2.1e-10 ***
## condition8Talker 1.2e-08 ***
## groupnonnative:condition1T 0.93245
## groupnonnative:condition2Talker 0.86226
## groupnonnative:condition8Talker 0.17063
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) grpnnn cndt1T cndt2T cndt8T grp:1T grp:2T
## groupnonntv -0.681
## condition1T -0.272 0.185
## condtn2Tlkr -0.262 0.178 0.348
## condtn8Tlkr -0.186 0.127 0.230 0.223
## grpnnntv:1T 0.165 -0.274 -0.606 -0.211 -0.139
## grpnnntv:2T 0.168 -0.278 -0.224 -0.644 -0.143 0.332
## grpnnntv:8T 0.096 -0.160 -0.118 -0.114 -0.514 0.182 0.180
```

```
anova(contentword)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## group           0.7043 0.70433     1    34.68 14.2114 0.0006101 ***
## condition       5.2148 1.73827     3 1189.56 35.0732 < 2.2e-16 ***
## group:condition 0.0946 0.03152     3 1189.56  0.6361 0.5918320
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Morphosyntactic-Level Analysis

```
morphemes <- lmer(error_rate~(1|subject_id)+group*condition,morphdat)
summary(morphemes)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: error_rate ~ (1 | subject_id) + group * condition
##   Data: morphdat
##
## REML criterion at convergence: -819.8
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -2.3372 -0.5674 -0.3074  0.6323  4.6723
##
## Random effects:
##   Groups      Name                Variance Std.Dev.
## subject_id (Intercept) 0.002383 0.04881
## Residual              0.027791 0.16671
## Number of obs: 1213, groups: subject_id, 29
##
## Fixed effects:
##              Estimate Std. Error      df t value
## (Intercept)      8.683e-02 1.547e-02 3.590e+01  5.611
## groupponnative    1.198e-01 2.293e-02 4.024e+01  5.223
## condition1T      -9.366e-03 1.567e-02 1.200e+03 -0.598
## condition2Talker  4.781e-02 1.630e-02 1.199e+03  2.934
## condition8Talker  1.480e-01 2.292e-02 1.182e+03  6.458
## groupponnative:condition1T 1.183e-02 2.584e-02 1.203e+03  0.458
## groupponnative:condition2Talker -2.422e-02 2.531e-02 1.198e+03 -0.957
## groupponnative:condition8Talker -9.462e-02 4.460e-02 1.188e+03 -2.121
##
##              Pr(>|t|)
## (Intercept)      2.32e-06 ***
## groupponnative    5.73e-06 ***
## condition1T       0.55006
## condition2Talker  0.00341 **
## condition8Talker  1.55e-10 ***
## groupponnative:condition1T 0.64724
## groupponnative:condition2Talker 0.33896
## groupponnative:condition8Talker 0.03409 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Correlation of Fixed Effects:
##          (Intr) grpnnn cndt1T cndt2T cndt8T grp:1T grp:2T
## groupnonntv -0.675
## condition1T -0.332  0.224
## condtn2Tlkr -0.319  0.215  0.345
## condtn8Tlkr -0.227  0.153  0.230  0.223
## grpnnntv:1T  0.201 -0.331 -0.606 -0.209 -0.139
## grpnnntv:2T  0.205 -0.336 -0.222 -0.644 -0.143  0.329
## grpnnntv:8T  0.117 -0.193 -0.118 -0.114 -0.514  0.181  0.180
```

```
anova(morphemes)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## group          0.46582  0.46582     1   38.19 16.7616  0.000212 ***
## condition      0.77410  0.25803     3 1192.62  9.2848 4.523e-06 ***
## group:condition 0.16739  0.05580     3 1192.62  2.0078  0.111092
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Perform planned and post-hoc tests

Post-hoc comparisons are performed on subject-level error rates for native vs. non-native participants

```
mydata_subj_bal <- ddply(mydata_subj, c('group','subject_id','error_type'),
  summarise,
  error_rate = mean(error_rate))
```

Content-word comparisons

```
t.test(
  mydata_subj_bal$error_rate[mydata_subj_bal$group=='nonnative' & mydata_subj_bal$error_type=='content'],
  mydata_subj_bal$error_rate[mydata_subj_bal$group=='native' & mydata_subj_bal$error_type=='content']
)
```

```
##
## Welch Two Sample t-test
##
## data:  mydata_subj_bal$error_rate[mydata_subj_bal$group == "nonnative" & and mydata_subj_bal$error_
## t = 3.4618, df = 26.901, p-value = 0.001808
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.05524142 0.21608599
## sample estimates:
## mean of x mean of y
## 0.3066182 0.1709545
```

```
cohen.d(
  mydata_subj_bal$error_rate[mydata_subj_bal$group=='nonnative' & mydata_subj_bal$error_type=='content'],
  mydata_subj_bal$error_rate[mydata_subj_bal$group=='native' & mydata_subj_bal$error_type=='content'],
  na.rm=TRUE
)
```

```
##
## Cohen's d
##
## d estimate: 1.280407 (large)
## 95 percent confidence interval:
##      inf      sup
## 0.4435177 2.1172957
```

Morphosyntactic comparisons

```
t.test(
  mydata_subj_bal$error_rate[mydata_subj_bal$group=='nonnative' & mydata_subj_bal$error_type=='morph'],
  mydata_subj_bal$error_rate[mydata_subj_bal$group=='native' & mydata_subj_bal$error_type=='morph']
)
```

```
##
## Welch Two Sample t-test
##
## data: mydata_subj_bal$error_rate[mydata_subj_bal$group == "nonnative" & and mydata_subj_bal$error_
## t = 2.8777, df = 25.111, p-value = 0.008063
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.02536379 0.15295363
## sample estimates:
## mean of x mean of y
## 0.2342757 0.1451170
```

```
cohen.d(
  mydata_subj_bal$error_rate[mydata_subj_bal$group=='nonnative' & mydata_subj_bal$error_type=='morph'],
  mydata_subj_bal$error_rate[mydata_subj_bal$group=='native' & mydata_subj_bal$error_type=='morph'],
  na.rm=TRUE
)
```

```
##
## Cohen's d
##
## d estimate: 1.077239 (large)
## 95 percent confidence interval:
##      inf      sup
## 0.2613873 1.8930914
```

Between-condition planned comparisons

Content-word level

Subject-level comparisons for mask types and error types are aggregated in another set of code detailed in the markdown file `Supplemental-Statistical_analyses_in_R.Rmd` (but not explicitly stated here) to prepare the data for the next set of tests:

```
mydata_paired = data.frame(subject_id = unique(mydata_subj$subject_id),Mask1T=NA,Mask2T=NA,Mask8T=NA,Mask
```

1-Talker vs. SSN


```
t.test(mydata_paired$Mask1T,  
       mydata_paired$MaskSSN,  
       paired=TRUE)
```

```
##  
## Paired t-test  
##  
## data: mydata_paired$Mask1T and mydata_paired$MaskSSN  
## t = 1.944, df = 26, p-value = 0.0628  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -0.005223646 0.187261774  
## sample estimates:  
## mean of the differences  
## 0.09101906
```

2-Talker vs. SSN

```
t.test(mydata_paired$Mask2T,  
       mydata_paired$MaskSSN,  
       paired=TRUE)
```

```
##  
## Paired t-test  
##  
## data: mydata_paired$Mask2T and mydata_paired$MaskSSN  
## t = 4.9566, df = 26, p-value = 3.769e-05  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 0.08748863 0.21146912  
## sample estimates:  
## mean of the differences  
## 0.1494789
```

8-Talker vs. SSN

```
t.test(mydata_paired$Mask8T,  
       mydata_paired$MaskSSN,  
       paired=TRUE)
```

```
##  
## Paired t-test  
##  
## data: mydata_paired$Mask8T and mydata_paired$MaskSSN  
## t = 9.2372, df = 25, p-value = 1.551e-09  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 0.1656539 0.2607190  
## sample estimates:  
## mean of the differences  
## 0.2131864
```

Morphosyntactic level

1-Talker vs. SSN

```
t.test(mydata_paired$Mask1T,
       mydata_paired$MaskSSN,
       paired=TRUE)

##
## Paired t-test
##
## data: mydata_paired$Mask1T and mydata_paired$MaskSSN
## t = 0.55177, df = 26, p-value = 0.5858
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.03332953 0.05778835
## sample estimates:
## mean of the differences
## 0.01222941
```

2-Talker vs. SSN

```
t.test(mydata_paired$Mask2T,
       mydata_paired$MaskSSN,
       paired=TRUE)

##
## Paired t-test
##
## data: mydata_paired$Mask2T and mydata_paired$MaskSSN
## t = 1.5831, df = 26, p-value = 0.1255
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.01053442 0.08114484
## sample estimates:
## mean of the differences
## 0.03530521
```

8-Talker vs. SSN

```
t.test(mydata_paired$Mask8T,
       mydata_paired$MaskSSN,
       paired=TRUE)

##
## Paired t-test
##
## data: mydata_paired$Mask8T and mydata_paired$MaskSSN
## t = 3.3545, df = 25, p-value = 0.002538
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.04780158 0.19984706
## sample estimates:
## mean of the differences
## 0.1238243
```