

Mixed-Effects Logistic Regression Analysis: Part 3

from Doing LVC with R*

Matt Hunt Gardner

2023-03-22

Table of contents

Correlations, Interactions, & Collinearity	1
Interactions	3
Collinearity	9
References	15

Before you proceed with this section, please make sure that you have your data loaded and modified based on the code here¹ and that `Dep.Var` is re-coded such that `Deletion` is the second factor². Next, you set the global R options to employ sum contrast coding³.

Correlations, Interactions, & Collinearity

Lets look again at the results of the most parsimonious analysis of the full data set.

```
library(lme4)
td.glmer.parsimonious <- glmer(Dep.Var ~ After.New +
  Morph.Type + Before + Stress + Phoneme + (1 | Speaker),
  data = td, family = "binomial", control = glmerControl(optCtrl = list(maxfun = 20000),
    optimizer = "bobyqa"))
summary(td.glmer.parsimonious)
```

```
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) [glmerMod]
Family: binomial ( logit )
Formula: Dep.Var ~ After.New + Morph.Type + Before + Stress + Phoneme +
(1 | Speaker)
Data: td
Control: glmerControl(optCtrl = list(maxfun = 20000), optimizer = "bobyqa")
```

AIC	BIC	logLik	deviance	df.resid
1114	1175	-545	1090	1177

Scaled residuals:

Min	1Q	Median	3Q	Max
-5.223	-0.488	-0.259	0.495	14.033

*https://lingmethodshub.github.io/content/R/lvc_r/

¹https://lingmethodshub.github.io/content/R/lvc_r/050_lvc.html

²https://lingmethodshub.github.io/content/R/lvc_r/110_lvc.html

³https://lingmethodshub.github.io/content/R/lvc_r/112_lvc.html

Random effects:

```
Groups Name      Variance Std.Dev.
Speaker (Intercept) 0.796    0.892
Number of obs: 1189, groups: Speaker, 66
```

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.277	0.207	-1.34	0.18034
After.New1	1.840	0.157	11.71	< 2e-16 ***
After.New2	-1.175	0.144	-8.14	4.1e-16 ***
Morph.Type1	0.426	0.140	3.05	0.00230 **
Morph.Type2	-1.892	0.213	-8.87	< 2e-16 ***
Before1	-0.575	0.202	-2.84	0.00447 **
Before2	0.526	0.193	2.72	0.00659 **
Before3	0.117	0.278	0.42	0.67370
Before4	0.731	0.190	3.85	0.00012 ***
Stress1	-0.799	0.137	-5.81	6.2e-09 ***
Phoneme1	0.287	0.128	2.25	0.02462 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	Aft.N1	Aft.N2	Mrp.T1	Mrp.T2	Befor1	Befor2	Befor3	Befor4
After.New1	0.064								
After.New2	-0.104	-0.430							
Morph.Type1	-0.434	0.203	-0.114						
Morph.Type2	-0.051	-0.221	0.178	-0.376					
Before1	-0.296	-0.223	0.293	0.052	0.429				
Before2	-0.164	0.191	-0.094	-0.110	0.247	0.029			
Before3	0.150	0.018	-0.060	0.319	-0.515	-0.421	-0.477		
Before4	0.250	0.304	-0.431	-0.202	0.051	-0.311	-0.090	-0.274	
Stress1	-0.434	-0.432	-0.064	0.050	0.097	0.056	0.125	-0.094	-0.250
Phoneme1	0.459	0.149	-0.307	-0.137	-0.265	-0.543	-0.263	0.149	0.438
Strss1									
After.New1									
After.New2									
Morph.Type1									
Morph.Type2									
Before1									
Before2									
Before3									
Before4									
Stress1									
Phoneme1									

Below the results for fixed effects is a table of the correlations of the fixed effects. This table is a good way to spot non-orthogonal⁴ effects you might not yet have caught (though you should have caught these effects if you thoroughly explored your data using summary statistics⁵). Look at only the coefficients for the correlations of levels of **different** parameters. Generally any value over $|0.3|$ ⁶ should be investigated further. If you have any correlations over $|0.7|$ you should be worried. In your table there is no correlation

⁴https://en.wikipedia.org/wiki/Orthogonality#Statistics,_econometrics,_and_economics

⁵https://lingmethodshub.github.io/content/R/lvc_r/060_lvc.html

⁶Any absolute value greater than 3, or rather any positive value higher than +3 or any negative value lower than -3.

higher than $|0.7|$, but there are a few over $|0.3|$: `After.New1*Before4` $|0.304|$; `After.New1*Stress1` $|0.432|$; `After.New2*Before4` $|0.431|$; `After.New2*Phoneme1` $|0.307|$; `Morph.Type1*Before3` $|0.319|$; `Morph.Type2*Before3` $|0.515|$; `Before1*Phoneme1` $|0.543|$; and `Before4*Phoneme1` $|0.438|$. These correlations suggest it might be worthwhile to re-check the summary statistics, looking especially at the cross-tab of `After.New` and `Before`, `After.New` and `Phoneme`, `Morph.Type` and `Before`, `Morph.Type` and `Phoneme`, and `Before` and `Phoneme`.⁷

There are two other methods for testing for a relationship between your fixed effect predictors that relate to the kind of relationship your fixed effects predictors might have. The first is that the predictors have an **interaction** the other is that they are (multi-) **collinear**.

Interactions

An interaction arises when two independent fixed effects work together to predict the variation of the application value. For example, based on the Conditional Inference Tree⁸ analysis you know that it is not case that gender itself explains the social variation in `Deletion` vs. `Realized` (this is confirmed by the analysis of data from just young speakers⁹, where `Sex` is not significant), nor is it that age explains the social variation (confirmed by the non-significance of both `Age.Group` and `Center.Age` in the full model¹⁰). Instead, it seems that older men use `Deletion` more frequently than everyone else. This is an interaction. It is the combination of `Age.Group` and `Sex` that (potentially) best explains the social variation. You can test this in your model by creating an interaction group with these two fixed effect predictors. You do this by including the interaction term `Sex*Age.Group` in your analysis. To make things easier here you can simplify and again consider middle-age and older speakers together. You can also drop `Phoneme` as it is non-significant among both cohorts. When you include an interaction term, the individual components of the interaction will also be included as singular predictors.

```
# Create a simplified Age.Group.Simple column
td <- td %>%
  mutate(Age.Group.Simple = cut(YOB, breaks = c(-Inf,
    1979, Inf), labels = c("Old/Middle", "Young")))

# Create a regression analysis with a
# Sex*Age.Group.Simple interaction group
td.glmer.sex.age.interaction <- glmer(Dep.Var ~ After.New +
  Morph.Type + Before + Stress + Sex * Age.Group.Simple +
  (1 | Speaker), data = td, family = "binomial",
  glmerControl(optCtrl = list(maxfun = 20000), optimizer = "bobyqa"))

summary(td.glmer.sex.age.interaction)
```

```
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) [glmerMod]
Family: binomial ( logit )
Formula:
Dep.Var ~ After.New + Morph.Type + Before + Stress + Sex * Age.Group.Simple +
(1 | Speaker)
Data: td
Control: glmerControl(optCtrl = list(maxfun = 20000), optimizer = "bobyqa")
```

AIC	BIC	logLik	deviance	df.resid
-----	-----	--------	----------	----------

⁷See also *Notes on Interactions* by Derek Denis, available at https://www.dropbox.com/s/7c4tzc8st5dmeit/Denis_2010_Notes_On_Interactions.pdf.

⁸https://lingmethodshub.github.io/content/R/lvc_r/080_lvc.html

⁹https://lingmethodshub.github.io/content/R/lvc_r/112_lvc.html

¹⁰https://lingmethodshub.github.io/content/R/lvc_r/112_lvc.html

```

      1117      1188      -545      1089      1175

Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.305 -0.492 -0.266  0.492 14.222

Random effects:
    Groups Name      Variance Std.Dev.
    Speaker (Intercept) 0.695   0.834
Number of obs: 1189, groups: Speaker, 66

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    -0.4344    0.1831  -2.37  0.01767 *
After.New1       1.7895    0.1554  11.51 < 2e-16 ***
After.New2     -1.0791    0.1371  -7.87  3.6e-15 ***
Morph.Type1      0.4618    0.1385   3.34  0.00085 ***
Morph.Type2     -1.7712    0.2055  -8.62 < 2e-16 ***
Before1        -0.3258    0.1695  -1.92  0.05454 .
Before2         0.6685    0.1870   3.58  0.00035 ***
Before3         0.0159    0.2750   0.06  0.95386
Before4         0.5365    0.1696   3.16  0.00156 **
Stress1        -0.7696    0.1368  -5.63  1.8e-08 ***
Sex1           -0.2626    0.1359  -1.93  0.05322 .
Age.Group.Simple1  0.1281    0.1371   0.93  0.35011
Sex1:Age.Group.Simple1 -0.1750    0.1363  -1.28  0.19902
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation matrix not shown by default, as p = 13 > 12.
Use print(x, correlation=TRUE) or
    vcov(x)          if you need it

```

```
Anova(td.glmer.sex.age.interaction)
```

Analysis of Deviance Table (Type II Wald chisquare tests)

```

Response: Dep.Var

              Chisq Df Pr(>Chisq)
After.New    144.21  2  < 2e-16 ***
Morph.Type   74.39  2  < 2e-16 ***
Before       36.42  4  2.4e-07 ***
Stress       31.67  1  1.8e-08 ***
Sex           3.71  1    0.054 .
Age.Group.Simple  0.71  1    0.399
Sex:Age.Group.Simple  1.65  1    0.199
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

What you can see from the `summary(td.glmer.sex.age.interaction)` and `Anova(td.glmer.sex.age.interaction)` results is that this interaction term is not significant and does not add explanatory value to the analysis. The negative polarity of the estimate coefficient of the interaction term `Sex1:Age.Group.Simple1` indicates that when the level of `Sex` is `Female` (1) and `Age.Group.Simple` is `Old/Middle` (1) the overall probability decreases by -0.1750 . This coefficient represents the extra effect of both predictors working together. The p -value of 0.19902, however, indicates that this change is not statistically different from zero/no

effect. In other words, even though we know older men use **Deletion** more frequently, the extra effect of combining age and sex does not emerge as significant when the influence of the linguistic predictors is considered. If you want to home in on the older/middle men in your results, you can reorder the **Sex** predictor. Using the `fct_rev()` function, which reverses the order of factors making the last “missing” factor first, is the easiest way to do this.

```
# Create a regression analysis with a
# Sex*Age.Group.Simple interaction group in which
# `Male` equals Sex1
td.glmer.sex.age.interaction <- glmer(Dep.Var ~ After.New +
  Morph.Type + Before + Stress + fct_rev(Sex) * Age.Group.Simple +
  (1 | Speaker), data = td, family = "binomial",
  glmerControl(optCtrl = list(maxfun = 20000), optimizer = "bobyqa"))

summary(td.glmer.sex.age.interaction)
```

```
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) [glmerMod]
Family: binomial ( logit )
Formula: Dep.Var ~ After.New + Morph.Type + Before + Stress + fct_rev(Sex) *
  Age.Group.Simple + (1 | Speaker)
Data: td
Control: glmerControl(optCtrl = list(maxfun = 20000), optimizer = "bobyqa")
```

AIC	BIC	logLik	deviance	df.resid
1117	1188	-545	1089	1175

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.305	-0.492	-0.266	0.492	14.222

Random effects:

Groups	Name	Variance	Std.Dev.
Speaker	(Intercept)	0.695	0.834

Number of obs: 1189, groups: Speaker, 66

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.4344	0.1831	-2.37	0.01767 *
After.New1	1.7895	0.1554	11.51	< 2e-16 ***
After.New2	-1.0791	0.1371	-7.87	3.6e-15 ***
Morph.Type1	0.4618	0.1385	3.34	0.00085 ***
Morph.Type2	-1.7712	0.2055	-8.62	< 2e-16 ***
Before1	-0.3258	0.1695	-1.92	0.05454 .
Before2	0.6685	0.1870	3.58	0.00035 ***
Before3	0.0159	0.2750	0.06	0.95385
Before4	0.5365	0.1696	3.16	0.00156 **
Stress1	-0.7696	0.1368	-5.63	1.8e-08 ***
fct_rev(Sex)1	0.2626	0.1359	1.93	0.05322 .
Age.Group.Simple1	0.1281	0.1371	0.93	0.35011
fct_rev(Sex)1:Age.Group.Simple1	0.1750	0.1363	1.28	0.19902

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation matrix not shown by default, as $p = 13 > 12$.
 Use `print(x, correlation=TRUE)` or
`vcov(x)` if you need it

```
Anova(td.glmer.sex.age.interaction)
```

Analysis of Deviance Table (Type II Wald chisquare tests)

Response: Dep.Var

	Chisq	Df	Pr(>Chisq)
After.New	144.21	2	< 2e-16 ***
Morph.Type	74.39	2	< 2e-16 ***
Before	36.42	4	2.4e-07 ***
Stress	31.67	1	1.8e-08 ***
fct_rev(Sex)	3.71	1	0.054 .
Age.Group.Simple	0.71	1	0.399
fct_rev(Sex):Age.Group.Simple	1.65	1	0.199

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

You can see that the coefficient for the interaction term is identical, but with reverse polarity. It indicates that when **Sex** is **Male** and **Age.Group.Simple** is **Old/Middle** the extra effect is $+0.1750$, but again, as you saw above, this difference is not significantly different from zero/no effect $p = 0.19902$.

An alternative way to test this interaction is to create a four-way **Sex:Age.Group.Simple** interaction group¹¹ and include it as a fixed effect. By doing this instead of testing for an extra effect caused by the interaction of these two variables, you are instead testing the difference in likelihood from the overall likelihood for each combination of age and sex, and determining whether this is significantly different from zero.

```
# Create a four-way interaction group
td <- td %>%
  unite("Sex.Age.Group.Simple", c(Sex, Age.Group.Simple),
        sep = ":", remove = FALSE)
levels(as.factor(td$Sex.Age.Group.Simple))
```

```
[1] "F:Old/Middle" "F:Young"      "M:Old/Middle" "M:Young"
```

The levels of the four-way interaction group are **F:Old/Middle**, **F:Young**, **M:Old/Middle**, and **M:Young**. If you recreate your `glmer()` analysis, you should find that the third level, **M:Old/Middle**, to have a positive coefficient (**Deletion** more likely than the mean), and the others to have a negative coefficient (**Deletion** less likely than the mean).

```
# Create a regression analysis with the
# Age.Simple:Sex interaction group
td.glmer.sex.age.interaction <- glmer(Dep.Var ~ After.New +
  Morph.Type + Before + Stress + Sex.Age.Group.Simple +
  (1 | Speaker), data = td, family = "binomial",
  glmerControl(optCtrl = list(maxfun = 20000), optimizer = "bobyqa"))

summary(td.glmer.sex.age.interaction)
```

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [glmerMod]

¹¹https://lingmethodshub.github.io/content/R/lvc_r/050_lvc.html

```
Family: binomial ( logit )
Formula:
Dep.Var ~ After.New + Morph.Type + Before + Stress + Sex.Age.Group.Simple +
(1 | Speaker)
Data: td
Control: glmerControl(optCtrl = list(maxfun = 20000), optimizer = "bobyqa")
```

AIC	BIC	logLik	deviance	df.resid
1117	1188	-545	1089	1175

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.305	-0.492	-0.266	0.492	14.222

Random effects:

Groups	Name	Variance	Std.Dev.
Speaker	(Intercept)	0.695	0.834

Number of obs: 1189, groups: Speaker, 66

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.4344	0.1831	-2.37	0.01767 *
After.New1	1.7895	0.1554	11.51	< 2e-16 ***
After.New2	-1.0791	0.1371	-7.87	3.6e-15 ***
Morph.Type1	0.4618	0.1385	3.34	0.00085 ***
Morph.Type2	-1.7712	0.2055	-8.62	< 2e-16 ***
Before1	-0.3258	0.1695	-1.92	0.05454 .
Before2	0.6685	0.1870	3.58	0.00035 ***
Before3	0.0159	0.2750	0.06	0.95386
Before4	0.5365	0.1696	3.16	0.00156 **
Stress1	-0.7696	0.1368	-5.63	1.8e-08 ***
Sex.Age.Group.Simple1	-0.3095	0.2161	-1.43	0.15206
Sex.Age.Group.Simple2	-0.2158	0.2441	-0.88	0.37667
Sex.Age.Group.Simple3	0.5658	0.2557	2.21	0.02692 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation matrix not shown by default, as p = 13 > 12.

Use print(x, correlation=TRUE) or
vcov(x) if you need it

```
Anova(td.glmer.sex.age.interaction)
```

Analysis of Deviance Table (Type II Wald chisquare tests)

Response: Dep.Var

	Chisq	Df	Pr(>Chisq)
After.New	144.21	2	< 2e-16 ***
Morph.Type	74.39	2	< 2e-16 ***
Before	36.42	4	2.4e-07 ***
Stress	31.67	1	1.8e-08 ***
Sex.Age.Group.Simple	5.62	3	0.13

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

By using this four-way interaction group you can see that the `M:Older/Middle (Sex.Age.Group.Simple3)` coefficient is negative, and it is significantly different from zero/no effect. To find the coefficient for the missing fourth value, re-create the analysis using `fct_rev()`.

```
# Create a regression analysis with the reversed
# Age.Simple:Sex interaction group
td.glmer.sex.age.interaction <- glmer(Dep.Var ~ After.New +
  Morph.Type + Before + Stress + fct_rev(Sex.Age.Group.Simple) +
  (1 | Speaker), data = td, family = "binomial",
  glmerControl(optCtrl = list(maxfun = 20000), optimizer = "bobyqa"))

summary(td.glmer.sex.age.interaction)
```

Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) [glmerMod]

Family: binomial (logit)

Formula:

Dep.Var ~ After.New + Morph.Type + Before + Stress + fct_rev(Sex.Age.Group.Simple) +
(1 | Speaker)

Data: td

Control: glmerControl(optCtrl = list(maxfun = 20000), optimizer = "bobyqa")

AIC	BIC	logLik	deviance	df.resid
1117	1188	-545	1089	1175

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.305	-0.492	-0.266	0.492	14.222

Random effects:

Groups	Name	Variance	Std.Dev.
Speaker	(Intercept)	0.695	0.834

Number of obs: 1189, groups: Speaker, 66

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.4344	0.1831	-2.37	0.01767 *
After.New1	1.7895	0.1554	11.51	< 2e-16 ***
After.New2	-1.0791	0.1371	-7.87	3.6e-15 ***
Morph.Type1	0.4618	0.1385	3.34	0.00085 ***
Morph.Type2	-1.7712	0.2055	-8.62	< 2e-16 ***
Before1	-0.3258	0.1695	-1.92	0.05454 .
Before2	0.6685	0.1870	3.58	0.00035 ***
Before3	0.0159	0.2750	0.06	0.95386
Before4	0.5365	0.1696	3.16	0.00156 **
Stress1	-0.7696	0.1368	-5.63	1.8e-08 ***
fct_rev(Sex.Age.Group.Simple)1	-0.0405	0.2273	-0.18	0.85860
fct_rev(Sex.Age.Group.Simple)2	0.5658	0.2557	2.21	0.02692 *
fct_rev(Sex.Age.Group.Simple)3	-0.2158	0.2441	-0.88	0.37668

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation matrix not shown by default, as p = 13 > 12.

Use `print(x, correlation=TRUE)` or


```
vcov(x)          if you need it
```

```
Anova(td.glmer.sex.age.interaction)
```

Analysis of Deviance Table (Type II Wald chisquare tests)

Response: Dep.Var

	Chisq	Df	Pr(>Chisq)
After.New	144.21	2	< 2e-16 ***
Morph.Type	74.39	2	< 2e-16 ***
Before	36.42	4	2.4e-07 ***
Stress	31.67	1	1.8e-08 ***
fct_rev(Sex.Age.Group.Simple)	5.62	3	0.13

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

As with the other levels, **Men:Young** (`fct_rev(Sex.Age.Group.Simple)` 1) is not significant. What you can conclude is that all women and young men are not significantly different from the overall probability (and by extension each other), but old/middle men are significantly different from the overall probability. Creating this four-way interaction group and including it as a fixed effect reveals this pattern in a way that including the interaction term **Sex:Age.Simple** does not. That being said, the results of the `Anova()` indicate that this predictor still does not add explanatory value to the analysis.

Collinearity

When fixed effects predictors are not independent we say they are (multi-) collinear¹². Collinearity and interactions are similar, but separate, phenomena.

Collinearity is the phenomenon whereby two or more predictor variables are highly correlated, such that the value/level of one can be predicted from the value/level of the other with a non-trivial degree of accuracy. Including both in an analysis 1) violates the assumptions of the model; and 2) can actually result in diminished likelihood estimates for both predictors, masking real effects. As discussed before¹³, in this Cape Breton data, **Education**, **Job**, and **Age.Group** are all collinear to various degrees. For example, if **Job** is **Student**, then the level of **Education** can be predicted (it will also be **Student**), and vice versa. For both, **Age.Group** can be predicted too (**Young**). These types of correlations are easy to see for social categories, but somewhat more difficult to tease out for linguistic categories. The first step is always a thorough cross tabulation¹⁴ of your independent variables. For a quick visual of cross tabulations you can employ a mosaic plot¹⁵. Here is the code for creating a quick mosaic plot using `ggplot2`, which you likely already have installed if you've followed along with previous chapters.

```
# Install ggmosaic package
install.packages("ggmosaic")

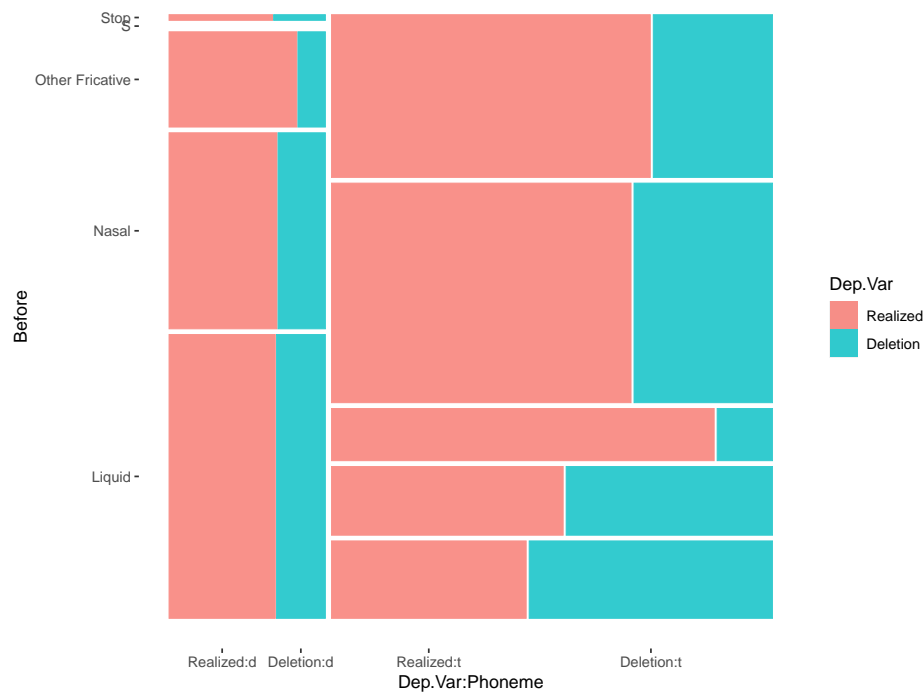
library(ggmosaic)
library(ggplot2)
# Create a quick mosaic plot of Phoneme and
# Before
ggplot(td) + geom_mosaic(aes(product(Dep.Var, Before,
  Phoneme), fill = Dep.Var)) + theme_mosaic()
```

¹²<https://www.britannica.com/topic/collinearity-statistics>

¹³https://lingmethodshub.github.io/content/R/lvc_r/080_lvc.html

¹⁴https://lingmethodshub.github.io/content/R/lvc_r/060_lvc.html

¹⁵<https://cran.r-project.org/web/packages/ggmosaic/vignettes/ggmosaic.html>

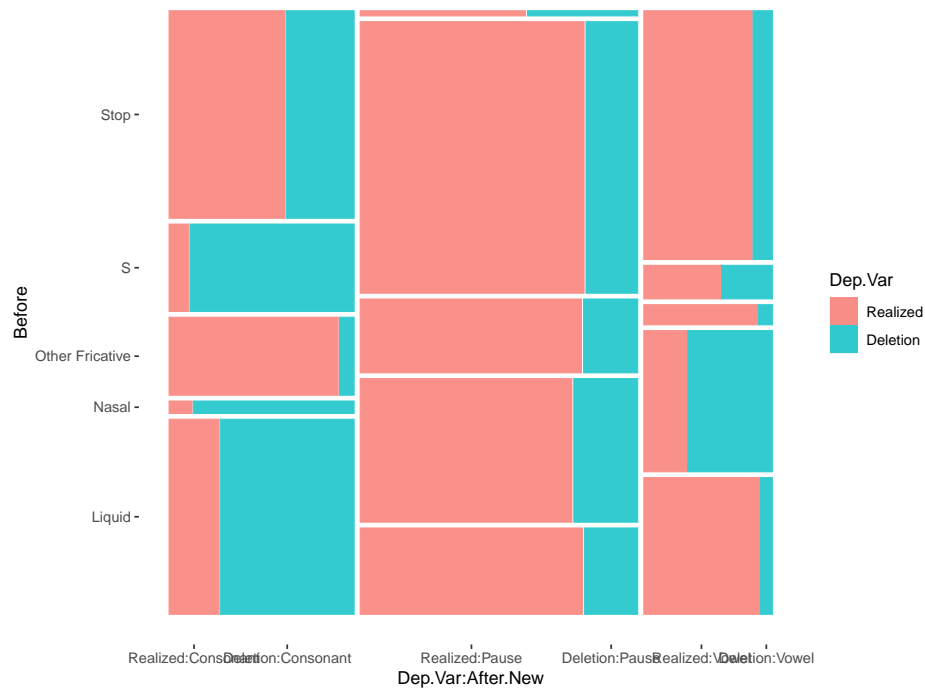


In a mosaic plot the size of the box for each combination of variables corresponds to the relative number of tokens of that combination. The first major observation from the mosaic plot is that there are no preceding /s/ tokens where the underlying phoneme is /d/, and there are remarkably few tokens in which /d/ is preceded by a non-nasal stop.¹⁶ This indicates that you shouldn't include both of these predictors in your model, or complexify the model by creating an interaction group of **Phoneme** and **Before**. This is because you can predict some of the values of **Phoneme** and **Before**. For example, if a token is underlyingly world-final /d/, the preceding segment will not be /s/. Likewise, if the preceding segment is /s/, the underlying phoneme must be /t/.

Lets look at another mosaic plot.

```
# Create a quick mosaic plot of Phoneme and
# Before
ggplot(td) + geom_mosaic(aes(product(Dep.Var, Before,
  After.New), fill = Dep.Var)) + theme_mosaic()
```

¹⁶I checked the data and there are only three such tokens: one token of *bugged* and two of *hugged*.



This plot is a little bit hard to read. To make the x-axis labels a little easier to read, you can use the binary version of `Dep.Var`. You'll remember that 1 is Deletion and 0 is Realized.

```
# Create a quick mosaic plot of Phoneme and
# Before
ggplot(td) + geom_mosaic(aes(product(Dep.Var.Binary,
  Before, After.New), fill = Dep.Var.Binary)) + theme_mosaic()
```



This mosaic plot shows that there are very few tokens with a preceding **Stop** and a following **Pause**. Though no apparent collinearity is present, this mosaic plot does reveal some interesting potential interactions. The effect of preceding /s/, liquids, and nasals appears to be specific to pre-consonantal contexts, and perhaps also pre-vowel contexts for nasals. This suggests further exploration of the data is warranted — perhaps by creating separate `glmer()` models for each following context, by complexifying your full model by creating a **Before** and **After.New** interaction group, or by simplifying your full model by collapsing these two categories¹⁷ into simpler grouped categories, e.g., **Pre-Pause**, **Liquid-Consonant**, **Liquid-Vowel**, **Nasal-Consonant**, **Nasal-Vowel**, **S-Consonant**, **S-Vowel**, **Other-Consonant**, **Other-Vowel**, or similar.

```
# Create a new model using insights from the
# mosaic plots
td <- td %>%
  mutate(Before.After = factor(paste(td$Before, td$After.New,
    sep = "."))) %>%
  mutate(Before.After = recode_factor(Before.After,
    Liquid.Pause = "Pause", Nasal.Pause = "Pause",
    `Other Fricative.Pause` = "Pause", S.Pause = "Pause",
    Stop.Pause = "Pause", `Other Fricative.Consonant` = "Other.Consonant",
    Stop.Consonant = "Other.Consonant", `Other Fricative.Vowel` = "Other.Vowel",
    Stop.Vowel = "Other.Vowel"))
```

¹⁷https://lingmethodshub.github.io/content/R/lvc_r/040_lvc.html

```
td.glmer.parsimonious.new <- glmer(Dep.Var ~ Before.After +
  Morph.Type + Stress + (1 | Speaker), data = td,
  family = "binomial", glmerControl(optCtrl = list(maxfun = 20000),
  optimizer = "bobyqa"))
```

```
# Compare fit of new parsimonious model with old
# parsimonious model
anova(td.glmer.parsimonious, td.glmer.parsimonious.new)
```

Data: td

Models:

td.glmer.parsimonious: Dep.Var ~ After.New + Morph.Type + Before + Stress + Phoneme + (1 | Speaker)

td.glmer.parsimonious.new: Dep.Var ~ Before.After + Morph.Type + Stress + (1 | Speaker)

	npar	AIC	BIC	logLik	deviance	Chisq	Df	Pr(>Chisq)
td.glmer.parsimonious	12	1114	1175	-545	1090			
td.glmer.parsimonious.new	13	1087	1153	-531	1061	28.6	1	8.7e-08

```
td.glmer.parsimonious
td.glmer.parsimonious.new ***
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

The `anova()` function shows that `td.glmer.parsimonious.new` is a better fit model. In other words, it does a better job of predicting the variation in the data.

It is important, however, to point out that collinearity does not reduce the predictive power or reliability of the `glmer()` model as a whole — it only affects calculations regarding individual predictors. That is, a `glmer()` model with correlated predictors can indicate how well the entire bundle of predictors predicts the outcome variable, but it may not give valid results about any individual predictor, or about which predictors are redundant with respect to others. In other words, collinearity prevents you from discovering the three lines of evidence.

So how can you test whether your predictors are collinear? There are two measures beyond just looking at the correlation matrix (which can point to either collinearity or interaction).

The first method to test collinearity is to find the **Condition Number** (κ a.k.a. kappa). The function to calculate this comes from a package¹⁸ created by linguist Jason Grafmiller, which adapts the `collin.fnc()` function from Baayen's `languageR`¹⁹ package to work with `lme4` mixed models. To install this package you need to first install the `devtools()` package, and then you can download it. We will return to the original `td.glmer.parsimonious` to do this test.

```
# Install JGmermod
install.packages("devtools")
devtools::install_github("jasongraf1/JGmermod")
```

```
library(JGmermod)
# Calculate Condition Number
collin.fnc.mer(td.glmer.parsimonious)$cnumber
```

[1] 5.2

¹⁸<https://rdrr.io/github/jasongraf1/JGmermod/>

¹⁹<https://cran.r-project.org/web/packages/languageR/index.html>

The Condition Number here is less than 6 indicating no collinearity Baayen (2008: 182). According to Baayen (citing Belsley & Kuh & Welsch 1980), when the condition number is between 0 and 6, there is no collinearity to speak of. Medium collinearity is indicated by condition numbers around 15, and condition numbers of 30 or more indicate potentially harmful collinearity.

The second measure of collinearity is determining the **Variable Inflation Factor** (VIF), which estimates how much the variance of a regression coefficient is inflated due to (multi)collinearity. The function `check_collinearity()` from the `performance` package is used to calculate the VIF.

```
install.packages("performance")

library(performance)
check_collinearity(td.glmer.parsimonious)
```

```
# Check for Multicollinearity
```

```
Low Correlation
```

Term	VIF	VIF 95% CI	Increased SE	Tolerance	Tolerance 95% CI
After.New	2.68	[2.45, 2.94]	1.64	0.37	[0.34, 0.41]
Morph.Type	2.06	[1.90, 2.25]	1.44	0.49	[0.44, 0.53]
Before	4.93	[4.46, 5.46]	2.22	0.20	[0.18, 0.22]
Stress	1.68	[1.56, 1.83]	1.30	0.59	[0.55, 0.64]
Phoneme	1.87	[1.73, 2.04]	1.37	0.53	[0.49, 0.58]

According to the `performance` package documentation²⁰, a VIF less than 5 indicates a low correlation of that predictor with other predictors. A value between 5 and 10 indicates a moderate correlation, while VIF values larger than 10 are a sign for high, not tolerable correlation of model predictors (James et al. 2013). The **Increased SE** column in the output indicates how much larger the standard error is due to the association with other predictors conditional on the remaining variables in the model.

Based on the Condition Number ($\kappa < 6$) and the VIF (< 5) you can report that any (multi-) collinearity in your model is within acceptably low limits. You can add this to your manuscript table, as in Table 1 (based on `td.glmer.parsimonious`), though you should always contextualize what these measures indicate (i.e., low collinearity) in the text too.

Keep in mind that if there are interaction terms (e.g., `Sex*Age.Group`) in your model high VIF values are expected. This is because you are explicitly expecting and testing a correlation between two predictors. The (multi-) collinearity among two components of the interaction term is also called “inessential ill-conditioning”, which leads to inflated VIF values.

Also keep in mind that (multi-) collinearity might arise when a third, unobserved variable has a causal effect on two or more predictors’ effect on the dependant variable. For example, correlated Education and Job Type effects may be caused by an underlying age effect, if older speakers are generally less educated and blue-collar workers and young speakers are generally more educated and white collar workers. In such cases, the actual relationship that matters is the association between the unobserved variable and the dependant variable. If confronted with a case like this, you should revisit what independent predictors are included in the model. Non-inferential tools that can include (multi-) collinear descriptors (like Conditional Inference Trees²¹ or Random Forests²²) may help you.

²⁰https://rdrr.io/cran/performance/man/check_collinearity.html

²¹https://lingmethodshub.github.io/content/R/lvc_r/080_lvc_r.html

²²https://lingmethodshub.github.io/content/R/lvc_r/090_lvc_r.html

Table 1: Mixed-effects logistic regression testing the fixed effect of FOLLOWING CONTEXT, MORPHEME TYPE, PRECEDING CONTEXT, STRESS and PHONEME and a random intercept of *Speaker* on the deletion of word-final /t, d/ in Cape Breton English

AIC = 1114, Marginal R^2 = .40, Conditional R^2 = .52					Observations	
Fixed Effects:	Estimate	Std. Error	z-value	p-value	n	% Deletion
INTERCEPT (Grand Mean)	-0.277	0.207	-1.34		1,189	32
FOLLOWING CONTEXT						
<i>Consonant</i>	1.840	0.157	11.71	***	372	54
<i>Vowel</i>	-0.665	0.161	-4.13	***	259	28
<i>Pause</i>	-1.175	0.144	-8.14	***	558	20
MORPHEME TYPE						
<i>Semi-Weak Simple Past</i>	1.466	0.207	7.10	***	116	63
<i>Mono-morpheme</i>	0.426	0.140	3.05	***	762	37
<i>Weak Simple Past</i>	-1.892	0.213	-8.87	***	311	10
STRESS						
<i>Unstressed</i>	0.799	0.137	5.81	***	142	47
<i>Stressed</i>	-1.598	0.275	-5.81	***	1,047	31
PRECEDING CONTEXT						
<i>/s/</i>	0.731	0.190	3.85	***	332	53
<i>Nasal</i>	0.526	0.193	2.72	**	209	39
<i>Other Fricative</i>	0.117	0.278	0.42		130	15
<i>Liquid</i>	-0.575	0.202	-2.84	**	269	42
<i>Stop</i>	-0.799	0.189	-4.22	***	249	27
PHONEME						
<i>/d/</i>	0.287	0.128	2.25	*	878	34
<i>/t/</i>	-0.287	0.128	-2.25	*	311	29
Random Effects:					<i>sd</i>	<i>n</i>
SPEAKER					0.892	66

*** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$

Sum contrast coding. Estimate coefficients reported in log-odds.

Model significantly better than null model (AIC = 1,456, $\chi^2 = 362$, df = 10, ***)

Correlation of Fixed Effects $\leq |0.54|$, $\kappa = 5.2$, Variable Inflation Factor ≤ 4.93

References

- Baayen, R. Harald. 2008. *Analyzing linguistic data: A practical introduction to statistics using R*. Cambridge: Cambridge University Press.
- Belsley, David A. & Kuh, Edwin & Welsch, Roy E. 1980. *Regression diagnostics: Identifying influential data and sources of collinearity*. New York: Wiley.
- James, Gareth & Witten, Daniela & Hastie, Trevor & Tibshirani, Robert. 2013. *An introduction to statistical learning: With applications in R*. New York: Springer. Retrieved from <https://link.springer.com/book/10.1007/978-1-4614-7138-7c>