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Common Issues and Solutions in Regression Modeling (Mixed or not)

Day 2

Florian Jaeger

May 4, 2010

Hypothesis testing in psycholinguistic research

- ▶ Typically, we make predictions not just about the existence, but also the *direction* of effects.
- ▶ Sometimes, we're also interested in effect *shapes* (non-linearities, etc.)
- ▶ Unlike in ANOVA, regression analyses reliably test hypotheses about effect direction and shape without requiring post-hoc analyses if (a) *the predictors in the model are coded appropriately* and (b) *the model can be trusted*.
- ▶ **Today:** Provide an overview of (a) and (b).

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Overview

- ▶ **Introduce sample data and simple models**
- ▶ **Towards a model with interpretable coefficients:**
 - ▶ outlier removal
 - ▶ transformation
 - ▶ coding, centering, ...
 - ▶ *collinearity*
- ▶ **Model evaluation:**
 - ▶ fitted vs. observed values
 - ▶ model validation
 - ▶ investigation of residuals
 - ▶ case influence, outliers
- ▶ **Model comparison**
- ▶ **Reporting the model:**
 - ▶ comparing effect sizes
 - ▶ back-transformation of predictors
 - ▶ visualization

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Data 1: Lexical decision RTs

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- ▶ **Outcome:** log lexical decision latency RT
- ▶ **Inputs:**
 - ▶ factors Subject (21 levels) and Word (79 levels),
 - ▶ factor NativeLanguage (*English* and *Other*)
 - ▶ continuous predictors Frequency (log word frequency), and Trial (rank in the experimental list).

	Subject	RT	Trial	NativeLanguage	Word	Frequency
1	A1	6.340359	23	English	owl	4.859812
2	A1	6.308098	27	English	mole	4.605170
3	A1	6.349139	29	English	cherry	4.997212
4	A1	6.186209	30	English	pear	4.727388
5	A1	6.025866	32	English	dog	7.667626
6	A1	6.180017	33	English	blackberry	4.060443

Data 2: Lexical decision response

- **Outcome:** Correct or incorrect response (Correct)
- **Inputs:** same as in linear model

```
> lmer(Correct == "correct" ~ NativeLanguage +  
+      Frequency + Trial +  
+      (1 | Subject) + (1 | Word),  
+      data = lexdec, family = "binomial")
```

Random effects:

Groups	Name	Variance	Std.Dev.
Word	(Intercept)	1.01820	1.00906
Subject	(Intercept)	0.63976	0.79985

Number of obs: 1659, groups: Word, 79; Subject, 21

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-1.746e+00	8.206e-01	-2.128	0.033344	*
NativeLanguageOther	-5.726e-01	4.639e-01	1.234	0.217104	
Frequency	5.600e-01	1.570e-01	-3.567	0.000361	* **
Trial	4.443e-06	2.965e-03	0.001	0.998804	

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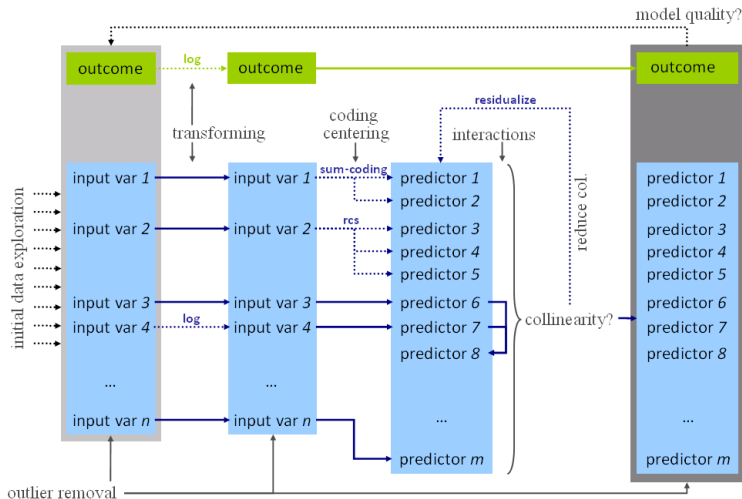
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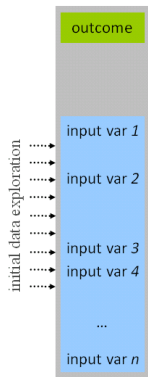
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Data exploration

- ▶ Select and *understand* input variables and outcome based on a-priori theoretical consideration
 - ▶ How many parameters does your data afford (↪overfitting)?
- ▶ Data exploration: *Before* fitting the model, explore inputs and outputs
 - ▶ Outliers due to missing data or measurement error (e.g. RTs in SPR < 80msecs).
 - ▶ **NB:** postpone distribution-based outlier exclusion until after **transformations**)
 - ▶ Skewness in distribution can affect the accuracy of model's estimates (↪transformations).

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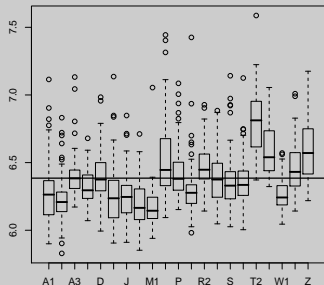
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Understanding variance associated with potential random effects

- explore candidate predictors (e.g., Subject or Word) for level-specific variation.



```
> boxplot(RT ~ Subject, data = lexdec)
```

→ Huge variance.

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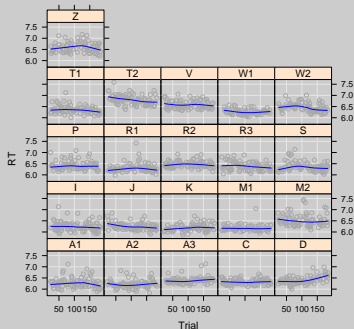
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Random effects (cnt'd)

- explore variation of level-specific slopes.



```
> xyloless.fnc(RT ~ Trial | Subject,  
> type = c("g", "smooth"), data = lexdec)
```

→ not too much variance.

- random effect inclusion test via ↪ **model comparison**

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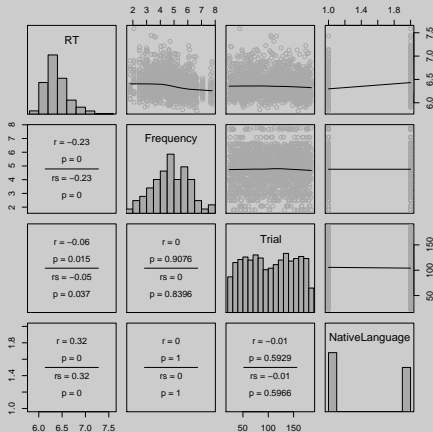
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Understanding input variables

► Explore:

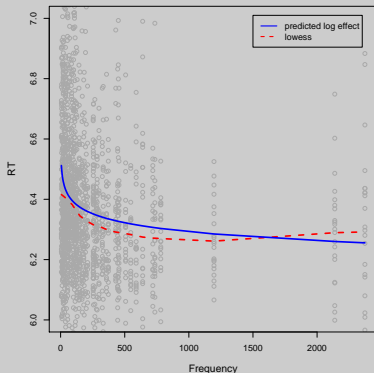
- correlations between predictors (\hookrightarrow **collinearity**).
- non-linearities may become obvious (lowess).



```
> pairscor.fnc(lexdec[,c("RT", "Frequency", "Trial", "NativeLanguage")])
```

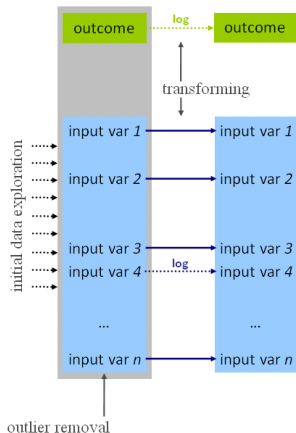
Non-linearities

- ▶ Consider Frequency (already log-transformed in `lexdec`) as predictor of RT:



- Assumption of a linearity may be inaccurate.
 - ▶ Select appropriate ↻ **transformation**: log, power, sinusoid, etc.
 - ▶ or use polynomial `poly()` or splines `rcs()`, `bs()`, etc. to ↻ **model non-linearities**.

Transformation



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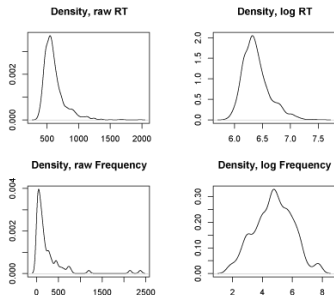
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Transformation

- Reasons to transform:
 - Conceptually motivated (e.g. log-transformed probabilities)
 - Can reduce non-linear to linear relations (cf. previous slide)
 - Remove skewness (e.g. by log-transform)
- Common transformation: log, square-root, power, or inverse transformation, etc.



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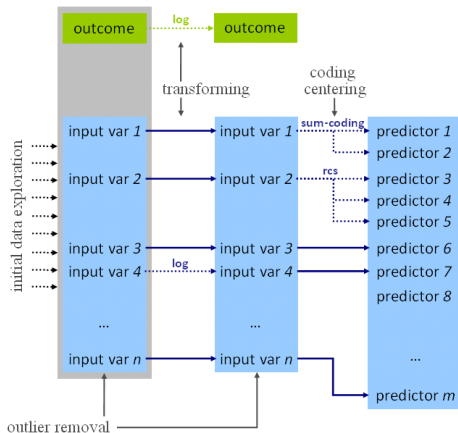
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Coding and centering predictors



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Coding affects interpretation

Consider a simpler model:

```
> lmer(RT ~ NativeLanguage +  
+       (1 | Word) + (1 | Subject), data = lexdec)
```

	AIC	BIC	logLik	deviance	REMLdev
	-886.1	-853.6	449.1	-926.6	-898.1

Random effects:

Groups	Name	Variance	Std.Dev.
Word	(Intercept)	0.0045808	0.067682
Subject	(Intercept)	0.0184681	0.135897
Residual		0.0298413	0.172746

Number of obs: 1659, groups: Word, 79; Subject, 21

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	6.32358	0.03783	167.14
NativeLanguageOther	0.15003	0.05646	2.66

- ▶ **Treatment (a.k.a. dummy) coding** is standard in most stats programs
 - ▶ NativeLanguage coded as 1 if “other”, 0 otherwise.
 - ▶ Coefficient for (Intercept) reflects reference level English of the factor NativeLanguage.
 - ▶ Prediction for NativeLanguage = Other is derived by $6.32358 + 0.15003 = 6.47361$ (log-transformed reaction times).

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Recoding

- ▶ Coding affects interpretation of coefficients.
- ▶ E.g., we can recode NativeLanguage into NativeEnglish:

```
> lexdec$NativeEnglish = ifelse(lexdec$NativeLanguage == "English", 1, 0)
> lmer(RT ~ NativeEnglish + Frequency +
+      (1 | Word) + (1 | Subject), data = lexdec)
<...>
      AIC      BIC logLik deviance REMLdev
-886.1 -853.6  449.1  -926.6  -898.1
Random effects:
Groups   Name             Variance Std.Dev.
Word     (Intercept)    0.0045808 0.067682
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Residual                    0.0298413 0.172746
Number of obs: 1659, groups: Word, 79; Subject, 21

Fixed effects:
              Estimate Std. Error t value
(Intercept)    6.32358    0.03783  167.14
NativeEnglish  -0.15003    0.05646   2.66
<...>
```

- ▶ NB: ↪ **Goodness-of-fit** (AIC, BIC, loglik, etc.) is *not* affected by choice between different sets of *orthogonal contrasts*.

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Other codings of factor

- ▶ Treatment coding ...
 - ▶ makes intercept hard to interpret.
 - ▶ leads to ↪ **collinearity** with interactions
- ▶ Sum (a.k.a. contrast) coding avoids that problem (in balanced data sets) and makes intercept interpretable (in factorial analyses of balanced data sets).
 - ▶ Corresponds to ANOVA coding.
 - ▶ Centers for balanced data set.
 - ▶ **Caution when reporting effect sizes!** (R contrast codes as -1 vs. $1 \rightarrow$ coefficient estimate is only half of estimated group difference).
- ▶ Other contrasts possible, e.g. to test hypothesis that levels are ordered (`contr.poly()`, `contr.helmert()`).

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Centering predictors

- ▶ **Centering:** removal of the mean out of a variable ...
 - ▶ makes coefficients more interpretable.
 - ▶ if all predictors are centered \rightarrow intercept is estimated grand mean.
 - ▶ reduces \curvearrowright **collinearity** of predictors
 - ▶ *with intercept*
 - ▶ *higher-order terms that include the predictor (e.g. interactions)*
- ▶ **Centering** does not change ...
 - ▶ coefficient estimates (it's a linear transformations); including random effect estimates.
 - ▶ \curvearrowright **Goodness-of-fit** of model (information in the model is the same)

Centering: An example

- Re-consider the model with NativeEnglish and Frequency. Now with a centered predictors:

```
> lexdec$cFrequency = lexdec$Frequency - mean(lexdec$Frequency)
> lmer(RT ~ cNativeEnglish + cFrequency +
+      (1 | Word) + (1 | Subject), data = lexdec)
<...>
```

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	6.385090	0.030570	208.87
cNativeEnglish	-0.155821	0.060532	-2.57
cFrequency	-0.042872	0.005827	-7.36

Correlation of Fixed Effects:

	(Intr)	cNtvEn
cNatvEnglsh	0.000	
cFrequency	0.000	0.000

<...>

- Correlation between predictors and intercept gone.
- Intercept changed (from 6.678 to 6.385 units): now grand mean (**previously: prediction for Frequency=0!**)
- NativeEnglish and Frequency coefs unchanged.

Centering: An interaction example

- ▶ Let's add an interaction between NativeEnglish and Frequency.
- ▶ Prior to centering: interaction is collinear with main effects.

```
> lmer(RT ~ NativeEnglish * Frequency +  
+       (1 | Word) + (1 | Subject), data = lexdec)
```

```
<...>
```

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	6.752403	0.056810	118.86
NativeEnglish	-0.286343	0.068368	-4.19
Frequency	-0.058570	0.006969	-8.40
NativeEnglish:Frequency	0.027472	0.006690	4.11

Correlation of Fixed Effects:

	(Intr)	NtvEng	Frgncy
NativeEnglish	-0.688		
Frequency	-0.583	0.255	
NtvEnglish:F	0.320	-0.465	-0.549

```
<...>
```

Centering: An interaction example (cnt'd)

► After centering:

```
<...>
Fixed effects:

```

	Estimate	Std. Error	t value
(Intercept)	6.385090	0.030572	208.85
cNativeEnglish	-0.155821	0.060531	-2.57
cFrequency	-0.042872	0.005827	-7.36
cNativeEnglish:cFrequency	0.027472	0.006690	4.11

```

Correlation of Fixed Effects:
      (Intr)  cNtvEn  cFrqnc
cNatvEnglsh  0.000
cFrequency   0.000   0.000
cNtvEngls:F  0.000   0.000   0.000
<...>
```

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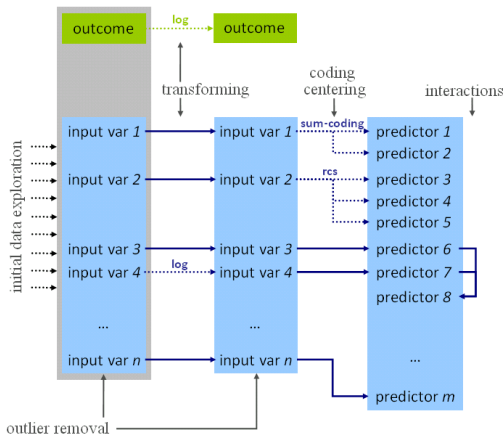
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Interactions and non-linearities

- ▶ Include interactions after variables are centered → avoids unnecessary ↪ **collinearity**.
- ▶ The same holds for higher order terms when non-linearities in continuous (or ordered) predictors are modeled. Though often centering will not be enough.
 - ▶ See for yourself: a polynomial of (back-transformed) frequency

```
> lexdec$rawFrequency <- round(exp(lexdec$Frequency), 0)
> lmer(RT ~ poly(rawFrequency, 2) +
+         (1 | Word) + (1 | Subject), data = lexdec)
```

- ▶ ... vs. a polynomial of the centered (back-transformed) frequency

```
> lexdec$crawFrequency = lexdec$rawFrequency - mean(lexdec$rawFrequency)
> lmer(RT ~ poly(crawFrequency, 2) +
+         (1 | Word) + (1 | Subject), data = lexdec)
```

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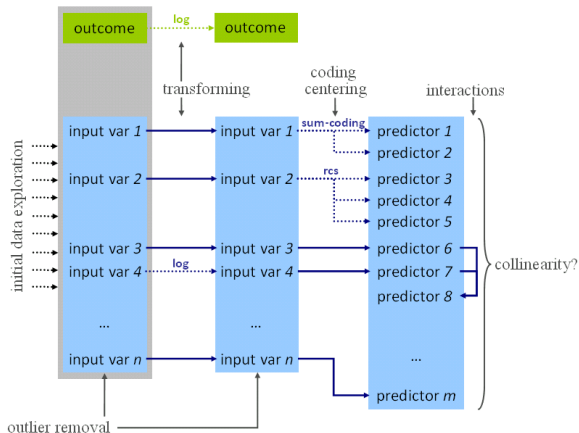
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Definition of collinearity

- ▶ **Collinearity**: a predictor is collinear with other predictors in the model if there are high (partial) correlations between them.
- ▶ Even if a predictor is not highly correlated with any single other predictor in the model, it can be highly collinear with the combination of predictors → collinearity will affect the predictor
- ▶ This is not uncommon!
 - ▶ in models with many predictors
 - ▶ when several somewhat related predictors are included in the model (e.g. word length, frequency, age of acquisition)

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Consequences of collinearity

- standard errors $SE(\beta)$ s of collinear predictors are biased (*inflated*).
 - *tends* to underestimate significance (but see below)
- coefficients β of collinear predictors become hard to interpret (though not biased)
 - ▶ ‘bouncing betas’: minor changes in data might have a major impact on β s
 - ▶ coefficients will flip sign, double, half
- coefficient-based tests don’t tell us anything reliable about collinear predictors!

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Extreme collinearity: An example

- ▶ **Drastic example of collinearity:** meanWeight (rating of the weight of the object denoted by the word, averaged across subjects) and meanSize (average rating of the object size) in lexdec.

```
lmer(RT ~ meanSize + (1 | Word) + (1 | Subject), data = lexdec)
```

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	6.3891053	0.0427533	149.44
meanSize	-0.0004282	0.0094371	-0.05

- ▶ n.s. correlation of meanSize with RTs.
- ▶ similar n.s. weak negative effect of meanWeight.
- ▶ The two predictors are highly correlated ($r > 0.999$).

Extreme collinearity: An example (cnt'd)

- If the two correlated predictors are included in the model ...

```
> lmer(RT ~ meanSize + meanWeight +  
+       (1 | Word) + (1 | Subject), data = lexdec)
```

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	5.7379	0.1187	48.32
meanSize	1.2435	0.2138	5.81
meanWeight	-1.1541	0.1983	-5.82

Correlation of Fixed Effects:

	(Intr)	meanSz
meanSize	-0.949	
meanWeight	0.942	-0.999

- $SE(\beta)$ s are hugely inflated (more than by a factor of 20)
- large and highly significant **significant counter-directed** effects (β s) of the two predictors
- collinearity needs to be investigated!

Extreme collinearity: An example (cnt'd)

- ▶ Objects that are perceived to be unusually heavy for their size tend to be more frequent (→ accounts for 72% of variance in frequency).
- ▶ Both effects apparently disappear though when frequency is included in the model (but cf. ↪ **residualization** → meanSize or meanWeight still has small expected effect beyond Frequency).

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	6.64846	0.06247	106.43
cmeanSize	-0.11873	0.35196	-0.34
cmeanWeight	0.13788	0.33114	0.42
Frequency	-0.05543	0.01098	-5.05

So what does collinearity do?

- Type II error increases → power loss

```
h <- function(n) {  
  x <- runif(n)  
  y <- x + rnorm(n, 0, 0.01)  
  z <- ((x + y) / 2) + rnorm(n, 0, 0.2)  
  
  m <- lm(z ~ x + y)  
  signif.m.x <- ifelse(summary(m)$coef[2,4] < 0.05, 1, 0)  
  signif.m.y <- ifelse(summary(m)$coef[3,4] < 0.05, 1, 0)  
  
  mx <- lm(z ~ x)  
  my <- lm(z ~ y)  
  signif.mx.x <- ifelse(summary(mx)$coef[2,4] < 0.05, 1, 0)  
  signif.my.y <- ifelse(summary(my)$coef[2,4] < 0.05, 1, 0)  
  return(c(cor(x,y), signif.m.x, signif.m.y, signif.mx.x, signif.my.y))  
}  
result <- sapply(rep(M,n), h)  
print(paste("x in combined model:", sum(result[2,])))  
print(paste("y in combined model:", sum(result[3,])))  
print(paste("x in x-only model:", sum(result[4,])))  
print(paste("y in y-only model:", sum(result[5,])))  
print(paste("Avg. correlation:", mean(result[1,])))
```

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So what does collinearity do?

- ▶ Type II error increases → power loss
- ▶ Type I error does not increase much (5.165% Type I error for two predictors with $r > 0.9989$ in joined model vs. 5.25% in separate models; 20,000 simulation runs with 100 data points each)

```
set.seed(1)
n <- 100
M <- 20000
f <- function(n) {
  x <- runif(n)
  y <- x + rnorm(n, 0, 0.01)
  z <- rnorm(n, 0, 5)
  m <- lm(z ~ x + y)
  mx <- lm(z ~ x)
  my <- lm(z ~ y)
  signifmin <- ifelse(min(summary(m)$coef[2:3,4]) < 0.05, 1, 0)
  signifx <- ifelse(min(summary(mx)$coef[2,4]) < 0.05, 1, 0)
  signify <- ifelse(min(summary(my)$coef[2,4]) < 0.05, 1, 0)
  signifxory <- ifelse(signifx == 1 | signify == 1, 1, 0)
  return(c(cor(x, y), signifmin, signifx, signify, signifxory))
}
result <- sapply(rep(n, M), f)
sum(result[2,])/M # joined model returns >=1 spurious effect
sum(result[3,])/M
sum(result[4,])/M
sum(result[5,])/M # two individual models return >=1 spurious effect
min(result[1,])
```

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So what does collinearity do?

- ▶ Type II error increases → power loss
- ▶ Type I error does not increase (much)
- ★ But small differences between highly correlated predictors can be highly correlated with another predictors and create 'apparent effects' (like in the case discussed).
 - Can lead to *misleading effects* (not technically spurious, but if they we interpret the coefficients *causally* we will have a misleading result!).
 - ▶ This problem is not particular to collinearity, but it frequently occurs in the case of collinearity.
- ▶ When coefficients are unstable (as in the above case of collinearity) treat this as a warning sign - check for **mediated effects**.

Detecting collinearity

- ▶ Mixed model output in R comes with correlation matrix (cf. previous slide).
 - ▶ Partial correlations of fixed effects *in the model*.
- ▶ Also useful: correlation matrix (e.g. `cor()`; use Spearman option for categorical predictors) or `pairscor.fnc()` in `languageR` for visualization.
 - ▶ **apply to predictors** (not to untransformed input variables)!

```
> cor(lexdec[,c(2,3,10, 13)])
```

	RT	Trial	Frequency	Length
RT	1.0000000	-0.052411295	-0.213249525	0.146738111
Trial	-0.0524113	1.000000000	-0.006849117	0.009865814
Frequency	-0.2132495	-0.006849117	1.000000000	-0.427338136
Length	0.1467381	0.009865814	-0.427338136	1.000000000

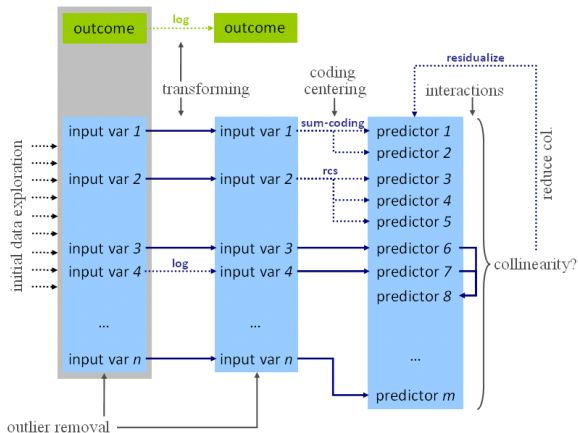
Formal tests of collinearity

- ▶ Variance inflation factor (VIF, `vif()`).
 - ▶ generally, $VIF > 10 \rightarrow$ absence of absolute collinearity in the model cannot be claimed.
 - ★ $VIF > 4$ are usually already problematic.
 - ★ but, for large data sets, even VIFs > 2 can lead inflated standard errors.
- ▶ Kappa (e.g. `collin.fnc()` in `languageR`)
 - ▶ generally, c-number (κ) over 10 \rightarrow mild collinearity in the model.
- ▶ Applied to current data set, ...

```
> collin.fnc(lexdec[, c(2, 3, 10, 13)])$cnumber
```

- ▶ ...gives us a kappa $> 90 \rightarrow$ Houston, we have a problem.

Dealing with collinearity



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Dealing with collinearity

- ▶ **Good news:** Estimates are only problematic for those predictors that are collinear.
- If collinearity is in the nuisance predictors (e.g. certain controls), nothing needs to be done.
- ▶ **Somewhat good news:** If collinear predictors are of interest but we are *not* interested in the direction of the effect, we can use ↪ **model comparison** (rather than tests based on the standard error estimates of coefficients).
- ▶ If collinear predictors are of interest and we *are* interested in the direction of the effect, we need to reduce collinearity of those predictors.

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Reducing collinearity

- ▶ **Centering** ↷: reduces collinearity of predictor with intercept and higher level terms involving the predictor.
 - ▶ **pros:** easy to do and interpret; often improves interpretability of effects.
 - ▶ **cons:** none?
- ▶ **Re-express the variable** based on conceptual considerations (e.g. ratio of spoken vs. written frequency in `lexdec`; rate of disfluencies per words when constituent length and fluency should be controlled).
 - ▶ **pros:** easy to do and relatively easy to interpret.
 - ▶ **cons:** only applicable in some cases.

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Reducing collinearity (cnt'd)

- ▶ **Stratification**: Fit separate models on **subsets** of data holding correlated predictor A constant.
- ▶ If effect of predictor B persists → effect is probably real.
 - ▶ **pros**: Still relatively easy to do and easy to interpret.
 - ▶ **cons**: harder to do for continuous collinear predictors; reduces power, → extra caution with null effects; doesn't work for multicollinearity of several predictors.
- ▶ **Principal Component Analysis (PCA)**: for n collinear predictors, extract $k < n$ most important orthogonal components that capture $> p\%$ of the variance of these predictors.
 - ▶ **pros**: Powerful way to deal with *multicollinearity*.
 - ▶ **cons**: Hard to interpret (→ better suited for control predictors that are not of primary interest); technically complicated; some decisions involved that affect outcome.

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Reduce collinearity (cnt'd)

- ▶ **Residualization**: Regress collinear predictor against combination of (partially) correlated predictors
 - ▶ usually using ordinary regression (e.g. `lm()`, `ols()`).
 - ▶ **pros**: systematic way of dealing with multicollinearity; directionality of (conditional) effect interpretable
 - ▶ **cons**: effect sizes hard to interpret; judgment calls: what should be residualized against what?

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An example of moderate collinearity (cnt'd)

- Consider two moderately correlated variables ($r = -0.49$), (centered) word length and (centered log) frequency:

```
> lmer(RT ~ cLength + cFrequency +  
+       (1 | Word) + (1 | Subject), data = lexdec)
```

```
<...>
```

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	6.385090	0.034415	185.53
cLength	0.009348	0.004327	2.16
cFrequency	-0.037028	0.006303	-5.87

Correlation of Fixed Effects:

	(Intr)	cLngh
cLength	0.000	
cFrequency	0.000	0.429

```
<...>
```

- Is this problematic? Let's remove collinearity via **residualization**

Residualization: An example

- ▶ Let's regress word length vs. word frequency.

```
> lexdec$rLength = residuals(lm(Length ~ Frequency, data = lexdec))
```

- ▶ `rLength`: difference between actual length and length as predicted by frequency. Related to actual length ($r > 0.9$), but crucially not to frequency ($r \ll 0.01$).
- ▶ Indeed, collinearity is removed from the model:

```
<...>
Fixed effects:
              Estimate Std. Error t value
(Intercept)  6.385090   0.034415  185.53
rLength      0.009348   0.004327    2.16
cFrequency   -0.042872   0.005693   -7.53

Correlation of Fixed Effects:
              (Intr) rLngth
rLength      0.000
cFrequency   0.000  0.000
<...>
```

- $SE(\beta)$ estimate for frequency predictor decreased
- larger t -value

Residualization: An example (cnt'd)

- ▶ **Q:** What precisely is `rLength`?
 - ▶ **A:** Portion of word length that is not explained by (a linear relation to `log`) word frequency.
- Coefficient of `rLength` needs to be interpreted as such
- ▶ No trivial way of back-transforming to `Length`.
- ▶ **NB:** We have granted frequency the entire portion of the variance that cannot unambiguously attributed to *either frequency or length*!
- If we choose to residualize frequency on length (rather than the inverse), we may see a different result.

Understanding residualization

- ▶ So, let's regress frequency against length.
- ▶ Here: no qualitative change, but word length is now *highly* significant (random effect estimates unchanged)

```
> lmer(RT ~ cLength + rFrequency +  
+       (1 | Word) + (1 | Subject), data = lexdec)  
<...>  
Fixed effects:  
                Estimate Std. Error t value  
(Intercept)    6.385090    0.034415   185.53  
cLength         0.020255    0.003908     5.18  
rFrequency     -0.037028    0.006303    -5.87  
  
Correlation of Fixed Effects:  
          (Intr) cLngth  
cLength    0.000  
rFrequency 0.000    0.000  
<...>
```

→ Choosing what to residualize, changes interpretation of β s and hence the hypothesis we're testing.

Extreme collinearity: ctn'd

- ▶ we can now residualize meanWeight against meanSize and Frequency, and
- ▶ and residualize meanSize against Frequency.
- ▶ include the transformed predictors in the model.

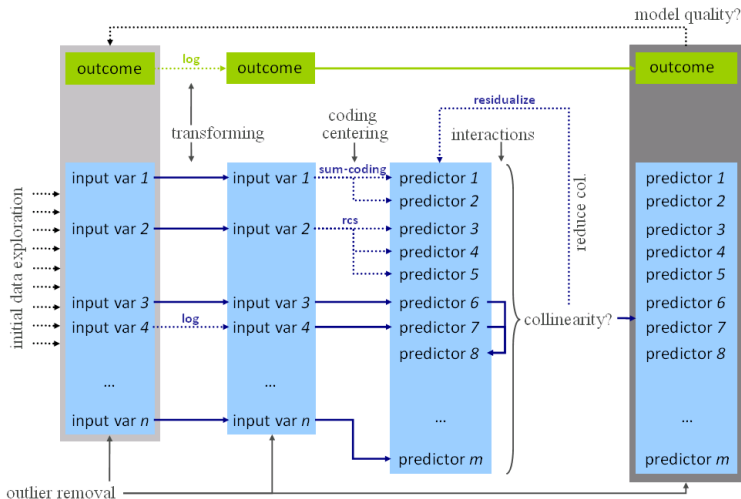
```
> lexdec$rmeanSize <- residuals(lm(cmeanSize ~ Frequency + cmeanWeight,  
+                               data=lexdec))  
> lexdec$rmeanWeight <- residuals(lm(cmeanWeight ~ Frequency,  
+                                  data=lexdec))  
> lmer(RT ~ rmeanSize + rmeanWeight + Frequency + (1|Subject) + (1|Word),  
+      data=lexdec)  
  
(Intercept)  6.588778    0.043077  152.95  
rmeanSize    -0.118731    0.351957   -0.34  
rmeanWeight   0.026198    0.007477    3.50  
Frequency    -0.042872    0.005470   -7.84
```

- ▶ NB: The frequency effect is stable, but the meanSize vs. meanWeight effect depends on what is residualized against what.

Residualization: Which predictor to residualize?

- ▶ What to residualize should be based on conceptual considerations (e.g. rate of disfluencies = number of disfluencies \sim number of words).
- ▶ **Be conservative** with regard to your hypothesis:
 - ▶ If the effect only holds under some choices about residualization, *the result is inconclusive*.
 - ▶ We usually want to show that a hypothesized effect holds *beyond what is already known* or that it *subsumes other effects*.
- **Residualize** effect of interest.
 - ▶ E.g. if we hypothesize that a word's predictability affects its duration beyond its frequency → `residuals(lm(Predictability ~ Frequency, data))`.
 - ▶ (if effect *direction* is not important, see also ↪ **model comparison**)

Modeling schema



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Overfitting

Overfitting: Fit might be too tight due to the exceeding number of parameters (coefficients). The maximal number of predictors that a model allows depends on their distribution and the distribution of the outcome.

► Rules of thumb:

- **linear models:** > 20 observations per predictor.
- **logit models:** the less frequent outcome should be observed > 10 times more often than there predictors in the model.
- Predictors count: one per each random effect + residual, one per each fixed effect predictor + intercept, one per each interaction.

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Validation allows us to detect **overfitting**:

- ▶ How much does our model depend on the exact data we have observed?
- ▶ Would we arrive at the same conclusion (model) if we had only slightly different data, e.g. a subset of our data?
- ▶ **Bootstrap-validate** your model by repeatedly sampling from the population of speakers/items with replacement. Get estimates and confidence intervals for fixed effect coefficients to see how well they generalize (Baayen, 2008:283; cf. `bootcov()` for ordinary regression models).

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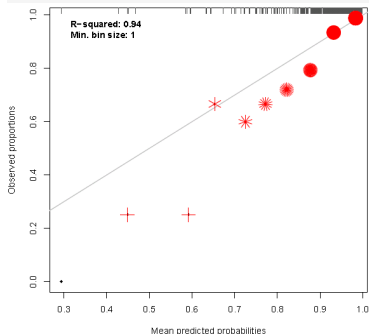
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Visualize validation

- ▶ Plot predicted vs. observed (averaged) outcome.
- ▶ E.g. for logit models, `plot.logistic.fit.fnc` in `languageR` or similar function (cf. <http://hlplab.wordpress.com>)
 - ▶ The following shows a badly fitted model:

```
> lexdec$NativeEnglish = ifelse(lexdec$NativeLanguage == "English", 1, 0)
> lexdec$cFrequency = lexdec$Frequency - mean(lexdec$Frequency)
> lexdec$cNativeEnglish = lexdec$NativeEnglish - mean(lexdec$NativeEnglish)
> lexdec$Correct = ifelse(lexdec$Correct == "correct", T, F)
> l <- glmer(Correct ~ cNativeEnglish * cFrequency + Trial +
+           (1 | Word) + (1 | Subject),
+           data = lexdec, family="binomial")
```



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Fitted values

So far, we've been worrying about coefficients, but the real model output are the **fitted values**.

Goodness-of-fit measures assess the relation between fitted (a.k.a. predicted) values and actually observed outcomes.

- **linear models**: Fitted values are predicted numerical outcomes.

	RT	fitted
1	6.340359	6.277565
2	6.308098	6.319641
3	6.349139	6.265861
4	6.186209	6.264447

- **logit models**: Fitted values are predicted log-odds (and hence predicted probabilities) of outcome.

	Correct	fitted
1	correct	0.9933675
2	correct	0.9926289
3	correct	0.9937420
4	correct	0.9929909

Goodness-of-fit measures: Linear Mixed Models

- ▶ $R^2 = \text{correlation}(\text{observed}, \text{fitted})^2$.
 - ▶ Random effects usually account for much of the variance
→ obtain separate measures for partial contribution of fixed and random effects (Gelman & Hill 2007:474).
 - ▶ E.g. for

```
> cor(l$RT, fitted(lmer(RT ~ cNativeEnglish * cFrequency + Trial +  
+ (1 | Word) + (1 | Subject), data = l)))^2
```

- ▶ ...yields $R^2 = 0.52$ for model, but only 0.004 are due to fixed effects!

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Measures built on data likelihood

- ▶ **Data likelihood**: What is the probability that we would observe the data we have given the model (i.e. given the predictors we chose and given the 'best' parameter estimates for those predictors).
- ▶ Standard model output usually includes such measures, e.g. in R:

AIC	BIC	logLik	deviance	REMLdev
-96.48	-63.41	55.24	-123.5	-110.5

- ▶ **log-likelihood**, $\text{logLik} = \log(L)$. This is the maximized model's log data likelihood, no correction for the number of parameters. **Larger (i.e. closer to zero) is better**. The value for log-likelihood should always be *negative*, and AIC, BIC etc. are positive. → current bug in the `lmer()` output for linear models.

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Measures built on data likelihood (contd')

- ▶ Other measures trade off goodness-of-fit (↪ **data likelihood**) and model complexity (number of parameters; cf. Occam's razor; see also ↪ **model comparison**).
 - ▶ **Deviance**: -2 times **log-likelihood** ratio. **Smaller is better.**
 - ▶ **Aikake Information Criterion**, $AIC = k - 2\ln(L)$, where k is the number of parameters in the model. **Smaller is better.**
 - ▶ **Bayesian Information Criterion**, $BIC = k * \ln(n) - 2\ln(L)$, where k is the number of parameters in the model, and n is the number of observations. **Smaller is better.**
 - ▶ also **Deviance Information Criterion**

Likelihood functions used for the fitting of linear mixed models

► Linear models:

- **Maximum Likelihood** function, ML: Find θ -vector for your model parameters that maximizes the probability of your data given the model's parameters and inputs. Great for point-wise estimates, but provides biased (anti-conservative) estimates for variances.
- **Restricted or residual maximum likelihood**, REML: default in `lmer` package. Produces unbiased estimates for variance.
- In practice, the estimates produced by ML and REML are nearly identical (Pinheiro and Bates, 2000:11).

→ hence the two deviance terms given in the standard model output in R.

Goodness-of-fit: Mixed Logit Models

- ▶ Best available right now:
 - ▶ some of the same measures based on data likelihood as for mixed models

AIC	BIC	logLik	deviance
499.1	537	-242.6	485.1

- ★ but **no known closed form solution** to likelihood function of mixed logit models → current implementations use **Penalized Quasi-Likelihoods** or better **Laplace Approximation** of the likelihood (default in R; cf. Harding & Hausman, 2007)

- ▶ Discouraged:

- ★ **pseudo- R^2** a la Nagelkerke (cf. along the lines of http://www.ats.ucla.edu/stat/mult_pkg/faq/general/Psuedo_RSquareds.htm)
- ★ **classification accuracy**: If the predicted probability is < 0.5 → predicted outcome = 0; otherwise 1. Needs to be compared against baseline. (cf. Somer's D_{xy} and C index of concordance).

Model comparison

- ▶ Models can be compared for performance using any goodness-of-fit measures. Generally, an advantage in one measure comes with advantages in others, as well.
- ▶ **To test whether one model is significantly better** than another model:
 - ▶ **likelihood ratio test** (for nested models only)
 - ▶ (DIC-based tests for non-nested models have also been proposed).

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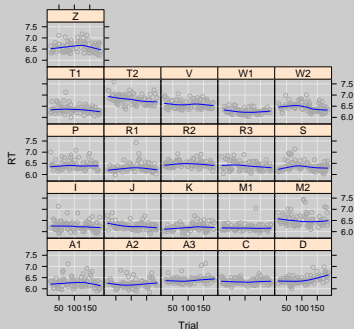
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Likelihood ratio test for nested models

- ▶ -2 times ratio of likelihoods (or difference of log likelihoods) of nested model and super model.
- ▶ Distribution of likelihood ratio statistic follows asymptotically the χ -square distribution with $DF(model_{super}) - DF(model_{nested})$ degrees of freedom.
- ▶ χ -square test indicates whether sparing extra df's is justified by the change in the log-likelihood.
 - ▶ in R: `anova(model1, model2)`
 - ▶ NB: **use restricted maximum likelihood-fitted models to compare models that differ in random effects.**

Example of model comparison



```
> super.lmer = lmer(RT ~ rawFrequency + (1 | Subject) + (1 | Word), data = lexdec)
> nested.lmer = lmer(RT ~ rawFrequency + (1 + Trial| Subject) + (1 | Word), data = lexdec)
> anova(super.lmer, nested.lmer)
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
super.lmer	5	-910.41	-883.34	460.20				
nested.lmer	7	-940.71	-902.81	477.35	34.302		2	3.56e-08 ***

→ change in log-likelihood justifies inclusion
Subject-specific **slopes** for Trial, and the **correlation parameter** between trial intercept and slope.

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Model comparison: Trade-offs

- ▶ Compared to tests based on $SE(\beta)$, model comparison

...

- ▶ robust against collinearity
- ▶ does not test directionality of effect

★ **Suggestion:** In cases of high collinearity ...

- ▶ first determine which predictors are subsumed by others (**model comparison**, e.g. $p > 0.7$) → remove them,
- ▶ then use $SE(\beta)$ -based tests (**model output**) to test effect *direction* on simple model (with reduced collinearity).

Reporting the model's performance

- ▶ for the overall performance of the model, report goodness-of-fit measures:
 - ▶ for linear models: report R^2 . Possibly, also the amount of variance explained by fixed effects over and beyond random effects, or predictors of interest over and beyond the rest of predictors.
 - ▶ for logistic models: report D_{xy} or concordance C-number. Report the increase in classification accuracy over and beyond the baseline model.
- ▶ for model comparison: report the p-value of the log-likelihood ratio test.

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Before you report the model coefficients

- ▶ **Transformations, centering**, (potentially ↪ **standardizing**), **coding, residualization** should be described as part of the predictor summary.
 - ▶ Where possible, give theoretical, and/or empirical arguments for any decision made.
 - ▶ Consider reporting scales for outputs, inputs and predictors (e.g., range, mean, sd, median).

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Some considerations for good science

- ▶ **Do not** report effects that heavily depend on the choices you have made;
- ▶ **Do not** fish for effects. There should be a strong theoretical motivation for what variables to include and in what way.
- ▶ To the extent that different ways of entering a predictor are investigated (without a theoretical reason), **do** make sure your conclusions hold for *all* ways of entering the predictor *or* that the model you choose to report is superior (**model comparison**↩).

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What to report about effects

- ▶ ↪ **Effect size** (What is that actually?)
- ▶ Effect direction
- ▶ Effect shape (tested by significance of non-linear components & superiority of transformed over un-transformed variants of the same input variable); plus visualization

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Reporting the model coefficients

- **Linear models:** report (at least) coefficient estimates, *MCMC-based* confidence intervals (HPD intervals) and *MCMC-based* p-values for each fixed and random effect (cf. `pvals.fnc()` in `languageR`).

```
$fixed
```

	Estimate	MCMCmean	HPD95lower	HPD95upper	pMCMC	Pr(> t)
(Intercept)	6.3183	6.3180	6.2537	6.3833	0.0001	0.0000
cFrequency	-0.0429	-0.0429	-0.0541	-0.0321	0.0001	0.0000
NativeLanguageOther	0.1558	0.1557	0.0574	0.2538	0.0032	0.0101


```
$random
```

Groups	Name	Std.Dev.	MCMCmedian	MCMCmean	HPD95lower	HPD95upper
1	Word (Intercept)	0.0542	0.0495	0.0497	0.0377	0.0614
2	Subject (Intercept)	0.1359	0.1089	0.1101	0.0824	0.1386
3	Residual	0.1727	0.1740	0.1741	0.1679	0.1802

- **Logit models:** for now, simply report the coefficient estimates given by the model output (but see e.g. Gelman & Hill 2006 for Bayesian approaches, more akin to the MCMC-sampling for linear models)

Interpretation of coefficients

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	6.323783	0.037419	169.00
NativeLanguageOther	0.150114	0.056471	2.66
cFrequency	-0.039377	0.005552	-7.09

- ▶ The increase in 1 log unit of cFrequency comes with a -0.039 log units decrease of RT.
- ▶ Utterly **uninterpretable**!
- ▶ To get estimates in sensible units we need to back-transform **both** our predictors and our outcomes.
 - ▶ decentralize cFrequency, and
 - ▶ exponentially-transform logged Frequency and RT.
 - ▶ if necessary, we de-residualize and de-standardize predictors and outcomes.

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Getting interpretable effects

- ▶ estimate the effect in ms across the frequency range and then the effect for a unit of frequency.

```
> intercept = as.vector(fixef(lexdec.lmer4)[1])
> betafreq = as.vector(fixef(lexdec.lmer4)[3])
> eff = exp(intercept + betafreq * max(lexdec$Frequency)) -
> exp(intercept + betafreq * min(lexdec$Frequency))
[1] -109.0357 #RT decrease across the entire range of Frequency
> range = exp(max(lexdec$Frequency)) -
> exp(min(lexdec$Frequency))
[1] 2366.999
```

- ▶ Report that the full effect of Frequency on RT is a 109 ms decrease.

★ But in this model there is no simple relation between RTs and frequency, so resist to report that “the difference in 100 occurrences comes with a 4 ms decrease of RT”.

```
> eff/range * 100
[1] -4.606494
```

The magic of the 'original' scale

- ★ What's the advantage of having an effect size in familiar units?
 - ▶ Comparability across experiments?
 - ▶ Intuitive idea of 'how much' factor (and mechanisms that predicts it to matter) accounts for?
- ★ But this may be misleadingly intuitive ...
 - ▶ If variables are related in non-linear ways, then *that's how it is*.
 - ▶ If residualization is necessary then it's applied for a good reason → back-translating will lead to misleading conclusions (there's only so much we can conclude in the face of collinearity).
 - ▶ Most theories don't make precise predictions about effect sizes on 'original' scale anyway.
 - ▶ Comparison across experiments/data sets often only legit if similar stimuli (with regard to values of predictors).

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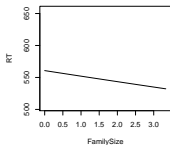
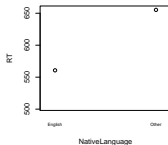
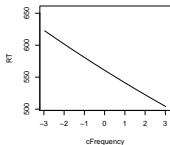
Comparing effect sizes

- ▶ It ain't trivial: What is meant by effect size?
 - ▶ Change of outcome if 'feature' is present? → coefficient
 - ▶ per unit?
 - ▶ overall range?
 - ▶ But that does not capture how much an effect affects language processing:
 - ▶ What if the feature is rare in *real language use* ('availability of feature')? Could use ...
 - Variance accounted for (**goodness-of-fit**) ↪ improvement associated with factor)
 - **Standardized coefficient** (gives direction of effect)
- ★ **Standardization**: subtract the mean and divide by two standard deviations.
 - ▶ standardized predictors are on the same scale as binary factors (cf. Gelman & Hill 2006).
 - ▶ makes all predictors (relatively) comparable.

Plotting coefficients of linear models

Plotting (partial) effects of predictors allows for comparison and reporting of their effect sizes:

- ▶ partial fixed effects can be plotted, using `plotLMER.fnc()`. Option `fun` is the back-transformation function for the outcome. Effects are plotted on the same scale, easy to compare their relative weight in the model.



- ▶ confidence intervals (obtained by MCMC-sampling of posterior distribution) can be added.

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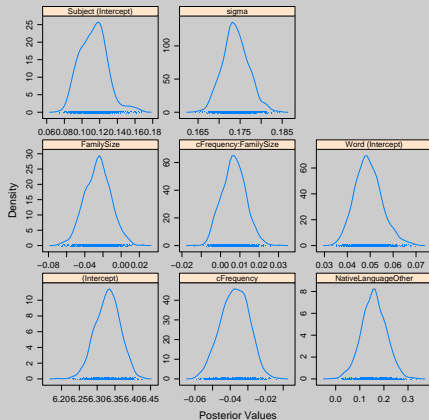
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Plotting posterior distributions (for linear mixed models)

- `pvals.fnc()` plots MCMC-sampling posterior distributions, useful for inspection of whether the distributions are well-bounded.



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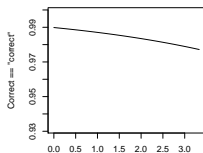
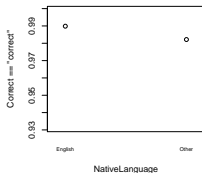
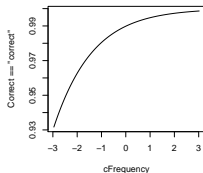
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Plotting coefficients of mixed logit models

- ▶ Log-odd units can be automatically transformed to probabilities.
 - ▶ **pros:** more familiar space
 - ▶ **cons:** effects are linear in log-odds space, but non-linear in probability space; linear slopes are hard to compare in probability space; non-linearities in log-odd space are hard to interpret



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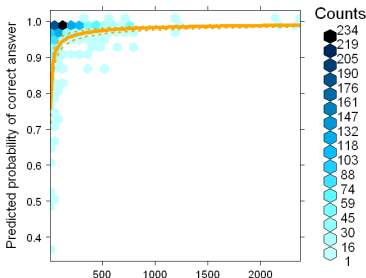
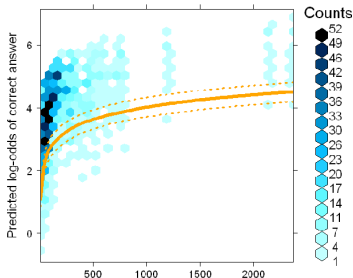
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Plotting coefficients of mixed logit models (contd')

- For an alternative way, see <http://hlplab.wordpress.com/>:

```
> data(lexdec)
> lexdec$NativeEnglish = ifelse(lexdec$NativeLanguage == "English", 1, 0)
> lexdec$rawFrequency = exp(lexdec$Frequency)
> lexdec$cFrequency = lexdec$Frequency - mean(lexdec$Frequency)
> lexdec$cNativeEnglish = lexdec$NativeEnglish - mean(lexdec$NativeEnglish)
> lexdec$Correct = ifelse(lexdec$Correct == "correct", T, F)
> l<- lmer(Correct ~ cNativeEnglish + cFrequency + Trial +
+         (1 | Word) + (1 | Subject), data = lexdec, family="binomial")
> my.glmerplot(1, "cFrequency", predictor= lexdec$rawFrequency,
+             predictor.centered=T, predictor.transform=log,
+             name.outcome="correct answer", xlab= ex, fun=plogis)
```



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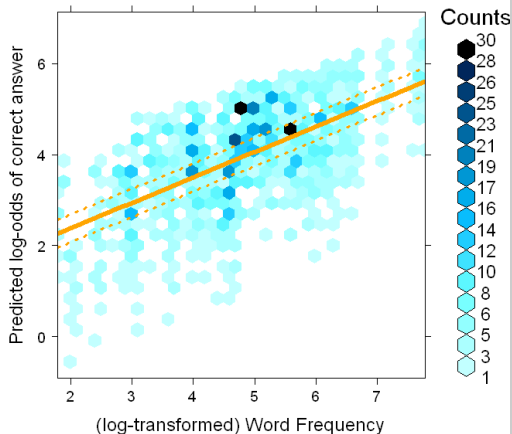
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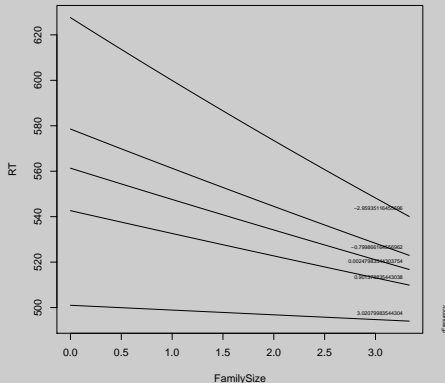
Plotting coefficients of mixed logit models (contd')

- Great for outlier detection. Plot of predictor in log-odds space (actual space in which model is fit):



Plotting interactions

```
> plotLMER.fnc(l, pred = "FamilySize", intr = list("cFrequency",  
> quantile(lexdec$cFrequency), "end"), fun = exp)
```



- Can also be plotted as the FamilySize effect for levels of cFrequency. Plotting and interpretation depends on research hypotheses.

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Reporting interactions

- ▶ Report the p-value for the interaction as a whole, not just p-values for specific contrasts. For linear models, use `aovlmer.fnc()` in `languageR`.

```
> aovlmer.fnc(lmer(RT ~ NativeLanguage + cFrequency * FamilySize +  
> (1| Subject) + (1|Word), data = lexdec), mcmcm = mcmcSamp)
```

Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value	F	Df2	p
NativeLanguage	1	0.20	0.20	6.5830	6.5830	1654.00	0.01
cFrequency	1	1.63	1.63	54.6488	54.6488	1654.00	2.278e-13
FamilySize	1	0.05	0.05	1.6995	1.6995	1654.00	0.19
cFrequency:FamilySize	1	0.03	0.03	1.0353	1.0353	1654.00	0.31

- FamilySize and its interaction with cFrequency do not reach significance in the model.

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Some thoughts for discussion

- ★ What do we do when *what's familiar* (probability space; original scales such as msec; linear effects) is not *what's best/better*?
- ★ More flexibility and power to explore and understand complex dependencies in the data do not come for free, they require additional education that is not currently standard in our field.
 - ▶ Let's distinguish challenges that relate to complexity of our hypothesis and data vs. issues with method (regression).
 - ▶ cf. What's the best measure of effect sizes? What to do when there is collinearity? Unbiased vs. biased variance estimates for ML-fitted models; accuracy of laplace approximation.

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