A very basic tutorial for performing linear mixed effects analyses

…with special reference to psycholinguistic experiments

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This is a tutorial for using linear mixed effects models. Quite a few introductions to these models already exist, but they are often very technical and can be daunting for readers who lack the appropriate mathematical background. This tutorial is different from other introductions by being decidedly *conceptual*; I will focus on *why* you want to use mixed models and *how* you should use them. The tutorial requires R – so if you haven't installed it yet, go and get it!

Although the examples come from the domain of psycholinguistics and phonetics, you can use the tutorial independent of these topics. I chose to take easy examples in order to make the tutorial accessible to people from other fields. Finally, the tutorial serves the dual function of not only showing you how to use linear mixed effects models, but along the way, a lot of basic terminology is revisited and clarified.

Introduction: Fixed and random effects

A good way to start thinking about mixed models is by looking at the "language-as-a-fixed-effect fallacy". In 1973, the Stanford psychologist Herbert Clark published a tremendously influential paper in which he complained about the then-common practice of performing only a *subjects analysis* in psycholinguistic experiments. To illustrate this, let's look at an example. In Table 1, you see raw data of a fictional psycholinguistic experiment:

[1] For updates and other tutorials, check my webpage www.bodowinter.com. If you have any suggestions, please write me an email: bodo@bodowinter.com

Table 1: Raw data from a psycholinguistic experiment

Subject	Item	Condition	Reaction Time
Frank	"car"	A	400ms
Frank	"car"	B	500ms
Frank	"elephant"	A	440ms
Frank	"elephant"	B	750ms
…	…	…	…
Peter	"car"	A	430ms
Peter	"car"	B	520ms
…			

There are several different subjects and each subject responded to multiple words (=items). Each item was presented in two contexts (A and B) – let's say that these were the critical conditions the experimenter was interested in. Now, by just looking at the raw data, we can already guess that in condition B, people responded somewhat slower than in A. To show that this difference between A and B is consistent across different subjects, people would perform a *subjects analysis*. How would they do it? The first step would be to re-order the data by taking *means by subject* such as in table 2:

Table 2: Data from the naming experiment by subjects

Subject	Condition A	Condition B
Frank	400ms	450ms
Peter	500ms	600ms
…		

Now, each row is not a single data entry but a summary of all of a particular subject's responses. Frank's "A" cell is filled with the mean of all of his responses in the A condition, and his "B" cell is filled with the mean of all of his responses in the B condition. If all of the other subjects behaved in a similar way, then a paired t-test run over this dataset would probably indicate a significant difference between condition A and B: it seems as if people responded slower in condition B.

However, we have to bear in mind that by taking the mean of a subject's responses to different items in condition A and condition B, we're essentially reducing the data – we're getting rid of the distribution that is underlying the different responses of a particular subject. Because of this, it could actually be the case that the difference between condition A and condition B seen in table 2 is only driven by a few items. If you look at "case 1" and "case 2" below, you'll see that the mean can be the same even though the underlying distributions look very different.

Case 1
400 400 400 400 ➔ mean: 400

Case 2
200 200 200 1000 ➔ mean: 400

Because both "case 1" and "case 2" are likely possibilities, and because table 2 does not allow us to see with which of these cases we're dealing, we need to construct a different table, one where we take the means by items:

Table 3: Data from our experiment with means by items

Item	Condition A	Condition B
"car"	220ms	210ms
"elephant"	230ms	1000ms
"pig"	190ms	200ms
"truck"	200ms	200ms
...		

Here, we're essentially ignoring the subject information. And in this hypothetical example, we can indeed see that the difference between A and B that was observed in the subjects analysis was due to just a few items. It seems to be the case that the one extreme value in condition B, the 1000ms response to the word "elephant" influenced the pattern that we observed by looking at the data by subjects. If we were to run a paired t-test on this dataset, it would probably not indicate a significant difference…

This example highlights that looking at data by subjects or by items can lead to vastly different conclusions. One of Herbert Clark's main contributions was to highlight the importance of the items analysis, and similar arguments have been made in other fields than just psycholinguistics.

Now, it's time to introduce some new terminology that will later help us with the linear mixed effects models. When we did the subjects analysis, we took "Subjects" as a *random effect*. Basically this means that we expect random variation from each subject, because after all, everybody will have slightly different reaction times based on a various reasons that we can't control in our experiments (e.g. some people are just slower than others, some subjects might be stoned when appearing to your experiment etc.). When we did the items analysis, we took "Items" as a random effect. Each word has a range of different features that might affect reaction times (frequency, word class, word length etc.), some of which we won't be able to control in our experiment. From the perspective of the experiment, both subjects and items will influence the reaction times in a way that is – at least to some extent – unpredictable or "random". Things that induce some

amount of random variation into your data, statisticians like to call "random effects".

The counter-term to "random effect" is "fixed effect". Things that you control in your experiment, where you *predict* or expect a certain systematic difference between conditions are called "fixed effects" or "factors". Fixed effects can be categorical and discontinuous (e.g. male vs. female) or numerical and continuous (e.g. articulation rate).

So, before we go on to the actual linear mixed effects models, let's just see what happened in response to Clark's paper. In the end, his critique led to the requirement that whenever you present multiple items to each subject, you have to perform a subjects analysis *and* an items analysis. Therefore, you'll find in almost all psycholinguistic publications that *two* test statistics are reported, e.g. F_1 and F_2 (ANOVA) or t_1 and t_2 (t-test). A result could read something like this:

> "We obtained a significant effect of Frequency for both subjects ($F_1(32)=16.43$, $p=0.0043$) and items ($F_2(16)=5.78$, $p=0.0032$)."

Or simply:

> "We obtained a significant effect of Frequency ($F_1(32)=16.43$, $p=0.0043$; $F_2(16)=5.78$, $p=0.0032$)."

The subscript 1 stands for the subjects analysis, the subscript 2 stands for the items analysis. Usually, it is required that both test statistics are significant (see Raaijmakers et al. 1999 for a critique of this standard). If, for example, the subjects analysis reaches an accepted significance level such as $\alpha=0.05$ but the items analysis does *not*, then this might indicate that only a few individual items lead to the effect observed in the subjects analysis. In other words, you could say the effect does not generalize over items.

Now, mixed models improve upon the common practice of doing separate tests for subjects and items by allowing you to *combine random effects*. In essence, this means that you can generalize across both subjects and items *with a single model*. So, you don't need to do two separate statistical tests anymore. Mixed models have several other advantages:

1. You can include categorical and numerical predictor variables in your experiment. For example, you could test the combined effect of the fixed effects Articulation Rate (numerical/continuous) and Gender (categorical/discontinuous) on a set of measures you've done.
2. You can use mixed models for both categorical/discontinuous and numerical/continuous data. For example, you can predict the

occurrence of a yes response (categorical/discontinuous), as well as reaction times and other numerical/continuous dependent measures.

Sounds cool? So let's do it! In the following, I present to you how to use mixed models in R. For this, you need to have R installed.

Linear mixed effects models in R

For a start, we need to install the R packages *lme4* (Bates & Maechler, 2009) and *languageR* (Baayen, 2009; cf. Baayen, 2008). While being connected to the internet, open R and type in:

```
install.packages( )
```

Select a server close to you and then choose the packages *lme4* and *languageR*. In order to be able to use the packages, you have to load them into the R environment with the following command:

```
library(lme4);library(languageR)
```

Now, you have several new commands available to you, among them *lmer( )*, which is the basic command for performing mixed effects models provided by the *lme4* package, and *pvals.fnc( )*, which is the a command for getting p-values from mixed models provided by the *languageR* package.

To go on, we need some data. For this tutorial, I'm using a dataset that is available on: http://www.bodowinter.com/tutorial/politeness_data.csv

This is a shortened version of a dataset that was used for Grawunder & Winter (2010) and Winter & Grawunder (submitted). Put the data into your /bin/ folder where you've installed R. Then, load the data into R:

```
politeness <- read.csv(file.choose( ))
```

Now, you have an object called "politeness" in your R environment. You can familiarize yourself with the data by using *head( )*, *summary( )*, *str( )*, *colnames( )*… or whatever commands you commonly use to get an overview of a dataset. Also, it is always good to check for missing values:

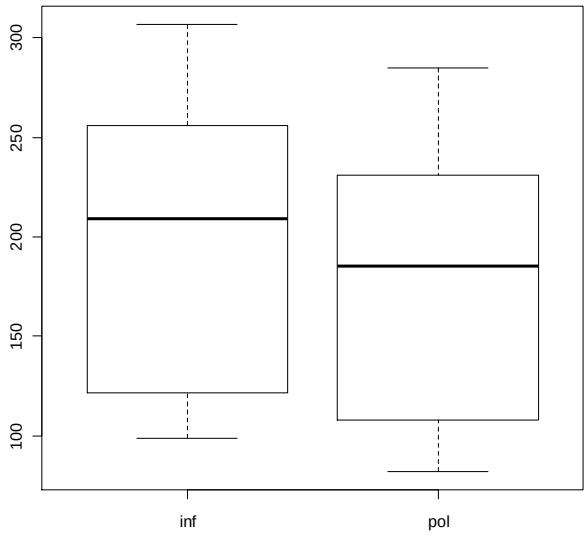
```
which(is.na(politeness)==T)
```

Apparently, there is a missing value in row 263. This is important to know but fortunately, missing values are automatically excluded when performing linear mixed effects model analyses.

With this data (which is from Korean speakers, by the way), we were interested in the phonetic difference between polite and informal speech. Whether a given response was in the polite or the informal condition is given in the column "attitude". The dependent measure in this example is voice pitch given in the column called "frequency". The units of frequency are given in Hertz (Hz). One last thing: you need to know that we took *repeated measures* from each subject, meaning that each subject was presented multiple context scenarios in the polite and informal condition. The number of the context scenario is given in the column "scenario".

Because the three most important rules of statistics are "Draw a picture, draw a picture, draw a picture" (Michael Starbird), let's make a boxplot before we start constructing mixed models. In fact, before you do any inferential statistics you should always explore the data extensively.

```
boxplot(frequency ~ attitude, data=politeness)
```



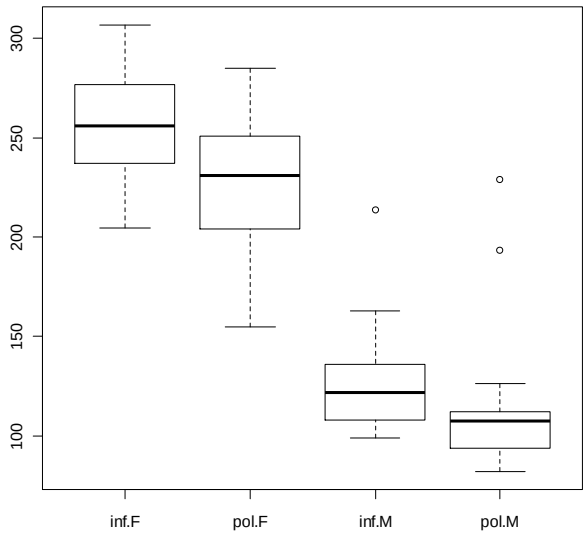
It looks like the voice pitch was lower in the polite condition. This is important because – before we do any statistical tests – we can formulate the expectation that the mixed model will show (if anything) a lowering of voice pitch in the polite condition. Let's also look at the medians of the two conditions.

```
median(politeness[which(politeness$attitude=="pol"
     ),]$frequency, na.rm=T)
median(politeness[which(politeness$attitude=="inf"
     ),]$frequency)
```

The reason why the first command includes the additional argument *na.rm=T* is that R is reluctant to give you a median value if there is a missing value, and as we pointed out before, there is a missing value in the polite condition in line 263.

The *median( )* commands give you the median 185.5 Hz for the polite condition and the median of 209.05 Hz for the informal condition. So, there seems to be a difference of about 23.55 Hz. Now, let's see whether this difference between the polite and the informal condition depends on whether the speaker is male or female; let's add the factor Gender to our boxplot.

```
boxplot(frequency ~ attitude*gender,
      data=politeness)
```



This graph indicates that there might be no interaction between attitude and gender: for both genders, politeness values are similar lower than informal values

What do we see? Well, the results for females and males do not look qualitatively different from each other: in both cases the voice pitch is lower in the polite condition. So, just by looking at this boxplot, there does not seem to be an interaction between the factors Politeness and Gender. Again, this is important for formulating expectations with respect to your mixed effects analysis. It cannot be emphasized enough how important it is to look at the data extensively before you start doing an analysis.

Now, let's start building a model. By doing so, we're leaving the domain of descriptive statistics (summarizing and displaying data) and we enter the domain of inferential statistics (testing whether the differences that we saw with descriptive statistics are chance results or not). By doing inferential statistics such

as linear mixed effects models, we want to know whether the difference in voice pitch between the polite and the informal condition are due to chance…

We will now use the function *lmer( )*. This command takes as its first argument a formula very similar to the one we used in the *boxplot( )* command. When we created the boxplots, we displayed frequency values with respect to the factor attitude, now we want to *predict* frequency values with respect the factor attitude. So, to the left of the tilde we put the thing that we seek to explain or predict, the dependent measure. To the right of the tilde, we put the fixed effect that we use to predict pitch, the *predictor variable* or the *fixed effect*. In the example below, there's no random effect and if you type in the command, you will retrieve an error:

```
lmer(frequency ~ attitude, data=politeness)
```

The reason for this error is that the linear mixed effect model *needs* a random effect. So we need to introduce a random effect, and the way this is done is a little bit cryptic:

```
(1|subject)
```

… means "Subject as a random effect" and likewise

```
(1|item)
```

… means "Item as a random effect".

In our example, the items are scenarios. Therefore, the command that we need to use is:

```
politeness.model = lmer(frequency ~ attitude +
    (1|subject) + (1|scenario), data=politeness)
```

With this command, we created a model that predicted frequency based on the fixed effect "attitude" and the random effects "subject" and "scenario", and we saved this model in the object *politeness.model*. Type in *politeness.model* and see what it gives you. Among other things, you see a t-value for the fixed effect which is -2.547. t-values approaching 2 or -2 usually reach significance if there's enough data. Usually, you would now look on a table (or use your computer) to find the p-value associated with that specific t-value. However, that's not possible in this case because you don't know the degrees of freedom. So, how can we assess the statistical significance of the results? Harald Baayen developed a function *pvals.fnc( )* that gives you p-values based on Markov-chain Monte Carlo sampling, so called MCMC-estimated p-values.

```
politeness.model.p = pvals.fnc(politeness.model)
```

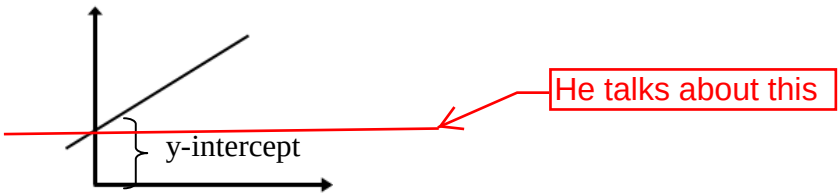
By typing in the above expression, you calculate the p-values based on the model that is saved in the object *politeness.model*. The p-values are saved in the object *politeness.model.p*. Type in the name of this object to see the following results:

```
> politeness.model.p
$fixed
             Estimate MCMCmean HPD95lower HPD95upper  pMCMC Pr(>|t|)
(Intercept)    192.05   191.76     155.73   226.6958 0.0001   0.0000
attitudepol    -19.19   -18.90     -37.91    -0.8898 0.0460   0.0138

$random
    Groups        Name Std.Dev. MCMCmedian MCMCmean HPD95lower HPD95upper
1 scenario (Intercept)  14.5440    10.3382  10.8097     0.0000    24.5176
2  subject (Intercept)  70.2687    30.9401  31.7243    20.7121    44.9968
3 Residual              27.8965    33.9510  34.3098    26.8123    42.6653
```

Right now, let's only look at the p-values for the fixed effects and not at the random effects (later on, you can access only the fixed effects by typing in *politeness.model.p$fixed*). So, what do we see? There are two rows, one is called "(Intercept)" and one is called "attitudepol". Then, there are several columns of which the two most important are "Estimate" and "pMCMC". Let's look at "attitudepol" first. "Attitudepol" is an abbreviation for "the polite level of the factor Attitude" (as opposed to the level informal). In the "Estimate" column, you see -19.19, which is actually a numerical value of our measurement (frequency in Hertz). So, the table says that for the polite condition (as opposed to the informal condition), you need to decrease frequency by 19.19 Hz. In the pMCMC, you see the value 0.0460. This is the MCMC-estimated p-value. So, by a standard α-level of 0.05, this result is significant … which means that it is relatively unlikely due to chance.

Now, the row "(Intercept") indicates your "starting point". If you think back to high school math, the intercept refers to the value where a line meets the y-axis of a plot:



The model takes the mean of all data points as the value that it would estimate "to start with". Then, all the other effects are predicted on the basis of this starting value, e.g. to arrive at a good estimate of pitch in the polite condition, you have to decrease the mean by 19 Hz.

In our example, the intercept has the estimate 192.05 Hz. This is the mean of all frequencies taken together, including both males and females. Since males have relatively low Hertz values and females relatively high Hertz values, you end up with a mean that is between the two. This is a classic example of a *bimodal distribution*, a distribution that has two modes (=the most frequent value). To see this, compare the mean of the complete dataset:

```
mean(politeness$frequency, na.rm=T)
```

To the mean of the mean of the male and female subsets:

```
mean(politeness[which(politeness$gender ==
     "F"),]$frequency)
mean(politeness[which(politeness$gender ==
     "M"),]$frequency, na.rm=T)
```

In some way, an intercept of 192.05 Hz does not make much sense. This is similar to the classic example of a farm with a dozen hens and a dozen cows …. where, if you were to take the arithmetic mean number of legs on the farm, you would make the meaningless statement that the animals of the farm have on average three legs. So, we should inform our model that multiple genders are present in our data and that therefore, vast differences in voice pitch are to be expected. Currently, our model does not account for Gender.

Should Gender be a fixed or a random effect? Some people might be tempted to put "gender" as a random effect because they want to "generalize over" genders… however, this is not a good idea because the variation in frequencies that you expect to come from male and female participants is not "random" but in fact quite systematic and predictable. So we want to add gender as a fixed effect, as if we were doing a controlled experiment with four conditions: male|polite, male|informal, female|polite and female|informal. What we're interested in is not only the effect of gender on frequencies in general, but also on the effect of gender on frequencies with respect to politeness. We can test this by adding gender to the model and putting a * between the fixed effects gender and politeness. This * says to the model that we're not only interested in the fixed effect gender and the fixed effect politeness, but also in the interaction of these two factors.

```
politeness.model = lmer(frequency ~
     attitude*gender + (1|subject) + (1|scenario),
     data=politeness)
politeness.model.p = pvals.fnc(politeness.model)
```

Note that you've overwritten the model and the p-value output object of the first mixed model analysis that we performed. Check the results by typing *politeness.model.p$fixed*.

```
> politeness.model.p$fixed
                    Estimate MCMCmean HPD95lower HPD95upper  pMCMC Pr(>|t|)
(Intercept)           256.02   256.24     217.84    294.659 0.0001   0.0000
attitudepol           -29.27   -29.43     -50.89     -7.814 0.0122   0.0071
genderM              -127.94  -128.11    -181.01    -77.333 0.0008   0.0000
attitudepol:genderM    20.38    20.46     -11.03     51.664 0.1916   0.1781
```

What do we see? The intercept is 256 Hz (the mean frequency of the female participants…). So the model takes the voice pitch of females as the starting value. Why does it take the females and not the males? If you type in the following…

```
levels(politeness$gender)
```

… you see that "F" for female is listed before "M". The model simply takes the first level of a factor as the intercept.

The fact that the intercept reaches significance ($p < 0.0001$) simply means that the intercept is significantly different from 0. It usually does not matter much if the intercept is significant or not.

Now, to accurately predict the frequency of the polite condition as opposed to the frequency of the informal condition, you need to lower the frequencies by 29.27 Hz. This result is unlikely due to chance as indicated by the low p-value (p=0.0122). Then, with respect to gender, you need to lower frequencies by 127.94 Hz for males. As we would expect, this difference is unlikely due to chance as well (p=0.0008). The "attitudepol" and "genderM" rows indicate so-called *main effects* (you only consider the effect of a single factor). The last column "attitudepol:genderM" indicates an *interaction effect* because it includes two factors. Whenever you include an interaction effect into your model with *, the model will automatically compute the corresponding main effects as well.

The estimate of the interaction effect is a little bit difficult to read: "for the polite condition you need to go up by 20.38 Hz for males". Interaction effects are often difficult to read and in order to see in which direction the effect is going,

you usually need to make extra graphs and tests rather than looking at the estimates output of the mixed models. Crucially however, the mixed model confirms an expectation that we had by looking at boxplot 2: The interaction between attitude and gender is not significant (p=0.1916), meaning that whatever interaction there is in the dataset right now is likely due to chance. We expected this result based on boxplot 2 where we didn't see a big difference of polite vs. informal for males and females.

However, what would happen if there were a significant interaction effect? In this case, the usual approach is to perform a number of *pairwise comparisons* (e.g. male|polite vs. female|polite, male|polite vs. male|informal etc.) with t-tests or Wilcoxon tests. A significant interaction only tells you that two factors interact; to get at the direction of the interaction, visualization of the interaction (e.g. boxplots), as well as a series of individual tests is needed. These tests, as well as the necessary corrections for multiple comparisons (e.g. Bonferroni correction, Dunn Sidak correction) might well be the topic of another tutorial and there's actually several other texts on this – I unfortunately can't cover them here.

So far, so cool. We see that attitude has a significant influence on frequency and so does gender, but these two factors don't interact. However, we need to check some extra things. In particular, two things **ALWAYS** need to be done when using linear mixed effects models:

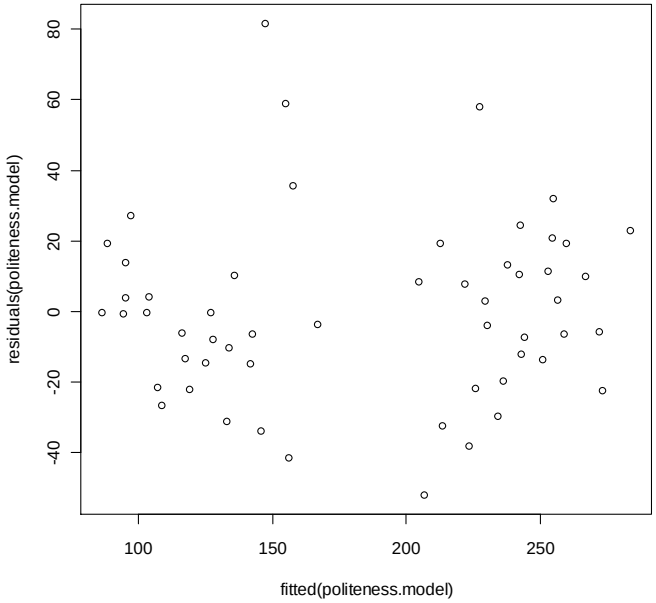
1. you need to check for normality and homogeneity
2. you need to construct a so-called "null model" and compare the performance of your mixed model to this null model

Let's address the first one first. Mixed effects models belong to the family of *parametric* statistical techniques (together with such tests as t-tests and ANOVAs). Parametric approaches require the difference between the conditions to be normally distributed, i.e. the differences between condition A and condition B need to approximate a bell-shaped curve. Non-parametric techniques do not have this restriction – they are "distribution-free" –, however, mixed models are parametric and therefore we need to check whether the differences actually follow the normal curve. Another requirement of mixed models is that the data is homogenous, namely that one part of your dataset is not vastly different from another with respect to e.g. variance.

There are several separate tests for homogeneity and normality, but the way mixed models are implemented in R, we can easily check both of these requirements visually without having to perform any extra tests. To do this, we will inspect so-called "residual plots". This plot depicts fitted values on the x-axis and residuals on the y-axis. "Fitted value" is simply another word for the value

that the model predicts, and a “residual” is the deviance of a predicted value from the actually observed value (= the error). This is how we get the plot:

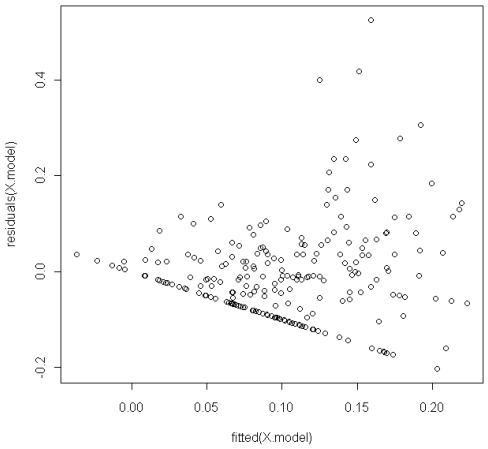
```
plot(fitted(politeness.model),residuals(politeness
     .model))
```



Now, what do we see? Well, we have the predicted values of voice pitch on the x-axis and the residuals on the y-axis. So the y-axis represents how much is left over if you take the difference of the fitted value and the actually observed value. Although somewhat difficult to see with so few values, there are two clouds in the plot… one to the right on the x-axis in the range of ~200-270 Hz, and one to the left in the range of ~90-160 Hz, with a small gap between these two. These two clouds are the responses from the female and the male subjects respectively.

Other than these two clouds, there does not seem to be a particular pattern. More importantly, there does not seem to be any indication of a linear trend – try to mentally fit a line through the dataset and you will see that the best line is probably a straight line going from left to right with a lot of spread around the line. The spread indicates that if we take a particular point on the x-axis, it’s difficult to say where you will lie on the y-axis. And for our residuals, that’s exactly what we want.

Let’s think about what it would mean if you saw a linear trend with a downwards going slope:



👎 **not good**

Such a linear trend would mean that the error of the model (the difference between observed and fitted values) is in some way systematic. On the figure above, lower fitted values have residuals that are more towards the 0 line. Higher fitted values are consistently more off, so the model is more wrong with larger values. So, ideally what you want is something that is akin towards a horizontal line.

In the case of the above graph, the data is somehow not homogenous maybe because one part of the data is more variable than another. If that is the case, you might need to transform the data in order to make it meet the assumptions that are necessary for mixed models. Again, transformations (e.g. logarithmic, quadratic, inverse transformations) are a pretty big topic that I cannot cover in this text. However, I do intend to write a tutorial on data cleaning with R in which a lot of transformations will be covered.

To sum up this section: whenever you check the residual plots, check for visual patterns. If there's no pattern and more importantly, if there are no linear trends, then your data is o.k. with respect to homogeneity and normality.

Now, we need to do one last thing. We need to check whether our model ("politeness.model") performs significantly better than a *null model*. A null model is a model that includes only the random effects and not the fixed effects we're interested in. You can think of this as a kind of "sanity check" in which we assess whether our fixed effects have any merit at all. The null model below has a single fixed effect "1".

```
politeness.null = lmer(frequency ~ 1 + (1|subject)
     + (1|scenario), data=politeness)
```

Then, we perform a so-called likelihood ratio test with the *anova( )* command. We simply put the test model as one argument and the null model as the other:

```
anova(politeness.model, politeness.null)
```

The result is a relatively low p-value of 0.00047, indicating that the difference between the models is unlikely due to chance… in other words: our model makes a difference and the results obtained by our model actually matter! If the likelihood ratio test would not reach significance, you should reject your results and not report them.

Writing up your results

You might have wondered that with the linear mixed effects analyses that we've performed so far, our results were only p-values and there were no test statistics (such as t-values or F-values), and there were no degrees of freedom. This is a problem because most journal publications require you to report at least three things: 1. the test statistics, 2. the degrees of freedom and 3. the p-value. Here's two examples of two typical results that include all three of these values:

$F_1(1,21)=6.14$, $p=0.02$ (ANOVA)

$t(17)=2.6579$, $p=0.0166$ (t-test)

There currently is a debate about whether degrees of freedom is a meaningful concept for linear mixed effects models, and there is no consensus or standard about which test-statistic to report (because the regular distributions such as t-distributions or F-distributions do not apply to linear mixed effects models). So, if the journal allows you, the simplest solution is to not report any test statistic and not report any degrees of freedom and simply report the MCMC-estimated p-values. However, if you run into problems with reviewers, you can calculate the degrees of freedom by hand (number of observations minus number of fixed effects) and take the t-test statistic of the *lmer( )* output. In a footnote, you should mention the fact that these values are only approximations or "shorthands" and that there is an ongoing "degrees of freedom debate". If you can, simply report p-values.

To finish, I'd like to give you a write-up example of the statistics section in a hypothetical paper that includes the data that we talked about. It's important to give credit to the people who developed the packages and the methods that you've used. Not enough people do this, so you should.

Write-up example

"All data were analyzed using R (R Development Core Team, 2009) and the R packages *lme4* (Bates & Maechler, 2009) and *languageR* (Baayen, 2009; cf. Baayen, 2008). We analyzed the data by using linear mixed effects models. In order to avoid the language-as-a-fixed-effect fallacy (Clark, 1973), we used both Subjects and Items as random effects (see Baayen et al., 2008). As fixed effects, we included Politeness, Gender and the interaction of Politeness and Gender into the model.

We checked for normality and homogeneity by visual inspections of plots of residuals against fitted values. To assess the validity of the mixed effects analyses, we performed likelihood ratio tests comparing the models with fixed effects to the null models with only the random effects. We rejected results in which the model including fixed effects did not differ significantly from the null model. Throughout the paper, we present MCMC-estimated p-values that are considered significant at the α=0.05 level."

I hope that you enjoyed this tutorial. As I intend to update this tutorial regularly, I'm always grateful for any suggestions.

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