Linear Mixed-Effects Models

(aka Statistics III)

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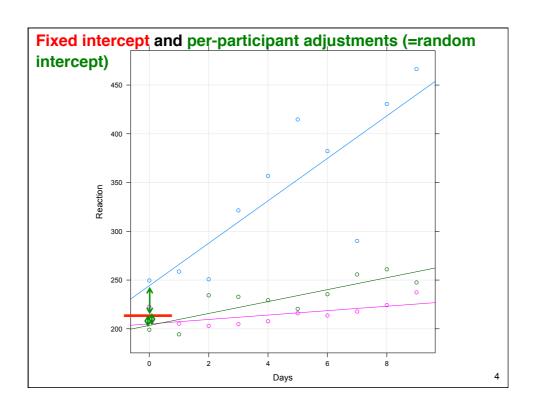
1

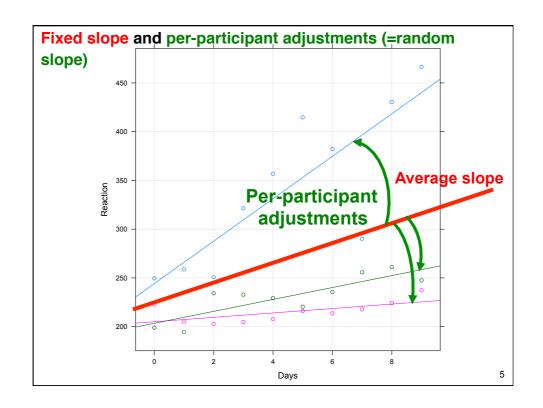
Today: p values

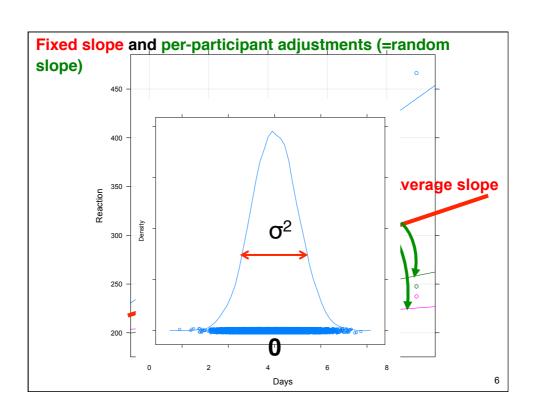
- · Recap: random slopes
- · HW/lab/BB-related stuff
- p values!
 - Many different roads leading to Rome...
 - Some detours (Type 2 vs 3; testing coefficients vs effects, multiple cores, ...)
- · Homework/lab session
 - -p values
 - Imer tutorial

Introducing our new friend Random slopes

- → Example: real data
- → sleepstudy







All put together

$$Y_{ij} = (b_0 + u_{0j}) + (b_1 + u_{1j})X_{ij} + \varepsilon_{ij}$$

- $b_0 + u_{0i}$
 - Fixed and random intercept
- $b_1 + u_{1i}$
 - Fixed and random slope
- X_{ij}
 - Days predictor
- · ε_{ij}
 - Error

Plus: We learned about "random correlations" (covariances between random effects)

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Today: p values

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Questions from HW?

- More questions and answers on BlackBoard!
- Warnings when doing profile-based CIs for the cherry pit data
- Was it too little? too much? too easy? too difficult?

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Today: p values

- · Recap: random slopes
- · HW/lab/BB-related stuff
- p values!
 - Many different roads leading to Rome...
 - Some detours (Type 2 vs 3; coefficients vs effects, ...)
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 - p values
 - Imer tutorial

p values!

What we did so far: Confidence intervals

- Fixed effects (i.e., regression coefficients): How much confidence can we have that the coefficient of interest is different from 0?
 - Factors: Each of the contrasts representing the factor gets their own CI (often not very meaningful)
- Random effects: How much confidence can we have that the variance/SD/correlation of interest is different from 0?

Thus, for example for fixed effect:

- Take point estimate (i.e., regression coefficient)
- · Quantify the (un)certainty around that estimate
- Can we be sufficiently sure (e.g., 95%) it differs from 0?
- If yes, we say the coefficient is significant (i.e., significantly different from 0, e.g., with p < .05)

What we do now: p values

Different idea

Does the predictor of interest significantly improve model fit?

Typical approach

- Run model with predictor of interest
 - Compute some model fit quantity for that model
- Run model without that predictor of interest (otherwise identical)
 - Compute some model fit quantity for that simplified model
- · Compare the two model fits
- If the more complex model (the one with the predictor) has a significantly better model fit: We conclude that the predictor is significant.

NOTE: You can compare only nested models

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Sounds simple, right?

· Well, it is

Except...

- There are a few things that make it a bit complicated sometimes, like:
 - Different methods (similar to different ways to get Cls)
 - Type 2 versus Type 3 tests
 - Tests of coefficients versus tests of effects
 - Factors (with more than 2 levels)
 - · Interaction effects including factors
 - Contrast coding scheme matters (e.g., sum-to-zero vs treatment etc)
- But we'll start simple

Sleepstudy hypothesis

 After more nights of sleep deprivation, participants have longer RTs

Our model from last week

s_1 <- lmer(Reaction ~ Days + (1 + Days!
f_Subject), data = sleepstudy2)</pre>

Hypothesis in terms of model

- → significant fixed effect of Days
- We did it with Cls, now we do it with model comparisons

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Model with predictor of interest

s_1 <- lmer(Reaction ~ Days + (1 + Days|
f_Subject), data = sleepstudy2)</pre>

Model without predictor of interest

s_1_noDay <- lmer(Reaction ~ (1 + Days|
f_Subject), data = sleepstudy2)</pre>

Please note:

 Random slope for Days still in the model!
 We want to test significance of fixed effect only (average effect; not whether there's individual variation)

summary(s_1_noDay)

[...]

Random effects:

Groups Name Variance Std.Dev. Corr

f_Subject (Intercept) 651.6 25.53

Days 142.2 11.93 -0.18

Residual 654.9 25.59 Number of obs: 180, groups: f_Subject, 18

Fixed effects:

Estimate Std. Error t value (Intercept) 257.76 6.76 38.13

Looks like no errors/warnings/problems etc, good!

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So how do we compare these two models?

- · Actually, there are many many ways...
- · Some more recommended, others less
- · Not all work in all cases etc
- I will show you several different ways, and we'll have to make some detours along the way
- In the end, I'll give you an overview of the methods with some recommendations
- But I promised we start simple, so let's do that

anova()

You know that from Stats II course anova() does model comparisons For Ime4 models: Likelihood Ratio Tests (LRTs) NOTES

- LRTs require models to be fit with ML instead of REML http://stats.stackexchange.com/questions/48671/what-is-restricted-maximum-likelihood-and-when-should-it-be-used
- If you fit your models with REML (as we always do), anova() will re-fit them for you with ML
- The command wants the "smaller" model first, followed by the "larger" model, but it will re-order them for you if you put them in the wrong order
- · You can compare more than 2 models at the same time

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$anova(s_1_noDays, s_1)$

Notes

- The test statistic (Chisquare) is difference between the two deviances
- The Dfs for the test: the difference between the Dfs of the two models (in our case the simpler model has 1 Df less)

Write-up example

[...] To determine *p* values, we computed Likelihood Ratio Tests using R's anova function to compare the model with the respective predictor of interest to the model without the respective predictor of interest (with models being identical otherwise). [...]

Reaction times increased significantly as a function of the number of days with sleep deprivation (Estimate = 10.47(1.55), Chisq(1) = 23.54, p < .001).

NOTES:

- Feel free to use the Greek letter Chi instead: χ^2
- You could remove the "Estimate = 10.47(1.55)" part
- You could add the CI for the estimate: "Estimate = 10.47(1.55), 99.9% CI [5.26, 15.39], Chisq(1) = 23.54, p < .001)"

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Bootstrapped Likelihood Ratio Tests

PBmodcomp() from package pbkrtest

General syntax

PBmodcomp(LargeModel, SmallModel)

- Wants 2 models as input: one with the predictor of interest, one without it
- PBmodcomp requires models to be fit with ML
- If you fit your models with REML (as we did),
 PBmodcomp() will re-fit them for you with ML
- PBmodcomp() wants the "larger" model first, followed by the "smaller" model. It will NOT reorder them for you! It will do some bootstrapping and even give you some results, but it will not make sense!!!

Notes continued

- Default number of simulations = 1000
- If you want a different number:
 PBmodcomp(s_1, s_1_noDays, nsim = 10000)
- PBmodcomp runs several tests, including a regular LRT; we're interested in the PBtest

→ ?PBmodcomp

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```
S_1Days_PB <- PBmodcomp(s_1, s_1_noDays)

→ Bootstrapping takes a while (40.41 sec in that case)

s_1Days_PB

Parametric bootstrap test; time: 40.41 sec; samples: 1000 extremes: 0;
large : Reaction ~ Days + (1 + Days | f_Subject)
small : Reaction ~ (1 + Days | f_Subject)
stat df p.value

LRT 23.516 1 1.239e-06 ***

PBtest 23.516 0.000999 ***</pre>
```

Several tests?

```
summary(s_1Days_PB)
```

```
Parametric bootstrap test; time: 40.41 sec; samples: 1000 extremes: 0;
```

```
large : Reaction \sim Days + (1 + Days | f_Subject)
```

small : Reaction ~ (1 + Days | f_Subject)

```
df
                         ddf
                               p.value
          stat
PBtest
        23.516
                              0.000999 ***
Gamma
        23.516
                             1.488e-05 ***
Bartlett 20.779 1.000
                             5.154e-06 ***
        23.516
                1.000 17.185 0.000146 ***
        23.516 1.000
                             1.239e-06 ***
LRT
```

If you're curious: ?PBmodcomp

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Write-up example

To determine p values, we used the PBmodcomp function of the package pbkrtest (Halekoh & Højsgaard, 2014)*, which performs model comparison of nested models using parametric bootstrap methods (i.e., bootstrapped Likelihood Ratio Tests).

Reaction times increased significantly as a function of the number of days with sleep deprivation (Estimate = 10.47(1.55), PBtest = 23.52, p < .001).

NOTES:

- *Citation information for a package: citation("pbkrtest")
- You could remove the "Estimate = 10.47(1.55)" part
- You could add the CI for the estimate: "Estimate = 10.47(1.55), 99.9% CI [5.26, 15.39], PBtest = 23.54, p < .001)"

Conditional F-tests with Kenward-Roger df correction

KRmodcomp() from package pbkrtest

General syntax

KRmodcomp(LargeModel, SmallModel)

- Only for Imer models, not glmer models
- Wants 2 models as input: one with the predictor of interest, one without it
- KRmodcomp requires models to be fit with REML (sic!)
- If you fit your models with ML, KRmodcomp() will re-fit them for you with REML
- KRmodcomp() wants the "larger" model first, followed by the "smaller" model. It seems like it reorders them for you, if you enter them in wrong order. (But I wouldn't trust it completely, so better enter them in right order!)

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Our example

```
s_1Days_KR <- KRmodcomp(s_1, s_1_noDays)</pre>
s_1Days_KR
F-test with Kenward-Roger approximation; computing time:
0.14 sec.
large : Reaction ~ Days + (1 + Days | f_Subject)
small : Reaction ~ (1 + Days | f_Subject)
        stat ndf ddf F.scaling p.value
                                     1 2.359e-07 ***
Ftest 45.853 1.000 27.997
summary(s_1Days_KR)
F-test with Kenward-Roger approximation; computing time: 0.14
large : Reaction ~ Days + (1 + Days | f_Subject)
small : Reaction ~ (1 + Days | f_Subject)
stat ndf ddf F.scaling p.value
Ftest 45.853 1.000 27.997 1 2.359e-07 ***
FtestU 45.853 1.000 27.997
                                    2.359e-07 ***
```

Write-up example

To determine *p* values, we used the KRmodcomp function of the package pbkrtest (Halekoh & Højsgaard, 2014), which performs conditional F tests with degrees of freedom based on Kenward-Roger approximation.

Reaction times increased significantly as a function of the number of days with sleep deprivation (Estimate = 10.47(1.55), F(1, 27.997) = 45.85, p < .001).

NOTES:

- You could remove the "Estimate = 10.47(1.55)" part
- You could add the CI for the estimate: "Estimate = 10.47(1.55), 99.9% CI [5.26, 15.39], F(1, 27.997) = 45.85, p < .001)"

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So far so good!

3 different ways to obtain *p* values

- LRT using anova()
- "Bootstrapped LRT" using pbkrtest::PBmodcomp()
- Conditional F test with K-R dfs using pbkrtest::KRmodcomp()

BUT...

- They work only for Type 2 (aka Type II) tests
- Not possible (at least not easy for us) to use them for Type 3 (aka Type III) tests
- Remember the difference between Type 2 and 3?

→ DETOUR AHEAD!

Type 2 versus Type 3 Tests

Example: model with main effects A and B and interaction A:B

Type 2 tests (aka Type II)

For interaction A:B (A:B | A, B)

For main effect A (A | B)

For main effect B (B | A)

Type 3 tests (aka Type III)

For interaction A:B (A:B | A, B)

For main effect A (A | B, A:B)

For main effect B (B | A, A:B)

Type 2 vs 3 differs only for models with interactions

http://goanna.cs.rmit.edu.au/~fscholer/anova.php https://mcfromnz.wordpress.com/2011/03/02/anova-type-iiiiii-ss-explained

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Many statisticians prefer **Type 2** tests: If there is a significant interaction, it doesn't make sense to test main effects.

Psychology (and SPSS default): Type 3 tests are very common; we are interested in main effects even if there are significant interactions.

In R

- Both are possible, but there is a bug/feature that tries to make it impossible to run models you need for Type 3 tests.
- Luckily, some experts wrote specific functions to make Type 3 tests possible.

Crucial: For Type 3 tests, you cannot use all contrast types: Sum-to-zero, Helmert, and polynomial are OK; treatment (= dummy) must not be used! For Type 2: All fine

http://www.mail-archive.com/r-help@stat.math.ethz.ch/msg69781.html http://talklab.psy.gla.ac.uk/tvw/catpred/

R/Imer example code

What Imer models do we need to get *p* values?

(1) Run full model (main effects and interaction)

```
m_full \leftarrow lmer(DV \sim A*B + (1 + A*B \mid ppID), ...)
```

- (2) Test significance of interaction (same for Type 2 and 3)
- (a) Run reduced model without fixed effect interaction term m_noInteract <- lmer(DV ~ A + B + (1 + A*B | ppID), ...)
- (b) Compare full model to model without interaction
 anova(m_noInteract, m_full)
 PBmodcomp(m_full, m_noInteract)
 KRmodcomp(m_full, m_noInteract)

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(2) Test significance of main effect A Type 2 test

We compare a model with A and B to a model with only B

(a) Model without *any* interaction term

```
m_AB \leftarrow lmer(DV \sim A + B + (1 + A + B \mid ppID), ...)
```

(b) Model with only B

```
m_B \leftarrow lmer(DV \sim B + (1 + A + B \mid ppID), ...)
```

(c) Compare the two models

anova(m_B, m_AB); or KRmodcomp or PBmodcomp

(3) Test significance of main effect B

Analoguous to test of main effect A anova(m_A , m_AB)

How would you do that for a Type 3 tests?

(2) Test significance of main effect A

We compare full model (A, B, A:B) to a model with B and A:B

```
(a) Full Model
```

```
m_{full} \leftarrow lmer(DV \sim A * B + (1 + A * B | ppID), ...)
```

- (b) Model from which main effect A has been removed
 m_noMainA <- lmer(DV ~ B + A:B + (1 + A * B | ppID), ...)</pre>
- (c) Compare the two models
 anova(m_noMainA, m_full)

BUT

- R doesn't let you run the model m_noMainA
- **Bug/feature:** Interaction term without its respective main effects doesn't make sense (well, if you are a Type 2 person...)
- Try it out (homework!): It does something, but not what you want to do

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So what should we do? We want Type 3!

Option 1: There are workarounds

- You can create your own interaction term so that R doesn't notice that the respective main effect is missing; i.e., the interaction term looks like it is a main effect
- You can dig into the R/lme4 machinery, grab the model matrix, and change it manually so R does what you want

Option 2: Thank others that did that for you

Several functions do the complicated stuff for you and run the correct Type 3 tests; **END OF DETOUR!**

- car::Anova()
 - F tests with K-R approx.
 - Wald Chiquare tests (not recommended! but fast)
 - Type 2 and Type 3
- afex:mixed()
 - F tests with K-R approx.
 - LRT
 - PB
 - Type 3 (also Type 2, but not same as car::Anova())
- others: e.g., package lmerTest
 - We will not cover them in the course

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car::Anova() and afex:mixed()

- Both use the pbkrtest package
- Both do some additional nice things for you:
- Both run ALL submodels (i.e., you don't have to create them yourself and then do comparisons)
- Anova() requires that you run your Imer model first and then put the model into the Anova command
- mixed() can replace the lmer command
- mixed() will check whether your continuous predictors are centered; if not, it will tell you so
- mixed() uses automatically sum-to-zero contrasts for all your factors (can be disabled)

How to use Anova()

library(car)

s_1 <- lmer(Reaction ~ Days + (1 + Days |
f_Subject), data = sleepstudy2)</pre>

For K-R F type 3 tests

Anova(s_1 , type = 3, test = "F")

Same, but type 2

Anova(s_1 , type = $\frac{2}{1}$, test = "F")

Wald Chisquare tests (not recommended, but fast)

Anova(s_1 , type = 3, test = "Chisq")

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Anova(s_1 , type = 3, test = "F")

Analysis of Deviance Table (Type III Wald F tests with Kenward-Roger df)

Response: Reaction

F Df Df.res Pr(>F)
(Intercept) 1357.061 1 25.688 < 2.2e-16 ***
Days 45.853 1 27.997 2.359e-07 ***

Anova(s_1 , type = $\frac{2}{2}$, test = "F")

Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df)

Response: Reaction

F Df Df.res Pr(>F)
Days 45.853 1 27.997 2.359e-07 ***

Write-up example

To determine *p* values, we computed Type 3 conditional F tests with Kenward-Roger approximation for degrees of freedom as implemented in the Anova function of the package car (Fox & Weisberg, 2011), which in turn calls the function KRmodcomp of the package pbkrtest (Halekoh & Højsgaard, 2014).

Reaction times increased significantly as a function of the number of days with sleep deprivation (Estimate = 10.47(1.55), F(1, 27.997) = 45.85, p < .001).

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mixed() and the package afex

install.packages("afex")
library(afex)

Several useful "convenience" functions

- mixed()
- allFit()
- plus lots more like rmANOVAs plotting, etc!

Convenience function?

mixed() calls:

- 1me4 to compute mixed models
- and then pbkrtest and/or anova() to compute p values
- it can also use parallel to use several cores

General syntax

```
m1 <- mixed(DV ~ IV1 + IV2 + (1 + IV2 |
f_group), data = mydata, type = 3, method =
c("KR", "PB", "LRT"), cl = mycluster)</pre>
```

Explanations

[..]

- type → Type 3 tests (also does kind of Type 2)
- method → KRmodcomp, PBmodcomp, anova only 1 method at a time!
- cl → cluster created with makeCluster()

```
Additional arguments when using method = "PB" args.test = list(nsim = 10000, cl = mycluster)
```

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For example our sleep data model: LRT

```
s_1_mixed_LRT <- mixed(Reaction ~ Days + (1 + Days |
f_Subject), data = sleepstudy2, type = 3, method = "LRT")
Numerical variables NOT centered on 0 (i.e., interpretation of
all main effects might be difficult if in interactions): Days
REML argument to lmer() set to FALSE for method = 'PB' or 'LRT'
Fitting 2 (q)lmer() models:</pre>
```

Different types of output (more or less info)

```
s_1_{mixed\_LRT} \rightarrow very short, only most essential info s_1_{mixed\_LRT} \rightarrow very short, of the full model s_1_{mixed\_LRT} \rightarrow very short, in the first essential info s_1_{mixed\_LRT} \rightarrow very short, of the full model s_1_{mixed\_LRT} \rightarrow very short, in the first essential info s_1_{mixed\_LRT} \rightarrow very short, in the first essential info s_1_{mixed\_LRT} \rightarrow very short, in the first essential info s_1_{mixed\_LRT} \rightarrow very short, in the first essential info s_1_{mixed\_LRT} \rightarrow very short, in the first essential info s_1_{mixed\_LRT} \rightarrow very short, in the first essential info s_1_{mixed\_LRT} \rightarrow very short.
```

 $str(s_1_mixed_LRT) \rightarrow LOTS$ of stuff in there!!

```
anova(s_1_mixed_LRT)
Mixed Model Anova Table (Type 3 tests)
Model: Reaction ~ Days + (1 + Days | f_Subject)
Data: sleepstudy2
Df full model: 6
     Df Chisq Chi Df Pr(>Chisq)
                   1 1.226e-06 ***
Days 5 23.537
s_1_mixed_LRT$tests
$Days
Data: sleepstudy2
Models:
fits[[c]]: Reaction \sim 0 + m.matrix[, -2L] + (1 + Days | f_Subject)
full.model: Reaction ~ Days + (1 + Days | f_Subject)
             AIC BIC logLik deviance Chisq Chi Df Pr(>Chisq)
fits[[c]] 5 1785.5 1801.4 -887.74 1775.5
full.model 6 1763.9 1783.1 -875.97 1751.9 23.537
                                                1 1.226e-06
                                                             45
```

Write-up example

To determine *p* values, we computed Type 3 Likelihood Ratio Tests as implemented in the mixed function of the package afex (Singmann, Bolker, & Westfall, 2015).

Reaction times increased significantly as a function of the number of days with sleep deprivation (Estimate = 10.47(1.55), Chisq(1) = 23.54, p < .001).

PB

```
s_1_mixed_PB <- mixed(Reaction ~ Days + (1 + Days |
f_Subject), data = sleepstudy2, type = 3, method = "PB")
Numerical variables NOT centered on 0 (i.e., interpretation of
all main effects might be difficult if in interactions): Days
REML argument to lmer() set to FALSE for method = 'PB' or 'LRT'
Fitting 2 (g)lmer() models:
Γ..]
Obtaining 1 p-values:
[.] > this takes a while! (bootstrapping)
anova(s_1_mixed_PB)
Model: Reaction ~ Days + (1 + Days | f_Subject)
Data: sleepstudy2
      Chisq Chi Df Pr(>Chisq) Pr(>PB)
                  1 1.2256e-06 0.000999 ***
Days 23.537
                                                            47
```

Write-up example

To determine *p* values, we computed Type 3 bootstrapped Likelihood Ratio Tests (using 1000 simulations) as implemented in the mixed function of the package afex (Singmann, Bolker, & Westfall, 2015), which in turn calls the function PBmodcomp of the package pbkrtest (Halekoh & Højsgaard, 2014).

Reaction times increased significantly as a function of the number of days with sleep deprivation (Estimate = 10.47(1.55), PBtest = 23.54, p < .001).

F test with K-R dfs

Write-up example

To determine *p* values, we computed Type 3 conditional F tests with Kenward-Roger approximation for degrees of freedom as implemented in the mixed function of the package afex (Singmann, Bolker, & Westfall, 2015), which in turn calls the function KRmodcomp of the package pbkrtest (Halekoh & Højsgaard, 2014).

Reaction times increased significantly as a function of the number of days with sleep deprivation (Estimate = 10.47(1.55), F(1, 27.997) = 45.85, p < .001).

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Speeding Up

- mixed() fits as many models as there are fixed effects (+1)
 → can take a long time for complex models
- · bootstrapping (PB only) also can take a long time
- Easy to use more than 1 CPU to do things in parallel

More generally (beyond just mixed()):

- Bootstrapping is S L O W
- Using more than 1 CPU speeds up things A LOT
- How to use several CPUs may differ between Mac/PC and different OS versions → google it for your situation!
- Necessary to install packages (snow, parallel, multicore, ...)
- The required packages change sometimes (different operating systems, different R versions, ...)
- But it's worth the hassle → saves a lot of time!
- Always leave at least 1 core unused by R!!

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What currently works for me

Mac, OS X 10.9.5

install.packages("parallel")

library(parallel)

detectCores()

→ Tells me that my laptop has 4 cores

Multiple Cores with mixed()

(1) Create the cluster

```
n_cores <- detectCores()
MyCluster <- makeCluster(rep("localhost",
n_cores - 1))</pre>
```

(2) Run your mixed() command (LRT, KR, PB)

```
mix1 <- mixed(DV ~ IV + (1 + IV | pp), type =
3, method = "LRT", data = mydata, cl =
MyCluster)</pre>
```

- → Each CPU runs a (sub)model! Can save a lot of time.
- (3) Once you're done, stop the cluster stopCluster(MyCluster)

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Multiple Cores with mixed("PB")

- PB first runs all the (sub)models, and then does a lot of bootstrapping to get p values
- You can use also several CPUs for the bootstrapping

```
mix1 <- mixed(DV ~ IV + (1 + IV | pp), type =
3, method = "PB", data = mydata, cl =
MyCluster, args.test = list(nsim = 1000, cl =
MyCluster))</pre>
```

→ Note: You can also change the number of simulations (also possible without the cluster command)

Once you're done, stop the cluster

stopCluster(MyCluster)

Multiple Cores with PBmodcomp()

n_cores <- detectCores()</pre>

Create the clusters

```
MyCluster <- makeCluster(rep("localhost",
n_cores - 1))</pre>
```

Run your model comparison

```
PB_1 <- PBmodcomp(mylarge_m, mysmall_m, nsim =
1000, cl = MyCluster)</pre>
```

Look at the result

PB_1

Stop the cluster

stopCluster(MyCluster)

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Multiple Cores with:

confint.merMod

```
confint(s_1, method = "boot", parallel =
"multicore", ncpus = 3)
confint(s_1, method = "boot", parallel =
"snow", ncpus = 3)
```

bootMer()

```
boot_s_1 <- bootMer(s_1, FUN_bootMer,
parallel = "multicore", ncpus = 3)
boot_s_1 <- bootMer(s_1, FUN_bootMer,
parallel = "snow", ncpus = 3)</pre>
```

An Overview of what we covered

(1) confint() \rightarrow Cls \rightarrow p values

- Wald (untrustworthy)
- Likelihood profile (method = "profile")
- bootstrapping (method = "boot"); bootMer()
- → Good, but only for coefficients, not effects

(2) Conditional F-tests with K-R dfs

- pbkrtest::KRmodcomp(); Type 2
- car::Anova(test="F"); Type 2 and 3
- afex::mixed(method = "KR"); Type 3 (and 2)
- → Often good (not available for generalized mixed models; might be available also for glmer in the near future?)

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(3) Bootstrapped Likelihood Ratio Tests

- pbkrtest::PBmodcomp(); Type 2
- afex::mixed(method = "PB"); Type 3 (and 2)
- → Good

(4) Likelihood Ratio Tests

- anova(); Type 2
- afex::mixed(method = "LRT"); Type 3 (2)
- → Some debate whether good or not

(5) Wald Chisquare Test

- car::Anova(test="Chisq"); Type 2 and 3
- → Bad

Significance Tests

- Typically only for fixed effects of interest
- Several options (we encountered 5)
- Tests of coefficents vs. test of effects
 - Coefficients → like regression: coefficient significantly different from 0?
 - Effects → For factors with 3 or more levels and interactions involving factors
 - → like ANOVA: Is the **whole** factor significant? Is the **whole** interaction term significant?
- Post-hoc tests (e.g., multiple pairwise comparisons)
 → later in the course

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Coefficients: familiar from regression framework Is the coefficient significantly different from 0?

- Continuous predictors, e.g., Days (1 coeff)
- Interactions between 2 continuous predictors (1 coeff)
- Factors with 2 levels (1 coeff)
- Interactions between continuous predictor and 2-level factor (1 coeff)
- Factors with 3 or more levels → Remember?
 - Factors with 3 or more levels (e.g., k levels)...
 - ... are represented as k-1 contrasts
 - Each contrast can be tested for significance, e.g.:
 - Level 1 vs. overall average
 - Level 2 vs. overall average
 - → Different coding schemes (sum-to-zero, treatment, Helmert, ...): different contrasts, different interpretation

"Effects:" familiar from ANOVA framework

Example: A factor with 3 (or more) levels, e.g., Mood induction: happy, neutral, sad

- · Is the whole factor significant?
 - → Does the mood induction influence the DV?
- Interactions between categorical factors
 - → Is the **whole interaction** significant? Is the effect of mood induction different for females vs. males?

BTW: After identifying a significant effect of a "whole" factor or "whole" interaction, we want to further investigate where this comes from (e.g., with post-hocs). This is again something different and will be discussed later in the course...

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Why is this distinction relevant?

- Confidence intervals: Only tests of coefficients possible
- Model comparisons: Test of regression coefficients and effects possible

Last p value slide for today

→ Many different methods (usually similar results)

(Douglas Bates: https://stat.ethz.ch/pipermail/r-help/2006-May/094765.html)

- · More available than we are going to cover
- We focus on methods recommended as being reliable

List ordered according to recommendations

http://glmm.wikidot.com/faq

newer version (will move to here in the future): https://rawgit.com/bbolker/mixedmodels-misc/master/ glmmFAQ.html

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Today: p values

- · Recap: random slopes
- HW/lab/BB-related stuff
- p values!
 - Many different roads leading to Rome...
 - Some detours (Type 2 vs 3; coefficients vs effects, ...)
- · Homework/lab session
 - -p values
 - Imer tutorial

Today's Homework/Lab Session

Instructions: BlackBoard → Week 4

Practice computing p values for a mixed model, using all the methods that we discussed today. Plus some reading/R'ing, also in preparation for next week.

(1) The Cherry Pit Spitting Data

Compute *p* values for the model with gender, trial, and their interaction

- Type II test of the interaction with anova, KRmodcomp, PBmodcomp
- Try (and fail!) doing a type III main effect test with anova
- Type III tests of main effects and interaction with Anova and mixed
- Practice your write-up skills

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(2) The Imer tutorial

· Part 2 of the tutorial by Bodo Winter

Winter, B. (2013). Linear models and linear mixed effects models in R with linguistic applications. arXiv:1308.5499. [http://arxiv.org/pdf/1308.5499.pdf]

available here:

http://www.bodowinter.com/tutorial/bw_LME_tutorial2.pdf

Data set available here:

www.bodowinter.com/tutorial/politeness_data.csv

• Do all the stuff yourself in R (the same way you did this for part 1 on linear regression)

What do you have to hand in?

- · Answers to questions, output, figures, R code
- · Paste everything into a word doc, print it and
- bring it to the lab session on March 7

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Questions or comments?

That's it for today's lecture!

See you in the basement at 13:45

SP A -1.55A+B