How to embrace variation and accept uncertainty in linguistic and psycholinguistic data

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I assume that the reader has at least glanced at the paper (https://www.degruyter.com/document/doi/10.15 15/ling-2019-0051/html) before working through this file. Otherwise the plots will make no sense.

If there are any problems in running this code, please contact Shravan Vasishth.

Set up libraries

```
## ----setup,include=FALSE,cache=FALSE,echo=FALSE-----
library(MASS)
library(knitr)
library(xtable)
library(ggplot2)
library(dplyr)
##
## Attaching package: 'dplyr'
## The following object is masked from 'package:MASS':
##
##
      select
## The following objects are masked from 'package:stats':
##
##
      filter, lag
## The following objects are masked from 'package:base':
      intersect, setdiff, setequal, union
library(tidyr)
library(tidyverse)
## -- Attaching packages -----
                                                     ----- tidyverse 1.3.1 --
## v tibble 3.1.6
                      v stringr 1.4.0
## v readr
            2.1.2
                      v forcats 0.5.1
## v purrr
            0.3.4
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                   masks stats::lag()
## x dplyr::select() masks MASS::select()
```

```
#library(sjPlot)
library(rstan)
## Loading required package: StanHeaders
## rstan (Version 2.21.3, GitRev: 2e1f913d3ca3)
## For execution on a local, multicore CPU with excess RAM we recommend calling
## options(mc.cores = parallel::detectCores()).
## To avoid recompilation of unchanged Stan programs, we recommend calling
## rstan options(auto write = TRUE)
##
## Attaching package: 'rstan'
## The following object is masked from 'package:tidyr':
##
##
       extract
options(mc.cores = parallel::detectCores())
library(brms)
## Loading required package: Rcpp
## Loading 'brms' package (version 2.16.3). Useful instructions
## can be found by typing help('brms'). A more detailed introduction
## to the package is available through vignette('brms_overview').
## Attaching package: 'brms'
## The following object is masked from 'package:rstan':
##
##
       100
## The following object is masked from 'package:stats':
##
##
       ar
library(gridExtra)
## Attaching package: 'gridExtra'
## The following object is masked from 'package:dplyr':
##
##
       combine
library(bayesplot)
## This is bayesplot version 1.8.1
## - Online documentation and vignettes at mc-stan.org/bayesplot
## - bayesplot theme set to bayesplot::theme_default()
      * Does _not_ affect other ggplot2 plots
##
      * See ?bayesplot_theme_set for details on theme setting
library(ggridges)
library(lme4)
```

```
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
## The following objects are masked from 'package:tidyr':
##
##
       expand, pack, unpack
##
## Attaching package: 'lme4'
## The following object is masked from 'package:brms':
##
       ngrps
library(reshape2)
##
## Attaching package: 'reshape2'
## The following object is masked from 'package:tidyr':
##
##
       smiths
library(magick)
## Linking to ImageMagick 6.9.12.3
## Enabled features: cairo, fontconfig, freetype, heic, lcms, pango, raw, rsvg, webp
## Disabled features: fftw, ghostscript, x11
library(xtable)
#theme_set(theme_apa())
# set global chunk options, put figures into folder
options(warn=-1, replace.assign=TRUE)
opts_chunk$set(fig.path='figures/figure-', fig.align='center', fig.show='hold')
options(replace.assign=TRUE, width=75)
opts_chunk$set(dev='postscript')
opts_chunk$set(echo = TRUE,purl=TRUE)
## ----loadfunctions, include=TRUE, echo=FALSE, warning=FALSE, error=TRUE, message=TRUE----
source("../R/createStanDat.R")
source("../R/createStanDatAcc.R")
source("../R/magnifytext.R")
source("../R/multiplot.R")
source("../R/plotresults.R")
source("../R/plotpredictions.R")
source("../R/stan_results.R")
```

Load existing data on agreement attraction.

```
## ---agrmtattrn,echo=FALSE,warning=FALSE,message=FALSE-----
#Dillon et al 2013 Expt 1
DillonE1<-read.table("../data/DillonE1.txt",header=TRUE)
#Lago et al 2015 data (all expts):</pre>
```

```
Lago<-read.csv("../data/Lago.csv",header=T)</pre>
##Wagers et al 2009 data (all expts):
load("../data/Wagers.Rdata")
load("../data/Tucker.RData")
#Dillon E1:
DillonE1$cond<-factor(DillonE1$cond)</pre>
DillonE1Mism<-subset(DillonE1,fixationtype=="tt" & region==5 & cond%in%c(3,4) & value!="NA")
DillonE1Mism$cond<-factor(DillonE1Mism$cond)</pre>
DillonE1Mism$int<-ifelse(DillonE1Mism$cond==3,"low","high")</pre>
DillonE1Mism$x<-ifelse(DillonE1Mism$cond==3,-1,1)</pre>
dillonE1 \leftarrow DillonE1Mism[,c(1,3,4,14,15)]
dillonE1$expt<-factor("dillonE1")</pre>
colnames(dillonE1)[3]<-"rt"</pre>
nsubj_dillonE1<-length(unique(dillonE1$subj))</pre>
#get critical region data:
#dillonE <- subset(dillonE1, roi==5 & cond!='filler')</pre>
##Lago:
dat<-Lago
#critical region: not used because published paper found
#significant effects in postcrit region only
e1<-subset(dat,Experiment=="Experiment1" & Region=="06v1")
e2<-subset(dat,Experiment=="Experiment2" & Region=="06aux")
e3a<-subset(dat,Experiment=="Experiment3A" & Region=="06aux")
e3b<-subset(dat,Experiment=="Experiment3B" & Region=="aux")
nsubj_lagoe1<-length(unique(e1$Subject))</pre>
nsubj_lagoe2<-length(unique(e2$Subject))</pre>
nsubj_lagoe3a<-length(unique(e3a$Subject))</pre>
nsubj_lagoe3b<-length(unique(e3b$Subject))</pre>
#postcritical region:
poste1<-subset(dat,Experiment=="Experiment1" & Region=="07prep")</pre>
poste2<-subset(dat,Experiment="Experiment2" & Region=="07adv")</pre>
poste3a<-subset(dat,Experiment=="Experiment3A" & Region=="07a")</pre>
poste3b<-subset(dat,Experiment=="Experiment3B" & Region=="a")</pre>
##e1: a,b
#-(a) Ungram , singular attractor (interference condition)
#La *nota* que la chica escribieron en la clase alegrC3 a su amiga
#The note that the girl wrotepl during class cheered her friend up
#-(b) Ungram , plural attractor (baseline condition)
#Las *notas* que la chica escribieron en la clase alegraron a su amiga
#The notes that the girl wrotepl during class cheered her friend up
poste1<-subset(poste1,Condition%in%c("a","b"))</pre>
poste1$Condition<-factor(poste1$Condition)</pre>
poste1$x<-ifelse(poste1$Condition=="a",-1,1)</pre>
poste1$int<-ifelse(poste1$Condition=="a","low","high")</pre>
poste1 < -poste1[,c(1,3,8,15,14)]
```

```
poste1$expt<-factor("lagoE1")</pre>
lagoE1<-poste1</pre>
colnames(lagoE1)<-c("subj","item","rt","int","x","expt")</pre>
#e2: c,d
poste2<-subset(poste2,Condition%in%c("c","d"))</pre>
poste2$Condition<-factor(poste2$Condition)</pre>
poste2$x<-ifelse(poste2$Condition=="c",-1,1)</pre>
poste2$int<-ifelse(poste2$Condition=="c","low","high")</pre>
#head(poste2)
poste2<-poste2[,c(1,3,8,15,14)]
poste2$expt<-factor("lagoE2")</pre>
lagoE2<-poste2
colnames(lagoE2)<-c("subj","item","rt","int","x","expt")</pre>
#e3a: e,f
poste3a<-subset(poste3a,Condition%in%c("e","f"))</pre>
poste3a$Condition<-factor(poste3a$Condition)</pre>
#-(e) Ungram, singular attractor (interference condition)
#La *nota* que la chica van a escribir en la clase alegrarC! a su amiga
#The note that the girl are going to write during class will cheer her friend up
#-(f) Ungram, plural attractor (baseline condition)
#Las *notas* que la chica van a escribir en la clase alegrarC!n a su amiga
#The notes that the girl are going to write during class will cheer her friend up
#boxplot(RT~Condition, poste3a)
poste3a$x<-ifelse(poste3a$Condition=="e",-1,1)</pre>
poste3a$int<-ifelse(poste3a$Condition=="e","low","high")</pre>
poste3a < -poste3a[,c(1,3,8,15,14)]
poste3a$expt<-factor("lagoE3a")</pre>
lagoE3a<-poste3a
colnames(lagoE3a)<-c("subj","item","rt","int","x","expt")</pre>
#e3b: e,f
poste3b<-subset(poste3b,Condition%in%c("e","f"))</pre>
poste3b$Condition<-factor(poste3b$Condition)</pre>
#-(e) Ungram, singular attractor (baseline condition)
#The player that the coach were always praising very enthusiastically decided to leave the team
#-(f) Ungram, plural attractor (interference condition)
#The players that the coach were always praising very enthusiastically decided to
                                                                                           leave the team
poste3b$x<-ifelse(poste3b$Condition=="e",-1,1)</pre>
poste3b$int<-ifelse(poste3b$Condition=="e","low","high")</pre>
poste3b < -poste3b[,c(1,3,8,15,14)]
poste3b$expt<-factor("lagoE3b")</pre>
lagoE3b<-poste3b
colnames(lagoE3b)<-c("subj","item","rt","int","x","expt")</pre>
#Wagers:
E2postcrit<-subset(Experiment2, Region==7)</pre>
nsubj_wagerse2<-length(unique(E2postcrit$Subj))</pre>
#E2$intr.au<-ifelse(E2$rchead=="pl" & E2$qramm=="unqram",1/2,
                     ifelse(E2$rchead=="sq" & E2$qramm=="unqram",-1/2,
#
                             0))
#d (sing),h (plu)
```

```
#unique(subset(E2postcrit,gramm=="ungram")$Condition)
E2postcrit<-subset(E2postcrit,Condition%in%c("d","h"))
E2postcrit$Condition<-factor(E2postcrit$Condition)</pre>
E2postcrit$x<-ifelse(E2postcrit$Condition=="d",-1,1)
E2postcrit$int<-ifelse(E2postcrit$Condition=="d","low","high")
#colnames(E2postcrit)
E2postcrit<-E2postcrit[,c(4,3,8,13,12)]</pre>
E2postcrit$expt<-factor("wagersE2")</pre>
wagersE2<-E2postcrit
colnames(wagersE2)<-c("subj","item","rt","int","x","expt")</pre>
E3postcrit<-subset(Experiment3, Region==7)</pre>
nsubj_wagerse3<-length(unique(E3postcrit$Subj))</pre>
#E3crit$intr.au.pl<-ifelse(E3crit$qramm=="unqram" & E3crit$rcsubj=="sq" &
                               E3crit$rchead=="pl",1/2,
#
                           ifelse(E3crit$gramm=="ungram" & E3crit$rcsubj=="sq" &
#
                                      E3crit$rchead=="sg",-1/2,0))
#E3crit$intr.au.sq<-ifelse(E3crit$qramm=="unqram" & E3crit$rcsubj=="pl" &
                               E3crit$rchead=="sq",1/2,
#
                             ifelse(E3crit$gramm=="ungram" & E3crit$rcsubj=="pl" &
#
                                      E3crit$rchead=="pl",-1/2,0))
E3postcrit pl<-subset(E3postcrit,gramm=="ungram" & rcsubj=="sg")
E3postcrit pl$Condition<-factor(E3postcrit pl$Condition)</pre>
E3postcrit_sg<-subset(E3postcrit,gramm=="ungram" & rcsubj=="pl")
E3postcrit_sg$Condition<-factor(E3postcrit_sg$Condition)</pre>
#unique(E3postcrit_pl$Condition) b,f
#unique(E3postcrit_sq$Condition) c,q
#head(subset(E3postcrit_sq,rchead=="sq"))
#head(E3postcrit_pl)
##plural:
E3postcrit_pl$x<-ifelse(E3postcrit_pl$Condition=="b",-1,1)
E3postcrit_pl$int<-ifelse(E3postcrit_pl$Condition=="b","low","high")</pre>
E3postcrit_pl \leftarrow E3postcrit_pl[,c(4,3,8,15,14)]
E3postcrit_pl$expt<-factor("wagersE3pl")</pre>
colnames(E3postcrit_pl)<-c("subj","item","rt","int","x","expt")</pre>
wagersE3pl<-E3postcrit_pl</pre>
##singular:
E3postcrit_sg$x<-ifelse(E3postcrit_sg$Condition=="c",-1,1)
E3postcrit_sg$int<-ifelse(E3postcrit_sg$Condition=="c","low","high")
E3postcrit_sg \leftarrow E3postcrit_sg[,c(4,3,8,15,14)]
E3postcrit_sg$expt<-factor("wagersE3sg")</pre>
colnames(E3postcrit_sg)<-c("subj","item","rt","int","x","expt")</pre>
wagersE3sg<-E3postcrit_sg</pre>
E4postcrit<-subset(Experiment4, Region==8) ##
```

```
nsubj_wagerse4<-length(unique(E4postcrit$Subj))</pre>
#head(subset(Experiment4, Condition=="c"), n=10)
#postcritical region
#E4postcrit$intr.au<-ifelse(E4postcrit$gramm=="ungram" & E4postcrit$match=="match",-1/2,
                              ifelse(E4postcrit$gramm=="ungram" & E4postcrit$match=="mismatch",1/2,0))
E4postcrit<-subset(E4postcrit,gramm=="ungram")</pre>
E4postcrit$Condition<-factor(E4postcrit$Condition)</pre>
E4postcrit$x<-ifelse(E4postcrit$Condition=="c",-1,1)
E4postcrit$int<-ifelse(E4postcrit$Condition=="c","low","high")
E4postcrit \leftarrow E4postcrit[,c(4,3,8,13,12)]
E4postcrit$expt<-factor("wagersE4")</pre>
colnames(E4postcrit)<-c("subj","item","rt","int","x","expt")</pre>
wagersE4<-E4postcrit
E5postcrit<-subset(Experiment5, Region==8) ##postcritical region
nsubj_wagerse5<-length(unique(E5postcrit$Subj))</pre>
E5postcrit<-subset(E5postcrit,gramm=="ungram")</pre>
E5postcrit$Condition<-factor(E5postcrit$Condition)</pre>
E5postcrit$x<-ifelse(E5postcrit$Condition=="c",-1,1)
E5postcrit$int<-ifelse(E5postcrit$Condition=="c","low","high")
E5postcrit<-E5postcrit[,c(4,3,8,13,12)]
colnames(E5postcrit)<-c("subj","item","rt","int","x")</pre>
E5postcrit$expt<-factor("wagersE5")</pre>
wagersE5<-E5postcrit
#head(wagersE5)
```

Assemble all the data into one data frame:

```
## subj item rt int x expt
## 77 dillonE11 dillonE119 195 low -1 dillonE1
## 203 dillonE11 dillonE135 479 low -1 dillonE1
## 539 dillonE11 dillonE143 2287 low -1 dillonE1
## 665 dillonE11 dillonE14 730 high 1 dillonE1
## 749 dillonE11 dillonE128 1246 high 1 dillonE1
## 791 dillonE11 dillonE127 4027 low -1 dillonE1
```

In the dat data frame above, int is the low/high interference condition, which is \pm 1 coded in the column x.

Note that if one uses all the data altogether one has to rename the subjects, because subject 1 in dillonE1 is not the same subject as in some other experiment with subject id 1.

This Stan+lmer code is not run here (results are precomputed and stored)

One can fit the Stan/lmer models to these data using these commands. The results needed in this file are stored in the data directory through these commands.

```
##----agrmtattrn2,echo=FALSE,warning=FALSE,message=FALSE,eval=FALSE------
#Dillon E1:
stanDat<-createStanDat(d=dillonE1,</pre>
                        rt=dillonE1$rt,
                        form=as.formula("~ 1 + x"))
#str(stanDat)
DillonE1 <- stan(file = "StanModels/maxModelTargetMismatch.stan",</pre>
              data = stanDat,
              iter = 2000,
              chains = 4)
#Int is Interference:
pars<-c("Int","beta[2]","sigma_u[1]","sigma_u[2]","sigma_w[1]","sigma_w[2]","sigma_e")</pre>
DillonE1_res<-stan_results(DillonE1, params=pars[1])</pre>
#with(dillonE1, tapply(rt,x,mean))
mDillonE1_lmer<-lmer(log(rt)~x+(1+x||subj)+(1+x||item),dillonE1,
        control=lmerControl(calc.derivs=FALSE))
mDillonE1_lmer_res<-summary(mDillonE1_lmer)$coefficients[2,]</pre>
stanDat<-createStanDat(d=lagoE1,</pre>
                         rt=lagoE1$rt,
                        form=as.formula("~ 1 + x"))
LagoE1 <- stan(file = "StanModels/maxModelTargetMismatch.stan",</pre>
                  data = stanDat,
                  iter = 2000,
                  chains = 4)
LagoE1 res<-stan results(LagoE1, params=pars[1])</pre>
mLagoE1_lmer<-lmer(log(rt)~x+(1+x||subj)+(1+x||item),lagoE1,</pre>
        control=lmerControl(calc.derivs=FALSE))
mLagoE1_lmer_res<-summary(mLagoE1_lmer)$coefficients[2,]</pre>
stanDat<-createStanDat(d=lagoE2,
                         rt=lagoE2$rt,
                        form=as.formula("~ 1 + x"))
LagoE2 <- stan(file = "StanModels/maxModelTargetMismatch.stan",</pre>
                data = stanDat,
                iter = 2000,
                chains = 4)
LagoE2_res<-stan_results(LagoE2,params=pars[1])</pre>
mLagoE2 lmer < -lmer(log(rt) \sim x + (1+x||subj) + (1+x||item), lagoE2,
        control=lmerControl(calc.derivs=FALSE))
mLagoE2_lmer_res<-summary(mLagoE2_lmer)$coefficients[2,]</pre>
```

```
stanDat<-createStanDat(d=lagoE3a,</pre>
                            rt=lagoE3a$rt,
                        form=as.formula("~ 1 + x"))
LagoE3a <- stan(file = "StanModels/maxModelTargetMismatch.stan",</pre>
                data = stanDat,
                iter = 2000,
                chains = 4)
LagoE3a_res<-stan_results(LagoE3a,params=pars[1])</pre>
mLagoE3a_lmer<-lmer(log(rt)~x+(1|subj)+(1|item),lagoE3a,</pre>
        control=lmerControl(calc.derivs=FALSE))
mLagoE3a_lmer_res<-summary(mLagoE3a_lmer)$coefficients[2,]</pre>
stanDat<-createStanDat(d=lagoE3b,</pre>
                            rt=lagoE3b$rt,
                        form=as.formula("~ 1 + x"))
LagoE3b <- stan(file = "StanModels/maxModelTargetMismatch.stan",</pre>
                 data = stanDat,
                 iter = 2000,
                 chains = 4)
LagoE3b_res<-stan_results(LagoE3b,params=pars[1])</pre>
mLagoE3b_lmer<-lmer(log(rt)~x+(1+x||subj)+(1|item),lagoE3b,</pre>
        control=lmerControl(calc.derivs=FALSE))
mLagoE3b_lmer_res<-summary(mLagoE3b_lmer)$coefficients[2,]</pre>
stanDat<-createStanDat(d=wagersE2,
                            rt=wagersE2$rt,
                        form=as.formula("~ 1 + x"))
WagersE2 <- stan(file = "StanModels/maxModelTargetMismatch.stan",</pre>
                 data = stanDat,
                 iter = 2000.
                 chains = 4)
WagersE2_res<-stan_results(WagersE2, params=pars[1])</pre>
mWagersE2_lmer<-lmer(log(rt)~x+(1+x||subj)+(1+x||item),wagersE2,
        control=lmerControl(calc.derivs=FALSE))
mWagersE2_lmer_res<-summary(mWagersE2_lmer)$coefficients[2,]</pre>
stanDat<-createStanDat(d=wagersE3pl,</pre>
                            rt=wagersE3pl$rt,
                        form=as.formula("~ 1 + x"))
WagersE3pl <- stan(file = "StanModels/maxModelTargetMismatch.stan",</pre>
                  data = stanDat,
                  iter = 2000,
                  chains = 4)
```

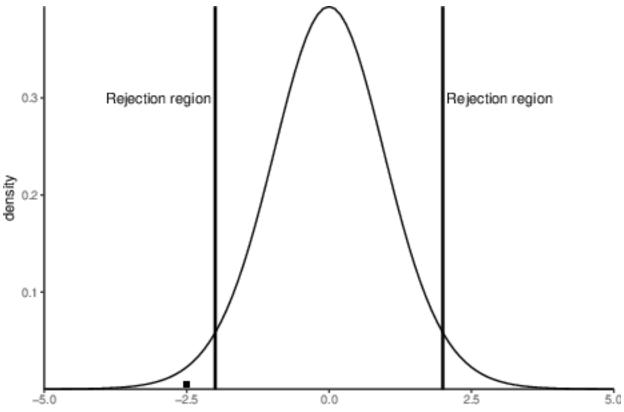
```
WagersE3pl_res<-stan_results(WagersE3pl,params=pars[1])</pre>
mWagersE3pl_lmer<-lmer(log(rt)~x+(1+x||subj)+(1+x||item),wagersE3pl,
        control=lmerControl(calc.derivs=FALSE))
mWagersE3pl_lmer_res<-summary(mWagersE3pl_lmer)$coefficients[2,]</pre>
stanDat<-createStanDat(d=wagersE3sg,</pre>
                           rt=wagersE3sg$rt,
                           form=as.formula("~ 1 + x"))
WagersE3sg <- stan(file = "StanModels/maxModelTargetMismatch.stan",</pre>
                    data = stanDat,
                    iter = 2000,
                    chains = 4)
WagersE3sg_res<-stan_results(WagersE3sg,params=pars[1])</pre>
mWagersE3sg_lmer<-lmer(log(rt)~x+(1+x||subj)+(1+x||item),wagersE3sg,
        control=lmerControl(calc.derivs=FALSE))
mWagersE3sg_lmer_res<-summary(mWagersE3sg_lmer)$coefficients[2,]
stanDat<-createStanDat(d=wagersE4,
                           rt=wagersE4$rt,
                           form=as.formula("~ 1 + x"))
WagersE4 <- stan(file = "StanModels/maxModelTargetMismatch.stan",</pre>
                    data = stanDat.
                    iter = 2000,
                    chains = 4)
WagersE4_res<-stan_results(WagersE4, params=pars[1])</pre>
mWagersE4_lmer<-lmer(log(rt)~x+(1|subj),wagersE4,</pre>
        control=lmerControl(calc.derivs=FALSE))
mWagersE4_lmer_res<-summary(mWagersE4_lmer)$coefficients[2,]</pre>
stanDat<-createStanDat(d=wagersE5,</pre>
                        rt=wagersE5$rt,
                        form=as.formula("~ 1 + x"))
WagersE5 <- stan(file = "StanModels/maxModelTargetMismatch.stan",</pre>
                  data = stanDat,
                  iter = 2000,
                  chains = 4)
WagersE5_res<-stan_results(WagersE5, params=pars[1])</pre>
mWagersE5_lmer<-lmer(log(rt)~x+(1+x|subj)+(1+x|item),wagersE5,
        control=lmerControl(calc.derivs=FALSE))
mWagersE5_lmer_res<-summary(mWagersE5_lmer)$coefficients[2,]</pre>
*posterior predicted data from Jaeger et al replication: See MethodsX paper:
load("../model/au_predicted_meansD13rep.Rda")
len_model<-length(au_predicted_means_rep)</pre>
```

```
agrmt_data<-data.frame(expt=factor(rep(c(1:10),</pre>
                                           each=4000)),
                        posterior=c(DillonE1_res[2][[1]][[1]],
                        LagoE1_res[2][[1]][[1]],
                        LagoE2_res[2][[1]][[1]],
                        LagoE3a_res[2][[1]][[1]],
                        LagoE3b_res[2][[1]][[1]],
                        WagersE2 res[2][[1]][[1]],
                        WagersE3pl_res[2][[1]][[1]],
                        WagersE3sg_res[2][[1]][[1]],
                        WagersE4_res[2][[1]][[1]],
                        WagersE5_res[2][[1]][[1]]))
means<-sort(with(agrmt_data,tapply(posterior,expt,mean)))</pre>
ordered_studies<-as.numeric(names(means))</pre>
model_pred<-data.frame(expt=rep("model",len_model),posterior=au_predicted_means_rep)</pre>
head(model_pred)
data_model<-rbind(agrmt_data,model_pred)</pre>
lvls<-levels(data_model$expt)</pre>
data_model$expt<-factor(data_model$expt,levels=lvls[c(11,ordered_studies
)])
save(data_model,file="../data/data_model.Rda")
#frequentist CIs:
lmer_estimates<-data.frame(rbind(mDillonE1_lmer_res,</pre>
mLagoE1_lmer_res,
mLagoE2_lmer_res,
mLagoE3a_lmer_res,
mLagoE3b_lmer_res,
mWagersE2_lmer_res,
mWagersE3pl_lmer_res,
mWagersE3sg_lmer_res,
mWagersE4_lmer_res,
mWagersE5_lmer_res))
lmer_estimates$lower<-lmer_estimates[,1]-2*lmer_estimates[,2]</pre>
lmer_estimates$upper<-lmer_estimates[,1]+2*lmer_estimates[,2]</pre>
lmer_estimates$id<-1:10</pre>
lmer_estimates2<-lmer_estimates[order(lmer_estimates[,1]), ]</pre>
lmer estimates3<-lmer estimates2[,c(6,1,4,5,3)]
save(lmer estimates2,file="../data/lmer estimates2.Rda")
save(lmer_estimates3,file="../data/lmer_estimates3.Rda")
```

t-test demo

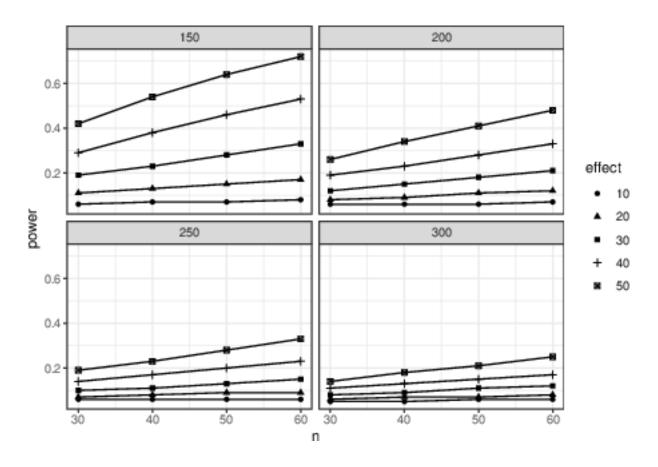
```
## ---ttestdemo,echo=FALSE,fig.height=3----
obst<- -2.5
xend<-5</pre>
```

```
degf<-20
x < -seq(-xend, xend, by=0.1)
y<-dt(x,df=degf)
dat<-data.frame(x=x,y=y)</pre>
p<-ggplot(data = dat,</pre>
          mapping = aes(x = x, y = y)) +
    geom_line()+
    scale_x_continuous(expand = c(0, 0))+
   scale_y_continuous(expand = c(0, 0)) +
   geom_vline(xintercept = -2,
                color = "black", size=1)+
   geom_vline(xintercept = 2,
                color = "black", size=1)+
  geom_point(aes(obst,0.005))+
  ylab("density")+xlab("")+theme_bw()+
  annotate("text", x = -3, y = 0.3, label = "Rejection region")+
  annotate("text", x = 3, y = 0.3, label = "Rejection region")
p + theme(panel.border = element_blank(),
        panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black"))
# Power
```



```
ylabl="",
                      titl="",
                      scl=1){
  ggplot(distrn,
       aes(x = power, y = nsubj,
           height = ..density..)) +
  geom_density_ridges(scale = scl,
                       stat = "density", rel_min_height = 0.01) +
  scale_y_discrete(expand = c(0.01, 0)) +
  xlim(0.05,1)+
  theme_ridges() + theme(legend.position = "none")+
  xlab(xlabl)+
  ggtitle(titl)+
  ylab(ylabl)+
  magnifytext(sze=12)
simulate_power<-function(nsim=10000,</pre>
                          stddev=NULL,
                          nsamps = seq(30,60,by=10),
                          d mean=30,
                          d sd=10){
##take nsim samples
##from "prior" on effect:
  d<-rnorm(nsim,mean=d_mean,sd=d_sd)</pre>
  powmatrix<-matrix(rep(NA,</pre>
                         nsim*length(nsamps)),ncol=length(nsamps))
for(i in 1:nsim){
  powmatrix[i,]<-power.t.test(delta=d[i],</pre>
                         n=nsamps,
                         type="one.sample",strict=TRUE)$power
power_df<-data.frame(nsubj=factor(rep(nsamps,</pre>
each=nsim)),
           stddev=rep(stddev,
           length(nsamps)*nsim),
power=as.vector(powmatrix))
power_df
}
## ----plotpower, echo=FALSE, fig. width=4, fig. height=5-----
simulate_power2<-function(nsamps=30,</pre>
                          d_{mean}=30,
                          d_sd=NULL,
                          nsim=100){
    pow<-power.t.test(delta=d_mean,</pre>
                                  n=nsamps,
                                  sd=d_sd,
                                  type="one.sample",strict=TRUE)$power
    pow
}
```

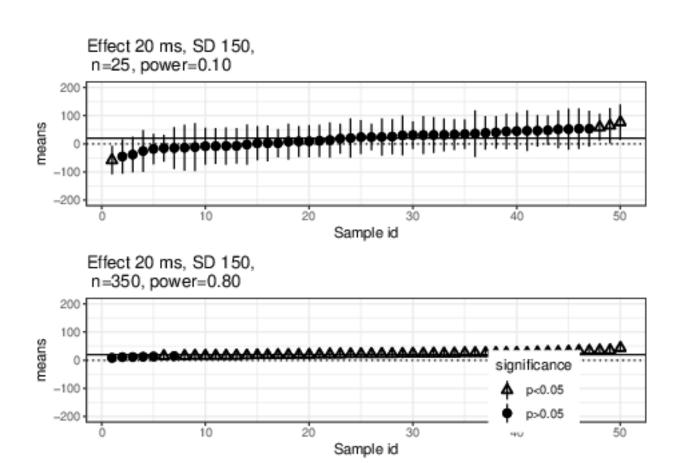
```
samps < -c(30,40,50,60)
sds<-c(150,200,250,300)
ds < -c(10,20,30,40,50)
powvals<-c()</pre>
## for each sample size:
for(i in 1:length(samps)){
  ## for each sd:
  for(j in 1:length(sds)){
    ## for each effect size:
    for(k in 1:length(ds)){
pwr<-simulate_power2(nsamps=samps[i],</pre>
                 d_mean=ds[k],
                 d_sd=sds[j])
powvals<-c(powvals,round(pwr,2))</pre>
    }
  }
}
power_calc<-data.frame(n=rep(samps,each=5*4),</pre>
                         sd=rep(rep(sds,each=5),4),
                         effect=rep(ds,16))
power_calc$powvals<-powvals</pre>
power_calc$sd<-factor(power_calc$sd)</pre>
power_calc$effect<-factor(power_calc$effect)</pre>
power_plot<-ggplot(power_calc, aes(x=n, y=powvals,</pre>
                         shape=effect)) + ylab("power")+geom_point()+geom_line()+theme_bw()+facet_wrap(~s
power_plot
```



Type M error demo

```
## ----demotypeM,echo=FALSE,fig.width=7,fig.height=6,include=TRUE----
set.seed(987654321)
d<-20
sd<-150
lown<-power.t.test(d=d,sd=sd,power=.10,type="one.sample",alternative="two.sided",strict=TRUE)$n
highn<-power.t.test(d=d,sd=sd,power=.80,type="one.sample",alternative="two.sided",strict=TRUE)$n
nsim < -50
\verb|tlow| < - thigh < - means | low < - CIuplow < - CIuplow < - CIuphigh < - CII whigh < - NULL | low < - CIuphigh < - CII whigh < - NULL | low < - CIUphigh < - CII whigh < - NULL | low < - CIUphigh < - CII whigh < - NULL | low < - CIUphigh < - CII whigh < - NULL | low < - CIUphigh < - CII whigh < - NULL | low < - CIUphigh < - CII whigh < - NULL | low < - CIUphigh < - CII whigh < - NULL | low < - CIUphigh < - CII whigh < - NULL | low < - CIUphigh < - CII whigh < - NULL | low < - CIUphigh < - CII whigh < - NULL | low < - CIUphigh < - CII whigh < - CII whigh
critlow<-abs(qt(0.025,df=lown-1))</pre>
crithigh<-abs(qt(0.025,df=highn-1))</pre>
for(i in 1:nsim){
       x<-rnorm(lown, mean=d, sd=sd)
       meanslow[i]<-mean(x)</pre>
       tlow[i]<-t.test(x)$statistic</pre>
       Cluplow[i] <-mean(x)+critlow*sd(x)/sqrt(length(x))</pre>
       CIlwlow[i] <-mean(x)-critlow*sd(x)/sqrt(length(x))</pre>
       x<-rnorm(highn, mean=d, sd=sd)
       meanshigh[i] <-mean(x)</pre>
       thigh[i]<-t.test(x)$statistic</pre>
       CIuphigh[i] <-mean(x)+crithigh*sd(x)/sqrt(length(x))</pre>
       CIlwhigh[i] <-mean(x)-crithigh*sd(x)/sqrt(length(x))</pre>
}
```

```
siglow<-ifelse(abs(tlow)>abs(critlow), "p<0.05", "p>0.05")
sighigh<-ifelse(abs(thigh)>abs(crithigh), "p<0.05", "p>0.05")
summarylow<-data.frame(means=meanslow, significance=siglow, CIupper=CIuplow, CIlower=CIlwlow)
summaryhigh <-data.frame(index=1:nsim, means=meanshigh, significance=sighigh, Clupper=Cluphigh, Cllower=Cl
# re-order data by mean effect size
summarylow<-summarylow[order(summarylow$means), ]</pre>
summarylow$index<-1:nrow(summarylow)</pre>
summaryhigh<-summaryhigh[order(summaryhigh$means), ]</pre>
summaryhigh$index<-1:nrow(summaryhigh)</pre>
p_low<-ggplot(summarylow, aes(y=means, x=index,</pre>
                               shape=significance,
                               ymax=Clupper, ymin=Cllower)) +
  geom_pointrange()+
  #coord_flip()+
  geom_point(size=2.5)+
  scale_shape_manual(values=c(2, 19))+
  magnifytext(sze=22)+
  geom_hline(yintercept=20) +
  theme bw() +
  scale_x_continuous(name = "Sample id")+
  scale_y_continuous(name = "means",limits=c(-200,200))+
  labs(title="Effect 20 ms, SD 150, \n n=25, power=0.10")+
  theme(legend.position="none")+geom_hline(yintercept=0, linetype="dotted")
p_hi<-ggplot(summaryhigh, aes(y=means, x=index,</pre>
                               shape=significance, ymax=Clupper, ymin=Cllower)) +
  geom_pointrange()+
  #coord_flip()+
  geom_point(size=2.5)+
  scale_shape_manual(values=c(2, 19))+
    scale_x_continuous(name = "Sample id")+
  magnifytext(sze=22)+
  geom_hline(yintercept=d) +
  theme bw() +
  scale_y_continuous(name = "means",limits=c(-200,200))+
  labs(title="Effect 20 ms, SD 150, \n n=350, power=0.80")+
  theme(legend.position=c(0.8,0.25))+geom_hline(yintercept=0, linetype="dotted")
multiplot(p_low,p_hi,cols=1)
```



t-values across the studies

```
## ----echo=FALSE, results=`asis'-----
load("../data/tvals.Rda")
rownames(tvals)<-""
xtable(round(tvals,2), caption="t-values from 10 published studies on the agreement attraction effect.",</pre>
```

% latex table generated in R 4.1.2 by xtable 1.8-4 package % Sat Mar 19 22:07:25 2022

| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| -2.56 | -2.25 | -1.67 | -1.83 | -1.40 | -2.22 | -1.33 | -0.22 | -2.81 | -1.74 |

Table 1: t-values from 10 published studies on the agreement attraction effect.

Meta-analysis

Given the data from different studies, one can do the meta-analysis by running the following commented out code. Please see https://github.com/vasishth/MetaAnalysisJaegerEngelmannVasishth2017 for more.

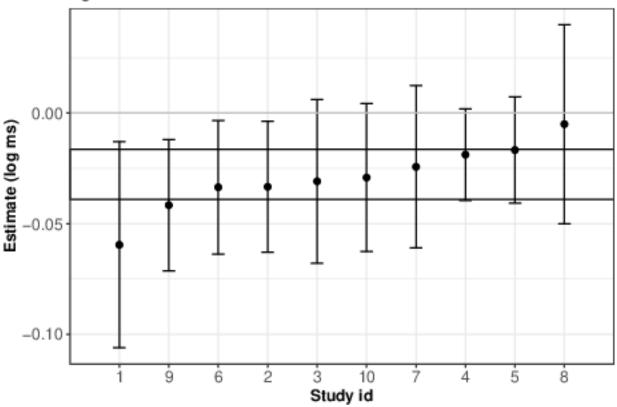
```
## ----metaanalysis,echo=FALSE,warning=FALSE,message=FALSE,eval=FALSE-----
## load("../data/lmer_estimates2.Rda")
## dat<-list(N=dim(lmer_estimates2)[1],
## y=lmer_estimates2$Estimate,
## sigma=lmer_estimates2$Std..Error)
##
## fit <- stan(file='../StanModels/rema.stan', data=dat,</pre>
```

```
## iter=2000, chains=4, seed=987654321,
## control = list(adapt_delta = 0.8))
## save(fit,file="../data/remafit.Rda")
```

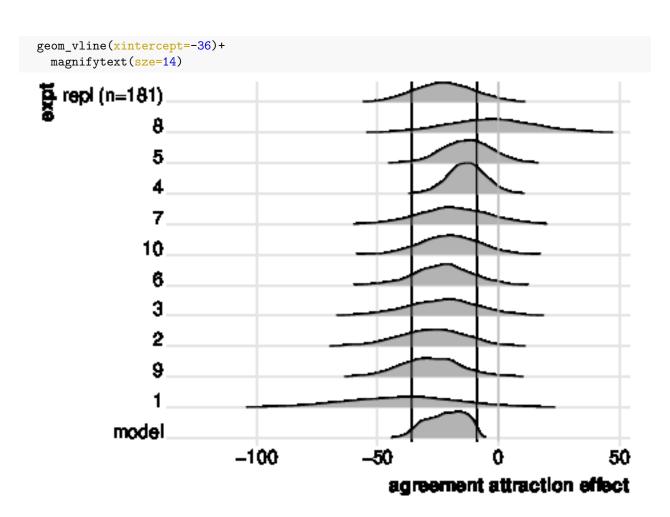
Load pre-computed meta-analysis values:

```
## ---remafitload.echo=FALSE-----
load("../data/remafit.Rda")
paramnames<-c("theta", "tau")</pre>
#print(fit,pars=paramnames)
params<-extract(fit,pars=paramnames)</pre>
#str(params)
mean_theta<-mean(params$theta)</pre>
lower theta<-quantile(params$theta, 0.025)
upper_theta<-quantile(params$theta, 0.975)
## ----dillonreprise,echo=FALSE-----
mean_dillonma<-round(exp(6.4376+mean_theta)-exp(6.4376-mean_theta))
upper_dillonma<-round(exp(6.4376+(upper_theta))-exp(6.4376-(upper_theta)))
lower_dillonma<-round(exp(6.4376+(lower_theta))-exp(6.4376-(lower_theta)))</pre>
## ----echo=FALSE, fig. width=5, fig. height=4------
load("../data/lmer_estimates3.Rda")
lmer_estimates3$id<-factor(lmer_estimates3$id,levels=lmer_estimates3$id)</pre>
pd<-position_dodge(0.6)
ggplot(lmer_estimates3, aes(x=id,
                               y=Estimate,group=id)) +
    geom_errorbar(aes(ymin=lower, ymax=upper),
                  width=.25, size=.5, position=pd) +
      annotate("rect",
            xmin = 0,
             xmax = 11,
             ymin = upper theta,
             ymax = lower_theta,
            color = "black",alpha=0.2)+
     geom_hline(yintercept=mean_theta,
                color="black",)+
   labs(title="Agreement attraction across 10 studies") +
   xlab("Study id")+
   ylab("Estimate (log ms)")+
   geom_hline(yintercept=0,col="gray")+
   geom_point(position=pd, size=2)+
   theme_bw()+
    magnifytext()
```

Agreement attraction across 10 studies



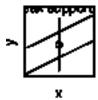
```
## ----ridgeplot,echo=FALSE,fig.width=9,fig.height=10--
## precomputed above:
load("../data/data_model.Rda")
load("../data/data_model_dillonrep.Rda")
modelquantiles<-quantile(subset(data_model,expt=="model")$posterior,prob=c(0.025,0.975))</pre>
expt_dillonrep<-subset(data_model_dillonrep,expt==11)</pre>
#head(expt_dillonrep)
expt dillonrep$expt<-factor("repl (n=181)")</pre>
data_model11studies<-rbind(data_model,expt_dillonrep)</pre>
scl<-1
ggplot(data_model11studies,
       aes(x = posterior, y = factor(expt), height = ..density..
  geom_density_ridges(scale = scl
                       ,stat = "density",
                      rel_min_height = 0.01) +
  scale_y_discrete(expand = c(0.01, 0)) +
  scale_x_continuous(expand = c(0.01, 0)) +
  #scale_fill_brewer(palette = "PuBuGn") +
  theme_ridges() + theme(legend.position = "none")+
  xlab("agreement attraction effect")+
  ylab("expt")+
  geom_vline(xintercept=0,col="gray")+
  ## meta-analysis based on frequentist estimates
  geom_vline(xintercept=-9)+
```

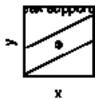


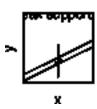
A graphical summary of the Roberts and Pashler 2000 criteria

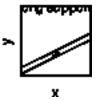
```
## ---rp,echo=FALSE,fig.height=6,fig.width=6-----
y < -seq(1,100,by=0.01)
op<-par(mfrow=c(2,2),pty="s")</pre>
plot(y,y,type="1",ylim=c(0,200),
    main="",xaxt="n",yaxt="n",xlab="",ylab="")
title(xlab="x",
      line=.5, cex.lab=1)
title(ylab="y",
      line=.5, cex.lab=1)
lines(y,y+80)
points(50,90)
arrows(x0=50,x1=50,y0=10,y1=170,
       angle=90,
       length=0)
text("weak support",x=40,y=200)
plot(y,y,type="l",ylim=c(0,200),
main="",xaxt="n",yaxt="n",xlab="",ylab="")
```

```
title(xlab="x",
      line=.5, cex.lab=1)
title(ylab="y",
      line=.5, cex.lab=1)
lines(y,y+80)
points(50,90)
arrows(x0=50,x1=50,y0=80,y1=100,
       angle=90,
       length=0)
text("weak support",x=40,y=200)
plot(y,y,type="1",ylim=c(0,200),
     main="",xaxt="n",yaxt="n",xlab="",ylab="")
title(xlab="x",
      line=.5, cex.lab=1)
title(ylab="y",
      line=.5, cex.lab=1)
lines(y,y+20)
points(50,60)
arrows(x0=50,x1=50,y0=60-50,y1=60+50,
       angle=90,
       length=0)
text("weak support",x=40,y=200)
plot(y,y,type="l",ylim=c(0,200),
     main="",xaxt="n",yaxt="n",xlab="",ylab="")
title(xlab="x",
      line=.5, cex.lab=1)
title(ylab="y",
      line=.5, cex.lab=1)
lines(y,y+20)
points(50,60)
arrows(x0=50,x1=50,y0=60-10,y1=60+10,
       angle=90,
       length=0)
text("strong support",x=40,y=200)
```









Computing power using simulation

```
## ----computepower,echo=FALSE-
source("../R/gen fake norm.R")
## maximal model, ignore correlations:
mDillonE1_lmer<-lmer(log(rt)~x+(1+x|subj)+(1+x|item),dillonE1,
                          control=lmerControl(calc.derivs=FALSE))
extract_parests_lmer<-function(</pre>
      mod=mDillonE1_lmer) {
      alpha<-summary(mod)$coefficients[1,1]</pre>
      beta<-summary(mod)$coefficients[2,1]</pre>
## extract standard deviation estimate:
sigma_e<-attr(VarCorr(mod),"sc")</pre>
## assemble variance covariance matrix for subjects:
subj_ranefsd<-attr(VarCorr(mod)$subj,"stddev")</pre>
sigma_u0<-subj_ranefsd[1]
sigma_u1<-subj_ranefsd[2]</pre>
item_ranefsd<-attr(VarCorr(mod)$item,"stddev")</pre>
sigma_w0<-item_ranefsd[1]</pre>
sigma_w1<-item_ranefsd[2]</pre>
## return list of params:
list(alpha=alpha,beta=beta,sigma_e=sigma_e,sigma_u0=sigma_u0,sigma_u1=sigma_u1,sigma_w0=sigma_w0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma_v0,sigma
parest<-extract_parests_lmer()</pre>
compute_power<-function(nsim=100,</pre>
                                                                              alpha=parest$alpha,
                                                                              beta=parest$beta,
                                                                              sigma_e=parest$sigma_e,
```

```
sigma_u0=parest$sigma_u0,
                         sigma_u1=parest$sigma_u1,
                 sigma_w0=parest$sigma_w0,
                         sigma_w1=parest$sigma_w1,
                         nsubj=48,
                         nitem=40){
tvals<-c()
for(i in 1:nsim){
fakedat<-gen_fake_norm(nitem=nitem,</pre>
                        nsubj=nsubj,
                alpha=alpha,
                beta=beta.
                sigma_u0=sigma_u0,
                sigma_u1=sigma_u1,
                sigma_w0=sigma_w0,
                sigma_w1=sigma_w1,
                sigma_e=sigma_e)
m<-lmer(rt~cond+(1+cond||subj)+(1+cond||item),</pre>
        control=lmerControl(calc.derivs=FALSE))
tvals[i] <-summary(m)$coefficients[2,3]</pre>
mean(abs(tvals)>2)
```

This code will take some time to run the first time round, but after that the results will be cached. If you change the code below in any way, I suggest deleting the cache directory and recomputing.

Chinese RC example (power analysis):

```
dat<-subset(gw,region=="headnoun")</pre>
## maximal model; switch off warnings, and ignore the correlations,
## which were not estimable.
m<-lmer(rt~cond+(1+cond|subj)+(1+cond|item),dat,</pre>
        control=lmerControl(calc.derivs=FALSE))
## function for extracting all parameter estimates:
extract_parests_lmer<-function(</pre>
  mod=m) {
  alpha<-summary(mod)$coefficients[1,1]</pre>
  beta<-summary(mod)$coefficients[2,1]</pre>
## extract standard deviation estimate:
sigma_e<-attr(VarCorr(mod), "sc")</pre>
## assemble variance covariance matrix for subjects and items:
subj_ranefsd<-attr(VarCorr(mod)$subj,"stddev")</pre>
sigma_u0<-subj_ranefsd[1]</pre>
sigma_u1<-subj_ranefsd[2]</pre>
item_ranefsd<-attr(VarCorr(mod)$item, "stddev")</pre>
sigma_w0<-item_ranefsd[1]</pre>
sigma_w1<-item_ranefsd[2]</pre>
## return list of params:
list(alpha=alpha,beta=beta,sigma_e=sigma_e,
     sigma u0=sigma u0,sigma u1=sigma u1,
     sigma_w0=sigma_w0,sigma_w1=sigma_w1)
}
parest<-extract_parests_lmer(mod=m)</pre>
```

Demonstrating Type M error

```
compute_typem<-function(nsim=100,</pre>
                         alpha=parest$alpha,
                         beta=parest$beta,
                         sigma_e=parest$sigma_e,
                         sigma u0=parest$sigma u0,
                         sigma_u1=parest$sigma_u1,
                 sigma_w0=parest$sigma_w0,
                         sigma_w1=parest$sigma_w1,
                         nsubj=40,
                         nitem=16){
beta_est<-tvals<-c()</pre>
for(i in 1:nsim){
fakedat<-gen_fake_norm(nitem=nitem,</pre>
                        nsubj=nsubj,
                alpha=alpha,
                beta=beta,
                sigma u0=sigma u0,
                sigma_u1=sigma_u1,
                sigma_w0=sigma_w0,
                sigma_w1=sigma_w1,
```

```
sigma_e=sigma_e)
m<-lmer(rt~cond+(1+cond||subj)+(1+cond||item),</pre>
        fakedat,
        control=lmerControl(calc.derivs=FALSE))
tvals[i] <-summary(m)$coefficients[2,3]</pre>
beta_est[i] <-summary(m)$coefficients[2,1]</pre>
}
beta_est[which(abs(tvals)>2)]
## ----effectestimates, echo=FALSE--
beta_estimates<-compute_typem(beta=120)</pre>
propoverestimated<-round(mean(beta_estimates>120),2)
inflation <- beta_estimates/120
beta_estimates60<-compute_typem(beta=60)</pre>
propoverestimated60<-round(mean(beta_estimates60>60),2)
inflation60<-beta_estimates60/60
## ----ploteffectestimates,echo=FALSE,cache=TRUE,fig.height=3,fig.width=3----
hist(beta_estimates,main="effect estimates",xlab="",freq=FALSE)
abline(v=120,lwd=2)
```

effect estimates

