Supplementary materials for

> Baayen, Vasishth, Kliegl, and Bates (2016), The cave of shadows: addressing the human factor with generalized additive mixed models. *Journal of Memory and Language.*

This document describes how data sets discussed in this paper can be obtained, and presents the R-code for the models and corresponding figures and tables.

Required software: R (>= 3.2.2) and R packages `devtools` (1.9.1 or later), `itsadug` (2.2 or later), `lattice` (0.20-33 or later), `lme4` (1.1-10 or later), `plotfunctions` (1.0 or later), `mgcv` (1.8-12 or later), `Rcurl` (1.95-4.7 or later), and `xtable` (1.7-4 or later).

Contents

1 Preliminaries

Once `R` is started up, the abovementioned packages must be activated. This accomplished in the following code snippet:

```
require(mgcv)
require(lme4)
require(xtable)
require(itsadug)
require(plotfunctions)
require(devtools)
require(RCurl)
require(RePsychLing)
```

The `RePsychLing` package is currently available on `github`. It is installed and made available as follows:

```
devtools::install_github("dmbates/RePsychLing",build_vignettes=FALSE)
require(RePsychLing)
```

All data sets analysed in this document are available in the `RePsychLing` package, with the exception of the `baldey` dataset, which is available at http://www.mirjamernestus.nl/Ernestus/Baldey/baldey_data.zip. After downloading and unpacking the zip file in a subfolder named `data`, the database can be loaded into `R`.

```
baldey = read.table("data/baldey.txt", header=TRUE)
```

One figure requires R code available on github:

```
source(textConnection(getURL(
"https://gist.github.com/mages/5339689/raw/576263b8f0550125b61f4ddba127f5aa00fa2014/add.alpha.R")))
```

Generalized additive models for the larger data sets (`baldey`, `poems`) may take up to several hours to fit.

The R code and R output given below make it possible to replicate all results reported in our manuscript, including tables and figures. Technical details on the figures illustrating regression splines in section 2 of the manuscript are not included as they are not part of actual data analysis.

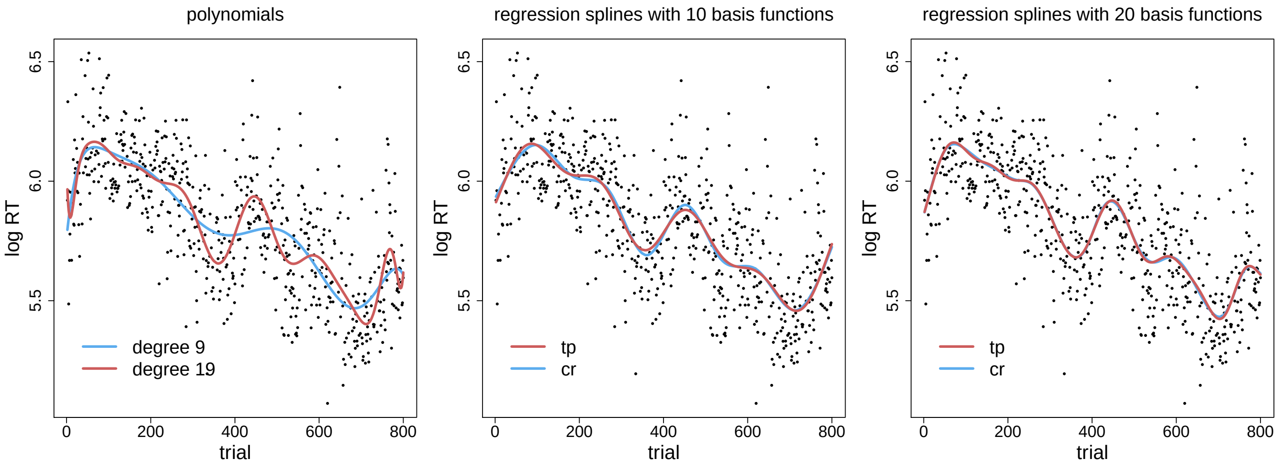
2 Introduction to the generalized additive mixed model

2.1 Figure 1

```
data("KKL")
dfr123 = KKL[KKL$subj==123,]

# set up one row of three plots
par(mfrow=c(1,3), oma=c(2,2,2,2), mar=c(5,5,2,1))

# two regression models with polynomials
poly10.lm = lm(lrt ~ poly(trial,9), data = dfr123)
poly20.lm = lm(lrt ~ poly(trial,19), data = dfr123)

# make left panel
cx=1.8
plot(dfr123$trial,  dfr123$lrt,
     pch=19, cex=0.5, cex.lab=cx+0.3, cex.axis=cx,
     xlab="trial", ylab="log RT")
lines(dfr123$trial, predict(poly10.lm),
     col="steelblue2", lwd=3, lty=1)
lines(dfr123$trial, predict(poly20.lm),
     col="indianred", lwd=3, lty=1)
mtext("polynomials", 3, 1.5, cex=cx-0.5)
legend(0.1, 5.4,
     legend = c("degree 9", "degree 19"),
     lty = rep(1, 2), lwd = rep(3,3),
     col = c("steelblue2", "indianred"), bty = "n", cex = cx+0.2)

# regression splines with 10 basis functions
dfr123.gam     = bam(lrt ~ s(trial, bs="cr", k=10),
                     data = dfr123, method="fREML")
dfr123$GamCR   = predict(dfr123.gam)
dfr123.gamTPRS = bam(lrt ~ s(trial, m=2, bs="tp", k=10),
                     data = dfr123, method="fREML")
dfr123$GamTPRS = predict(dfr123.gamTPRS)

# make center panel
plot(dfr123$trial,  dfr123$lrt,
     pch=19, cex=0.5,cex.lab=cx+0.3, cex.axis=cx,
     xlab="trial", ylab="log RT")
lines(dfr123$trial, dfr123$GamCR,
     col="steelblue2", lwd=3)
lines(dfr123$trial, dfr123$GamTPRS,
     col="indianred", lwd=3)
legend(0.1, 5.4,
     legend=rev(c("cr", "tp")),
     lty=rep(1, 2), lwd=rep(3,2),
     col=c("indianred", "steelblue2"), bty="n", cex=cx+0.2)
mtext("regression splines with 10 basis functions", 3, 1.5, cex=cx-0.5)

# regression splines with 20 basis functions
```

```
dfr123.gam      = bam(lrt ~ s(trial, bs="cr", k=20),
                       data=dfr123, method="fREML")
dfr123$GamCR    = predict(dfr123.gam)
dfr123.gamTPRS = bam(lrt ~ s(trial, m=2, bs="tp", k=20),
                       data=dfr123, method="fREML")
dfr123$GamTPRS = predict(dfr123.gamTPRS)

# make right panel
plot(dfr123$trial,  dfr123$lrt,
     pch=19, cex=0.5, cex.lab=cx+0.3, cex.axis=cx,
     xlab="trial", ylab="log RT")
lines(dfr123$trial, dfr123$GamCR,
     col="steelblue2", lwd=3)
lines(dfr123$trial, dfr123$GamTPRS,
     col="indianred", lwd=3)
mtext("regression splines with 20 basis functions", 3, 1.5, cex=cx-0.5)
legend(0.1, 5.4,
     legend=rev(c("cr", "tp")),
     lty=rep(1, 2), lwd=rep(3,2),
     col=c("indianred", "steelblue2"), bty="n", cex=cx+0.2)
```

Figure 1



AIC values for the models discussed with respect to Figure 1.

```
# a model with a linear effect of trial
AIC(lm(lrt  ~ trial, data=dfr123))

[1] -206.4587

# the models with polynomials
AIC(lm(lrt  ~ poly(trial, 9), data=dfr123))
```

```
[1] -274.739

AIC(lm(lrt  ~ poly(trial, 19), data=dfr123))

[1] -332.2674

# the models with restricted cubic splines
AIC(bam(lrt ~ s(trial, bs="cr", k=10), data=dfr123, method="fREML"))

[1] -316.748

AIC(bam(lrt ~ s(trial, bs="cr", k=20), data=dfr123, method="fREML"))

[1] -331.5204

# the models with thin plate regression splines
AIC(bam(lrt ~ s(trial, bs="tp", k=10), data=dfr123, method="fREML"))

[1] -311.4005

AIC(bam(lrt ~ s(trial, bs="tp", k=20), data=dfr123, method="fREML"))

[1] -334.0553
```

Comparison of restricted cubic splines with 10 and 20 basis functions.

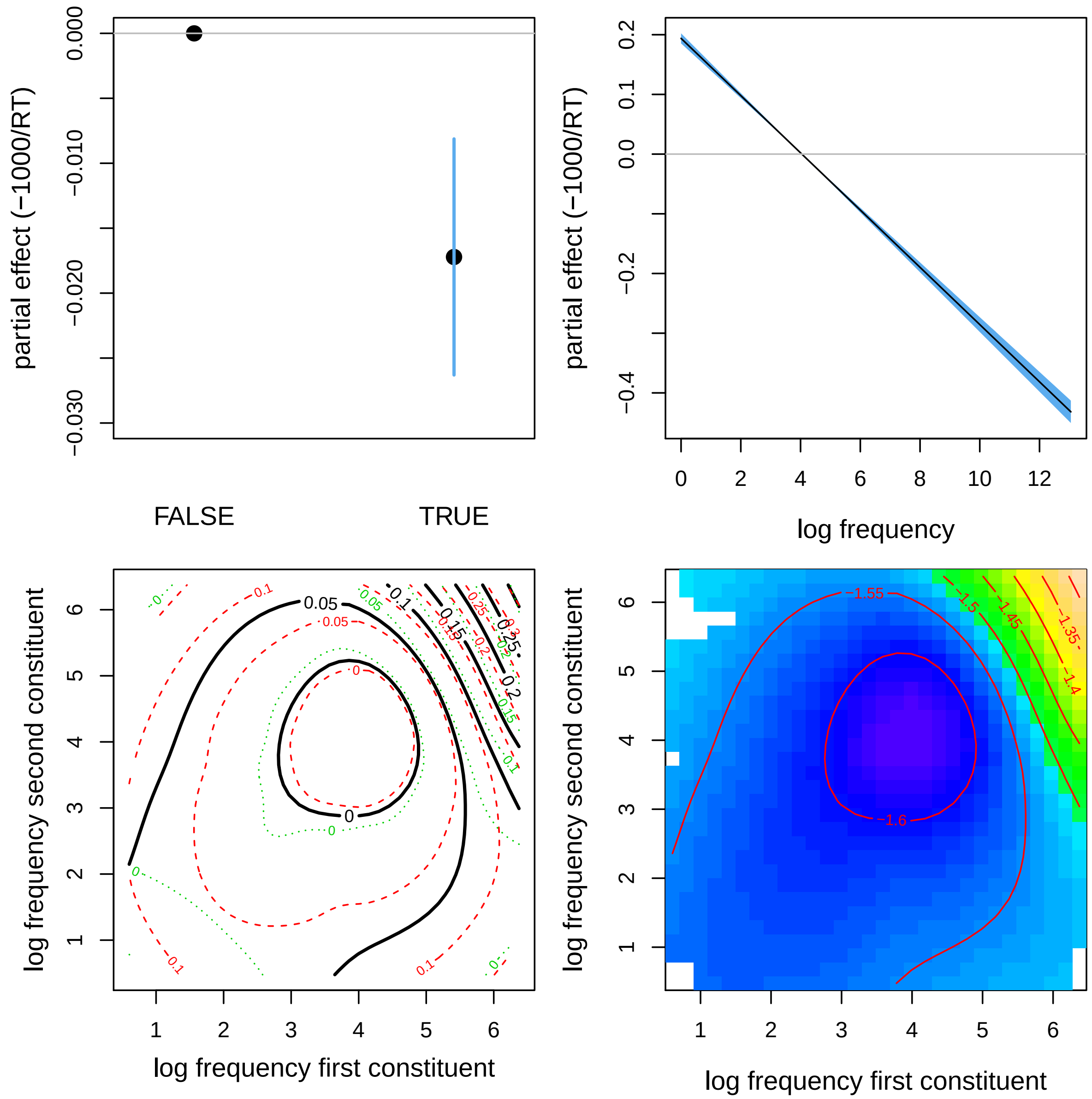
```
dfr123.10 = bam(lrt ~ s(trial, k=10), data=dfr123, method="fREML")
dfr123.20 = bam(lrt ~ s(trial, k=20), data=dfr123, method="fREML")
anova(dfr123.10, dfr123.20, test="F")

Analysis of Deviance Table

Model 1: lrt ~ s(trial, k = 10)
Model 2: lrt ~ s(trial, k = 20)
  Resid. Df Resid. Dev     Df Deviance      F    Pr(>F)
1    624.36     21.944
2    618.58     20.778 5.7799   1.1664 6.0082 5.676e-06
```

2.2 Figure 5 and the model for the `vietnamese` dataset

```
data(vietnamese)

# a GAM for this single-subject data set
vietnamese.gam = bam(RTinv ~ MidLevelTone +
                             s(LogFreq) +
                             te(LogFreqSyl1, LogFreqSyl2),
                             data=vietnamese, method="ML")
# a summary of the parametric part of the model
summary(vietnamese.gam)$p.table
# a summary of the smooths in the model
summary(vietnamese.gam)$s.table
```

```
# the corresponding figure
par(mfrow = c(2,2), mar = c(4,4,1,1))
plot(c(0.5,2.5), c(0, -0.017215), xlim=c(0, 3), ylim=c(-0.03, 0), xaxt="n",
     xlab=" ", ylab="partial effect (-1000/RT)", pch=19, cex=1.5)
abline(h=0, col="gray")
lines(c(2.5, 2.5), c(-0.017215+2*0.004544, -0.017215-2*0.004544), lwd=2, col="steelblue2")
mtext(c("FALSE", "TRUE"), side=1, line=2.5, at=c(0.5, 2.5))

plot(vietnamese.gam, select=1, scheme=1, shade.col="steelblue2", rug=FALSE,
     xlab="log frequency", ylab="partial effect (-1000/RT)")
abline(h=0, col="gray")
plot(vietnamese.gam, select=2, rug=FALSE,
        xlab="log frequency first constituent", ylab="log frequency second constituent",
        main=" ")
vis.gam(vietnamese.gam, view=c("LogFreqSyl1", "LogFreqSyl2"),
        color="topo", plot.type="contour", too.far=0.1,
        xlab="log frequency first constituent", ylab="log frequency second constituent",
        main=" ")
```

Figure 5.


partial effect (−1000/RT)
0.000
−0.010
−0.020
−0.030
FALSE
TRUE
partial effect (−1000/RT)
0.2
0.1
0.0
−0.2
−0.4
0
2
4
6
8
10
12
log frequency
log frequency second constituent
1
2
3
4
5
6
log frequency first constituent
0.05
0
0.1
0.15
0.2
0.25
log frequency second constituent
log frequency first constituent
−1.55
−1.6
−1.5
−1.45
−1.4
−1.35

3 The `KKL` dataset

3.1 Table 1 (main text) and Table 3 (appendix)

```
data(KKL)
# identify starting point for time series of RTs
KKL$FirstTrial = KKL$first==1
# scale trial and soa
KKL$Trial = scale(KKL$trial)
KKL$Soa  = scale(KKL$SOA)
# add a quadratic term for trial
KKL$TrialQ = KKL$Trial^2
# define interaction of size by orientation
KKL$Int = interaction(KKL$size, KKL$cardinal)
```

A sequence of linear mixed models and pairwise likelihood ratio tests:

```
kkl.lmer0 = lmer(lrt ~ sze * (spt + obj + grv) * orn +
                 (1|subj)+
                 (0+spt|subj)+
                 (0+grv|subj)+
                 (0+obj|subj)+
                 (0+orn|subj)+
                 (0+spt_orn|subj)+
                 poly(Soa,2,raw=TRUE),
                 data=KKL, REML=FALSE)

fixed-effect model matrix is rank deficient so dropping 3 columns / coefficients

# add in Trial and its interactios with sze and orn
kkl.lmer1 = lmer(lrt ~ sze * (spt + obj + grv) * orn +
                 (1|subj)+
                 (0+spt|subj)+
                 (0+grv|subj)+
                 (0+obj|subj)+
                 (0+orn|subj)+
                 (0+spt_orn|subj)+
                 Trial*(sze+orn)+
                 poly(Soa,2,raw=TRUE),
                 data=KKL, REML=FALSE)

fixed-effect model matrix is rank deficient so dropping 3 columns / coefficients

anova(kkl.lmer0, kkl.lmer1)

Data: KKL
Models:
kkl.lmer0: lrt ~ sze * (spt + obj + grv) * orn + (1 | subj) + (0 + spt |
kkl.lmer0:     subj) + (0 + grv | subj) + (0 + obj | subj) + (0 + orn |
kkl.lmer0:     subj) + (0 + spt_orn | subj) + poly(Soa, 2, raw = TRUE)
kkl.lmer1: lrt ~ sze * (spt + obj + grv) * orn + (1 | subj) + (0 + spt |
kkl.lmer1:     subj) + (0 + grv | subj) + (0 + obj | subj) + (0 + orn |
kkl.lmer1:     subj) + (0 + spt_orn | subj) + Trial * (sze + orn) + poly(Soa,
kkl.lmer1:     2, raw = TRUE)
```

```
          Df    AIC    BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
kkl.lmer0 25 -25088 -24865  12569   -25138
kkl.lmer1 28 -25885 -25636  12970   -25941 802.96      3  < 2.2e-16

# add in quadratic effect of Trial
kkl.lmer2 = lmer(lrt ~ sze * (spt + obj + grv) * orn +
                 (1|subj)+
                 (0+spt|subj)+
                 (0+grv|subj)+
                 (0+obj|subj)+
                 (0+orn|subj)+
                 (0+spt_orn|subj)+
                 Trial*(sze+orn)+
                 TrialQ*(sze+orn)+
                 poly(Soa,2,raw=TRUE),
                 data=KKL, REML=FALSE)

fixed-effect model matrix is rank deficient so dropping 3 columns / coefficients

anova(kkl.lmer1, kkl.lmer2)

Data: KKL
Models:
kkl.lmer1: lrt ~ sze * (spt + obj + grv) * orn + (1 | subj) + (0 + spt |
kkl.lmer1:     subj) + (0 + grv | subj) + (0 + obj | subj) + (0 + orn |
kkl.lmer1:     subj) + (0 + spt_orn | subj) + Trial * (sze + orn) + poly(Soa,
kkl.lmer1:     2, raw = TRUE)
kkl.lmer2: lrt ~ sze * (spt + obj + grv) * orn + (1 | subj) + (0 + spt |
kkl.lmer2:     subj) + (0 + grv | subj) + (0 + obj | subj) + (0 + orn |
kkl.lmer2:     subj) + (0 + spt_orn | subj) + Trial * (sze + orn) + TrialQ *
kkl.lmer2:     (sze + orn) + poly(Soa, 2, raw = TRUE)
          Df    AIC    BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
kkl.lmer1 28 -25885 -25636  12970   -25941
kkl.lmer2 31 -26174 -25899  13118   -26236 295.77      3  < 2.2e-16

# and allow slope of Trial to vary by subject
kkl.lmer3 = lmer(lrt ~ sze * (spt + obj + grv) * orn +
                 (1+Trial|subj)+
                 (0+spt|subj)+
                 (0+grv|subj)+
                 (0+obj|subj)+
                 (0+orn|subj)+
                 (0+spt_orn|subj)+
                 Trial*(sze+orn)+
                 TrialQ*(sze+orn)+
                 poly(Soa,2,raw=TRUE),
                 data=KKL, REML=FALSE)

fixed-effect model matrix is rank deficient so dropping 3 columns / coefficients

anova(kkl.lmer2, kkl.lmer3)

Data: KKL
Models:
kkl.lmer2: lrt ~ sze * (spt + obj + grv) * orn + (1 | subj) + (0 + spt |
```

```
kkl.lmer2:     subj) + (0 + grv | subj) + (0 + obj | subj) + (0 + orn |
kkl.lmer2:     subj) + (0 + spt_orn | subj) + Trial * (sze + orn) + TrialQ *
kkl.lmer2:     (sze + orn) + poly(Soa, 2, raw = TRUE)
kkl.lmer3: lrt ~ sze * (spt + obj + grv) * orn + (1 + Trial | subj) + (0 +
kkl.lmer3:     spt | subj) + (0 + grv | subj) + (0 + obj | subj) + (0 +
kkl.lmer3:     orn | subj) + (0 + spt_orn | subj) + Trial * (sze + orn) +
kkl.lmer3:     TrialQ * (sze + orn) + poly(Soa, 2, raw = TRUE)
          Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
kkl.lmer2 31 -26174 -25899  13118   -26236
kkl.lmer3 33 -26989 -26696  13528   -27055 818.5      2  < 2.2e-16

# show the model (Table 3 in the manuscript)
print(summary(kkl.lmer3),corr=FALSE)

Linear mixed model fit by maximum likelihood  ['lmerMod']
Formula: lrt ~ sze * (spt + obj + grv) * orn + (1 + Trial | subj) + (0 +
    spt | subj) + (0 + grv | subj) + (0 + obj | subj) + (0 +
    orn | subj) + (0 + spt_orn | subj) + Trial * (sze + orn) +
    TrialQ * (sze + orn) + poly(Soa, 2, raw = TRUE)
   Data: KKL

     AIC      BIC   logLik deviance df.resid
-26988.9 -26695.5  13527.5 -27054.9    53732

Scaled residuals:
    Min      1Q  Median      3Q     Max
-5.2071 -0.6203 -0.0982  0.5029  6.4808

Random effects:
 Groups   Name        Variance  Std.Dev. Corr
 subj     (Intercept) 0.0261682 0.16177
          Trial       0.0026194 0.05118  -0.27
 subj.1   spt         0.0044635 0.06681
 subj.2   grv         0.0011434 0.03381
 subj.3   obj         0.0006558 0.02561
 subj.4   orn         0.0058135 0.07625
 subj.5   spt_orn     0.0011040 0.03323
 Residual             0.0344439 0.18559
Number of obs: 53765, groups:  subj, 86

Fixed effects:
                             Estimate Std. Error t value
(Intercept)                 5.659e+00  1.753e-02   322.9
sze                         1.843e-01  3.501e-02     5.3
spt                         7.408e-02  7.698e-03     9.6
obj                         4.259e-02  4.524e-03     9.4
grv                        -8.957e-04  5.122e-03    -0.2
orn                         1.375e-02  9.109e-03     1.5
Trial                      -4.299e-02  5.755e-03    -7.5
TrialQ                      1.532e-02  9.031e-04    17.0
poly(Soa, 2, raw = TRUE)1.0 -1.009e-02  8.036e-04   -12.6
poly(Soa, 2, raw = TRUE)2.0  1.853e-02  8.991e-04    20.6
sze:spt                     4.837e-02  1.540e-02     3.1
sze:obj                    -1.177e-02  9.048e-03    -1.3
```

```
sze:grv                     -3.750e-02  1.024e-02    -3.7
sze:orn                      3.931e-02  1.785e-02     2.2
spt:orn                      2.028e-02  6.499e-03     3.1
obj:orn                      9.050e-03  7.168e-03     1.3
grv:orn                      1.093e-02  7.192e-03     1.5
sze:Trial                    1.835e-02  1.145e-02     1.6
orn:Trial                    2.785e-02  3.225e-03     8.6
sze:TrialQ                  -9.166e-05  1.790e-03    -0.1
orn:TrialQ                  -6.078e-03  4.794e-03    -1.3
sze:spt:orn                 -1.425e-02  1.300e-02    -1.1
sze:obj:orn                 -3.466e-03  1.434e-02    -0.2
sze:grv:orn                 -4.680e-02  1.438e-02    -3.3
fit warnings:
fixed-effect model matrix is rank deficient so dropping 3 columns / coefficients
```

The summary of `kkl.lmer3` is reported as **Table 3** in the Appendix. The above log likelihood ratio tests are summarized in **Table 1**.

3.2 Table 4 (appendix)

Table 4 (in the appendix) reports the summary of the following GAMM:

```
kkl.gamD = bam(lrt ~ sze * (spt + obj + grv) * orn +
                        s(Trial, subj, bs="fs", m=1)+
                        s(subj, spt, bs="re") +
                        s(subj, grv, bs="re") +
                        s(subj, obj, bs="re") +
                        s(subj, orn, bs="re") +
                        s(subj, spt_orn, bs="re") +
                        s(Trial, by=Int)+
                        s(Soa),
                        AR.start=FirstTrial, rho=0.15,
                  data=KKL, method="fREML", discrete=TRUE)
summary(kkl.gamD)
```

```
Family: gaussian
Link function: identity

Formula:
lrt ~ sze * (spt + obj + grv) * orn + s(Trial, subj, bs = "fs",
    m = 1) + s(subj, spt, bs = "re") + s(subj, grv, bs = "re") +
    s(subj, obj, bs = "re") + s(subj, orn, bs = "re") + s(subj,
    spt_orn, bs = "re") + s(Trial, by = Int) + s(Soa)

Parametric coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  5.6850584  0.0189221 300.445  < 2e-16
sze          0.1839522  0.0378441   4.861 1.17e-06
spt          0.0729251  0.0079223   9.205  < 2e-16
obj          0.0410758  0.0041140   9.984  < 2e-16
grv         -0.0004952  0.0049377  -0.100 0.920111
orn          0.0374653  0.0141694   2.644 0.008193
sze:spt      0.0482519  0.0158446   3.045 0.002326
sze:obj     -0.0088449  0.0082283  -1.075 0.282407
sze:grv     -0.0366134  0.0098757  -3.707 0.000210
sze:orn      0.0095644  0.0283388   0.338 0.735741
spt:orn      0.0213368  0.0063789   3.345 0.000824
obj:orn      0.0082761  0.0068235   1.213 0.225181
grv:orn      0.0077985  0.0068488   1.139 0.254848
sze:spt:orn -0.0097831  0.0127578  -0.767 0.443181
sze:obj:orn -0.0075086  0.0136470  -0.550 0.582183
sze:grv:orn -0.0482719  0.0136977  -3.524 0.000425

Approximate significance of smooth terms:
                             edf  Ref.df       F  p-value
s(Trial,subj)            557.867 774.000 661.847  < 2e-16
s(spt,subj)               77.793  86.000  31.591  < 2e-16
s(grv,subj)               47.606  84.000   2.164 1.82e-10
s(obj,subj)               29.571  84.000   1.340  0.00114
s(orn,subj)               44.080  84.000   1.148  < 2e-16
s(spt_orn,subj)           47.373  84.000   1.315 1.68e-10
```

```
s(Trial):Intbig.cardinal     8.349   8.679  13.402  < 2e-16
s(Trial):Intsmall.cardinal   8.053   8.489   9.837 1.44e-14
s(Trial):Intbig.diagonal     5.887   6.574   5.856 8.00e-06
s(Trial):Intsmall.diagonal   7.997   8.453   8.862 6.39e-08
s(Soa)                       5.602   6.747 103.115  < 2e-16

R-sq.(adj) =  0.532   Deviance explained =   54%
fREML = -15136  Scale est. = 0.032571  n = 53765
```

```
AIC(kkl.gamD)

[1] -31890
```

3.3 Figure 9

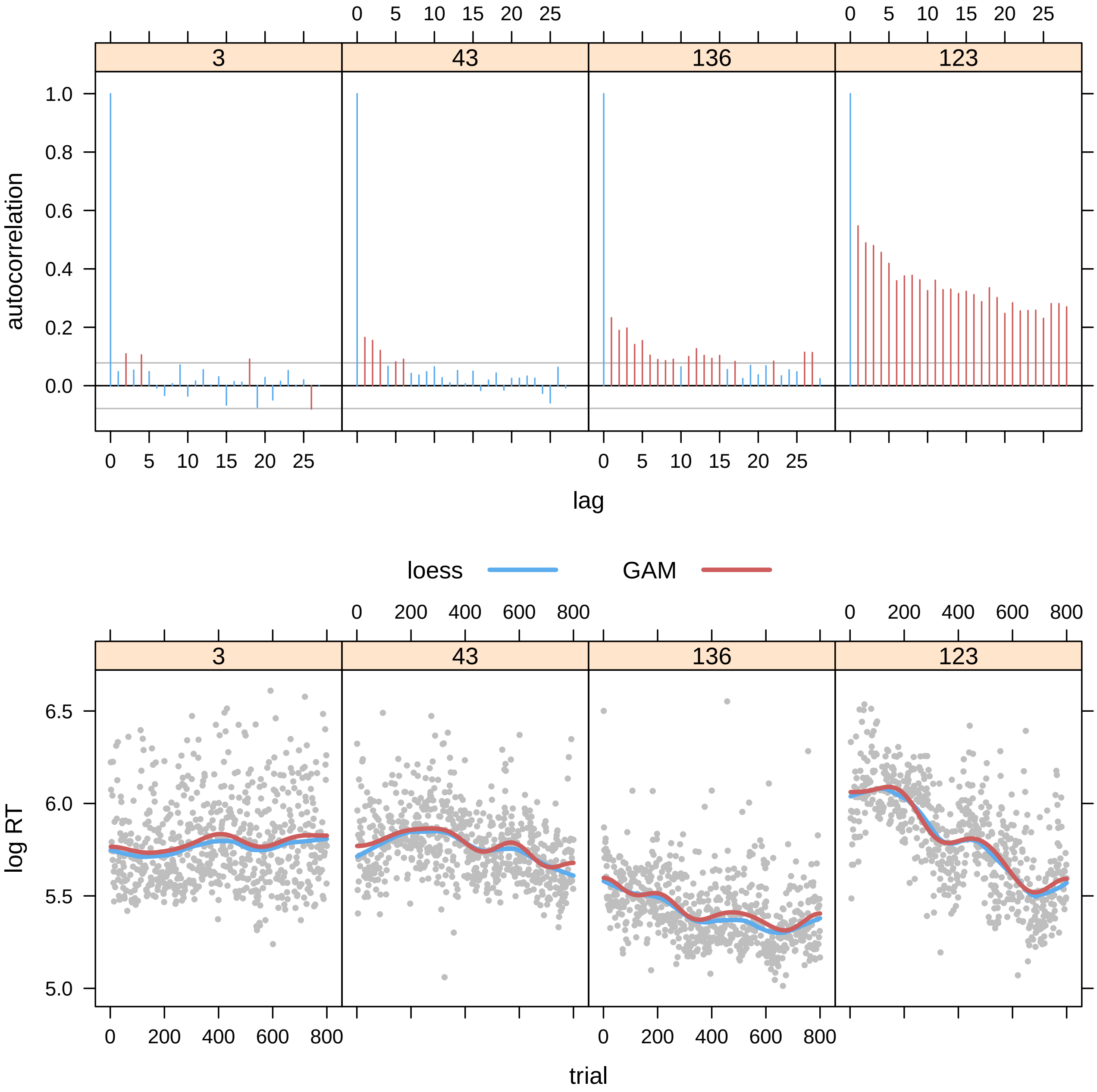
```r
# For Figure 9, we first define a function for acf plots with lattice
acfs = function(m=dat.gamA, s=selectedSubjects, mydata=dat, add_NA=FALSE,
                ci=0.95, rawplot=FALSE) {
  mydata$resids = resid(m)
  res = list()
  n.used = rep(0,length(s))
  for (i in 1:length(s)) {
    tmp = mydata[mydata$subj == s[i],]
    if (!add_NA) {
      x = acf(tmp$resids, plot=rawplot)
    } else {
      v = rep(NA, max(tmp$trial))
      v[tmp$trial] = tmp$resids
      x = acf(v, na.action=na.pass, plot=rawplot)
    }
    res[[i]] = data.frame(
      lag = x$lag,
      acf = x$acf,
      subj = factor(s[i]))
    n.used[i] = x$n.used
  }
  Dfr = do.call(rbind, res)

  civec = qnorm((1 + ci)/2)/sqrt(n.used)


  theplot = xyplot(acf ~ lag | subj, type = "h", data = Dfr, #col.line = "black",
    panel = function(x, y, subscripts, ...) {
      panel.abline(h = civec[panel.number()], col.line = "grey")
      panel.abline(h = -civec[panel.number()], col.line = "grey")
      panel.abline(h = 0, col.line = "black")
      d=Dfr[subscripts,]
      panel.xyplot(d$lag, d$acf,
        col=ifelse(abs(d$acf)>civec[panel.number()] & d$lag > 0,
                   "indianred", "steelblue2"),
                   ...)
    },
    #strip = strip.custom(bg = "grey90"),
    #par.strip.text = list(cex = 0.8),
    xlab="lag", ylab="autocorrelation",
    layout=c(4,1,1))

  return(list(vals=Dfr, plot=theplot))
}
# a LMM
kkl.lmer = lmer(lrt ~ sze * (spt + obj + grv) * orn +
                 (1|subj)+
                 (0+spt|subj)+
                 (0+grv|subj)+
                 (0+obj|subj)+
                 (0+orn|subj)+
```

```
                 (0+spt_orn|subj)+
                 poly(Soa,2,raw=TRUE), data=KKL, REML=FALSE)

# make plot for selected subjects
selectedSubjects = c(3, 43, 136, 123)
x = acfs(kkl.lmer, selectedSubjects, KKL)
print(x[[2]])  # this produces the plot
```

Figure 9, lower panels.

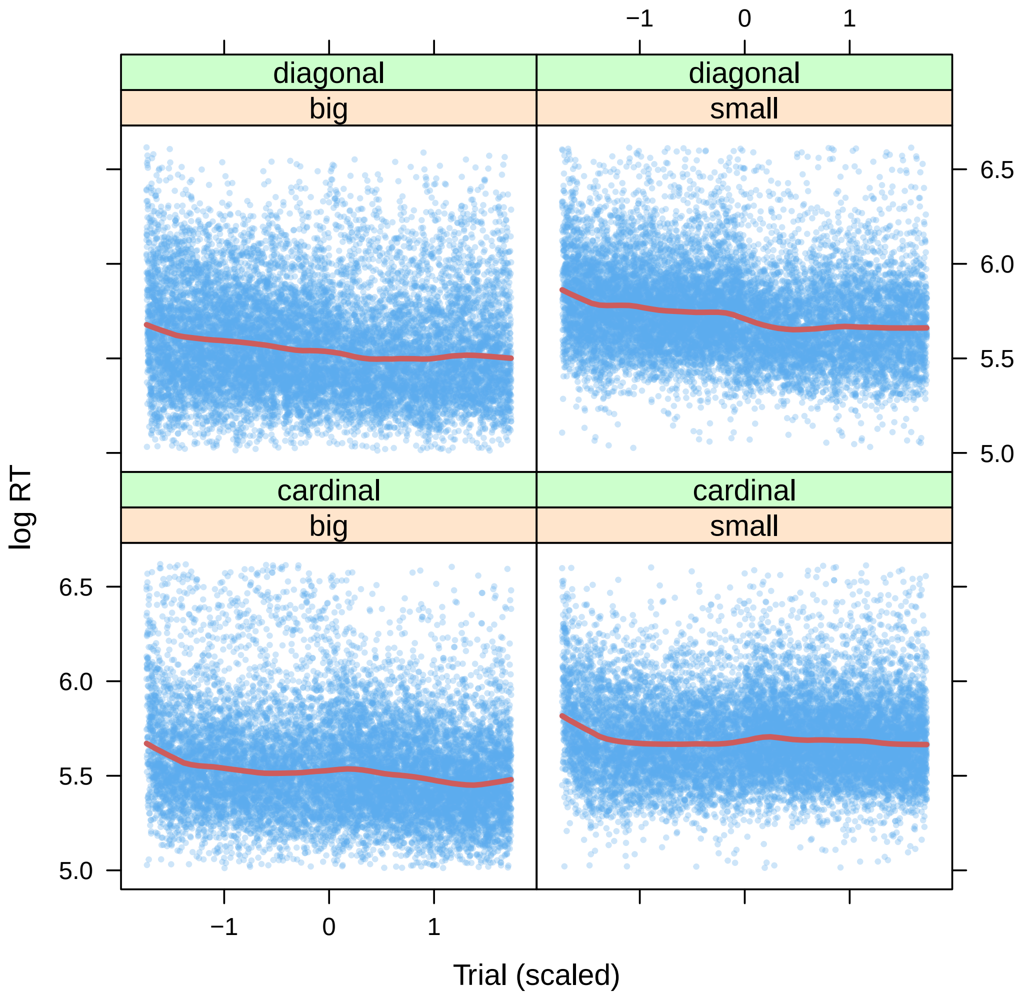
```
selectedSubjects = c(3, 43, 136, 123)
dfr = droplevels(KKL[KKL$subj %in% selectedSubjects,])
dfr$subj = ordered(dfr$subj, selectedSubjects)
dfr.gam = bam(lrt~1+s(trial, subj, bs="fs", m=1), data=dfr, method="fREML")
dfr$Gam = predict(dfr.gam)

keys = list(space="top", text=list(c("loess", "GAM")), columns=2,
            lines=list(lty=c(1,1), col=c("steelblue2", "indianred"), lwd=3))
xyplot(lrt ~ trial | subj, data = dfr, #col.line = "indianred",
  panel = function(x, y, subscripts, ...) {
    panel.xyplot(x, y, pch=19, col="gray", cex=0.4, ...)
    panel.loess(x, y, lwd=3, span=0.3, col="steelblue2", ...)
    d = dfr[subscripts,]
    panel.lines(d$trial, d$Gam, col="indianred", lwd=3)
  },
  #strip = strip.custom(bg = "grey90"),
  #par.strip.text = list(cex = 0.8),
  xlab="trial", ylab="log RT",
  layout=c(4,1,1),
  key=keys)
```

Figure 9.


3
43
136
123
autocorrelation
1.0
0.8
0.6
0.4
0.2
0.0
0 5 10 15 20 25
lag
loess
GAM
log RT
6.5
6.0
5.5
5.0
0 200 400 600 800
trial

3.4 Figure 10

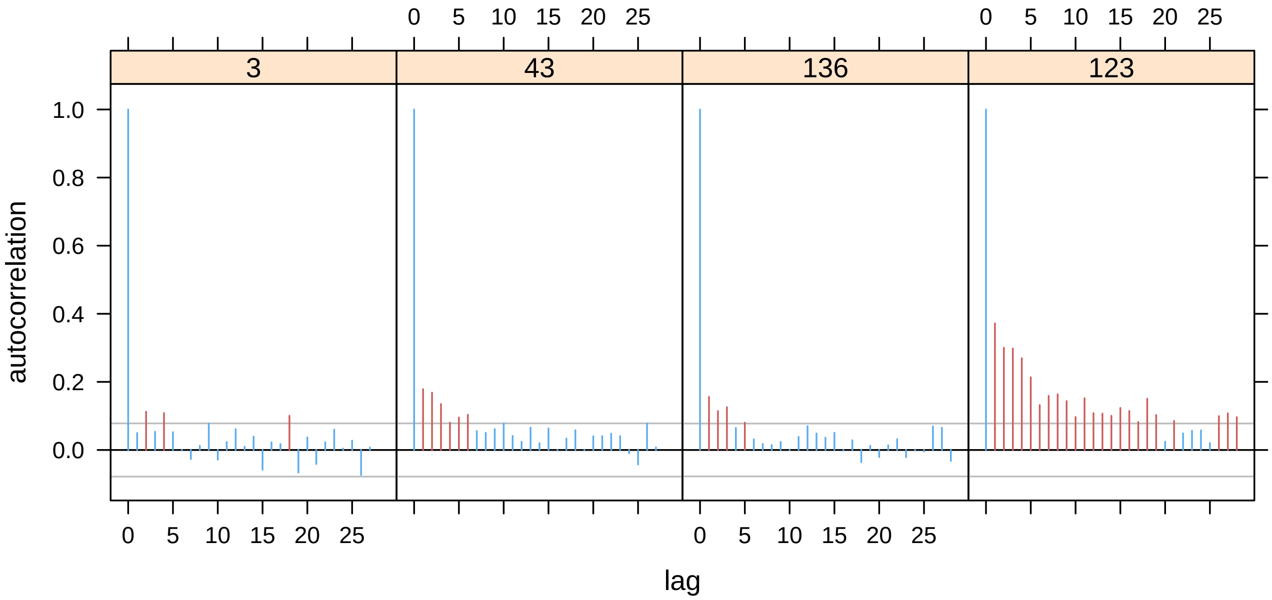
```r
selectedSubjects = c(3, 43, 136, 123)
myColor="steelblue2"
add.alpha <- function(col=NULL, alpha=1){
  if(missing(col)) stop("Please provide a vector of colours.")
  apply(sapply(col, col2rgb)/255, 2,
        function(x) rgb(x[1], x[2], x[3], alpha=alpha))
}

myColorAlpha = add.alpha(myColor, alpha=0.3)

xyplot(lrt~Trial|size+cardinal, data=KKL, type=c("p", "smooth"),span=0.2,
       col.line="indianred", cex=0.3, pch=19, col=myColorAlpha, lwd=3,
       xlab="Trial (scaled)", ylab="log RT")
```



3.5 Figure 11

```
x = acfs(kkl.lmer3, selectedSubjects, KKL)
print(x[[2]])
```

```
load("models/kkl.lmer3.rda")
x = acfs(kkl.lmer3, selectedSubjects, KKL)
pdf("figs/Figure11.pdf", he=4, wi=8)
print(x[[2]])
dev.off()
```

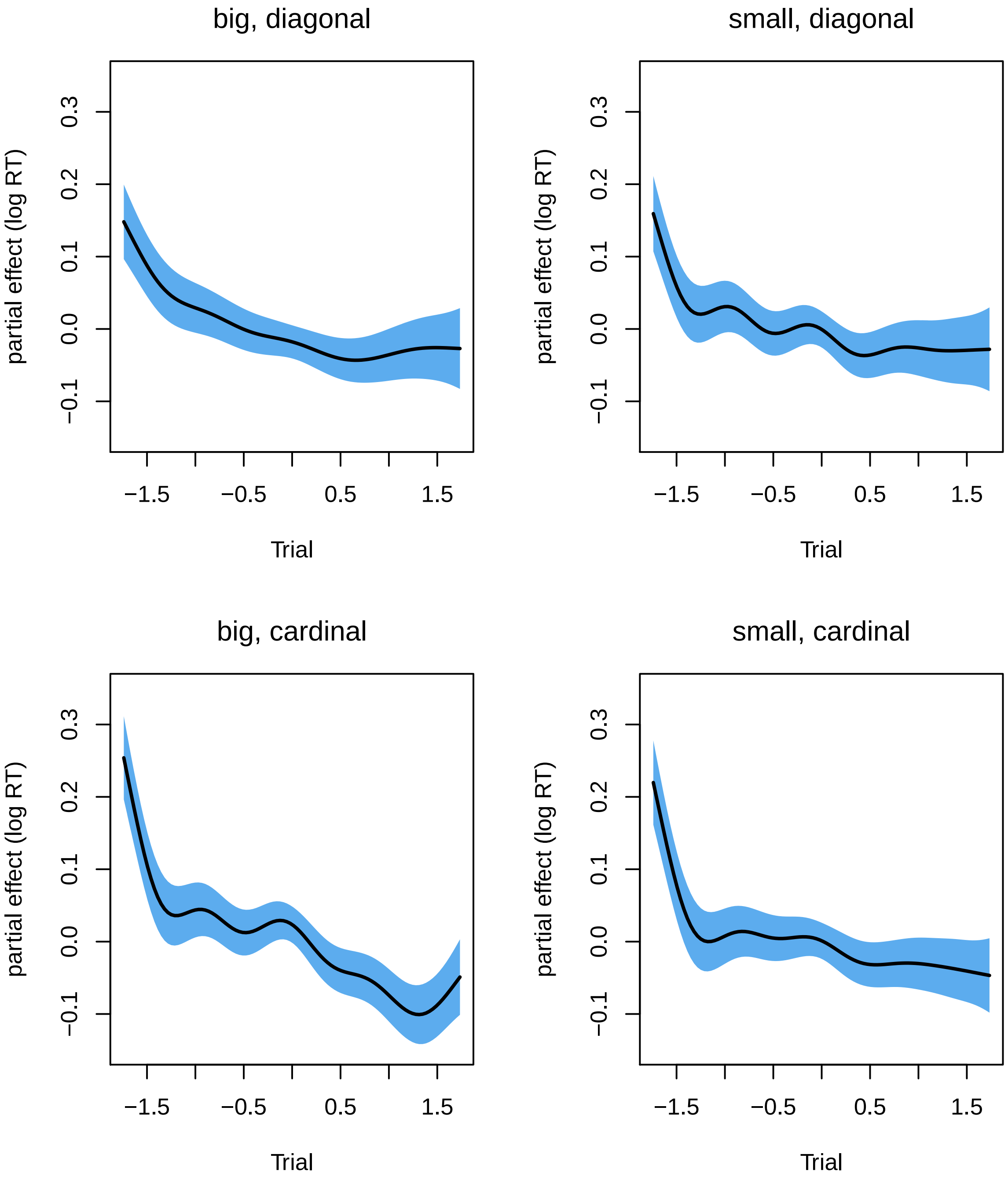


3.6 Figure 12

```
par(mfrow=c(2,2),mar=c(5,5,3,1),oma=rep(2,4))
ylimit=c(-0.15, 0.35)
plot(kkl.gamD, select=7, rug=F, ylim=ylimit, scheme=1,
     xlab="Trial", ylab="partial effect (log RT)",
     shade.col="steelblue2", col="indianred", lwd=2)
mtext("big, cardinal", 3, 1.0)
plot(kkl.gamD, select=8, rug=F, ylim=ylimit, scheme=1,
     xlab="Trial", ylab="partial effect (log RT)",
     shade.col="steelblue2", col="indianred", lwd=2)
mtext("small, cardinal", 3, 1.0)
plot(kkl.gamD, select=9, rug=F, ylim=ylimit, scheme=1,
     xlab="Trial", ylab="partial effect (log RT)",
     shade.col="steelblue2", col="indianred", lwd=2)
mtext("big, diagonal", 3, 1.0)
plot(kkl.gamD, select=10, rug=F, ylim=ylimit, scheme=1,
     xlab="Trial", ylab="partial effect (log RT)",
     shade.col="steelblue2", col="indianred", lwd=2)
mtext("small, diagonal", 3, 1.0)
```

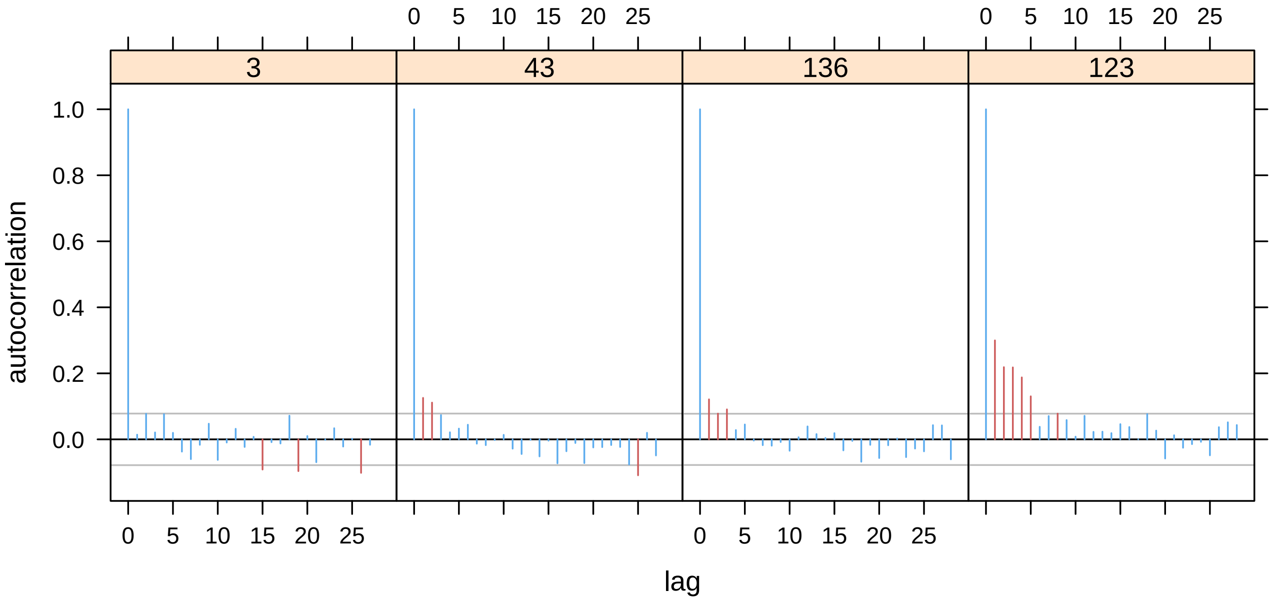
```
pdf("figs/Figure12.pdf", he=8,wi=7)
par(mfrow=c(2,2),mar=c(5,5,3,1),oma=rep(2,4))
ylimit=c(-0.15, 0.35)
plot(kkl.gamD, select=9, rug=F, ylim=ylimit, scheme=1,
     xlab="Trial", ylab="partial effect (log RT)",
     shade.col="steelblue2", col="indianred", lwd=2)
mtext("big, diagonal", 3, 1.0)
plot(kkl.gamD, select=10, rug=F, ylim=ylimit, scheme=1,
     xlab="Trial", ylab="partial effect (log RT)",
     shade.col="steelblue2", col="indianred", lwd=2)
mtext("small, diagonal", 3, 1.0)
plot(kkl.gamD, select=7, rug=F, ylim=ylimit, scheme=1,
     xlab="Trial", ylab="partial effect (log RT)",
     shade.col="steelblue2", col="indianred", lwd=2)
mtext("big, cardinal", 3, 1.0)
plot(kkl.gamD, select=8, rug=F, ylim=ylimit, scheme=1,
     xlab="Trial", ylab="partial effect (log RT)",
     shade.col="steelblue2", col="indianred", lwd=2)
mtext("small, cardinal", 3, 1.0)

dev.off()
```

Figure 12.


big, diagonal
small, diagonal
big, cardinal
small, cardinal
partial effect (log RT)
−0.1
0.0
0.1
0.2
0.3
−1.5
−0.5
0.5
1.5
Trial

3.7 Figure 13

```
x = acfs(kkl.gamD, selectedSubjects, KKL)
print(x[[2]])
```



3.8 Table 2

Table 2 is based on the following models:

```
# reference model
kkl.ref.gam <- bam(lrt ~ sze * (spt + obj + grv) * orn +
                         s(subj, bs="re") +
                         s(subj, spt, bs="re") +
                         s(subj, grv, bs="re") +
                         s(subj, obj, bs="re") +
                         s(subj, orn, bs="re") +
                         s(subj, spt_orn, bs="re") +
                         poly(Soa,2,raw=TRUE),
                   data=KKL, method="fREML", discrete=TRUE)
# 'linear' model
kkl.lin.gam <- bam(lrt ~ sze * (spt + obj + grv) * orn +
                         s(subj, bs="re") +
                         s(subj, Trial, bs="re") +
                         s(subj, spt, bs="re") +
                         s(subj, grv, bs="re") +
                         s(subj, obj, bs="re") +
                         s(subj, orn, bs="re") +
                         s(subj, spt_orn, bs="re") +
                         Trial*(sze+orn)+
                         TrialQ*(sze+orn)+
                         poly(Soa,2,raw=TRUE),
                   data=KKL, method="fREML", discrete=TRUE)
# model with factor smooths
kkl.fs.gam =    bam(lrt ~ sze * (spt + obj + grv) * orn +
                         s(Trial, subj, bs="fs", m=1)+
                         s(subj, spt, bs="re") +
                         s(subj, grv, bs="re") +
                         s(subj, obj, bs="re") +
                         s(subj, orn, bs="re") +
                         s(subj, spt_orn, bs="re") +
                         Trial*(sze+orn)+
                         TrialQ*(sze+orn)+
                         s(Soa),
                   data=KKL, method="fREML", discrete=TRUE)
# model with smooths for the interactions with trial
kkl.trial.gam = bam(lrt ~ sze * (spt + obj + grv) * orn +
                         s(Trial, subj, bs="fs", m=1)+
                         s(subj, spt, bs="re") +
                         s(subj, grv, bs="re") +
                         s(subj, obj, bs="re") +
                         s(subj, orn, bs="re") +
                         s(subj, spt_orn, bs="re") +
                         s(Trial, by=Int)+
                         s(Soa),
                    data=KKL, method="fREML", discrete=TRUE)
```

Model comparison was carried out with `compareML` from the `itsadug` package.

```
compareML(kkl.ref.gam, kkl.lin.gam)$table

        Model     Score Edf   Chisq    Df  p.value Sig.
1 kkl.ref.gam -12495.77  27
2 kkl.lin.gam -13422.25  34 926.484 7.000  < 2e-16  ***

compareML(kkl.lin.gam, kkl.fs.gam)$table

        Model     Score Edf Difference    Df p.value Sign.
1 kkl.lin.gam -13422.25  34
2  kkl.fs.gam -14500.08  31  -1077.822 3.000    <NA>

compareML(kkl.fs.gam, kkl.trial.gam)$table

          Model     Score Edf  Chisq    Df  p.value Sig.
1    kkl.fs.gam -14500.08  31
2 kkl.trial.gam -14582.64  33 82.565 2.000  < 2e-16  ***

AIC(kkl.ref.gam)

[1] -26009.55

AIC(kkl.lin.gam)

[1] -28047.29

AIC(kkl.fs.gam)

[1] -30876.72

AIC(kkl.trial.gam)

[1] -31040.29
```

These stats are brought together in Table 2.

4 The `baldey` dataset

4.1 Model and code for Table 5

For the `baldey` dataset, we restricted ourselves to correct responses to words.

```
baldey = droplevels(baldey[baldey$response=="correct" &
                    baldey$word_status=="word",])
```

A transform $-1000/RT$ for the reaction times brings a distribution with a strong rightward skew closer to normality. Outlier reaction times (less than 600 ms) are removed.

```
baldey = baldey[baldey$RT > 600,]    # 0.4% data loss
baldey$RTinv = -1000/baldey$RT
```

We add information about the initial trials for the subjects, and then scale trial.

```
mintrials = tapply(baldey$trial, baldey$subject, min)
baldey$MinTrial = mintrials[as.character(baldey$subject)]
baldey$AR.start = baldey$MinTrial==baldey$trial
```

We log-transform lemma frequency to avoid outlier effects of high-frequency ‘outliers’.

```
baldey$LemmaFreq = log(baldey$CELEX_lemma_freq+1)
```

After scaling predictors,

```
baldey$LemmaFreq = log(baldey$CELEX_lemma_freq+1)
baldey$LemmaFreqSc = as.numeric(scale(baldey$LemmaFreq))
baldey$WordDurSc = as.numeric(scale(baldey$word_duration))
baldey$TrialSc = as.numeric(scale(baldey$trial))
```

we fit a GAMM to the data.

```
baldey.gam <- bam(RTinv ~ gender +
                          s(LemmaFreqSc, by=gender, bs="cr") +
                          te(WordDurSc, TrialSc) +
                          s(word, bs="re") +
                          s(word, gender, bs="re") +
                          s(subject, WordDurSc, bs="re") +
                          s(session, subject, bs="fs", m=1),
                          AR.start=AR.start, rho=0.2,
                          data=baldey, discrete=TRUE)
```

The subtable of the parametric part of the model (see Table 5):

```
summary(baldey.gam)$p.table
```

```
              Estimate Std. Error    t value     Pr(>|t|)
(Intercept) -1.0381929 0.06834953 -15.189467 5.555810e-52
gendermale   0.3732205 0.08909260   4.189131 2.805468e-05
```

The subtable of the smooths of the model (also in Table 5):

```
summary(baldey.gam)$s.table
```

```
                                  edf      Ref.df            F       p-value
s(LemmaFreq):genderfemale    3.012133    3.430126 5.511694e+01  1.612847e-38
s(LemmaFreq):gendermale      1.014891    1.021960 1.247278e+02  3.398336e-29
te(word_duration,Trial)      8.705616   10.406449 2.271702e+01  4.892898e-44
s(word)                   1735.807042 2777.000000 2.015884e+00  0.000000e+00
s(gender,word)             495.787366 5544.000000 1.108202e-01  1.967590e-07
s(word_duration,subject)    18.744049   19.000000 7.988325e+01 1.592307e-293
s(session,subject)         154.417238  178.000000 1.263994e+05  0.000000e+00
```

The `fREML` score,

```
baldey.gam$gcv.ubre
```

```
   fREML 
-14903.7 
```

and the `AIC`:

```
AIC(baldey.gam)
```

```
[1] -31728.01
```

4.2 Table 6: the model with linear effects only

The GAMM with linear effects only (Table 6).

```
baldey.lin <- bam(RTinv ~ gender +
                          LemmaFreqSc*gender+
                          WordDurSc*TrialSc +
                          s(word, bs="re") +
                          s(word, gender, bs="re") +
                          s(subject, bs="re")+
                          s(subject, WordDurSc, bs="re") +
                          s(subject, session, bs="re"),
                          data=baldey, discrete=TRUE)
```

The subtable of the parametric part of the model (Table 6).

```
summary(baldey.lin.gam)$p.table
```

```
                         Estimate   Std. Error    t value      Pr(>|t|)
(Intercept)           -0.942629376 0.0406017546 -23.216469 1.485951e-118
gendermale             0.237397743 0.0574021321   4.135696  3.545059e-05
LemmaFreqSc           -0.020886829 0.0016662431 -12.535283  5.478266e-36
WordDurSc              0.061461226 0.0070232829   8.751068  2.183294e-18
TrialSc                0.006232360 0.0008371858   7.444417  9.906287e-14
gendermale:LemmaFreqSc 0.002426149 0.0017620096   1.376922  1.685431e-01
WordDurSc:TrialSc     -0.005362875 0.0008329795  -6.438183  1.220947e-10
```

The subtable of the smooths of the model (Table 6).

```
summary(baldey.lin.gam)$s.table
```

```
                           edf Ref.df            F       p-value
s(word)             1668.12107   2777 2.790862e+00 2.023020e-214
s(gender,word)       451.76914   5544 1.021730e-01  4.817559e-09
s(subject)            17.93030     18 9.009013e+05  0.000000e+00
s(WordDurSc,subject)  18.73591     19 1.213828e+02 6.843180e-178
s(session,subject)    19.89525     20 7.170278e+05  0.000000e+00
```

The `fREML` and AIC scores:

```
baldey.lin.gam$gcv.ubre
```

```
    fREML
-13027.88
```

```
AIC(baldey.lin.gam)
```

```
[1] -27582.51
```

Very similar results are obtained with the LMM:

```
baldey.lmer <- lmer(RTinv ~ gender +
                         LemmaFreqSc*gender+
                         WordDurSc*TrialSc +
                         (1+gender|word) +
                         (1+WordDurSc+session|subject),
                         data=baldey)
```

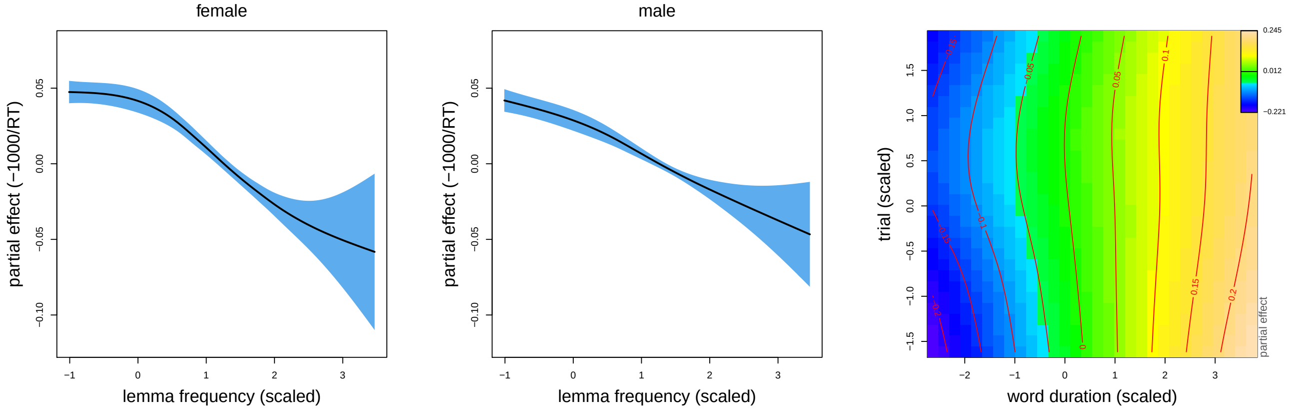
```
print(summary(baldey.lmer),corr=F)

Linear mixed model fit by REML ['lmerMod']
Formula: RTinv ~ gender + LemmaFreqSc * gender + WordDurSc * TrialSc +
    (1 + gender | word) + (1 + WordDurSc + session | subject)
   Data: baldey

REML criterion at convergence: -26072.5

Scaled residuals:
    Min      1Q  Median      3Q     Max
-5.3489 -0.5975 -0.0130  0.6110  4.3265

Random effects:
 Groups   Name        Variance  Std.Dev. Corr
 word     (Intercept) 0.0034549 0.05878
          gendermale  0.0009739 0.03121  -0.13
 subject  (Intercept) 0.0254792 0.15962
          WordDurSc   0.0009483 0.03079  -0.82
          session     0.0003140 0.01772  -0.22  0.06
 Residual             0.0316786 0.17798
Number of obs: 48385, groups:  word, 2780; subject, 20

Fixed effects:
                         Estimate Std. Error t value
(Intercept)            -0.8558065  0.0402314 -21.272
gendermale              0.0479604  0.0401551   1.194
LemmaFreqSc            -0.0208485  0.0016369 -12.737
WordDurSc               0.0619134  0.0070152   8.826
TrialSc                 0.0062278  0.0008371   7.440
gendermale:LemmaFreqSc  0.0023540  0.0017618   1.336
WordDurSc:TrialSc      -0.0053851  0.0008328  -6.466
```

```
compareML(baldey.gam, baldey.lin)
```

```
       Model     Score Edf    Chisq    Df  p.value Sig.
1 baldey.lin -13027.88  12
2 baldey.gam -14911.48  16 1883.594 4.000  < 2e-16  ***
```

4.3 Figure 14

```
par(mfrow=c(1,3),mar=c(4,4,3,4))
plot(baldey.gam, select=1, scheme=1, ylim=c(-0.12, 0.08), rug=FALSE,
     shade.col="steelblue2", col="indianred", lwd=2, xlab="lemma frequency",
     ylab="partial effect (-1000/RT)")
mtext("female", 3, 1)
plot(baldey.gam, select=2, scheme=1, ylim=c(-0.12, 0.08), rug=FALSE,
     shade.col="steelblue2", col="indianred", lwd=2, xlab="lemma frequency",
     ylab="partial effect (-1000/RT)")
mtext("male", 3, 1)
pvisgam(baldey.gam, select=3, view=c("WordDurSc", "TrialSc"),
     xlab="word duration (scaled)", ylab="trial (scaled)", main = " ")
```



Coefficient of variation for RTs and error rate.

```r
library(RePsychLing)
data(baldey)
# analysis 1: error proportions and cv calculated for RTs exceeding 600 ms
baldey = baldey[baldey$RT > 600,]
baldey$RTinv=-1000/baldey$RT

incor = tapply(baldey$response=="incorrect", baldey$subject, sum)
corr = tapply(baldey$response=="correct", baldey$subject, sum)
pincor = incor/(incor+corr)

sds = tapply(baldey$RTinv, baldey$subject, sd)
means = tapply(baldey$RTinv, baldey$subject, mean)
cvs = sds/means

cor.test(pincor, cvs)


Pearson's product-moment correlation

data:  pincor and cvs
t = -2.2054, df = 18, p-value = 0.04067
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.75055279 -0.02349328
sample estimates:
       cor
-0.4612191
```

```
# analysis 2: error proportions calculated across all observations,
# whereas cv is calculated over data points with RTs exceeding 600 ms
data(baldey)

incor = tapply(baldey$response=="incorrect", baldey$subject, sum)
corr = tapply(baldey$response=="correct", baldey$subject, sum)
pincor = incor/(incor+corr)

baldey = baldey[baldey$RT > 600,]
baldey$RTinv=-1000/baldey$RT
sds = tapply(baldey$RTinv, baldey$subject, sd)
means = tapply(baldey$RTinv, baldey$subject, mean)
cvs = sds/means

cor.test(pincor, cvs)


Pearson's product-moment correlation

data:  pincor and cvs
t = -3.5808, df = 18, p-value = 0.002136
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.8460326 -0.2833349
sample estimates:
       cor
-0.6449863
```

5 The `poems` dataset

5.1 The full GAMM

```
data(poems)  # available in RePsychLing, which was required above
# log-transform and scale frequency
poems$Fre = scale(log(poems$WordFormFrequency+1))
# log-transform reading time
poems$Lrt = log(poems$ReadingTime)
# scale frequency
poems$FreSc = as.numeric(scale(poems$Fre))
# scale trial
poems$TrialSc = as.numeric(scale(poems$Trial))
# order by subject and trial, and mark initial trial as the start
# of a new time series; this is necessary for
poems = poems[order(poems$Subject, poems$Trial),]
pos = tapply(poems$Trial, poems$Subject, min)
poems$MinTrial = pos[as.character(poems$Subject)]
poems$Start = poems$MinTrial==poems$Trial
```

A model with a tensor product smooth of frequency by trial. (Fitting this model takes about 30 minutes, and producing the summary takes another 30 minutes.) This model is summarized in Table 7.

```
poems.gam  = bam(Lrt ~ te(Fre, TrialSc) +
                       s(Poem, bs="re") +
                       s(TrialSc, Subject, bs="fs", m=1) +
                       s(Subject, Fre, bs="re"),
                       AR.start = poems$Start, rho = 0.30,
                       data = poems, discrete=TRUE)
summary(poems.gam)
```

```

Family: gaussian
Link function: identity

Formula:
Lrt ~ te(Fre, TrialSc) + s(Poem, bs = "re") + s(TrialSc, Subject,
    bs = "fs", m = 1) + s(Subject, Fre, bs = "re")

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  6.04636    0.01739   347.7   <2e-16

Approximate significance of smooth terms:
                       edf Ref.df      F p-value
te(Fre,TrialSc)      10.29   11.4  80.59  <2e-16
s(Poem)              81.19   87.0  19.45  <2e-16
s(TrialSc,Subject) 2163.53 2934.0 329.42  <2e-16
s(Fre,Subject)      304.11  326.0  14.88  <2e-16

R-sq.(adj) =  0.498   Deviance explained = 50.3%
fREML =  49642  Scale est. = 0.08918   n = 275996
```

5.2 A decompositional GAMM

A decompositional model with main effects for frequency and trial and a 'tinsor' product smooth for the interaction of frequency by trial (summarized in Table 8).

```
poems.gam2 = bam(Lrt ~ ti(Fre) + ti(TrialSc) + ti(Fre, TrialSc) +
                       s(Poem, bs="re") +
                       s(TrialSc, Subject, bs="fs", m=1) +
                       s(Subject, Fre, bs="re"),
                       AR.start = poems$Start, rho = 0.30,
                       data = poems, discrete=TRUE)
summary(poems.gam2)
```

```
Family: gaussian
Link function: identity

Formula:
Lrt ~ ti(Fre) + ti(TrialSc) + ti(Fre, TrialSc) + s(Poem, bs = "re") +
    s(TrialSc, Subject, bs = "fs", m = 1) + s(Subject, Fre, bs = "re")

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   6.0461     0.0174   347.4   <2e-16

Approximate significance of smooth terms:
                        edf   Ref.df       F p-value
ti(Fre)               1.566    1.880 247.865  <2e-16
ti(TrialSc)           3.899    3.915  90.924  <2e-16
ti(Fre,TrialSc)       8.051   10.187   9.931  <2e-16
s(Poem)              81.180   87.000  19.405  <2e-16
s(TrialSc,Subject) 2163.630 2934.000 323.821  <2e-16
s(Fre,Subject)      304.082  326.000  14.874  <2e-16

R-sq.(adj) =  0.498   Deviance explained = 50.3%
fREML =  49636  Scale est. = 0.089175  n = 275996
```

5.3 A model with linear effects only

Table 9 summarizes a LMM for the `poems` data.

```
poems.lmer = lmer(Lrt ~ FreSc * TrialSc +
                        (1|Poem) +
                        (1+FreSc+TrialSc|Subject),
                        data = poems, REML=TRUE)
print(summary(poems.lmer),corr=FALSE)

Linear mixed model fit by REML ['lmerMod']
Formula: Lrt ~ FreSc * TrialSc + (1 | Poem) + (1 + FreSc + TrialSc | Subject)
   Data: poems

REML criterion at convergence: 150493.3

Scaled residuals:
    Min      1Q  Median      3Q     Max
-5.9258 -0.6089 -0.1266  0.4605  5.6861

Random effects:
 Groups   Name        Variance Std.Dev. Corr
 Subject  (Intercept) 0.059568 0.24407
          FreSc       0.001176 0.03430  -0.61
          TrialSc     0.009619 0.09808   0.01  0.04
 Poem     (Intercept) 0.002534 0.05034
 Residual             0.099396 0.31527
Number of obs: 275996, groups:  Subject, 326; Poem, 87

Fixed effects:
                Estimate Std. Error t value
(Intercept)    6.0389852  0.0145774   414.3
FreSc         -0.0525598  0.0019991   -26.3
TrialSc       -0.0782900  0.0054865   -14.3
FreSc:TrialSc  0.0038955  0.0006195     6.3
```

Informal comparison of `poems.gam` and `poems.lmer`:

```
# AIC scores
AIC(poems.gam)

[1] 92688.55

AIC(poems.lmer)

[1] 150517.3

# REML scores
poems.gam$gcv.ubre

   fREML
49642.31

# 150493.3 for lmer, see summary above
cor(fitted(poems.gam), poems$Lrt)^2

[1] 0.5030827

cor(fitted(poems.lmer), poems$Lrt)^2

[1] 0.4292628
```

5.4 Figure 15

```r
# an ancillary function for acfs with lattice
acfs = function(dat=poems, model = poems.gam) {
  dat$Resid = resid_gam(model,AR_start=poems$Start,incl_na=TRUE)
  res=list()
  for (i in 1:nlevels(dat$Subject)) {
    tmp = dat[dat$Subject==levels(dat$Subject)[i],]
    acfmod = acf(tmp$Resid, na.action=na.pass, plot=F)
    acfobs = acf(tmp$Lrt, plot=F)
    res[[i]] = data.frame(lag    = acfmod$lag,
                          acf    = acfmod$acf,
                          acfObs = acfobs$acf)
    res[[i]]$subj = levels(dat$Subject)[i]
    res[[i]]$n.used.mod = acfmod$n.used
    res[[i]]$n.used.obs = acfobs$n.used
    res[[i]]$ci95obs = qnorm((1+0.95)/2)/sqrt(acfobs$n.used)
    res[[i]]$ci95mod = qnorm((1+0.95)/2)/sqrt(acfmod$n.used)
  }
  res = do.call(rbind, res)
  return(res)
}

acfdat = acfs()
```

```r
load("models/acfdat.poems.rda")
```

The top panel of Figure 15 is produced by the following code snippet.

```r
selectedSubjects = c("Subj265", "Subj176", "Subj19","Subj183")
tmp = acfdat[acfdat$subj %in% selectedSubjects,]
tmp$subj = ordered(tmp$subj, selectedSubjects)
ci = unname(tapply(tmp$ci95obs, tmp$subj, mean))
theplotObs = xyplot(acfObs ~ lag | subj, type = "h", dat = tmp, ylim=c(0,1),
    panel = function(x, y, subscripts, ...) {
      panel.abline(h =  ci[panel.number()], col.line = "grey")
      panel.abline(h = -ci[panel.number()], col.line = "grey")
      panel.abline(h = 0, col.line = "black")
      d=tmp[subscripts,]
      panel.xyplot(d$lag, d$acfObs,
        col=ifelse(abs(d$acfObs)> ci[panel.number()] & d$lag > 0,
                   "indianred", "steelblue2"),
                   ...)
    },
    xlab="lag", ylab="autocorrelation",
    layout=c(4,1,1))
print(theplotObs)  # show plot
```

The center panel of Figure 15 has a smooth based on a simple GAM with only a factor smooth:

```r
Lrt ~ s(Trial, Subject, bs="fs", m=1)
```

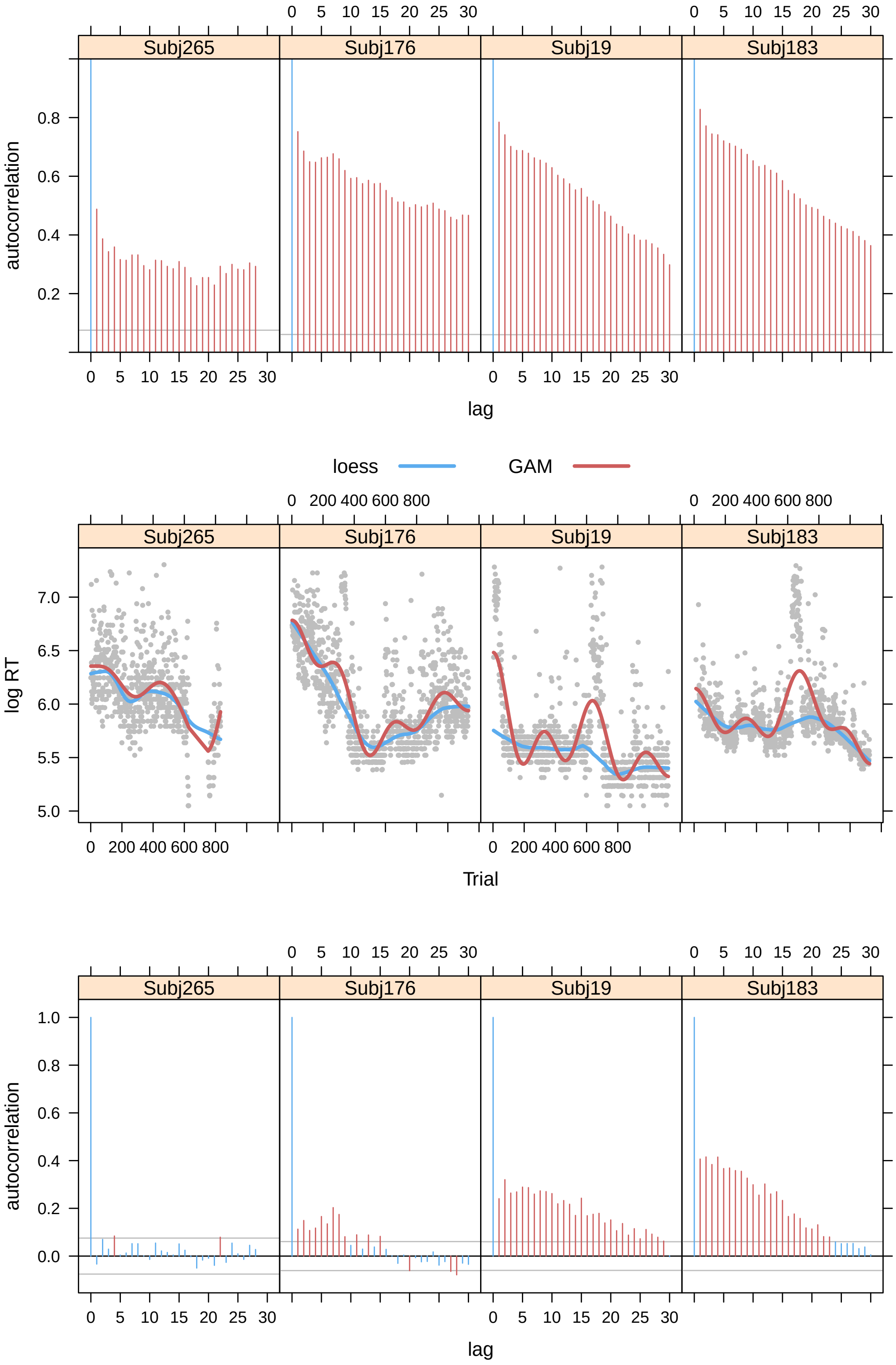
The following code produces the center panel:

```
selectedSubjects = c("Subj265", "Subj176", "Subj19","Subj183")
dfr = droplevels(poems[poems$Subject %in% selectedSubjects,])
dfr$Subject = ordered(dfr$Subject, selectedSubjects)
dfr.gam = bam(Lrt~1+s(Trial, Subject, bs="fs", m=1), data=dfr, method="fREML")
dfr$Gam = predict(dfr.gam)

keys = list(space="top", text=list(c("loess", "GAM")), columns=2,
            lines=list(lty=c(1,1), col=c("steelblue2", "indianred"), lwd=3))
xyplot(Lrt ~ Trial | Subject, data = dfr,
  panel = function(x, y, subscripts, ...) {
    panel.xyplot(x, y, pch=19, col="gray", cex=0.4, ...)
    panel.loess(x, y, lwd=3, span=0.3, col="steelblue2", ...)
    d = dfr[subscripts,]
    panel.lines(d$Trial, d$Gam, col="indianred", lwd=3)
  },
  xlab="Trial", ylab="log RT",
  layout=c(4,1,1),
  key=keys)
```

The bottom panel of Figure 15 is obtained in a similar way, but now using the model predictions.

```
tmp = acfdat[acfdat$subj %in% selectedSubjects,]
tmp$subj = ordered(tmp$subj, selectedSubjects)
ci = unname(tapply(tmp$ci95mod, tmp$subj, mean))
theplot = xyplot(acf ~ lag | subj, type = "h", dat = tmp,
    panel = function(x, y, subscripts, ...) {
      panel.abline(h =  ci[panel.number()], col.line = "grey")
      panel.abline(h = -ci[panel.number()], col.line = "grey")
      panel.abline(h = 0, col.line = "black")
      d=tmp[subscripts,]
      panel.xyplot(d$lag, d$acf,
        col=ifelse(abs(d$acf)> ci[panel.number()] & d$lag > 0,
                   "indianred", "steelblue2"),
                   ...)
    },
    xlab="lag", ylab="autocorrelation",
    layout=c(4,1,1))
print(theplot)
```

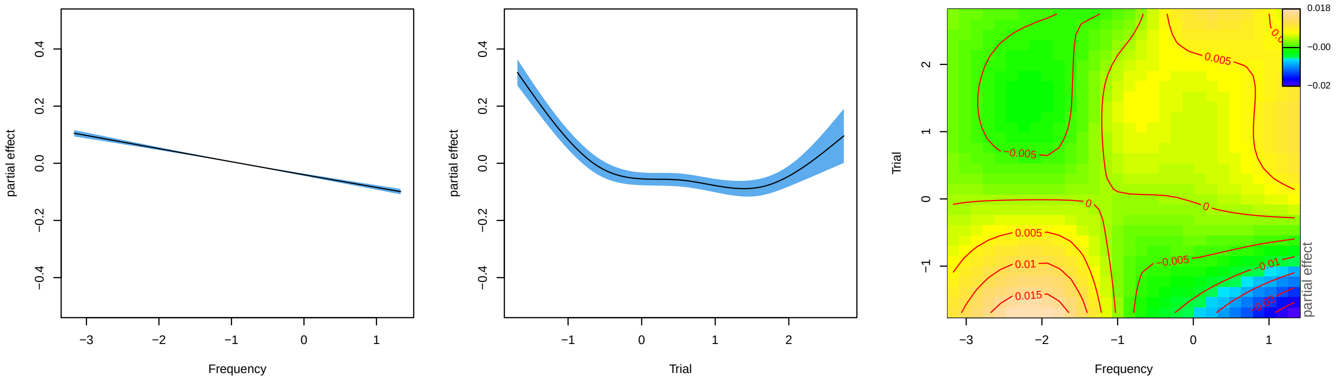
Figure 15.


Subj265
Subj176
Subj19
Subj183
autocorrelation
0.2
0.4
0.6
0.8
lag
0
5
10
15
20
25
30
loess
GAM
log RT
5.0
5.5
6.0
6.5
7.0
Trial
0
200
400
600
800
autocorrelation
0.0
0.2
0.4
0.6
0.8
1.0
lag

5.5 Figure 16

This takes about 10 minutes to complete.

```
par(mfrow=c(1,3),oma=rep(0,4))
plot(poems.gam2, select=1, rug=FALSE,
     scheme=1, shade.col="steelblue2",
     ylab="partial effect", xlab="Frequency")
plot(poems.gam2, select=2, rug=FALSE,
     scheme=1, shade.col="steelblue2",
     ylab="partial effect", xlab="Trial")
pvisgam(poems.gam2, select=3, view=c("Fre", "TrialSc"),
     xlab="Frequency", ylab="Trial", main=" ")
```



5.6 Figure 17 and corresponding LMMs

First, we fit a sequence of models with more complex by-subject random effects structure, and show that by-subject random slopes for frequency receive good support.

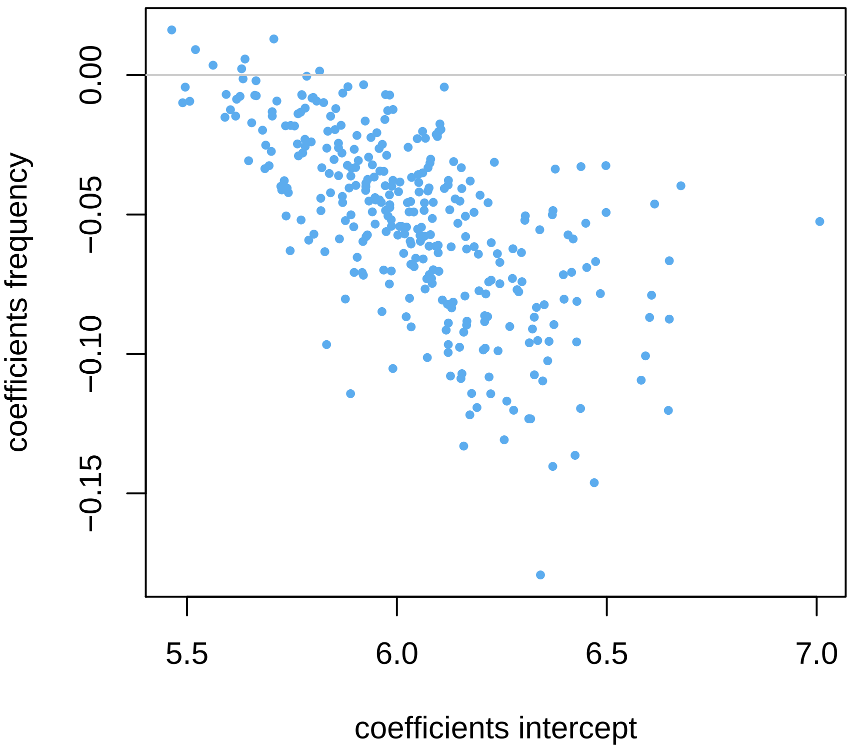
```
# by-subject random intercepts
poems.lmer1 = lmer(Lrt ~ FreSc * TrialSc +
                        (1|Poem) +
                        (1|Subject),
                        data = poems, REML=FALSE)
# by-subject random intercepts and by-subject random slopes for trial
poems.lmer2 = lmer(Lrt ~ FreSc * TrialSc +
                        (1|Poem) +
                        (1+TrialSc|Subject),
                        data = poems, REML=FALSE)
# by-subject random intercepts and by-subject random slopes for trial
# and in addition by-subject random slopes for frequency
poems.lmer3 = lmer(Lrt ~ FreSc * TrialSc +
                        (1|Poem) +
                        (1+FreSc+TrialSc|Subject),
                        data = poems, REML=FALSE)
# a simpler model without correlation parameters for frequency
poems.lmer4 = lmer(Lrt ~ FreSc * TrialSc +
                        (1|Poem) +
                        (1+TrialSc|Subject) +
                        (0+FreSc|Subject),
                        data = poems, REML=FALSE)
```

```
# compare the first three models
anova(poems.lmer1, poems.lmer2, poems.lmer3)

Data: poems
Models:
poems.lmer1: Lrt ~ FreSc * TrialSc + (1 | Poem) + (1 | Subject)
poems.lmer2: Lrt ~ FreSc * TrialSc + (1 | Poem) + (1 + TrialSc | Subject)
poems.lmer3: Lrt ~ FreSc * TrialSc + (1 | Poem) + (1 + FreSc + TrialSc | Subject)
            Df    AIC    BIC logLik deviance   Chisq Chi Df Pr(>Chisq)
poems.lmer1  7 172200 172274 -86093   172186
poems.lmer2  9 152934 153029 -76458   152916 19270.2      2  < 2.2e-16
poems.lmer3 12 150478 150605 -75227   150454  2461.7      3  < 2.2e-16
```

```
# and test for the correlation parameters for frequency
anova(poems.lmer4, poems.lmer3)

Data: poems
Models:
poems.lmer4: Lrt ~ FreSc * TrialSc + (1 | Poem) + (1 + TrialSc | Subject) +
poems.lmer4:     (0 + FreSc | Subject)
poems.lmer3: Lrt ~ FreSc * TrialSc + (1 | Poem) + (1 + FreSc + TrialSc | Subject)
            Df    AIC    BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
poems.lmer4 10 150608 150713 -75294   150588
poems.lmer3 12 150478 150605 -75227   150454 133.66      2  < 2.2e-16

# note that the summary of poems.lmer3 indicates the frequency
# correlational structure is carried almost exclusively by
# the frequency by intercept correlation
print(summary(poems.lmer3),corr=FALSE)

Linear mixed model fit by maximum likelihood  ['lmerMod']
Formula: Lrt ~ FreSc * TrialSc + (1 | Poem) + (1 + FreSc + TrialSc | Subject)
   Data: poems

     AIC      BIC   logLik deviance df.resid
150478.3 150604.6 -75227.1 150454.3   275984

Scaled residuals:
    Min      1Q  Median      3Q     Max
-5.9261 -0.6089 -0.1266  0.4605  5.6860

Random effects:
 Groups   Name        Variance Std.Dev. Corr
 Subject  (Intercept) 0.059408 0.24374
          FreSc       0.001172 0.03424  -0.61
          TrialSc     0.009589 0.09792   0.01  0.04
 Poem     (Intercept) 0.002528 0.05028
 Residual             0.099396 0.31527
Number of obs: 275996, groups:  Subject, 326; Poem, 87

Fixed effects:
                Estimate Std. Error t value
(Intercept)    6.0389850  0.0145582   414.8
FreSc         -0.0525595  0.0019960   -26.3
TrialSc       -0.0782901  0.0054780   -14.3
FreSc:TrialSc  0.0038961  0.0006195     6.3
```

Figure 17 is obtained with the following code, extracting the coefficients from `poems.lmer3`:

```
coefs = coef(poems.lmer3)[[1]]
plot(coefs[,1], coefs[,2],
     xlab="coefficients intercept", ylab="coefficients frequency",
     pch=19, cex=0.5, col="steelblue2")
abline(h=0, col="gray80")
```


0.00
−0.05
−0.10
−0.15
coefficients frequency
5.5
6.0
6.5
7.0
coefficients intercept

5.7 Figure 18

```r
par(mfrow=c(1,2))
plot(poems.gam, select=1, rug=FALSE,
     xlab="Frequency", ylab="Trial", main=" ")
pvisgam(poems.gam, select=1, view=c("Fre", "TrialSc"),
     xlab="Frequency", ylab="Trial", main=" ")
```