

Toward a discrimination-based account of unprimed and primed lexical decision

Petar Milin, Laurie B. Feldman, Michael Ramscar, Peter Hendrix, R. Harald Baayen
to appear in PLOS-one

1 general

```
library(xtable)
library(mgcv)
library(itsadug)
infoMessages(FALSE) # reduces the voluminous output of itsadug
```

```
sessionInfo()

## R version 3.3.2 (2016-10-31)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 14.04.5 LTS
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=de_DE.UTF-8  LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=de_DE.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=de_DE.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] itsadug_2.2      plotfunctions_1.0 xtable_1.8-2    Cairo_1.5-9
## [5] mgcv_1.8-16      nlme_3.1-128      knitr_1.15.1
##
## loaded via a namespace (and not attached):
## [1] lattice_0.20-34  codetools_0.2-15 digest_0.6.11   grid_3.3.2
## [5] magrittr_1.5     evaluate_0.10    highr_0.6       stringi_1.1.2
## [9] Matrix_1.2-7.1  tools_3.3.2     stringr_1.1.0
```

Analyses were run with `discrete=TRUE`, which allows for much faster model fitting. Results may differ slightly from those reported in the manuscript.

2 analyses English Lexicon Project

```
load('elp.rda')
```

1. RTinv: $-1000/RT$
2. Voice: voicing of initial segment
3. PC1: first principal component of orthographic consistency measures
4. MeanBigramFrequency: mean frequency of letter bigrams
5. AgeSubject: age group of subject
6. Sub1BilFreq: frequency in 1 billion subtitle corpus
7. FamilySize: morphological family size
8. WrittenSpokenFrequencyRatio: ratio of written to spoken frequency (BNC)
9. NVratio: ratio of noun and verb frequency
10. Ncount: count of orthographic neighbors at Hamming distance 1
11. WordCategory: word category
12. InflectionalEntropy: inflectional entropy
13. NumberComplexSynsets: number of complex synsets in WordNet
14. LogSubNorm1cG2L: G2L prior
15. SubNorm1aG2L: G2L activation diversity
16. LogBncNorm1ColL2L: L2L prior
17. BncNorm1RowL2L: L2L l-diversity
18. BncCossimRowL2L: semantic typicality
19. LogBncL2LCossimMatDensity09: semantic density
20. LogSubActG2L: G2L activation
21. ConceptFreq: estimated concept frequency

```

elp.classic.gam = bam(RTinv ~
  Voice + PC1 + MeanBigramFrequency +
  AgeSubject +
  te(Sub1BilFreq, FamilySize, by=AgeSubject) +
  s(WrittenSpokenFrequencyRatio) +
  NVratio +
  Ncount+
  WordCategory +
  te(InflectionalEntropy, NumberComplexSynsets),
  data = elp, method='ML')

```

```
summary(elp.classic.gam)
```

```

##
## Family: gaussian
## Link function: identity
##
## Formula:
## RTinv ~ Voice + PC1 + MeanBigramFrequency + AgeSubject + te(Sub1BilFreq,
##   FamilySize, by = AgeSubject) + s(WrittenSpokenFrequencyRatio) +
##   NVratio + Ncount + WordCategory + te(InflectionalEntropy,
##   NumberComplexSynsets)
##
## Parametric coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -1.4121128   0.0256522  -55.048   < 2e-16
## Voicevoiceless -0.0104417   0.0036464   -2.864  0.004212
## PC1             0.0030807   0.0009269    3.324  0.000897
## MeanBigramFrequency 0.0117673   0.0029074    4.047  5.29e-05
## AgeSubjectyoung -0.3224199   0.0034542  -93.341   < 2e-16
## NVratio        -0.0018037   0.0007912   -2.280  0.022680
## Ncount          0.0008987   0.0004150    2.166  0.030402
## WordCategoryV  -0.0119740   0.0051255   -2.336  0.019535
##
## Approximate significance of smooth terms:
##               edf Ref.df      F  p-value
## te(Sub1BilFreq,FamilySize):AgeSubjectold    7.555   9.417  52.750   < 2e-16
## te(Sub1BilFreq,FamilySize):AgeSubjectyoung  9.973  12.059  88.866   < 2e-16
## s(WrittenSpokenFrequencyRatio)              5.303   6.521   8.204  2.86e-09
## te(InflectionalEntropy,NumberComplexSynsets) 3.001   3.003  29.188   < 2e-16
##
## R-sq.(adj) =  0.749   Deviance explained = 75.1%
## -ML = -3096.8   Scale est. = 0.011281   n = 3782

AIC(elp.classic.gam)

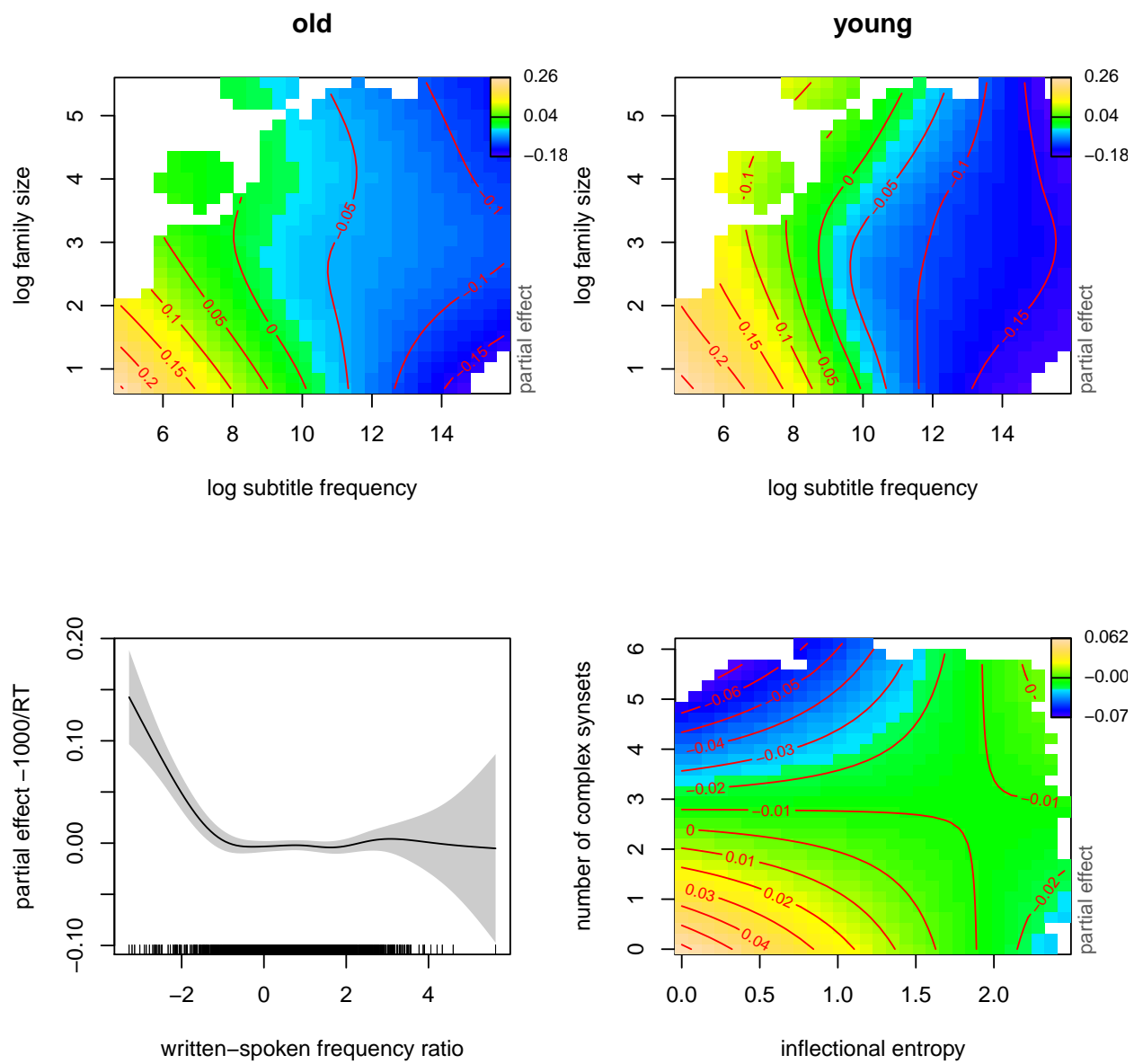
## [1] -6185.183

```

```

par(mfrow=c(2,2))
pvisgam(elp.classic.gam, select=1, main='old',
        view=c('SubiBilFreq','FamilySize'),
        cond=list(AgeSubject='old'), too.far=0.1, zlim=c(-0.18,0.26),
        xlab='log subtitle frequency', ylab='log family size')
pvisgam(elp.classic.gam, select=2, main='young',
        view=c('SubiBilFreq','FamilySize'),
        cond=list(AgeSubject='young'), too.far=0.1, zlim=c(-0.18,0.26),
        xlab='log subtitle frequency', ylab='log family size')
plot(elp.classic.gam, select=3,scheme=1,
     xlab='written-spoken frequency ratio', ylab='partial effect -1000/RT')
pvisgam(elp.classic.gam, select=4, main=' ',
        view=c('InflectionalEntropy','NumberComplexSynsets'),
        xlab='inflectional entropy', ylab='number of complex synsets',
        too.far=0.1)

```



```

elp.ndl.gam = bam(RTinv~AgeSubject                                +
  te(LogSubNorm1cG2L, SubNorm1aG2L)                             + # G2L rows and columns
  te(LogBncNorm1ColL2L, BncNorm1RowL2L, by=AgeSubject)          + # L2L rows and columns
  te(BncCossimRowL2L, LogBncL2LCossimMatDensity09)              + # sem. sim and density
  s(LogSubActG2L, by=AgeSubject)                                 + # activation
  s(WrittenSpokenFrequencyRatio)                                + # register
  s(ConceptFreq),                                                + # concept frequency
data=elp, method='ML')

```

```

summary(elp.ndl.gam)

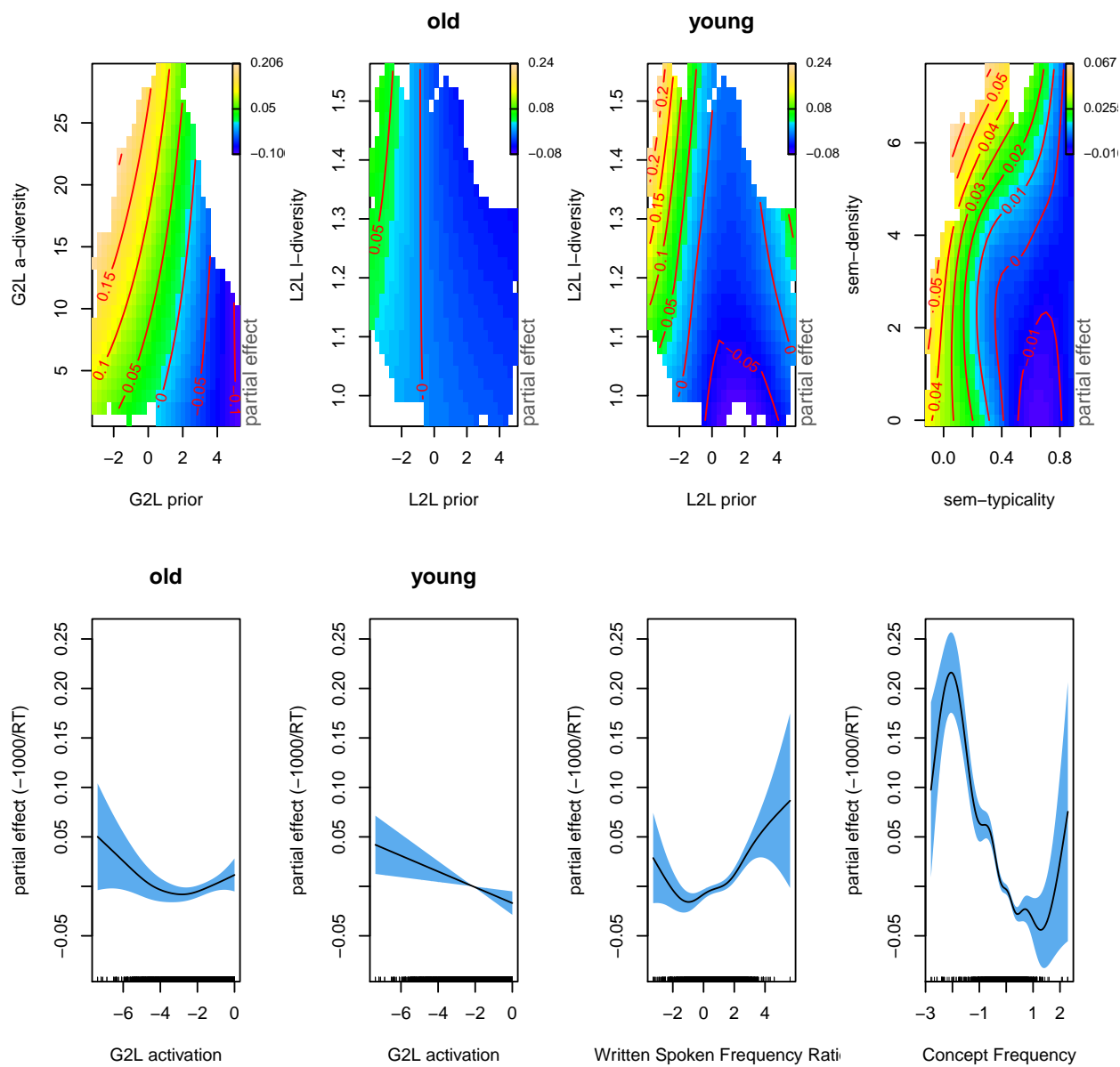
##
## Family: gaussian
## Link function: identity
##
## Formula:
## RTinv ~ AgeSubject + te(LogSubNorm1cG2L, SubNorm1aG2L) + te(LogBncNorm1Col...
##      BncNorm1RowL2L, by = AgeSubject) + te(BncCossimRowL2L, LogBncL2LCossim...
##      s(LogSubActG2L, by = AgeSubject) + s(WrittenSpokenFrequencyRatio) +
##      s(ConceptFreq)
##
## Parametric coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.318585    0.002428 -543.04  <2e-16
## AgeSubjectyoung -0.322389    0.003434  -93.88  <2e-16
##
## Approximate significance of smooth terms:
##                                     edf Ref.df      F
## te(LogSubNorm1cG2L,SubNorm1aG2L)      3.002   3.004 44.616
## te(LogBncNorm1ColL2L,BncNorm1RowL2L):AgeSubjectold 4.123   4.800   5.993
## te(LogBncNorm1ColL2L,BncNorm1RowL2L):AgeSubjectyoung 6.884   8.264 17.317
## te(BncCossimRowL2L,LogBncL2LCossimMatDensity09)    7.069   8.842   5.434
## s(LogSubActG2L):AgeSubjectold                2.487   3.184   2.742
## s(LogSubActG2L):AgeSubjectyoung               1.000   1.000   8.131
## s(WrittenSpokenFrequencyRatio)               4.192   5.270   8.166
## s(ConceptFreq)                               8.139   8.801 27.330
##                                     p-value
## te(LogSubNorm1cG2L,SubNorm1aG2L)             < 2e-16
## te(LogBncNorm1ColL2L,BncNorm1RowL2L):AgeSubjectold 3.22e-05
## te(LogBncNorm1ColL2L,BncNorm1RowL2L):AgeSubjectyoung < 2e-16
## te(BncCossimRowL2L,LogBncL2LCossimMatDensity09)    2.41e-07
## s(LogSubActG2L):AgeSubjectold                   0.03804
## s(LogSubActG2L):AgeSubjectyoung                  0.00437
## s(WrittenSpokenFrequencyRatio)                  8.81e-08
## s(ConceptFreq)                                  < 2e-16
##
## R-sq.(adj) = 0.751   Deviance explained = 75.4%
## -ML = -3106.3   Scale est. = 0.011149   n = 3782
AIC(elp.ndl.gam)
## [1] -6219.214

```

```

par(mfrow=c(2,4))
pvisgam(elp.ndl.gam, select=1,view=c('LogSubNorm1cG2L', 'SubNorm1aG2L'),
        xlab='G2L prior', ylab='G2L a-diversity',
        too.far=0.1, main=' ')
pvisgam(elp.ndl.gam, select=2,view=c('LogBncNorm1ColL2L', 'BncNorm1RowL2L'),
        xlab='L2L prior', ylab='L2L 1-diversity', main='old',
        cond=list(AgeSubject='old'), too.far=0.1, xlim=c(-0.08,0.24))
pvisgam(elp.ndl.gam, select=3,view=c('LogBncNorm1ColL2L', 'BncNorm1RowL2L'),
        xlab='L2L prior', ylab='L2L 1-diversity', main='young',
        cond=list(AgeSubject='young'), too.far=0.1, xlim=c(-0.08,0.24))
pvisgam(elp.ndl.gam, select=4,view=c('BncCossimRowL2L', 'LogBncL2LCossimMatDensity09'),
        xlab='sem-typicality', ylab='sem-density',
        too.far=0.1, main=' ')
plot(elp.ndl.gam, cex.lab=1, select=5, main='old',
     xlab='G2L activation', scheme=1, shade.col="steelblue2",
     ylab='partial effect (-1000/RT)')
plot(elp.ndl.gam, cex.lab=1, select=6, main='young',
     xlab='G2L activation', scheme=1, shade.col="steelblue2",
     ylab='partial effect (-1000/RT)')
plot(elp.ndl.gam, cex.lab=1, select=7, main=' ',
     xlab='Written Spoken Frequency Ratio', scheme=1, shade.col="steelblue2",
     ylab='partial effect (-1000/RT)')
plot(elp.ndl.gam, cex.lab=1, select=8, main=' ',
     xlab='Concept Frequency', scheme=1, shade.col="steelblue2",
     ylab='partial effect (-1000/RT)')

```



3 analyses Experiment 1

Table 1: Prime and target pairs used in the statistical analyses.

	Prime		Target
Exhaustive	Partial	Unrelated	
army	armoire	acquire	ARM
artery	article	cubicle	ART
askance	askew	sinew	ASK
bandage	bandit	pulpit	BAND
barren	baron	lemon	BAR
bath	batik	lasik	BAT
bitter	bitch	notch	BIT
bully	bullet	helmet	BULL
center	central	lateral	CENT
cower	cowl	furl	COW
endive	endure	manure	END
figment	figure	impure	FIG
filly	fillet	pullet	FILL
finish	finicky	panicky	FIN
fluent	fluid	timid	FLU
hammer	hamlet	carpet	HAM
jigger	jiggle	dangle	JIG
limber	limbo	gazebo	LIMB
palate	pallid	horrid	PAL
pastor	pasta	dogma	PAST
petal	petrol	mongol	PET
pineal	pinch	hunch	PIN
pinky	pinko	gumbo	PINK
poppy	poplin	goblin	POP
ratify	rattan	median	RAT
sandal	sandwich	ostrich	SAND
scarier	scarlet	triplet	SCAR
sear	seal	veal	SEA
sitar	situate	equate	SIT
spurious	spurn	drawn	SPUR
stagger	stagnate	neonate	STAG
tactual	tactile	hostile	TACT
tartar	tartan	orphan	TART
tenant	tennis	mantis	TEN
tender	tendon	rayon	TEND
testify	testicle	cuticle	TEST
textile	texture	conjure	TEXT

```
load("exp1.rda")
```

1. RTinv: $-1000/RT$
2. PRIMETYPE: unrelated, exhaustive, partial
3. Spelling: spelling score from dictation test
4. PC1: first principal component of classical predictors, words with high scores have few neighbors at greater distances
5. PC2: second principal component of classical predictors, high values indicate high frequency of use
6. Subject: participant
7. Trial: scaled trial number
8. PrevTarget: the preceeding target word in the experimental list
9. prime: the prime
10. target: the target
11. Unrelated: unrelated versus related priming condition
12. LogSubNorm1cG2L: G2L prior
13. SubNorm1aG2L: G2L activation diversity
14. LogBncNorm1Coll2L: L2L prior
15. BncNorm1RowL2L: L2L l-diversity
16. Experiment: sub-experiment

```
exp1.threelevel.gam <- bam(RTinv ~  
  Experiment + PRIMETYPE +  
  Spelling +  
  te(PC1, PC2) +  
  s(Subject, PC2, bs='re') +  
  s(Trial, Subject, bs='fs', m=1) +  
  s(PrevTarget, bs='re') +  
  s(prime, bs='re') +  
  s(target, bs='re'), discrete=TRUE,  
  data=exp1, method='fREML')
```

```
summary(exp1.threelevel.gam)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## RTinv ~ Experiment + PRIMETYPE + Spelling + te(PC1, PC2) + s(Subject,
##      PC2, bs = "re") + s(Trial, Subject, bs = "fs", m = 1) + s(PrevTarget,
##      bs = "re") + s(prime, bs = "re") + s(target, bs = "re")
##
## Parametric coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.48608    0.03773  -39.391  <2e-16
## ExperimentExp1 -0.05469    0.02783   -1.965  0.0494
## PRIMETYPEexhaustive -0.02005    0.01092   -1.836  0.0664
## PRIMETYPEpartial -0.01544    0.01089   -1.418  0.1562
## Spelling      -0.14468    0.05915   -2.446  0.0145
##
## Approximate significance of smooth terms:
##              edf   Ref.df       F    p-value
## te(PC1,PC2)     4.724     4.776  8.693 7.02e-08
## s(PC2,Subject)  25.215    169.000  0.177 0.03275
## s(Trial,Subject) 393.081   1527.000  2.100 < 2e-16
## s(PrevTarget)    42.566    139.000  0.448 0.00033
## s(prime)         28.111    105.000  0.488 0.00131
## s(target)        27.883     33.000 17.096 < 2e-16
##
## R-sq.(adj) = 0.441   Deviance explained = 49.1%
## fREML = 888.74   Scale est. = 0.066372   n = 5783
```

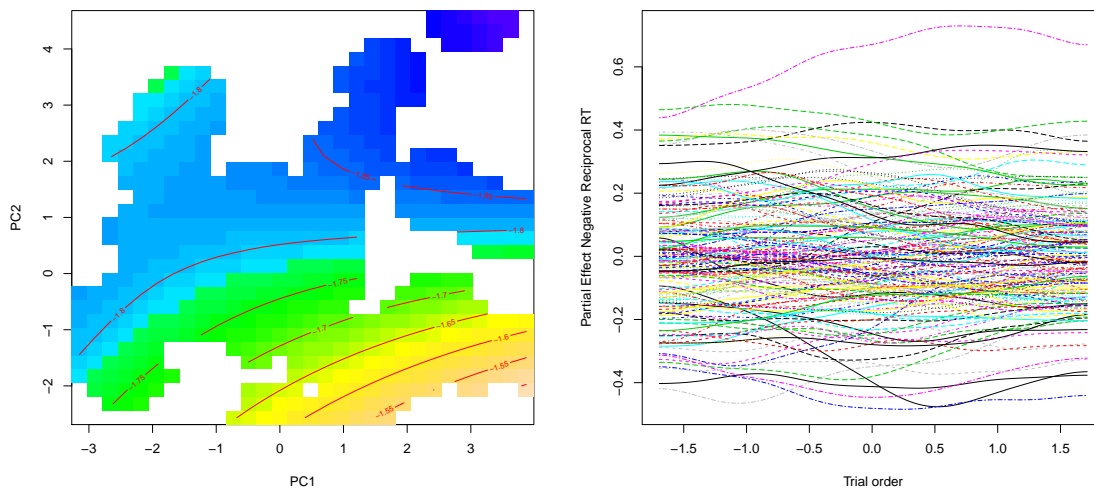
```
expl.classic.gam <- bam(RTinv ~
  Experiment + Unrelated + Spelling +
  te(PC1, PC2) +
  s(Trial, Subject, bs = 'fs', m = 1) +
  s(PrevTarget, bs = 're') +
  s(prime, bs = 're') +
  s(target, bs = 're'),
  data=expl, method='fREML', discrete=TRUE)
```

```
summary(expl.classic.gam)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## RTinv ~ Experiment + Unrelated + Spelling + te(PC1, PC2) + s(Trial,
##      Subject, bs = "fs", m = 1) + s(PrevTarget, bs = "re") + s(prime,
##      bs = "re") + s(target, bs = "re")
##
```

```
## Parametric coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -1.486334   0.037711 -39.413  <2e-16
## ExperimentExp1  -0.054347   0.027814  -1.954  0.0508
## Unrelatedrelated -0.017700   0.009414  -1.880  0.0601
## Spelling        -0.144206   0.059124  -2.439  0.0148
##
## Approximate significance of smooth terms:
##               edf   Ref.df     F  p-value
## te(PC1,PC2)      4.724    4.777  8.768 5.97e-08
## s(Trial,Subject) 393.607 1527.000  2.083 < 2e-16
## s(PrevTarget)    43.066   139.000  0.454 0.000278
## s(prime)         28.048   106.000  0.474 0.001440
## s(target)        27.905    33.000 16.875 < 2e-16
##
## R-sq.(adj) =  0.438   Deviance explained = 48.6%
## fREML = 886.39   Scale est. = 0.066724   n = 5783
```

```
vis.gam(expl.classic.gam, view=c('PC1','PC2'), color='topo',
        plot.type='contour', main='', xlab='PC1', ylab='PC2', too.far=0.1)
plot.gam(expl.classic.gam, select=2, xlab='Trial order',
        ylab='Partial Effect Negative Reciprocal RT', main='')
```



```

expl.nd1 <- bam(RTinv ~
  Experiment + Unrelated +
  te(LogSubNorm1cG2L, SubNorm1aG2L, Spelling) +
  te(LogBncNorm1ColL2L, BncNorm1RowL2L) +
  s(target, bs='re')+
  s(prime, bs='re')+
  s(PrevTarget, bs='re')+
  s(Trial, Subject, bs='fs', m=1),
  data=expl, method='fREML', discrete=TRUE)

```

```
summary(expl.nd1)
```

```

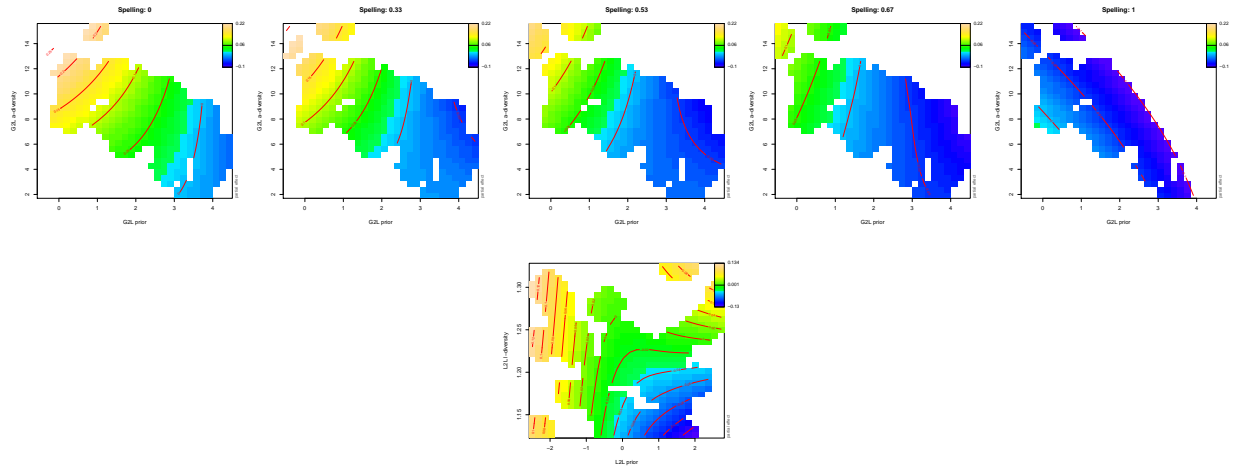
##
## Family: gaussian
## Link function: identity
##
## Formula:
## RTinv ~ Experiment + Unrelated + te(LogSubNorm1cG2L, SubNorm1aG2L,
##   Spelling) + te(LogBncNorm1ColL2L, BncNorm1RowL2L) + s(target,
##   bs = "re") + s(prime, bs = "re") + s(PrevTarget, bs = "re") +
##   s(Trial, Subject, bs = "fs", m = 1)
##
## Parametric coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.566851   0.025806 -60.717   <2e-16
## ExperimentExp1 -0.054595   0.027816  -1.963   0.0497
## Unrelatedrelated -0.017801   0.009409  -1.892   0.0586
##
## Approximate significance of smooth terms:
##               edf    Ref.df      F  p-value
## te(LogSubNorm1cG2L,SubNorm1aG2L,Spelling) 11.176   13.699  2.231 0.005211
## te(LogBncNorm1ColL2L,BncNorm1RowL2L)      4.604    4.667  3.479 0.004687
## s(target)                                24.520   30.000 12.297 < 2e-16
## s(prime)                                  28.249  103.000  0.486 0.001009
## s(PrevTarget)                             43.473  139.000  0.460 0.000204
## s(Trial,Subject)                           392.923 1527.000  2.070 < 2e-16
##
## R-sq.(adj) =  0.439   Deviance explained = 48.8%
## fREML = 877.51   Scale est. = 0.066528   n = 5783

```

```

qntls = quantile(exp1$Spelling)
for (i in 1:length(qntls)) {
  pvisgam(exp1.nd1, select=1, view=c('LogSubNorm1cG2L', 'SubNorm1aG2L'),
    cond=list(Spelling=qntls[i]), too.far=0.1,
    zlim=c(-0.1,0.22),
    xlab='G2L prior', ylab = 'G2L a-diversity',
    main=paste('Spelling: ', round(qntls[i],2), sep=''))
}
pvisgam(exp1.nd1, select=2, view=c('LogBncNorm1ColL2L', 'BncNorm1RowL2L'),
  xlab='L2L prior', ylab = 'L2L l-diversity',
  too.far=0.1, main=' ')

```



4 analyses Experiment 2

```
load("exp2.rda")
```

1. RTinv: $-1000/RT$
2. Identical: identical prime
3. PRIMETYPE: unrelated, exhaustive, partial
4. Spelling: spelling score from dictation test
5. Vocabulary: vocabulary score
6. PC1: first principal component of classical predictors, words with high scores have few neighbors at greater distances
7. PC2: second principal component of classical predictors, high values indicate high frequency of use
8. Subject: participant
9. Trial: scaled trial number
10. PrevTarget: the preceding target word in the experimental list
11. prime: the prime
12. target: the target
13. LogSubNorm1cG2L: G2L prior
14. SubNorm1aG2L: G2L activation diversity
15. LogBncNorm1ColL2L: L2L prior
16. BncNorm1RowL2L: L2L l-diversity

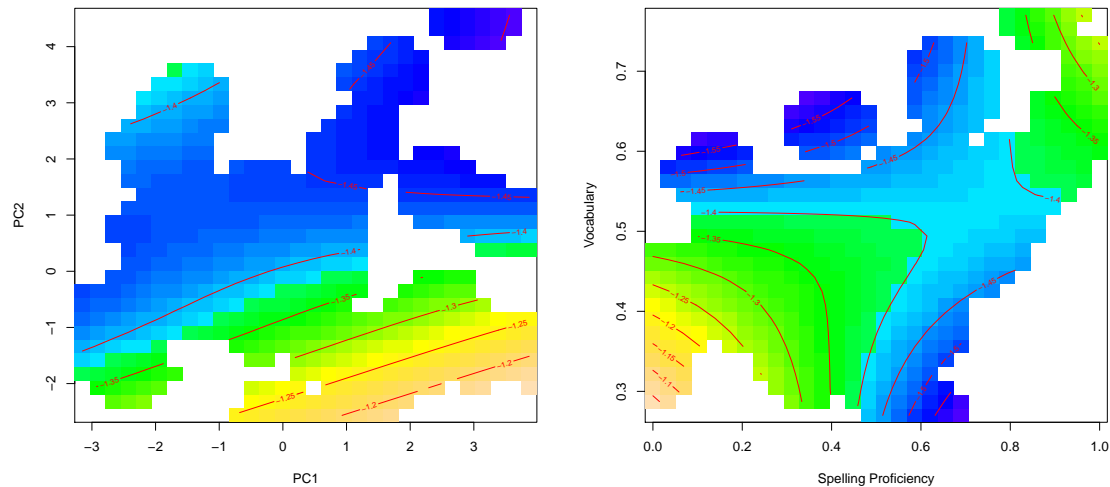
```
exp2.classic.gam = bam(RTinv ~  
  Identical +  
  te(Spelling, Vocabulary) +  
  te(PC1, PC2) +  
  s(Subject, PC2, bs='re') +  
  s(Trial, Subject, bs='fs', m=1) +  
  s(PrevTarget, bs='re') +  
  s(prime, bs='re') +  
  s(target, bs='re'),  
  data=exp2, method='fREML', discrete=TRUE)
```

```
summary(exp2.classic.gam)

##
## Family: gaussian
## Link function: identity
##
## Formula:
## RTinv ~ Identical + te(Spelling, Vocabulary) + te(PC1, PC2) +
##      s(Subject, PC2, bs = "re") + s(Trial, Subject, bs = "fs",
##      m = 1) + s(PrevTarget, bs = "re") + s(prime, bs = "re") +
##      s(target, bs = "re")
##
## Parametric coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.69145    0.03849 -43.946 < 2e-16
## Identicalrelated  0.04661    0.01559   2.991  0.00282
##
## Approximate significance of smooth terms:
##              edf   Ref.df      F  p-value
## te(Spelling,Vocabulary)  4.408    4.487  2.479 0.041067
## te(PC1,PC2)             4.923    5.063  4.778 0.000242
## s(PC2,Subject)          19.485   58.000  0.514 0.005797
## s(Trial,Subject)        155.074 527.000  1.687 < 2e-16
## s(PrevTarget)           27.667 139.000  0.255 0.017261
## s(prime)                20.870 106.000  0.290 0.021262
## s(target)              23.492   33.000  4.477 2.72e-12
##
## R-sq.(adj) =  0.42   Deviance explained = 49.4%
## fREML = 474.8   Scale est. = 0.073963   n = 2017
```



```
vis.gam(exp2.classic.gam, view=c('PC1','PC2'), color='topo',
        plot.type='contour', main='', xlab='PC1', ylab='PC2', too.far=0.1)
vis.gam(exp2.classic.gam, view=c('Spelling', 'Vocabulary'),
        xlab='Spelling Proficiency', ylab='Vocabulary',
        plot.type='contour', main='', color='topo', too.far=0.1)
```



```
exp2.ndl.gam <- bam(RTinv ~
  Identical +
  te(LogSubNorm1cG2L, SubNorm1aG2L, IndDiff, k=10) +
  s(target, bs='re') +
  s(prime, bs='re') +
  s(PrevTarget, bs='re') +
  s(Trial, Subject, bs='fs', m=1),
  data=exp2, method='fREML', discrete=TRUE)
```

```
summary(exp2.ndl.gam)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## RTinv ~ Identical + te(LogSubNorm1cG2L, SubNorm1aG2L, IndDiff,
##   k = 10) + s(target, bs = "re") + s(prime, bs = "re") + s(PrevTarget,
##   bs = "re") + s(Trial, Subject, bs = "fs", m = 1)
##
## Parametric coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.65479    0.03222  -51.364   <2e-16
## Identicalrelated  0.04746    0.01555   3.053   0.0023
##
```

```
## Approximate significance of smooth terms:
##
##          edf Ref.df      F  p-value
## te(LogSubNorm1cG2L,SubNorm1aG2L,IndDiff) 28.93  40.78  1.554  0.0144
## s(target)                                23.50  33.00  3.805  1.05e-10
## s(prime)                                  20.87 106.00  0.284   0.0204
## s(PrevTarget)                             27.98 139.00  0.256   0.0147
## s(Trial,Subject)                          156.99 529.00  1.903  < 2e-16
##
## R-sq.(adj) =  0.422   Deviance explained = 49.7%
## fREML = 464.51   Scale est. = 0.073648   n = 2017
```

```
qntls = quantile(exp2$IndDiff, seq(0,1,by=0.1))
qntls = qntls[c(2,4,6,8,10)]
for (i in 1:length(qntls)) {
  pvisgam(exp2.ndl.gam, select=1,
    view=c('LogSubNorm1cG2L','SubNorm1aG2L'),
    cond=list(IndDiff=qntls[i]), too.far=0.1,
    main=paste('Spe.Voc Score: ', round(qntls[i],2), sep=''),
    xlab='G2L prior', ylab='G2L a-diversity',
    zlim=c(-0.1,0.25))
}
```

