

Language and earings management: controlling for linguistic history

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Introduction

Test the relationship between strong/weak FTR and AAM, with and without controls for language family.

Load libraries

```
library(lme4)
library(sjPlot)
library(REEMtree)
library(rpart)
library(rpart.plot)
library(MASS)
library(ggplot2)
library(RColorBrewer)
library(MCMCglmm)
library(ape)
library(caper)
library(stargazer)
```

Load data

```
d = read.csv("../data/clean/data.csv",
             fileEncoding = "utf-8",
             encoding = 'utf-8')
```

Match each country to its main language and language family:

```
countryMainLanguageFamily =
  read.csv("../data/raw/CountryMainLanguageToLanguageFamily.csv",
           stringsAsFactors = F)

d$mainLanguageFamily =
  countryMainLanguageFamily[
    match(as.character(d$loc),
          countryMainLanguageFamily$Country.Code),
    ]$Family
```

Remove countries with many main language families:

```
d$CountryHasManyMainLanguages = countryMainLanguageFamily[
  match(as.character(d$loc),
        countryMainLanguageFamily$Country.Code),
  ]$ManyLanguages=="Y"
d2 = d[!d$CountryHasManyMainLanguages,]

d2 = d2[!is.na(d2$AAM),]
```

Remove cases with missing data:

```
keyVar = c("invpro", "pd", "indiv", "mas",
           "ua", "lto", "indul", "ggr", "SIZE",
           "BTM", "LEV", "ROA", "MEET", "LOSS")
d2 = d2[complete.cases(d2[,keyVar]),]
```

Table of languages:

```
data.frame(
  tapply(d2$strongftr, as.character(d2$loc), head, n=1)
)
```

```
##      tapply.d2.strongftr..as.character.d2.loc...head..n...1.
## AUS                                     1
## AUT                                     0
## BEL                                     0
## BGR                                     1
## BRA                                     0
## CAN                                     1
## CHE                                     0
## CHL                                     1
## CHN                                     0
## COL                                     1
## CZE                                     1
## DEU                                     0
## DNK                                     0
## EGY                                     1
```

## ESP	1
## FIN	0
## FRA	1
## GBR	1
## GRC	1
## HKG	0
## HUN	1
## IDN	0
## IND	1
## IRL	1
## ITA	1
## JOR	1
## JPN	0
## KOR	1
## LTU	1
## LUX	0
## LVA	1
## MAR	1
## MEX	1
## MYS	0
## NLD	0
## NOR	0
## NZL	1
## PAK	1
## PER	1
## PHL	1
## POL	1
## PRT	1
## ROU	1
## RUS	1
## SGP	1
## SWE	0
## THA	1
## TUR	1
## TWN	0
## USA	1

Convert to factors:

```
d2$mainLanguageFamily = factor(d2$mainLanguageFamily)
d2$MEET = factor(d2$MEET)
d2$LOSS = factor(d2$LOSS)
d2$strongftr = factor(d2$strongftr)
```

Scale variables:

```
d2Orig = d2
# Take log of AAM
d2$logAAM = log(1+d2$AAM)
#d2$logAAM = d2$logAAM - median(d2$logAAM,na.rm = T)
# Scale and center continuous variables
for(v in c("pd",'indiv','mas',
          'ua','lto','indul','ggr',
          'SIZE',"BTM","LEV","ROA")){
  d2[,v] = scale(d2[,v])
}
```

```
d2$AAM.scaled = scale(d2$AAM)
```

Mixed effects modelling

Model A: no controls for language family

Model `mA0` is a baseline model and model `mA1` adds the effect for FTR.

```
mA0 = lmer(AAM.scaled ~ 1 +
            invpro +
            pd + indiv + mas + ua + lto + indul +
            ggr +
            SIZE + BTM + LEV + ROA +
            MEET + LOSS +
            (1 | fyear) +
            (1 | indus),
            data = d2)
mA1 = update(mA0, ~. + strongftr)
```

Look at the estimates for variables within model `mA1`:

```
summary(mA1)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## AAM.scaled ~ invpro + pd + indiv + mas + ua + lto + indul + ggr +
##      SIZE + BTM + LEV + ROA + MEET + LOSS + (1 | fyear) + (1 |
##      indus) + strongftr
## Data: d2
##
## REML criterion at convergence: 256954.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.4990 -0.3712 -0.1335  0.1310 14.2360
##
## Random effects:
## Groups Name Variance Std.Dev.
## fyear (Intercept) 0.04171 0.2042
## indus (Intercept) 0.01484 0.1218
## Residual 0.88034 0.9383
## Number of obs: 94707, groups: fyear, 20; indus, 9
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  0.153654  0.063448  2.422
## invpro      -0.100554  0.003510 -28.644
## pd           0.012819  0.006140  2.088
## indiv        0.013771  0.009557  1.441
## mas          0.063738  0.003837 16.610
## ua          -0.062749  0.004456 -14.081
## lto          -0.124885  0.007243 -17.241
## indul        0.031991  0.006528  4.901
## ggr          -0.091870  0.005601 -16.401
## SIZE         0.036230  0.003744  9.677
## BTM          -0.010561  0.003274 -3.225
## LEV          0.006785  0.003353  2.023
```

```

## ROA          0.014690   0.003787   3.879
## MEET1        0.031684   0.006293   5.035
## LOSS1        0.167342   0.011696  14.308
## strongftr1   0.149591   0.010309  14.511

##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)       if you need it

Compare the fit of the two models to assess the effect of FTR:

anova(mA0,mA1)

## refitting model(s) with ML (instead of REML)

## Data: d2
## Models:
## mA0: AAM.scaled ~ 1 + invpro + pd + indiv + mas + ua + lto + indul +
## mA0:      ggr + SIZE + BTM + LEV + ROA + MEET + LOSS + (1 | fyear) +
## mA0:      (1 | indus)
## mA1: AAM.scaled ~ invpro + pd + indiv + mas + ua + lto + indul + ggr +
## mA1:      SIZE + BTM + LEV + ROA + MEET + LOSS + (1 | fyear) + (1 |
## mA1:      indus) + strongftr
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## mA0 18 257063 257234 -128514 257027
## mA1 19 256855 257035 -128409 256817 210.38      1 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

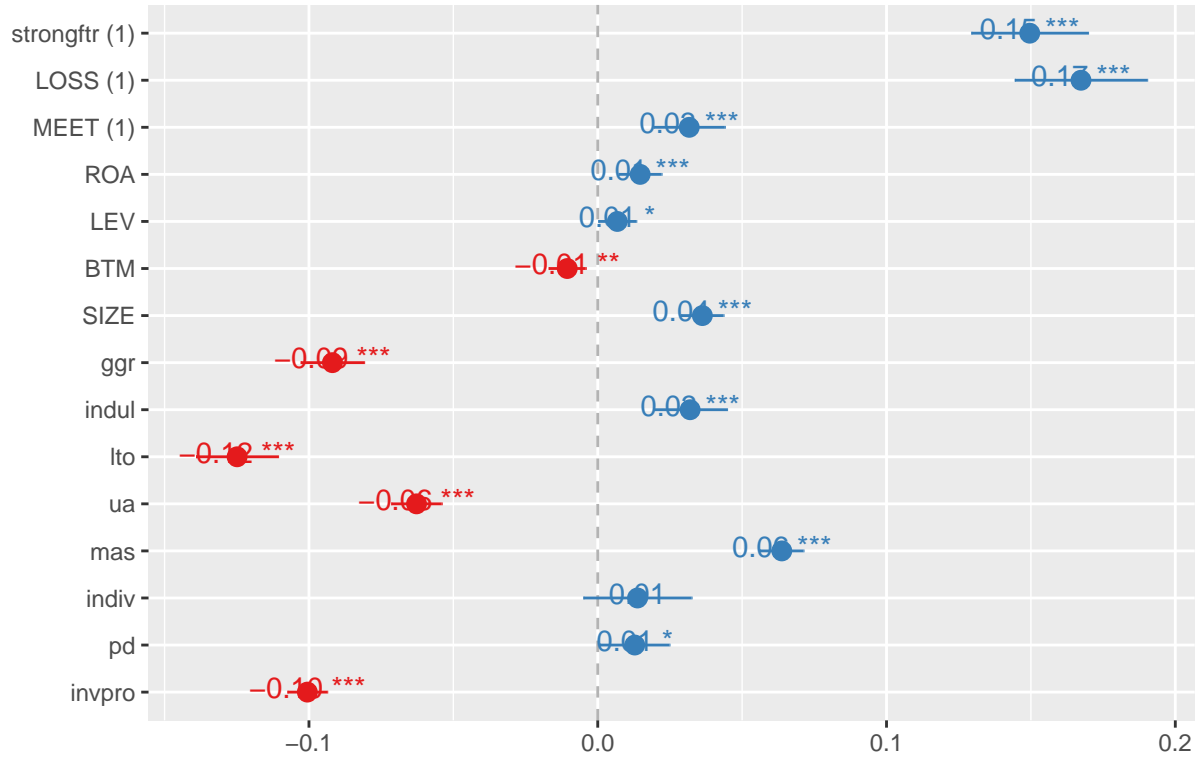
```

Plot fixed effects:

```
sjp.lmer(mA1,type="fe",p.kr = F)
```

```
## Computing p-values via Wald-statistics approximation (treating t as Wald z).
```

Fixed effects



Model B: with controls for language family

Model mB0 is the same as mA0, but with controls for language family. Model mB1 adds the FTR variable to the model for comparison.

```
mB0= update(mA0, ~.+(1 | mainLanguageFamily))
mB1= update(mB0, ~.+strongftr)
```

Look at the estimates for mB1:

```
summary(mB1)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## AAM.scaled ~ invpro + pd + indiv + mas + ua + lto + indul + ggr +
##      SIZE + BTM + LEV + ROA + MEET + LOSS + (1 | fyear) + (1 |
##      indus) + (1 | mainLanguageFamily) + strongftr
## Data: d2
##
## REML criterion at convergence: 256343.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.4757 -0.3765 -0.1269  0.1357 14.2536
##
## Random effects:
## Groups              Name            Variance Std.Dev.
## fyear                (Intercept)  0.04165   0.2041
## indus                (Intercept)  0.01531   0.1237
## mainLanguageFamily (Intercept)  0.10016   0.3165
## Residual                        0.87436   0.9351
## Number of obs: 94707, groups:  fyear, 20; indus, 9; mainLanguageFamily, 9
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  0.246953   0.124554   1.983
## invpro      -0.099264   0.004529 -21.919
## pd           0.055776   0.009174   6.079
## indiv        0.162885   0.014282  11.405
## mas          0.039045   0.006110   6.390
## ua          -0.047815   0.006584  -7.262
## lto         -0.220394   0.009085 -24.259
## indul        0.016509   0.007498   2.202
## ggr         -0.102036   0.005758 -17.720
## SIZE         0.020040   0.003848   5.207
## BTM         -0.010632   0.003271  -3.251
## LEV          0.009026   0.003355   2.690
## ROA          0.015726   0.003775   4.165
## MEET1        0.030613   0.006273   4.880
## LOSS1        0.140498   0.011720  11.988
## strongftr1   0.021657   0.016910   1.281
##
##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)      if you need it
```


Compare the two models to assess the significance of the FTR variable:

```
anova(mB0,mB1)
```

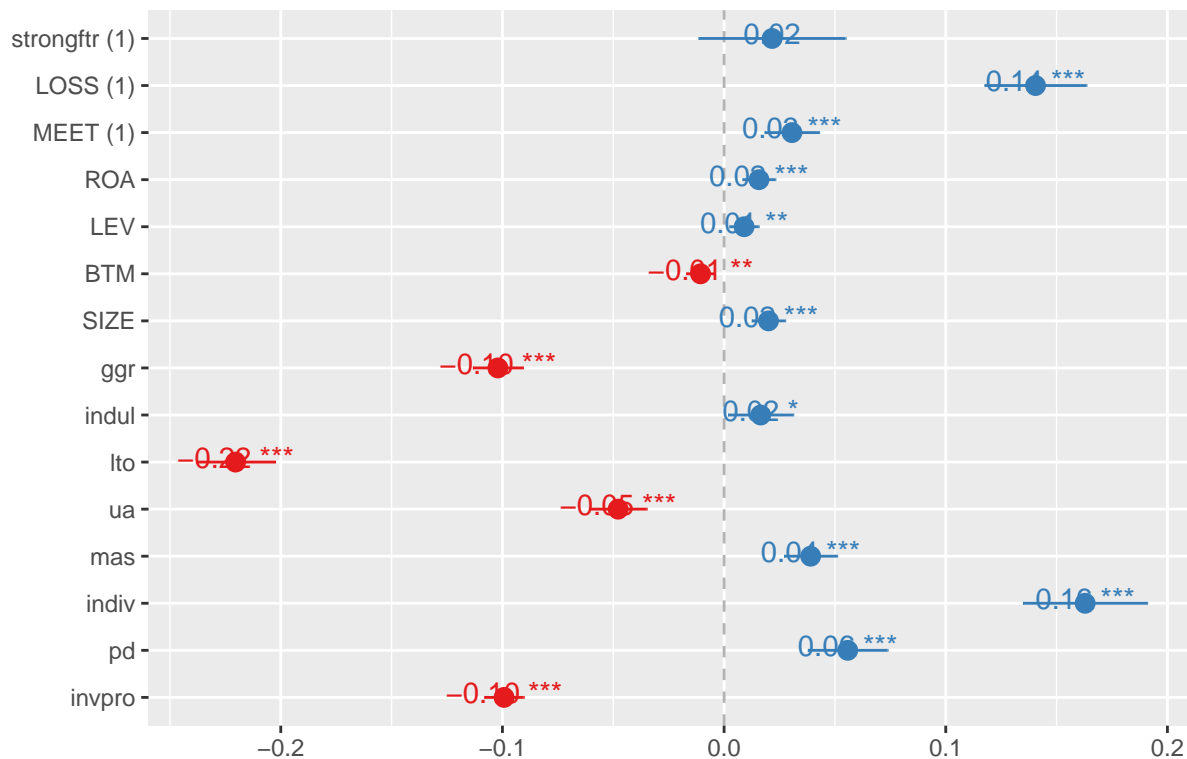
```
## refitting model(s) with ML (instead of REML)
## Data: d2
## Models:
## mB0: AAM.scaled ~ invpro + pd + indiv + mas + ua + lto + indul + ggr +
## mB0:      SIZE + BTM + LEV + ROA + MEET + LOSS + (1 | fyear) + (1 |
## mB0:      indus) + (1 | mainLanguageFamily)
## mB1: AAM.scaled ~ invpro + pd + indiv + mas + ua + lto + indul + ggr +
## mB1:      SIZE + BTM + LEV + ROA + MEET + LOSS + (1 | fyear) + (1 |
## mB1:      indus) + (1 | mainLanguageFamily) + strongftr
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## mB0 19 256254 256434 -128108 256216
## mB1 20 256254 256443 -128107 256214 1.6614      1      0.1974
```

Plot fixed effects with controls for language family:

```
sjp.lmer(mB1,type="fe",p.kr = F)
```

Computing p-values via Wald-statistics approximation (treating t as Wald z).

Fixed effects



Random slopes for FTR

Test if adding a random slope for FTR by language family significantly improves the fit of the model:

```
mB2 = lmer(AAM.scaled ~ 1 +
            invpro +
```

```

pd + indiv + mas + ua + lto + indul +
ggr +
SIZE + BTM + LEV + ROA +
MEET + LOSS +
strongftr +
(1 | fyear) +
(1 | indus) +
(1 + strongftr | mainLanguageFamily),
data = d2)

```

```
anova(mB1,mB2)
```

```

## refitting model(s) with ML (instead of REML)
## Data: d2
## Models:
## mB1: AAM.scaled ~ invpro + pd + indiv + mas + ua + lto + indul + ggr +
## mB1:      SIZE + BTM + LEV + ROA + MEET + LOSS + (1 | fyear) + (1 |
## mB1:      indus) + (1 | mainLanguageFamily) + strongftr
## mB2: AAM.scaled ~ 1 + invpro + pd + indiv + mas + ua + lto + indul +
## mB2:      ggr + SIZE + BTM + LEV + ROA + MEET + LOSS + strongftr +
## mB2:      (1 | fyear) + (1 | indus) + (1 + strongftr | mainLanguageFamily)
##      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## mB1 20 256254 256443 -128107 256214
## mB2 22 256180 256388 -128068 256136 78.319      2 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Yes, model fit significantly improves. The effect of FTR is even weaker:

```
summary(mB2)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: AAM.scaled ~ 1 + invpro + pd + indiv + mas + ua + lto + indul +
##      ggr + SIZE + BTM + LEV + ROA + MEET + LOSS + strongftr +
##      (1 | fyear) + (1 | indus) + (1 + strongftr | mainLanguageFamily)
##      Data: d2
##
## REML criterion at convergence: 256260.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.4711 -0.3755 -0.1230  0.1344 14.2610
##
## Random effects:
##      Groups             Name             Variance Std.Dev. Corr
##      fyear              (Intercept)  0.04226   0.2056
##      indus              (Intercept)  0.01570   0.1253
##      mainLanguageFamily (Intercept)  0.04331   0.2081
##                      strongftr1  0.07240   0.2691   0.60
##      Residual                      0.87352   0.9346
## Number of obs: 94707, groups:  fyear, 20; indus, 9; mainLanguageFamily, 9
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  0.2949671  0.1012065   2.915

```

```

## invpro      -0.1061720  0.0045830 -23.166
## pd          0.0499995  0.0093404  5.353
## indiv       0.1890531  0.0147841 12.788
## mas         0.0464442  0.0062111  7.478
## ua         -0.0248142  0.0071356 -3.477
## lto        -0.2406900  0.0094705 -25.415
## indul       0.0007693  0.0076795  0.100
## ggr        -0.0950665  0.0058169 -16.343
## SIZE        0.0181446  0.0038528  4.709
## BTM        -0.0105549  0.0032700 -3.228
## LEV         0.0094880  0.0033542  2.829
## ROA         0.0161278  0.0037749  4.272
## MEET1       0.0295640  0.0062706  4.715
## LOSS1       0.1391878  0.0117246 11.871
## strongftr1 -0.0366087  0.1089072 -0.336

##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)      if you need it

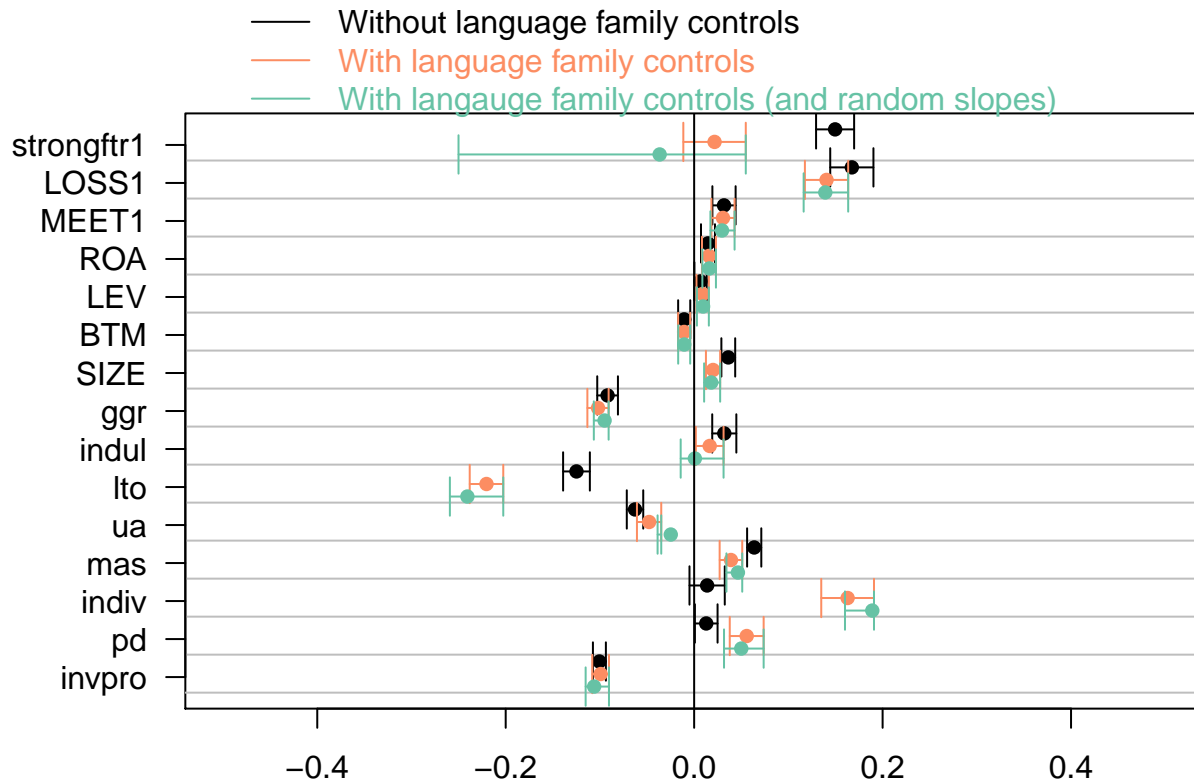
Calculate p-value for effect of FTR:
mB2_noFTR = update(mB2, ~. - strongftr)
anova(mB2,mB2_noFTR)

## refitting model(s) with ML (instead of REML)

## Data: d2
## Models:
## mB2_noFTR: AAM.scaled ~ invpro + pd + indiv + mas + ua + lto + indul + ggr +
## mB2_noFTR:      SIZE + BTM + LEV + ROA + MEET + LOSS + (1 | fyear) + (1 |
## mB2_noFTR:      indus) + (1 + strongftr | mainLanguageFamily)
## mB2: AAM.scaled ~ 1 + invpro + pd + indiv + mas + ua + lto + indul +
## mB2:      ggr + SIZE + BTM + LEV + ROA + MEET + LOSS + strongftr +
## mB2:      (1 | fyear) + (1 | indus) + (1 + strongftr | mainLanguageFamily)
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## mB2_noFTR 21 256178 256377 -128068 256136
## mB2       22 256180 256388 -128068 256136 0.1409      1      0.7073

```

Plot both models (code hidden):



```
## pdf
## 2
## pdf
## 2
```

Summary

Without a random intercept by main language family: There was a significant main effect of FTR ($\beta = 0.15$, log likelihood difference = 110 , $df = 1$, Chi Squared = 210.38 , $p = 1.1e-47$).

With a random intercept by main language family: There was no significant main effect of FTR ($\beta = 0.022$, log likelihood difference = 0.83 , $df = 1$, Chi Squared = 1.66 , $p = 0.2$).

Below are some statistics for other effects, using the same method as above:

[illegible]

##	Label	Beta	loglikDiff	df	chisq.test	p
## 2	pd : No controls	0.013	2.2	1	4.36	0.037
## 3	pd : With Controls	0.056	18	1	36.94	1.2e-09
## 4	indiv : No controls	0.014	1	1	2.08	0.15
## 5	indiv : With Controls	0.16	65	1	129.88	4.3e-30

## 6	mas : No controls	0.064	140	1	275.51	7.1e-62
## 7	mas : With Controls	0.039	20	1	40.87	1.6e-10
## 8	ua : No controls	-0.063	99	1	198.09	5.4e-45
## 9	ua : With Controls	-0.048	26	1	52.77	3.7e-13
## 10	lto : No controls	-0.12	150	1	296.83	1.6e-66
## 11	lto : With Controls	-0.22	290	1	581.64	1.6e-128
## 12	indul : No controls	0.032	12	1	24.01	9.6e-07
## 13	indul : With Controls	0.017	2.4	1	4.87	0.027
## 14	ggr : No controls	-0.092	130	1	268.69	2.2e-60
## 15	ggr : With Controls	-0.1	160	1	313.39	4e-70
## 16	SIZE : No controls	0.036	47	1	93.62	3.8e-22
## 17	SIZE : With Controls	0.02	14	1	27.15	1.9e-07
## 18	BTM : No controls	-0.011	5.2	1	10.41	0.0013
## 19	BTM : With Controls	-0.011	5.3	1	10.57	0.0012
## 20	LEV : No controls	0.0068	2	1	4.09	0.043
## 21	LEV : With Controls	0.009	3.6	1	7.23	0.0072
## 22	ROA : No controls	0.015	7.5	1	15.04	0.00011
## 23	ROA : With Controls	0.016	8.7	1	17.35	3.1e-05

```
resOther2 = cbind(
  resOther[seq(1,nrow(resOther)-1,by=2),c("Label","Beta","p")],
  resOther[seq(2,nrow(resOther),by=2),c("Beta","p")])
write.csv(resOther2,"../results/BetaResults_OtherVariables.csv",row.names = F)
```

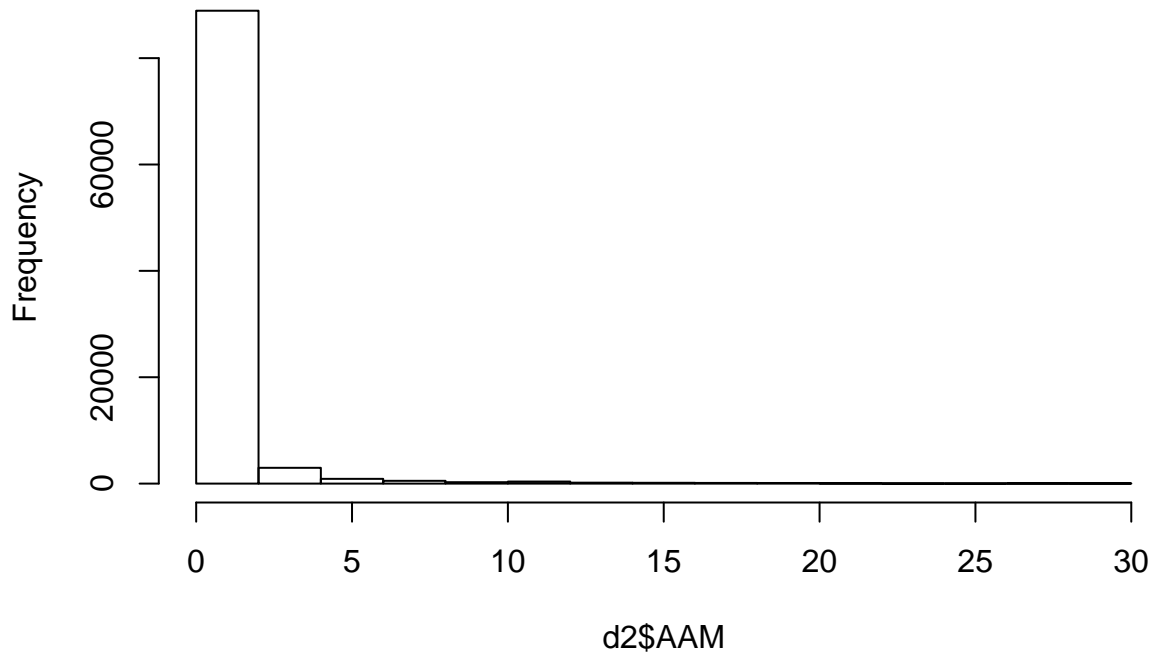
Alternative tests

Gamma distribution model

The distribution of the AAM variable is highly skewed and values below zero are not permitted:

```
hist(d2$AAM)
```

Histogram of d2\$AAM



```
normalDist = rnorm(n=length(d2$AAM),  
                  mean = mean(d2$AAM),  
                  sd = sd(d2$AAM))  
ks.test(d2$AAM,normalDist)
```

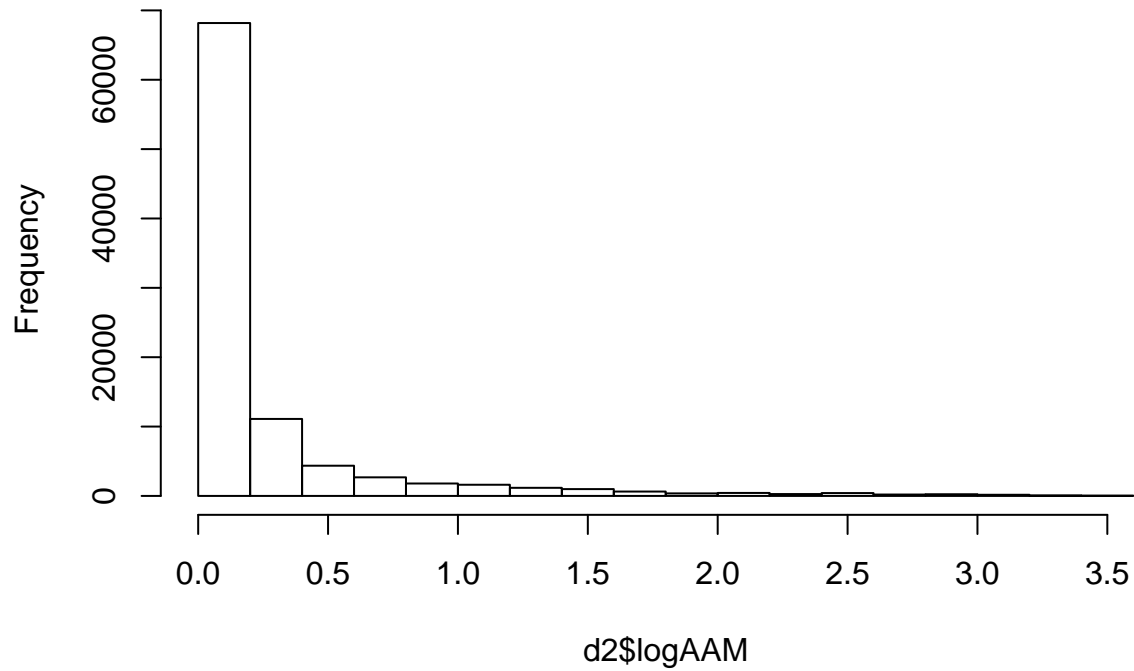
```
## Warning in ks.test(d2$AAM, normalDist): p-value will be approximate in the  
## presence of ties
```

```
##  
## Two-sample Kolmogorov-Smirnov test  
##  
## data: d2$AAM and normalDist  
## D = 0.3916, p-value < 2.2e-16  
## alternative hypothesis: two-sided
```

Even the log-transformed variable is skewed:

```
hist(d2$logAAM)
```


Histogram of d2\$logAAM

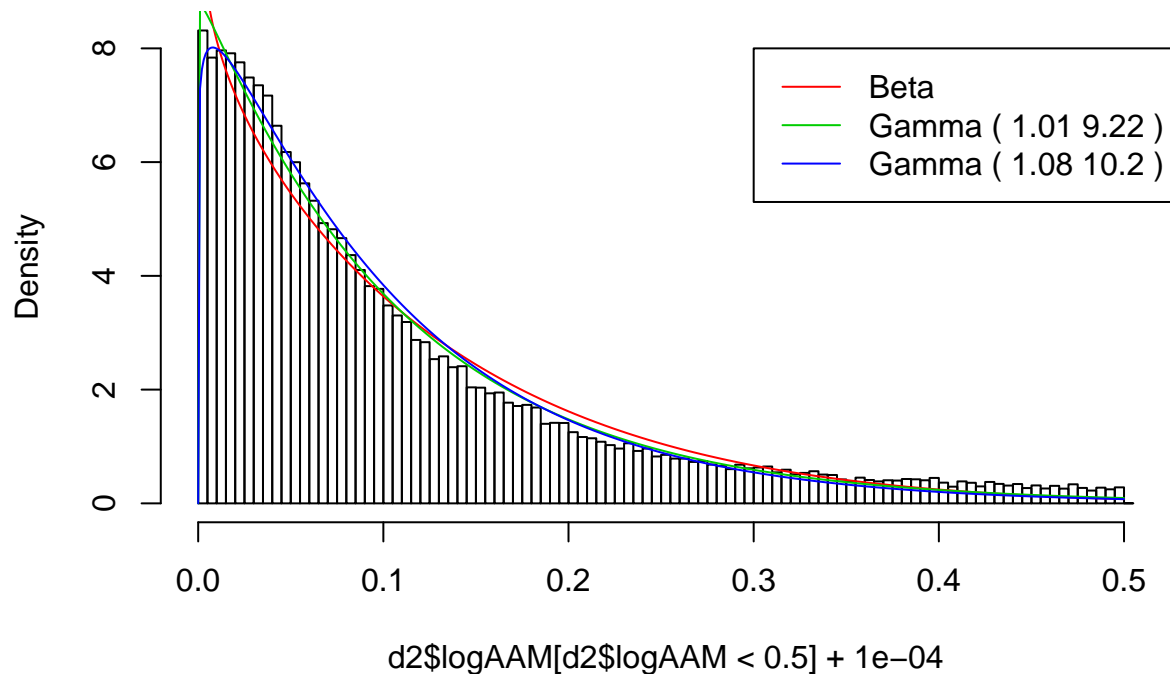


This leads to the models above (which use Gaussian distributions) producing very poor fits:

```
## pdf
## 2
```

Here we compare how Beta and Gamma distributions fit the log data:

Log AAM



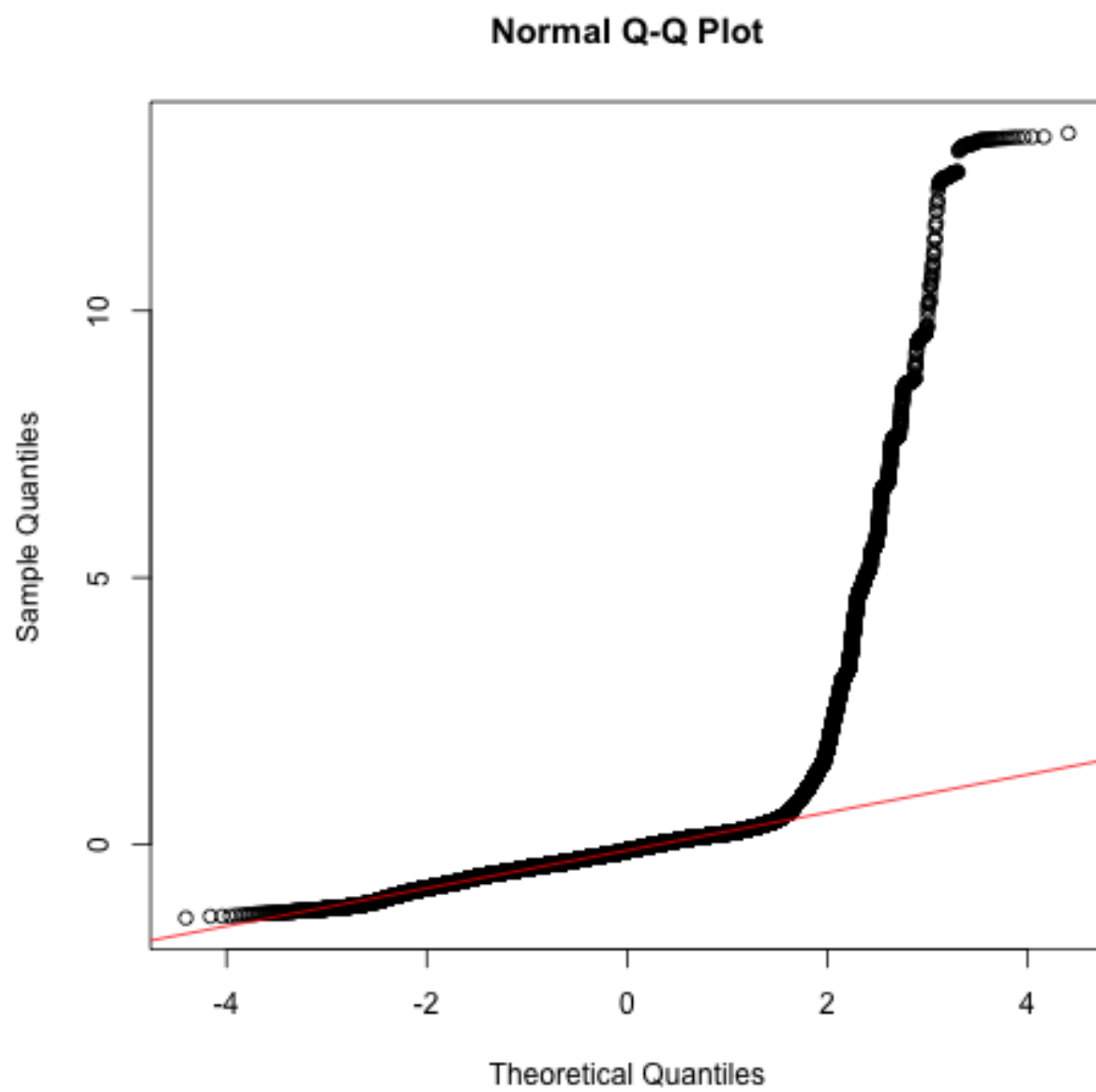


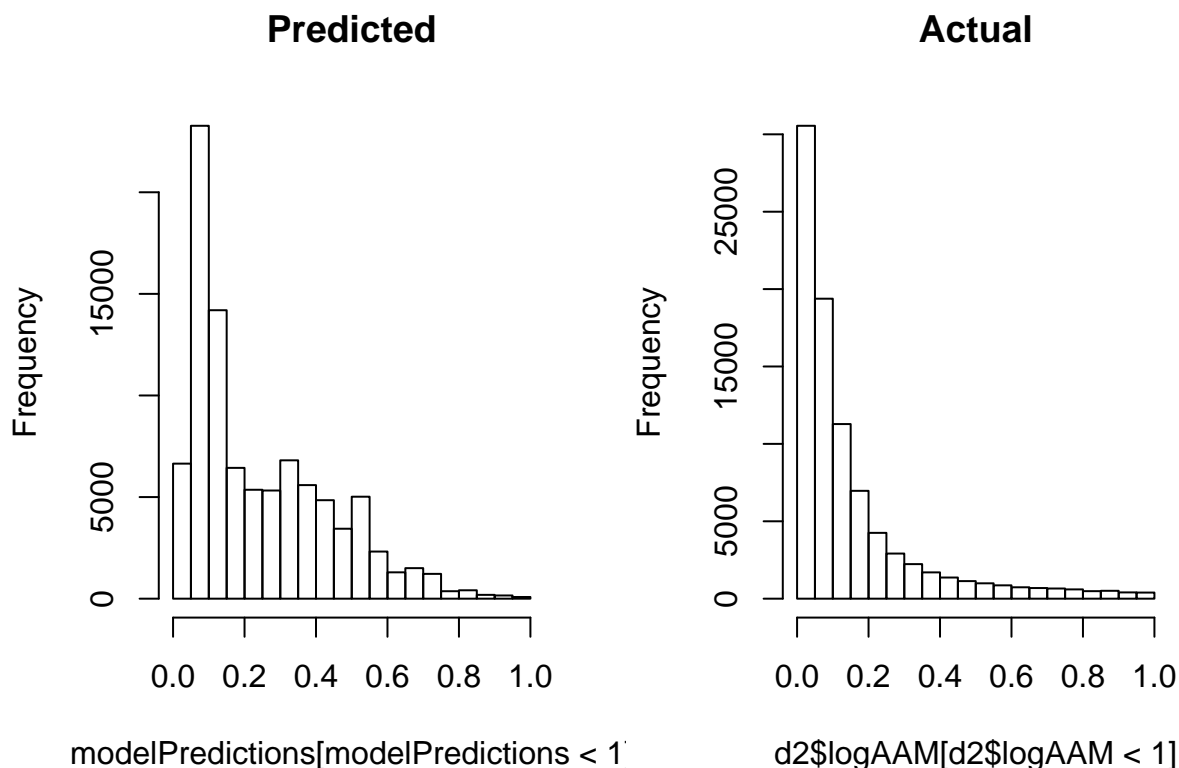
Figure 1:

The Gamma distribution seems to fit best. Fit a model with a Gamma distribution (without language family controls, with a random intercept by family and with a random intercept and slope):

```
mA1Gamma = glmer(logAAM+0.0001 ~ 1 +
  invpro +
  pd + indiv + mas + ua + lto + indul +
  ggr +
  SIZE + BTM + LEV + ROA +
  MEET + LOSS +
  strongftr +
  (1 | fyear) +
  (1 | indus),
  data = d2,
  family=Gamma(link="log"))
mB1Gamma = update(mA1Gamma, ~.+(1 | mainLanguageFamily))
mB2Gamma= update(mB1Gamma,
  ~.+(0+strongftr|mainLanguageFamily))
```

Check that the model is producing a sensible distribution:

```
modelPredictions = exp(predict(mB1Gamma))-0.0001
par(mfrow=c(1,2))
hist(modelPredictions[modelPredictions<1],main="Predicted")
hist(d2$logAAM[d2$logAAM<1],main="Actual")
```



```
par(mfrow=c(1,1))
png("../results/misc/qqplot_Gamma.png")
qqnorm(resid(mB1Gamma))
qqline(resid(mB1Gamma),col=2)
dev.off()
```

```
## pdf
## 2
```

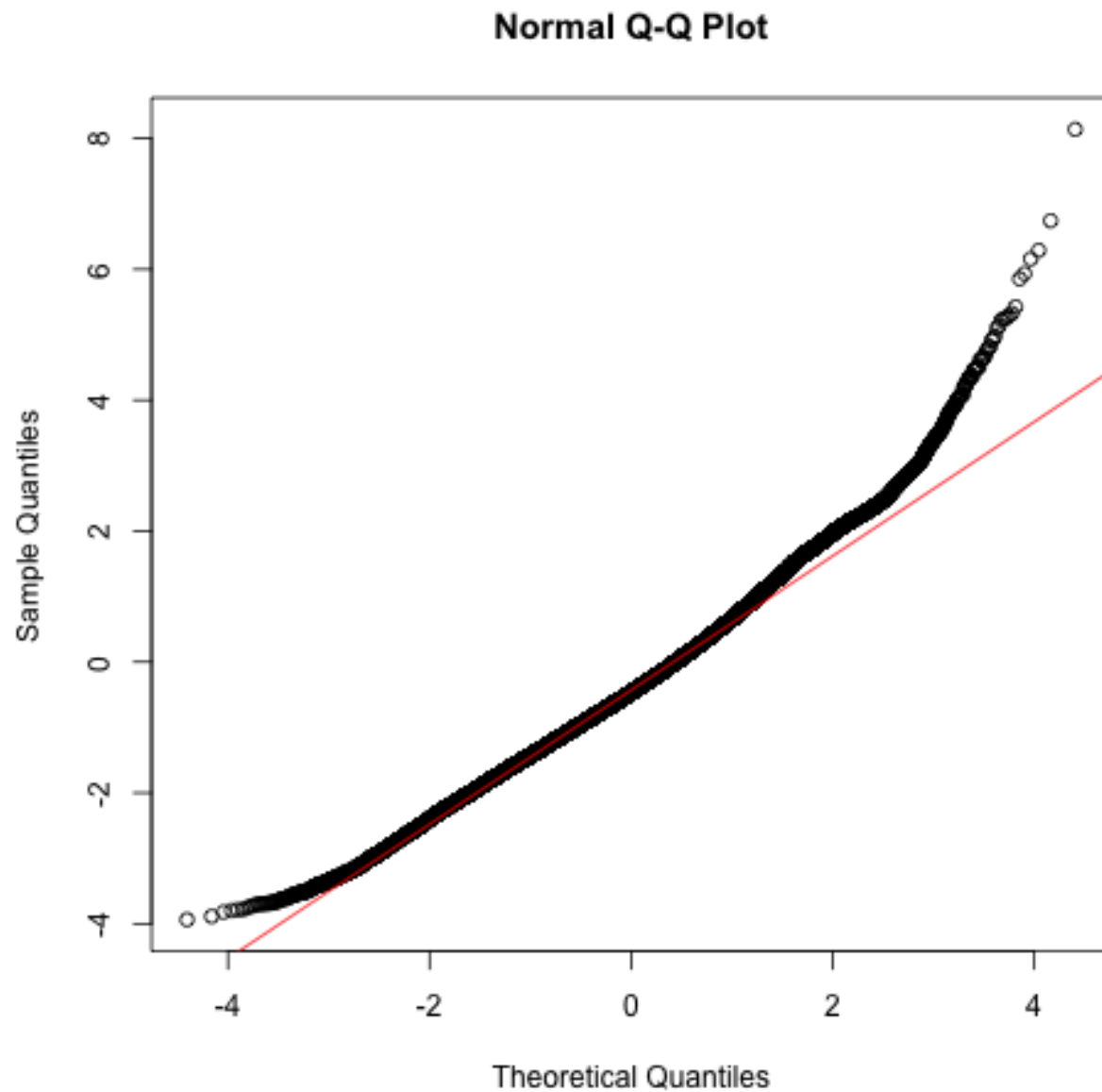


Figure 2:

Still not perfect at higher levels, but much better than the Gaussian models.

Model results:

```
summary(mA1Gamma)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: Gamma ( log )
## Formula:
```

```

## logAAM + 1e-04 ~ 1 + invpro + pd + indiv + mas + ua + lto + indul +
##   ggr + SIZE + BTM + LEV + ROA + MEET + LOSS + strongftr +
##   (1 | fyear) + (1 | indus)
## Data: d2
##
##      AIC      BIC    logLik deviance df.resid
## -135644.9 -135465.2  67841.5 -135682.9    94688
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.821 -0.619 -0.338  0.225  34.398
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   fyear    (Intercept) 0.2003   0.4476
##   indus     (Intercept) 0.1181   0.3436
##   Residual                1.4813   1.2171
## Number of obs: 94707, groups:  fyear, 20; indus, 9
##
## Fixed effects:
##              Estimate Std. Error t value Pr(>|z|)
## (Intercept) -1.6280301  0.1266208  -12.86 < 2e-16 ***
## invpro      -0.2124855  0.0043007  -49.41 < 2e-16 ***
## pd          -0.0867836  0.0075234  -11.54 < 2e-16 ***
## indiv       -0.0513334  0.0122957   -4.17 2.98e-05 ***
## mas          0.1074145  0.0047423   22.65 < 2e-16 ***
## ua          -0.1914821  0.0055205  -34.69 < 2e-16 ***
## lto         -0.3641583  0.0094341  -38.60 < 2e-16 ***
## indul        0.0719161  0.0075237    9.56 < 2e-16 ***
## ggr         -0.0838851  0.0064592  -12.99 < 2e-16 ***
## SIZE         0.0083879  0.0042610    1.97  0.049 *
## BTM         -0.0446026  0.0034390  -12.97 < 2e-16 ***
## LEV         -0.0021147  0.0036797   -0.57  0.565
## ROA          0.0003773  0.0039579    0.10  0.924
## MEET1        0.0521151  0.0071332    7.31 2.75e-13 ***
## LOSS1        0.3089023  0.0131382   23.51 < 2e-16 ***
## strongftr1   0.5389408  0.0118434   45.51 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)      if you need it
summary(mB1Gamma)

## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##   Family: Gamma ( log )
## Formula: logAAM + 1e-04 ~ invpro + pd + indiv + mas + ua + lto + indul +
##   ggr + SIZE + BTM + LEV + ROA + MEET + LOSS + strongftr +
##   (1 | fyear) + (1 | indus) + (1 | mainLanguageFamily)
## Data: d2
##

```

```

##           AIC           BIC      logLik deviance df.resid
## -138252.8 -138063.7   69146.4 -138292.8     94687
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.8377 -0.6265 -0.3331  0.2380 30.7850
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
##   fyear              (Intercept)  0.1944     0.4409
##   indus              (Intercept)  0.1172     0.3424
##   mainLanguageFamily (Intercept)  1.0053     1.0027
##   Residual                                1.4246     1.1936
## Number of obs: 94707, groups:  fyear, 20; indus, 9; mainLanguageFamily, 9
##
## Fixed effects:
##              Estimate Std. Error t value Pr(>|z|)
## (Intercept) -1.810443   0.306027  -5.92 3.30e-09 ***
## invpro      -0.140605   0.005364 -26.21 < 2e-16 ***
## pd          -0.019084   0.010442  -1.83 0.067622 .
## indiv       0.368243   0.018088  20.36 < 2e-16 ***
## mas         0.104654   0.007575  13.82 < 2e-16 ***
## ua         -0.027409   0.007689  -3.56 0.000364 ***
## lto        -0.576459   0.010866 -53.05 < 2e-16 ***
## indul      0.018232   0.009269   1.97 0.049184 *
## ggr        -0.079520   0.006515 -12.21 < 2e-16 ***
## SIZE       -0.017009   0.004316  -3.94 8.11e-05 ***
## BTM        -0.036027   0.003404 -10.58 < 2e-16 ***
## LEV         0.002056   0.003653   0.56 0.573598
## ROA        -0.002173   0.003933  -0.55 0.580592
## MEET1       0.049931   0.007059   7.07 1.51e-12 ***
## LOSS1       0.257498   0.013082  19.68 < 2e-16 ***
## strongftr1  0.179186   0.018865   9.50 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)      if you need it
summary(mB2Gamma)

## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##   Family: Gamma ( log )
## Formula: logAAM + 1e-04 ~ invpro + pd + indiv + mas + ua + lto + indul +
##   ggr + SIZE + BTM + LEV + ROA + MEET + LOSS + strongftr +
##   (1 | fyear) + (1 | indus) + (1 | mainLanguageFamily) + (0 +
##   strongftr | mainLanguageFamily)
##   Data: d2
##
##           AIC           BIC      logLik deviance df.resid
## -138420.8 -138203.2   69233.4 -138466.8     94684
##

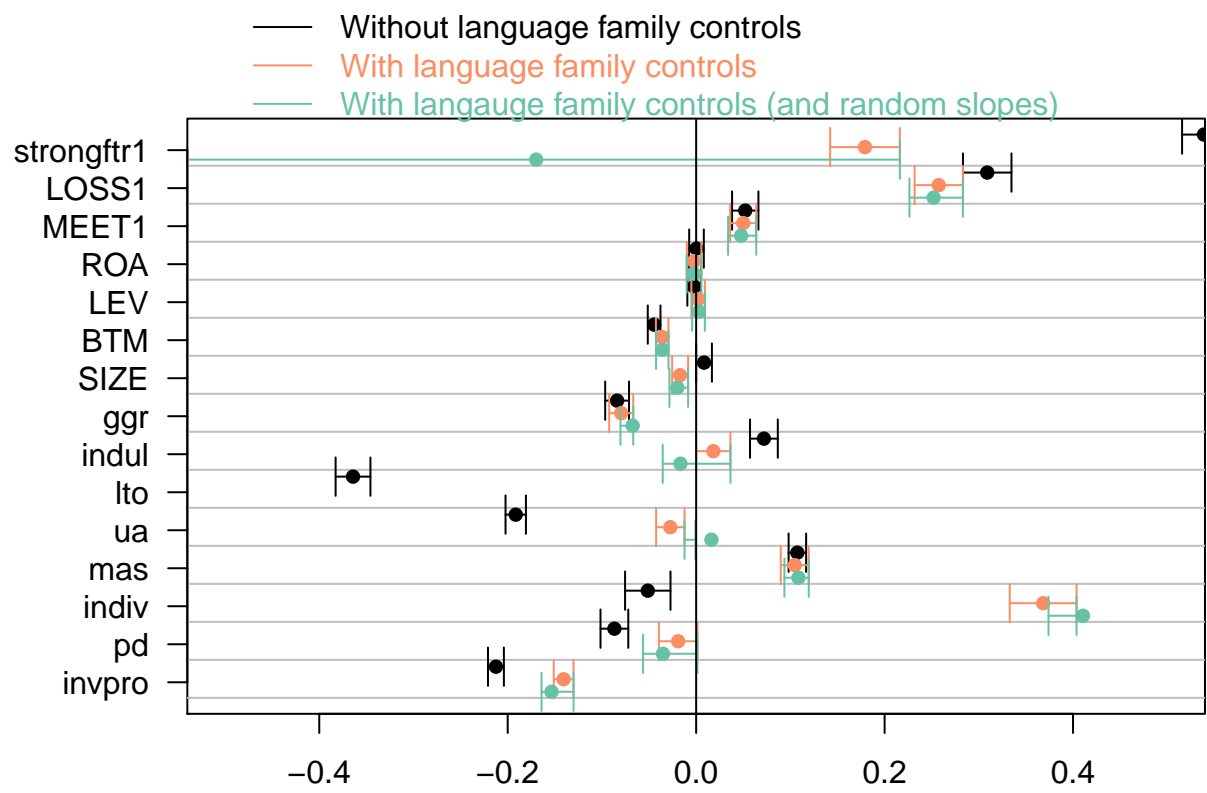
```

```

## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -0.8383 -0.6263 -0.3326  0.2380 31.1752
##
## Random effects:
##      Groups                Name         Variance Std.Dev. Corr
##      fyear                (Intercept) 0.2067261 0.45467
##      indus                (Intercept) 0.1191341 0.34516
##      mainLanguageFamily    (Intercept) 0.0003559 0.01887
##      mainLanguageFamily.1 strongftr0 0.6283060 0.79266
##                        strongftr1 1.7129177 1.30878 0.94
##      Residual                        1.4226490 1.19275
## Number of obs: 94707, groups:  fyear, 20; indus, 9; mainLanguageFamily, 9
##
## Fixed effects:
##              Estimate Std. Error t value Pr(>|z|)
## (Intercept) -1.620158   0.266232  -6.09 1.16e-09 ***
## invpro      -0.153494   0.005415 -28.35 < 2e-16 ***
## pd          -0.035222   0.010760  -3.27 0.00106 **
## indiv       0.410556   0.018690  21.97 < 2e-16 ***
## mas         0.108590   0.007622  14.25 < 2e-16 ***
## ua          0.016180   0.008635   1.87 0.06096 .
## lto         -0.612745   0.011464 -53.45 < 2e-16 ***
## indul       -0.016607   0.009616  -1.73 0.08417 .
## ggr         -0.067387   0.006620 -10.18 < 2e-16 ***
## SIZE        -0.019870   0.004320  -4.60 4.24e-06 ***
## BTM         -0.035865   0.003402 -10.54 < 2e-16 ***
## LEV          0.002873   0.003653   0.79 0.43153
## ROA         -0.002389   0.003930  -0.61 0.54320
## MEET1        0.047749   0.007056   6.77 1.31e-11 ***
## LOSS1        0.252019   0.013080  19.27 < 2e-16 ***
## strongftr1  -0.169744   0.212595  -0.80 0.42461
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

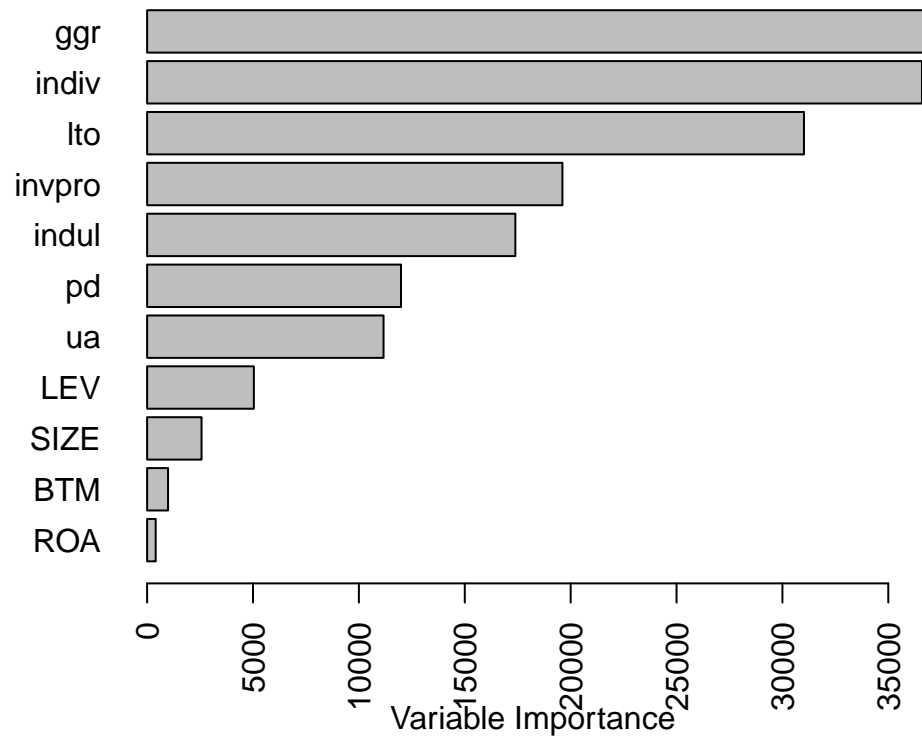
##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)      if you need it

```



pdf
2


```
barplot(sort(varimp), horiz=T, las=2,
        xlab="Variable Importance")
```



```
par(mar=c(5, 4, 4, 2) + 0.1)
```

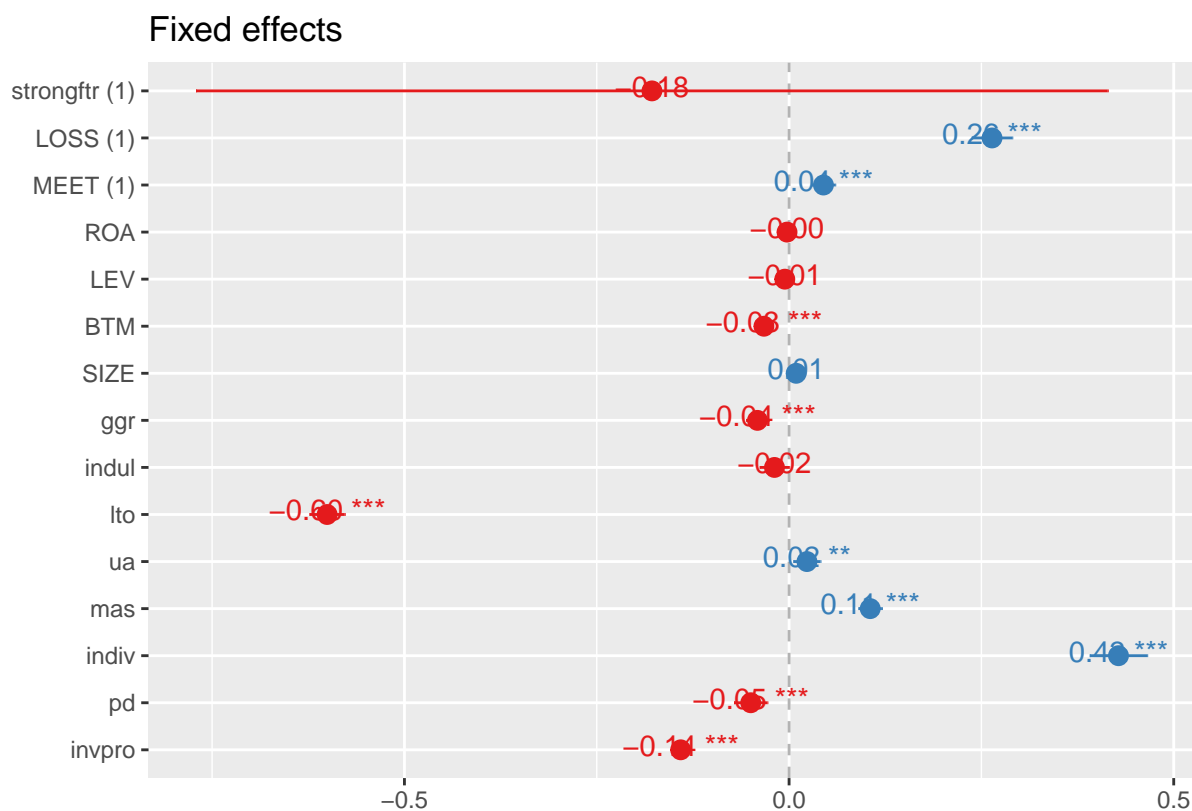
Random slopes

We can take a closer look at the random slopes for each language family:

```
d3 = d2[d2$mainLanguageFamily %in%  
  c("Austronesian", "Indo-European",  
    "Sino-Tibetan", "Uralic"),]  
mB2GammaFamily = update(mB2Gamma, data = d3)
```

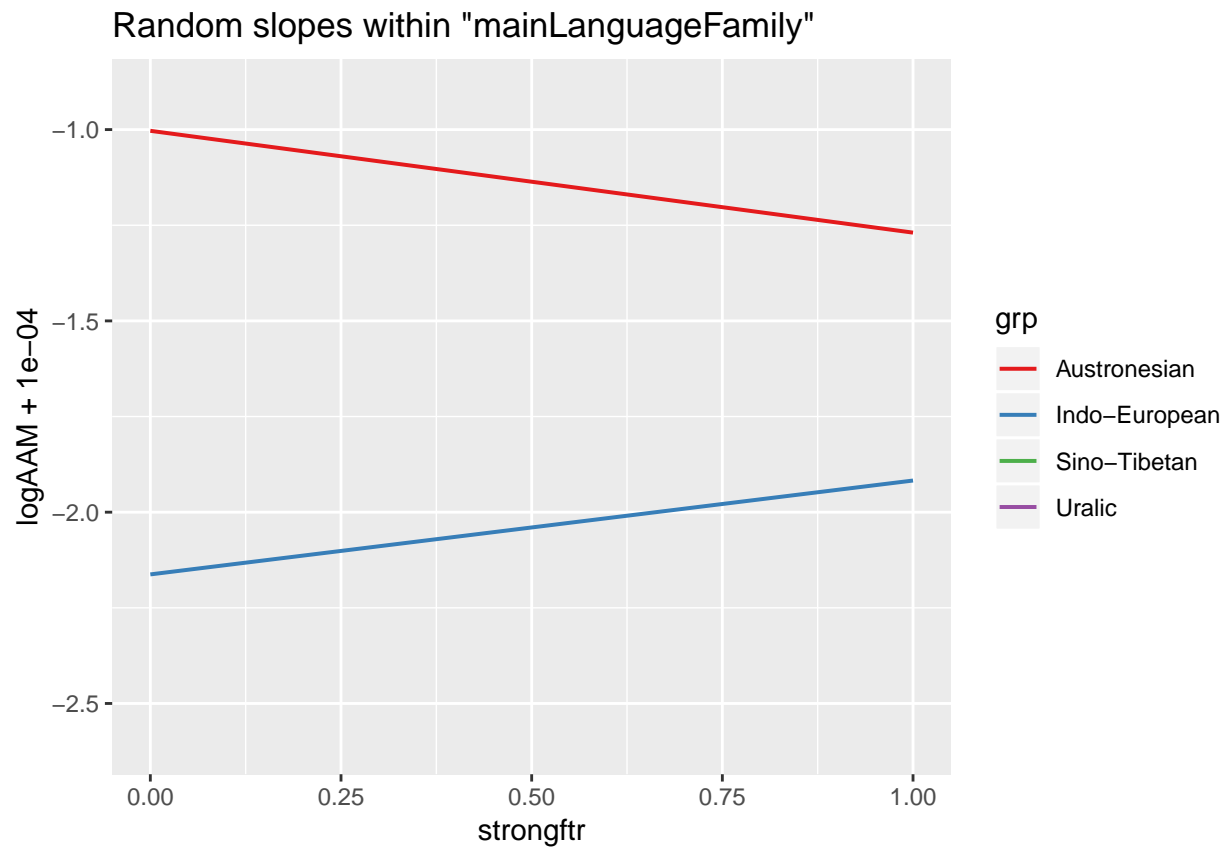
```
## Warning in checkConv(attr("derivs"), opt$par, ctrl = control  
## $checkConv, : Model failed to converge with max|grad| = 0.0013761 (tol =  
## 0.001, component 1)
```

```
sjp.lmer(mB2GammaFamily, type = "fe", p.kr = F)
```

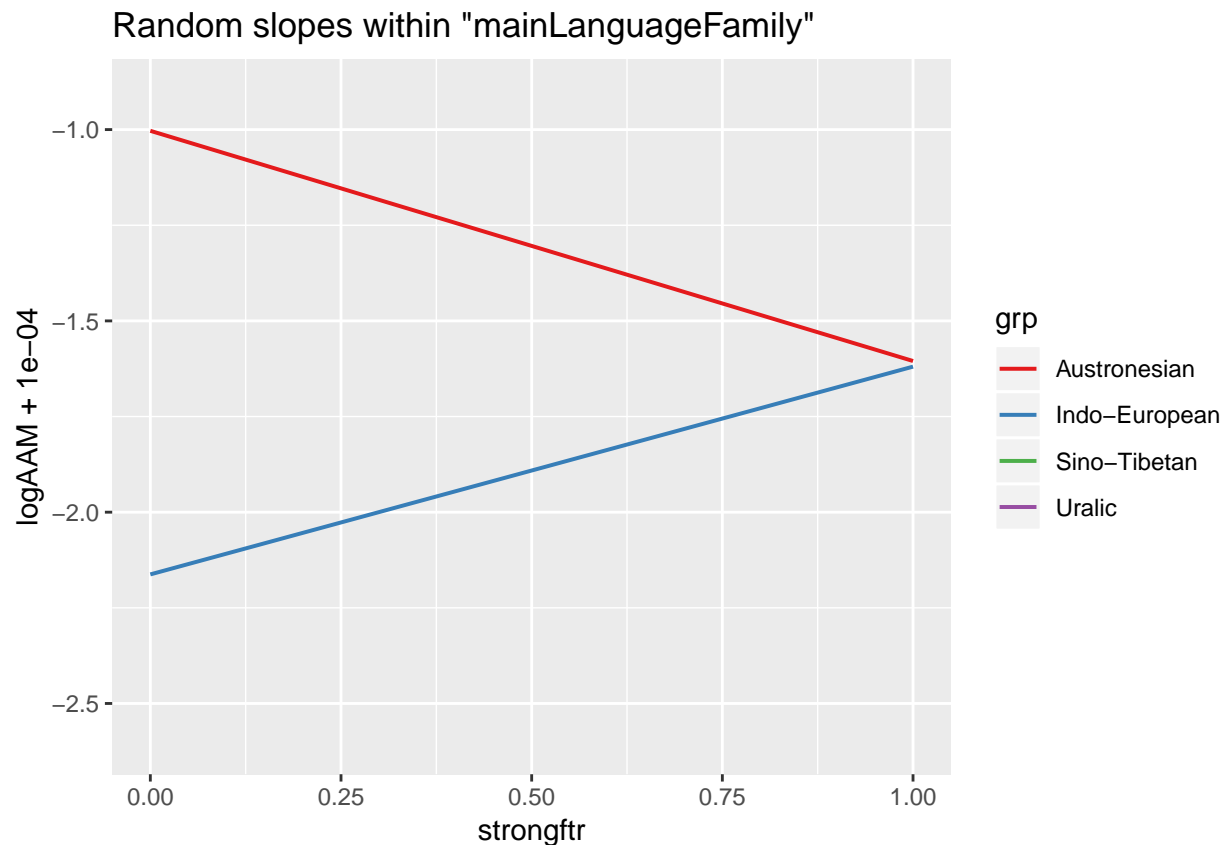


```
sjp.lmer(mB2GammaFamily, type = "rs.ri", vars = "strongftr", show.legend = T)
```

```
## Warning: Removed 2 rows containing missing values (geom_path).
```



Warning: Removed 2 rows containing missing values (geom_path).

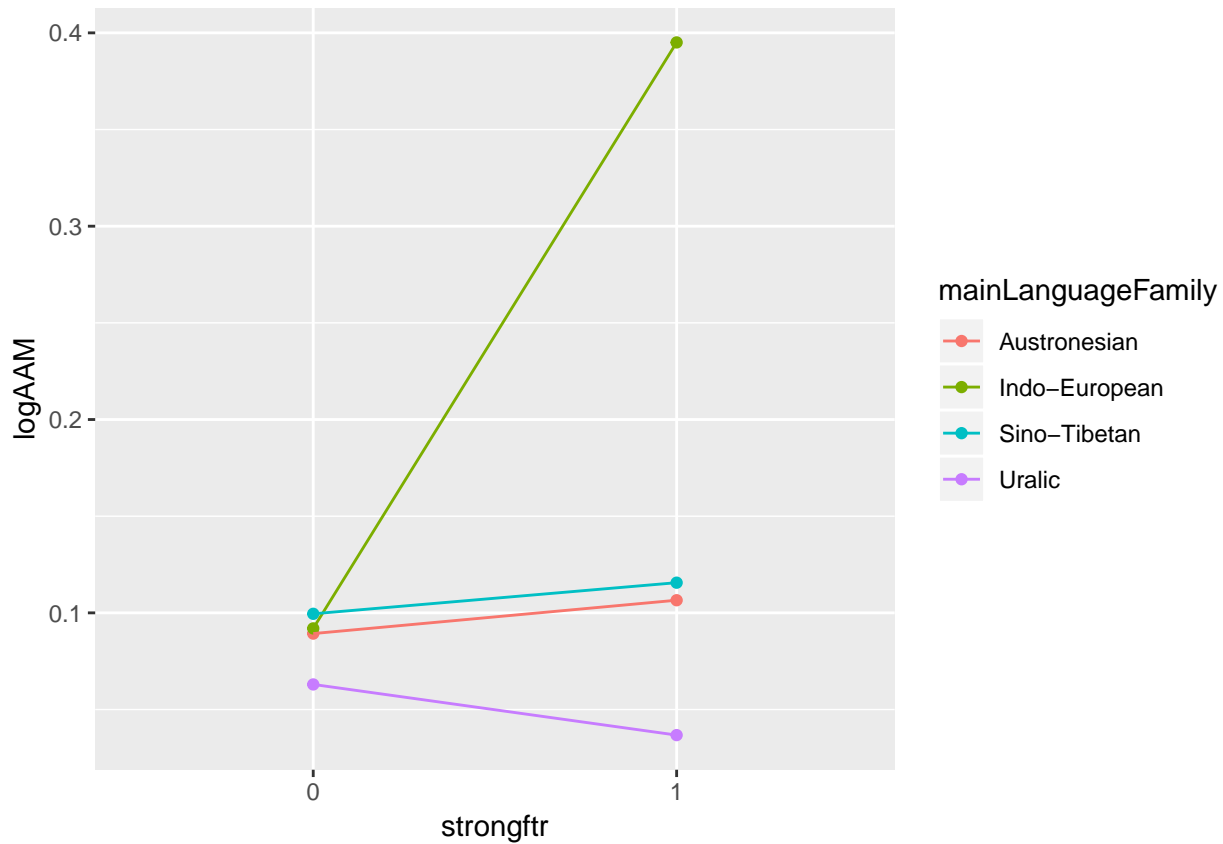


```
library(dplyr)

## Warning: package 'dplyr' was built under R version 3.3.2
##
## Attaching package: 'dplyr'
##
## The following object is masked from 'package:MASS':
##
##   select
##
## The following object is masked from 'package:nlme':
##
##   collapse
##
## The following objects are masked from 'package:stats':
##
##   filter, lag
##
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

x = d2[d2$mainLanguageFamily %in%
      c("Austronesian", "Indo-European",
        "Sino-Tibetan", "Uralic"),] %>%
  group_by(mainLanguageFamily, strongftr) %>%
  summarise(logAAM=mean(logAAM))
ggplot(x, aes(x=strongftr, y=logAAM, color=mainLanguageFamily)) +
  geom_point() +
```

```
geom_line(aes(group=mainLanguageFamily))
```



Model just for Indo-European languages:

```
mB1GammaIE = update(mA1Gamma, data=d2[d2$mainLanguageFamily=="Indo-European",])
summary(mB1GammaIE)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: Gamma ( log )
## Formula:
## logAAM + 1e-04 ~ 1 + invpro + pd + indiv + mas + ua + lto + indul +
## ggr + SIZE + BTM + LEV + ROA + MEET + LOSS + strongftr +
## (1 | fyear) + (1 | indus)
## Data: d2[d2$mainLanguageFamily == "Indo-European", ]
##
##      AIC      BIC    logLik deviance df.resid
## -39726.8 -39555.3  19882.4 -39764.8    61616
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -0.828 -0.632 -0.348  0.239 32.297
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## fyear    (Intercept) 0.2689    0.5186
## indus    (Intercept) 0.2729    0.5224
```

```

## Residual          1.4590   1.2079
## Number of obs: 61635, groups:  fyear, 20; indus, 9
##
## Fixed effects:
##           Estimate Std. Error t value Pr(>|z|)
## (Intercept) -0.326903   0.179472  -1.82 0.068535 .
## invpro      -0.460479   0.010504 -43.84 < 2e-16 ***
## pd          0.369501   0.013969  26.45 < 2e-16 ***
## indiv       0.222799   0.021596  10.32 < 2e-16 ***
## mas         0.244860   0.008143  30.07 < 2e-16 ***
## ua         -0.534175   0.013591 -39.30 < 2e-16 ***
## lto         -0.483771   0.016042 -30.16 < 2e-16 ***
## indul      -0.002515   0.013145  -0.19 0.848292
## ggr         -0.184346   0.013150 -14.02 < 2e-16 ***
## SIZE       -0.006981   0.005361  -1.30 0.192843
## BTM        -0.034560   0.004684  -7.38 1.61e-13 ***
## LEV        -0.014920   0.004513  -3.31 0.000947 ***
## ROA        -0.020073   0.004390  -4.57 4.81e-06 ***
## MEET1       0.015266   0.008982   1.70 0.089208 .
## LOSS1       0.176986   0.013648  12.97 < 2e-16 ***
## strongftr1 -0.105782   0.026847  -3.94 8.14e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)      if you need it

```

Phylogenetic test

Much of the data is linked to the Indo-European language family. We can use a phylogenetic tree (Bourckaert et al., 2012) to investigate the relationship between AAM and FTR when taking more fine-grained distinctions in linguistic history.

Subset of variables for the indo-european language family:

```
dIE = d[d$mainLanguageFamily=="Indo-European",]
dIE$DPlaceLang =
  countryMainLanguageFamily[
    match(as.character(dIE$loc),
          countryMainLanguageFamily$Country.Code),
  ]$DPlaceLang
```

Load tree and drop languages that are not in the dataset:

```
tree = read.nexus(file = "../data/raw/trees/bouckaert_et_al2012-d-place_2.NEXUS")
dplaceLangs = countryMainLanguageFamily$DPlaceLang[countryMainLanguageFamily$DPlaceLang!=""]
tree = drop.tip(tree,tree$tip.label[!tree$tip.label %in% dplaceLangs])
lx = read.csv("../data/raw/langftr.csv",stringsAsFactors = F)
countryMainLanguageFamily[countryMainLanguageFamily$FTR=="",]$FTR =
  c("Weak","Strong")[lx[match(countryMainLanguageFamily[countryMainLanguageFamily$FTR=="",]$Country.Code,
    lx$loc),]$strongftr+1]
```

```
## pdf
## 2
```

Collapse AAM and FTR within languages, and scale and center the AAM variable.

```
DP.FTR = factor(tapply(dIE$strongftr,dIE$DPlaceLang,head,n=1))
DP.LTO = scale(tapply(dIE$lto,dIE$DPlaceLang,mean,na.rm=T))
DP.AAM = scale(tapply(dIE$AAM,dIE$DPlaceLang,mean,na.rm=T))

cdata = data.frame(
  FTR = DP.FTR,
  AAM = DP.AAM,
  LTO = DP.LTO,
  lang = names(DP.FTR)
)
cdata = cdata[cdata$lang!="",]
```

Run a regression using the phylogenetic tree as a variance-covariance matrix.

```
# Priors
prior.PN<-list(
  G=list(
    G1=list(V=1,nu=0.002)),
  R=list(V=1,nu=0.002))
# Chain length
burnin = 100000
postBurnin =100000
thin = 10
# Run the model
set.seed(1289)
phyloModel0<-MCMCglmm(
  AAM ~ FTR,
  random=~lang,
```



```
ginverse=list(
  lang=inverseA(tree)$Ainv),
prior = prior.PN,
verbose=FALSE,
family="gaussian",
data = cdata,
nitt=burnin+postBurnin,
thin=thin,
burnin=burnin)
```

Results:

```
summary(phylModel0)
```

```
##
## Iterations = 100001:199991
## Thinning interval = 10
## Sample size = 10000
##
## DIC: 24.39859
##
## G-structure: ~lang
##
##      post.mean  1-95% CI u-95% CI eff.samp
## lang      1.395 0.0002236    4.025    578.1
##
## R-structure: ~units
##
##      post.mean  1-95% CI u-95% CI eff.samp
## units      0.597 0.0001479    1.568    494.9
##
## Location effects: AAM ~ FTR
##
##      post.mean 1-95% CI u-95% CI eff.samp pMCMC
## (Intercept)  -0.7944 -2.4719  0.6958  1485.2 0.310
## FTR1          0.9332 -0.4488  2.3000   905.9 0.188
```

There is no significant relationship between AAM and FTR.

Do the same test for Long-Term Orientation:

```
set.seed(12829)
phylModelLTO<-MCMCglmm(
  AAM ~ LTO,
  random=~lang,
  ginverse=list(
    lang=inverseA(tree)$Ainv),
  prior = prior.PN,
  verbose=FALSE,
  family="gaussian",
  data = cdata,
  nitt=burnin+postBurnin,
  thin=thin,
  burnin=burnin)
summary(phylModelLTO)
```

```

##
## Iterations = 100001:199991
## Thinning interval = 10
## Sample size = 10000
##
## DIC: 49.44665
##
## G-structure: ~lang
##
##      post.mean  1-95% CI u-95% CI eff.samp
## lang    0.4891 0.0001196    2.849    446.1
##
## R-structure: ~units
##
##      post.mean  1-95% CI u-95% CI eff.samp
## units    0.8295 0.0003182    1.571    1090
##
## Location effects: AAM ~ LTO
##
##      post.mean 1-95% CI u-95% CI eff.samp pMCMC
## (Intercept) -0.02423 -0.78404  0.72067    9630 0.9426
## LTO         -0.44768 -0.89869 -0.01900    8875 0.0476 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

OLS with clustered errors

Run a robust OLS regression, then print the results when clustering standard errors by language family. The results below were run using STATA code:

```
# No clustering
. reg AAM_scaled strongftr1 invpro pd
    indiv mas ua lto indul ggr size btm
    lev roa meet1 loss1,
    robust
```

Linear regression

```
Number of obs    =    94,707
F(15, 94691)     =    451.86
Prob > F         =    0.0000
R-squared        =    0.0731
Root MSE        =    .96283
```

		Coef.	Robust Std. Err.	t	P> t	[95% Conf. Interval]
AAM_scaled	strongftr1	.1317505	.0033255	39.62	0.000	.1252326 .1382685

```
# With clustering by language family
. reg AAM_scaled strongftr1 invpro pd
    indiv mas ua lto indul ggr size btm
    lev roa meet1 loss1,
    robust cluster(mainLanguageFamily)
```

Linear regression

```
Number of obs    =    94,707
F(7, 8)          =    .
Prob > F         =    .
R-squared        =    0.0731
Root MSE        =    .96283
```

(Std. Err. adjusted for 9 clusters in mainLanguageFamily)

		Coef.	Robust Std. Err.	t	P> t	[95% Conf. Interval]
AAM_scaled	strongftr1	.1317505	.079045	1.67	0.134	-.0505275 .3140286