

# Predicting semantic alignment by cultural similarity

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## Introduction

We compare cultural distances between societies with linguistic similarities between societies, controlling for shared history in two ways.

The first test uses mixed effects modelling. The pairing of the language family of each language (according to Glottolog) is used as a random effect. That means that the model can capture the likelihood that two languages from the Indo-European language family will be more similar to each other than two languages from different language families. The same is done with geographic area according to Autotyp.

The second test controls for history using distances from a phylogenetic tree. The tree comes from Bouckaert et al. (2012). Patristic distances between languages are used as a measure of historical distance between societies in a Mantel test. Note that the Mantel test assumes a strict distance metric, which is not necessarily the case with this data, but there are few other ways to deal with continuous pairwise distances.

## Load libraries

```
library(ape)
library(ecodist)
library(lme4)
library(sjPlot)
library(ggplot2)
library(igraph)
library(lattice)
library(dplyr)
```

Parameters (using data from Northuralex and Wikipedia, k=100, unfiltered):

```
datasetName = "wikipedia-main"
lingDistancesFile = "../data/FAIR/nel-wiki-k100-alignments-by-language-pair.csv"
lingDistancesFileNK = "../data/FAIR/nel-wiki-k100-alignments-by-language-pair-without-kinship.csv"
lingDistancesByDomainFile = "../results/EA_distances/nel-wiki-k100_with_ling.csv"
# (generated by ../processing/combineCultAndLingDistances.R)
```

## All domains

### Load data

Read the cultural distances:

```
cult = read.csv("../results/EA_distances/CulturalDistances_Long.csv", stringsAsFactors = F)
names(cult) = c("l1", "l2", "cult.dist")
```

Add language family:

```
l = read.csv("../data/FAIR_langauges_glottol_xdid.csv", stringsAsFactors = F)
g = read.csv("../data/glottolog-languoid.csv/languoid.csv", stringsAsFactors = F)
l$family = g[match(l$glotto, g$id),]$family_pk
l$family = g[match(l$family, g$pk),]$name
```

Read the semantic distances

```
ling = read.csv(lingDistancesFile, stringsAsFactors = F)
```

There are very few possible comparisons for Slovenian and Northern Sami, so we'll remove these:

```
ling = ling[!(ling$l1=="se" | ling$l2 == "se"),]
ling = ling[!(ling$l1=="sl" | ling$l2 == "sl"),]
```

Combine the linguistic and cultural distances. Note that we flip the cultural measure from a distance measure to a similarity measure.

```
cult$l1.iso2 = l[match(cult$l1, l$Language2),]$iso2
cult$l2.iso2 = l[match(cult$l2, l$Language2),]$iso2

fairisos = unique(c(ling$l1, ling$l2))
cultisos = unique(c(cult$l1.iso2, cult$l2.iso2))

cult = cult[(cult$l1.iso2 %in% fairisos) & (cult$l2.iso2 %in% fairisos),]
ling = ling[(ling$l1 %in% cultisos) & (ling$l2 %in% cultisos),]

matches = sapply(1:nrow(ling), function(i){
  which(cult$l1.iso2==ling$l1[i] & cult$l2.iso2==ling$l2[i])
})

ling$cult.dist = cult[matches,]$cult.dist
# Flip
ling$cult.dist = 1 - ling$cult.dist
# Scale
ling$cult.dist.center = scale(ling$cult.dist)
cdc.s = attr(ling$cult.dist.center, "scaled:scale")
cdc.c = attr(ling$cult.dist.center, "scaled:center")
ling$cult.dist.center = as.numeric(ling$cult.dist.center)
ling$comparison_count.center =
  scale(ling$comparison_count)

ling$family1 = l[match(ling$l1, l$iso2),]$family
ling$family2 = l[match(ling$l2, l$iso2),]$family
l[l$Language=="Arabic",]$autotyp.area= "Greater Mesopotamia"
l[l$Language=="Persian",]$autotyp.area= "Greater Mesopotamia"
ling$area1 = l[match(ling$l1, l$iso2),]$autotyp.area
```

```
ling$area2 = l[match(ling$l2, l$iso2),]$autotyp.area
```

```
fgroup = cbind(ling$family1,ling$family2)
fgroup = apply(fgroup,1,sort)
ling$family.group = apply(fgroup,2,paste,collapse=":")
agroup = cbind(ling$area1,ling$area2)
agroup = apply(agroup,1,sort)
ling$area.group = apply(agroup,2,paste,collapse=":")

ling$rho.center = scale(ling$local_alignment)
```

Each observation is now associated with a language family pair:

```
head(ling[,c("l1","l2","local_alignment","family.group")])
```

```
##      l1 l2 local_alignment      family.group
## 7   ja ab      0.01930414  Abkhaz-Adyge:Japonic
## 8   ab zh      0.02225169  Abkhaz-Adyge:Sino-Tibetan
## 10  cv xal      0.02765860      Mongolic:Turkic
## 11 xal ja      0.02832668      Japonic:Mongolic
## 12 xal zh      0.02895876      Mongolic:Sino-Tibetan
## 14  bn ab      0.03192066  Abkhaz-Adyge:Indo-European
```

And the same is true for area:

```
tail(ling[,c("l1","l2","local_alignment","area.group")])
```

```
##      l1 l2 local_alignment      area.group
## 2522 fr es      0.3936442      Europe:Europe
## 2524 cs uk      0.4023323      Europe:Inner Asia
## 2528 cs ru      0.4082099      Europe:Inner Asia
## 2529 be ru      0.4129814 Inner Asia:Inner Asia
## 2532 uk be      0.4276664 Inner Asia:Inner Asia
## 2535 uk ru      0.5079911 Inner Asia:Inner Asia
```

Number of observations:

```
# Number of datapoints:
nrow(ling)
```

```
## [1] 731
```

```
# Number of unique languages:
length(unique(unlist(ling[,c("l1","l2")])))
```

```
## [1] 39
```

```
# Number of unique language families:
uniqueFamilies = unique(unlist(ling[,c("family1","family2")]))
length(uniqueFamilies)
```

```
## [1] 10
```

```
# Number of unique areas:
uniqueAreas = unique(unlist(ling[,c("area1","area2")]))
length(uniqueAreas)
```

```
## [1] 6
```

Cross-over between language families and areas:

```
tx = data.frame(lang= c(ling$l1,ling$l2),
                 fam = c(ling$family1,ling$family2),
                 area= c(ling$area1,ling$area2))
tx = tx[!duplicated(tx),]
table(tx$fam,tx$area)
```

```
##
##           Europe Greater Mesopotamia Indic Inner Asia N Coast Asia
## Abkhaz-Adyge      0                1    0          0          0
## Afro-Asiatic      0                1    0          0          0
## Dravidian         0                0    3          0          0
## Indo-European    11                2    1          5          0
## Japonic           0                0    0          0          1
## Koreanic          0                0    0          0          1
## Mongolic          0                0    0          1          0
## Sino-Tibetan      0                0    0          0          0
## Turkic            0                1    0          5          0
## Uralic            1                0    0          4          0
##
##           Southeast Asia
## Abkhaz-Adyge      0
## Afro-Asiatic      0
## Dravidian         0
## Indo-European     0
## Japonic           0
## Koreanic          0
## Mongolic          0
## Sino-Tibetan      1
## Turkic            0
## Uralic            0
```

## LMER models

Mixed effects model, predicting Linguistic similaritys from cultural similarity, with random intercept for family and area and random slope for cultural similarity for family and area.

We start with a null model with random intercepts for family and area, and random slopes for cultural similarity by both. We add a fixed effect of the number of comparisons made for each datapoint (number of concepts that were available to compare). Then we add a fixed effect of cultural similarity

```
m0 = lmer(
  rho.center ~ 1 +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = ling
)
```

```
## boundary (singular) fit: see ?isSingular
```

```
m0.5 = lmer(
  rho.center ~ 1 +
    comparison_count.center +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = ling
)
```

```
## boundary (singular) fit: see ?isSingular
```

```
m1 = lmer(
  rho.center ~ 1 +
    comparison_count.center +
    cult.dist.center +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = ling
)
```

```
## boundary (singular) fit: see ?isSingular
```

```
an1 = anova(m0,m0.5,m1)
```

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

```
an1
```

```
## Data: ling
## Models:
## m0: rho.center ~ 1 + (1 + cult.dist.center | family.group) + (1 +
## m0:      cult.dist.center | area.group)
## m0.5: rho.center ~ 1 + comparison_count.center + (1 + cult.dist.center |
## m0.5:      family.group) + (1 + cult.dist.center | area.group)
## m1: rho.center ~ 1 + comparison_count.center + cult.dist.center +
## m1:      (1 + cult.dist.center | family.group) + (1 + cult.dist.center |
## m1:      area.group)
##      Df    AIC    BIC logLik deviance   Chisq Chi Df Pr(>Chisq)
## m0      8 1654.6 1691.3 -819.30   1638.6
## m0.5    9 1293.0 1334.3 -637.50   1275.0 363.597      1 < 2.2e-16 ***
## m1     10 1278.4 1324.4 -629.22   1258.4  16.564      1 4.704e-05 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Cultural similarity is not significantly correlated with Linguistic similarity. Here are the model estimates:

```
summary(m1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: rho.center ~ 1 + comparison_count.center + cult.dist.center +
##      (1 + cult.dist.center | family.group) + (1 + cult.dist.center |
##      area.group)
## Data: ling
##
## REML criterion at convergence: 1271.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6249 -0.6167  0.1103  0.6571  4.7402
##
## Random effects:
## Groups      Name                Variance Std.Dev. Corr
## family.group (Intercept)         0.1612630 0.40158
##              cult.dist.center 0.0001817 0.01348  1.00
## area.group   (Intercept)         0.0510850 0.22602
##              cult.dist.center 0.0036658 0.06055 -1.00
## Residual                        0.2885416 0.53716
## Number of obs: 731, groups:  family.group, 48; area.group, 20
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    -0.39270    0.09073  -4.328
## comparison_count.center 0.61196    0.02688  22.770
## cult.dist.center  0.19678    0.03275   6.008
##
## Correlation of Fixed Effects:
##              (Intr) cmpr_.
## cmprsn_cnt.  0.090
## clt.dst.cnt -0.194 -0.201
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Plot the estimates, rescaling the variables back to the original units:

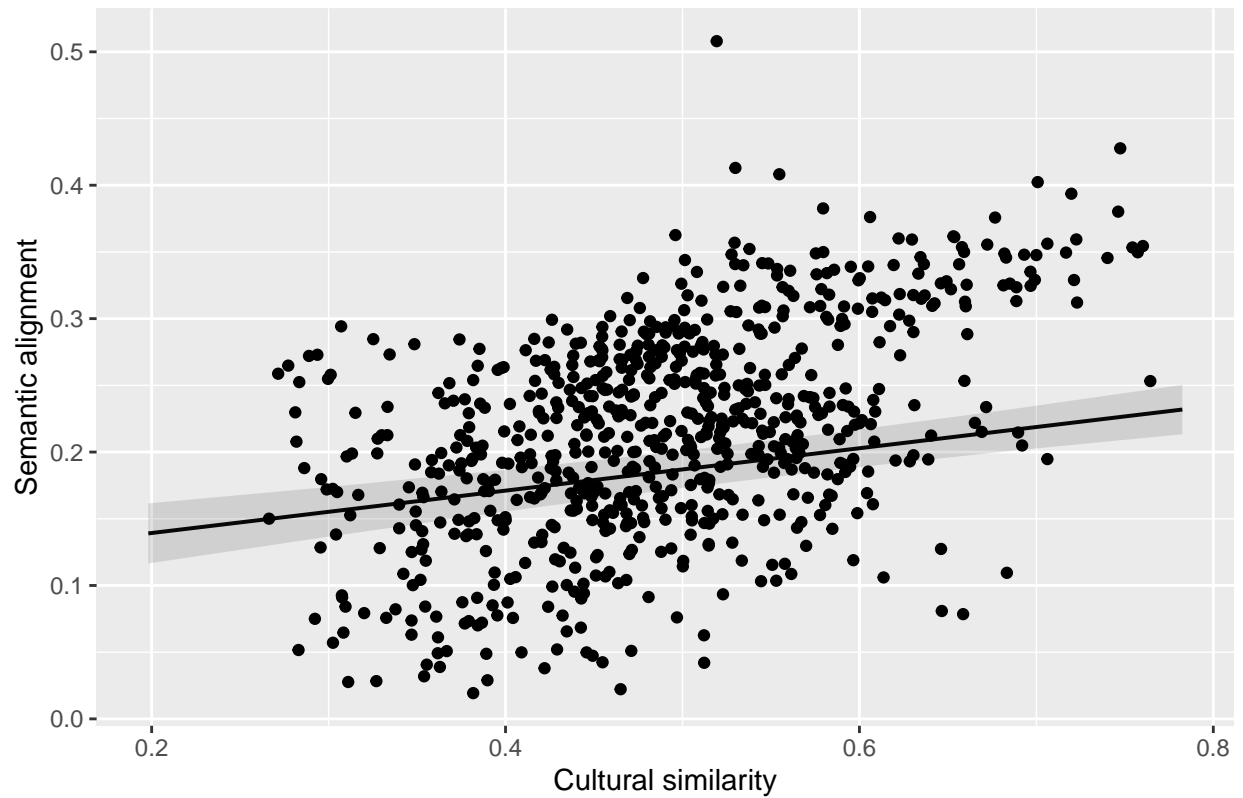
```
trans = function(X){
  X * attr(ling$rho.center,"scaled:scale") +
  attr(ling$rho.center,"scaled:center")
}

gx = plot_model(m1,'pred',terms='cult.dist.center')
gx$data$predicted = trans(gx$data$predicted)
gx$data$conf.low = trans(gx$data$conf.low)
gx$data$conf.high = trans(gx$data$conf.high)
gx$data$x = gx$data$x *
  cdc.s +cdc.c
gx = gx + #coord_cartesian(ylim=c(0,0.5),
  # xlim=c(0.15,0.85)) +
  xlab("Cultural similarity") +
```

```

ylab("Semantic alignment") +
ggtitle("") +
geom_point(data=ling,aes(x=cult.dist,y=local_alignment))
gx

```



```

pdf(paste0("../results/stats/",datasetName,"/CulturalDistance_Rho_Graph.pdf"),
    height=2.5, width=2.5)
gx
dev.off()

```

```

## pdf
## 2

```

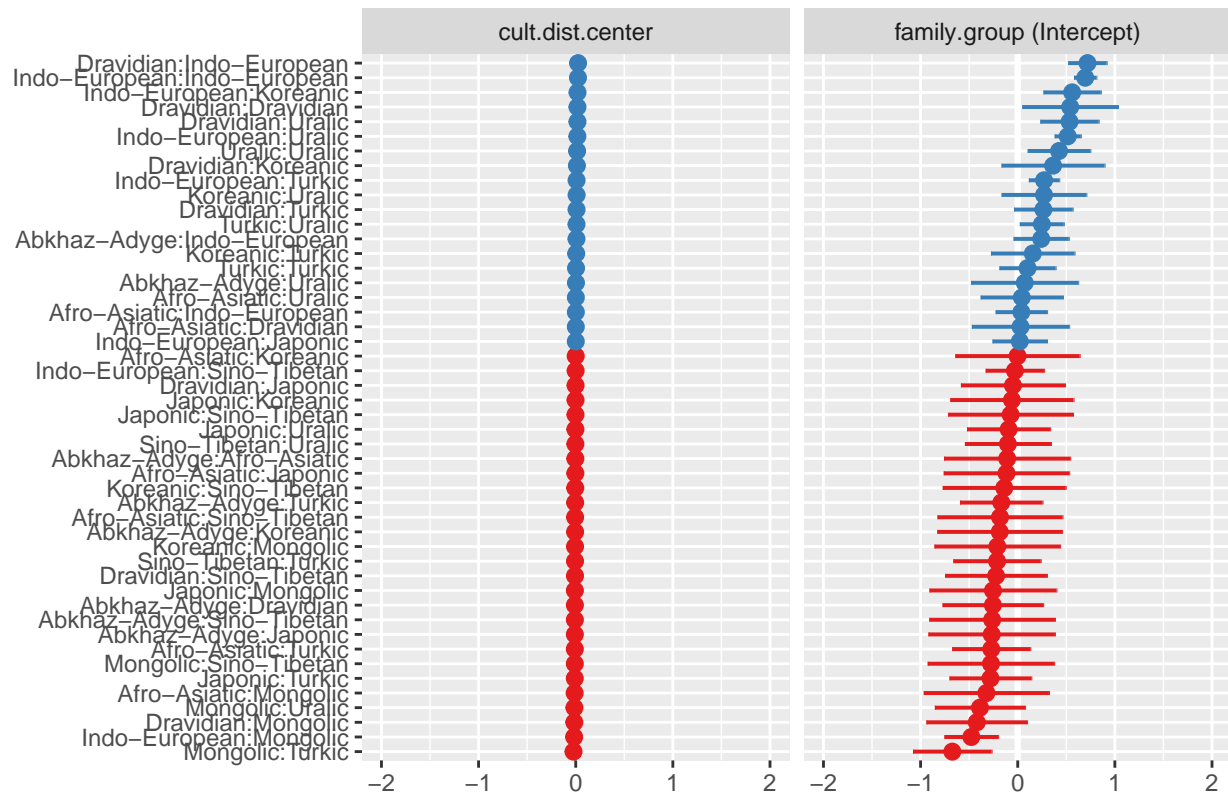
Plot the random effects:

```
plot_model(m1,'re', sort.est = "cult.dist.center")
```

```
## [[1]]
```



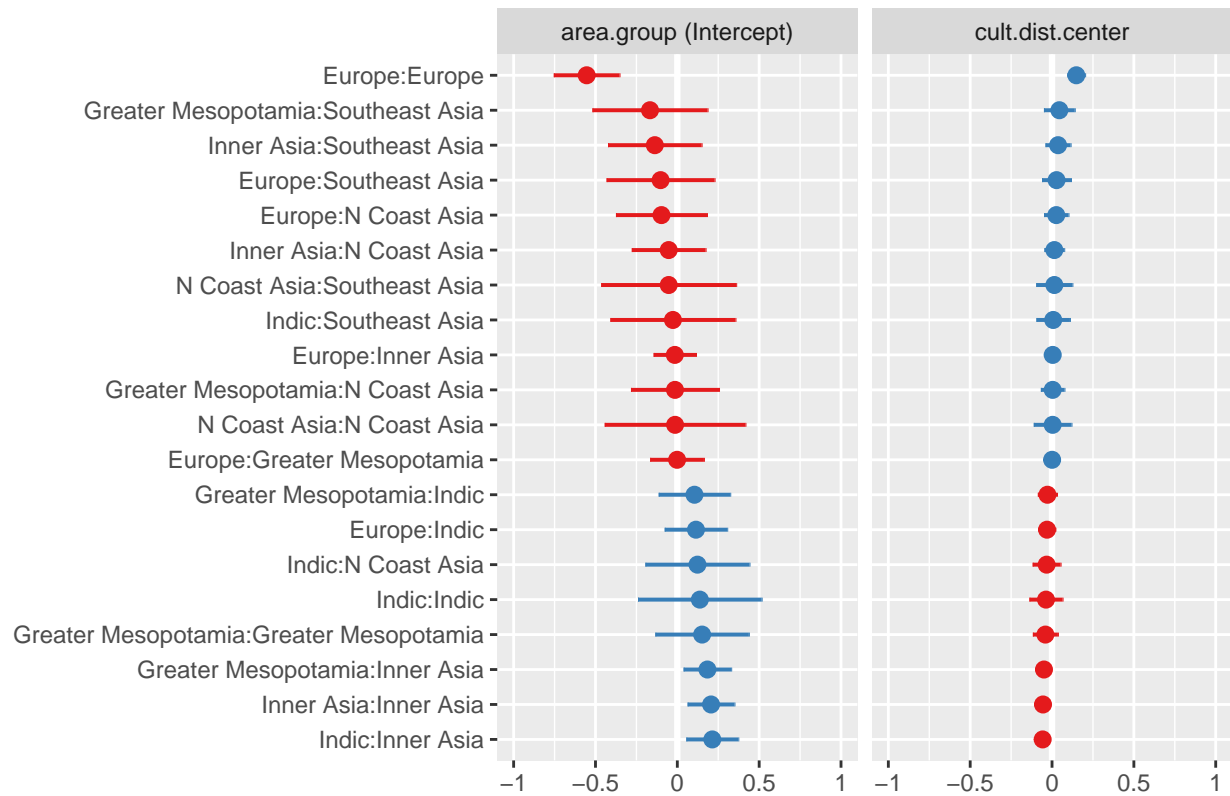
## Random effects



##

## [[2]]

## Random effects



## Without Kinship data

The analyses below show that the strongest relationship is with Kinship. Here we run the analysis as above, but using semantic distances computed without concepts that relate to kinship. Note that the local alignment values correlate with  $r > 0.99$ .

Code for constructing the data is hidden, but it is the same as above and available in the Rmd file:

Run the lmer models:

```
mONK = lmer(
  rho.center ~ 1 +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = lingNK
)

## boundary (singular) fit: see ?isSingular

m0.5NK = lmer(
  rho.center ~ 1 +
    comparison_count.center +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = lingNK
)

## boundary (singular) fit: see ?isSingular

m1NK = lmer(
  rho.center ~ 1 +
    comparison_count.center +
    cult.dist.center +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = lingNK
)

## boundary (singular) fit: see ?isSingular

anova(mONK,m0.5NK,m1NK)

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

## Data: lingNK
## Models:
## mONK: rho.center ~ 1 + (1 + cult.dist.center | family.group) + (1 +
## mONK:      cult.dist.center | area.group)
## m0.5NK: rho.center ~ 1 + comparison_count.center + (1 + cult.dist.center |
## m0.5NK:      family.group) + (1 + cult.dist.center | area.group)
## m1NK: rho.center ~ 1 + comparison_count.center + cult.dist.center +
## m1NK:      (1 + cult.dist.center | family.group) + (1 + cult.dist.center |
## m1NK:      area.group)
##      Df    AIC    BIC logLik deviance   Chisq Chi Df Pr(>Chisq)
## mONK   8 1654.6 1691.3 -819.30   1638.6
## m0.5NK  9 1293.0 1334.3 -637.50   1275.0 363.597      1 < 2.2e-16 ***
## m1NK  10 1278.4 1324.4 -629.22   1258.4  16.564      1 4.704e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(m1NK)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: rho.center ~ 1 + comparison_count.center + cult.dist.center +
##      (1 + cult.dist.center | family.group) + (1 + cult.dist.center |
##      area.group)
## Data: lingNK
##
## REML criterion at convergence: 1271.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6249 -0.6167  0.1103  0.6571  4.7402
##
## Random effects:
##   Groups             Name                Variance Std.Dev. Corr
##   family.group (Intercept)            0.1612630 0.40158
##               cult.dist.center 0.0001817 0.01348  1.00
##   area.group   (Intercept)            0.0510850 0.22602
##               cult.dist.center 0.0036658 0.06055 -1.00
## Residual                        0.2885416 0.53716
## Number of obs: 731, groups:  family.group, 48; area.group, 20
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)      -0.39270    0.09073  -4.328
## comparison_count.center 0.61196    0.02688 22.770
## cult.dist.center    0.19678    0.03275   6.008
##
## Correlation of Fixed Effects:
##              (Intr) cmpr_
## cmprsn_cnt.  0.090
## clt.dst.cnt -0.194 -0.201
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

## MRM

Use multiple regression on distance matrices (Lichstein, 2007) to do the same test as above. The code below loads the data into a matrix format:

```
# Use graph method to make distance matrix
grph <- graph.data.frame(ling[,c("l1", 'l2', 'local_alignment')], directed=FALSE)
# add value as a weight attribute
ling.m = get.adjacency(grph, attr="local_alignment", sparse=FALSE)
rownames(ling.m) = 1[match(rownames(ling.m), l$iso2), l$Language2]
colnames(ling.m) = 1[match(colnames(ling.m), l$iso2), l$Language2]
# Same for comparison_count.center
grph <- graph.data.frame(ling[,c("l1", 'l2', 'comparison_count')], directed=FALSE)
# add value as a weight attribute
cc.m = get.adjacency(grph, attr="comparison_count", sparse=FALSE)
rownames(cc.m) = 1[match(rownames(cc.m), l$iso2), l$Language2]
colnames(cc.m) = 1[match(colnames(cc.m), l$iso2), l$Language2]

cult.m = read.csv("../results/EA_distances/CulturalDistances.csv", stringsAsFactors = F)
rownames(cult.m) = cult.m[,1]
cult.m = cult.m[,2:ncol(cult.m)]
cult.m = as.matrix(cult.m)
# Flip cultural value to distance
cult.m = 1-cult.m
mx = match(rownames(ling.m), rownames(cult.m))
cult.m = cult.m[mx, mx]
colnames(cult.m) = rownames(cult.m)

# Same/different matrix for language family
family.matrix = 1[match(rownames(ling.m), l$Language), l$family]
family.matrix = outer(family.matrix, family.matrix, "!=") * 1

# Load ASJP distances for second test
asjp = readRDS("../data/ASJP/asjp17-dists_FAIR.RData")
ling.m.glotto = 1[match(rownames(cult.m), l$Language2), l$glotto]
ling.m.glotto = ling.m.glotto[ling.m.glotto %in% rownames(asjp)]
asjp.m = asjp[ling.m.glotto, ling.m.glotto]
asjp.lang.names = 1[match(rownames(asjp.m), l$glotto), l$Language2]
# Matrices for second analysis with asjp
ling.m2 = ling.m[asjp.lang.names, asjp.lang.names]
cult.m2 = cult.m[asjp.lang.names, asjp.lang.names]
cc.m2 = cc.m[asjp.lang.names, asjp.lang.names]

# Load the geographic distances:
geoDist = read.csv("../data/GeographicDistances.csv", stringsAsFactors = F)
geoDist.m = as.matrix(geoDist)
geoDist.m = geoDist.m[!is.na(geoDist.m[,1]), !is.na(geoDist.m[1,])]
# Convert to log distance in thousand km
geoDist.m = log10(geoDist.m/1000)
geoDist.m[is.infinite(geoDist.m)] = 0
colnames(geoDist.m) = gsub("\\.", " ", colnames(geoDist.m))
rownames(geoDist.m) = colnames(geoDist.m)
geoDist.m1 = geoDist.m[rownames(ling.m), rownames(ling.m)]
geoDist.m2 = geoDist.m[rownames(ling.m2), rownames(ling.m2)]
```

```

# center and scale values
ling.m = matrix(scale(as.vector(ling.m)),nrow=nrow(ling.m))
cc.m = matrix(scale(as.vector(cc.m)),nrow=nrow(cc.m))
cult.m = matrix(scale(as.vector(cult.m)),nrow=nrow(cult.m))
geoDist.m1 = matrix(scale(as.vector(geoDist.m1)),nrow=nrow(geoDist.m1))

asjp.m = matrix(scale(as.vector(asjp.m)),nrow=nrow(asjp.m))
ling.m2 = matrix(scale(as.vector(ling.m2)),nrow=nrow(ling.m2))
cc.m2 = matrix(scale(as.vector(cc.m2)),nrow=nrow(cc.m2))
cult.m2 = matrix(scale(as.vector(cult.m2)),nrow=nrow(cult.m2))
geoDist.m2 = matrix(scale(as.vector(geoDist.m2)),nrow=nrow(geoDist.m2))

```

Run the MRM model, predicting semantic alignment by cultural distance, controlling for family distance, geographic distance, and the comparison count (number of observations). Here, the family distance between two languages is just whether they are part of the same family. Note that this does not take into account particular values for particular families, nor the random slopes within families.

```
set.seed(1282)
ecodist::MRM(as.dist(ling.m) ~
              as.dist(cult.m) +
              as.dist(family.matrix) +
              as.dist(geoDist.m1) +
              as.dist(cc.m), nperm = 10000)

## $coef
##               as.dist(ling.m)    pval
## Int               0.22628455 0.0452
## as.dist(cult.m)      0.27056532 0.0117
## as.dist(family.matrix) -0.22892903 0.1053
## as.dist(geoDist.m1)    0.00141692 0.9863
## as.dist(cc.m)         0.60941424 0.0001
##
## $r.squared
##      R2      pval
## 0.6104647 0.0001000
##
## $F.test
##      F    F.pval
## 288.3577 0.0001
```

Semantic alignment is significantly correlated with cultural distance.

In the result above, geographic distance is not correlated with semantic distance. Geographic distance turns out to be moderately correlated with cultural distance:

```
ecodist::MRM(as.dist(geoDist.m1) ~
              as.dist(cult.m),
              nperm = 10000)

## $coef
##               as.dist(geoDist.m1)    pval
## Int               -0.02111026 0.7707
## as.dist(cult.m)    -0.50170516 0.0001
##
## $r.squared
##      R2      pval
## 0.1529605 0.0001000
##
## $F.test
##      F    F.pval
## 133.4504 0.0001
```

Even when testing for non-linear geographic effects, the main result still holds:

```
ecodist::MRM(as.dist(ling.m) ~
              as.dist(cult.m) +
              as.dist(family.matrix) +
              as.dist(geoDist.m1) +
              as.dist(geoDist.m1^2) +
```

```
as.dist(geoDist.m1^3) +
as.dist(cc.m),nperm = 10000)
```

```
## $coef
##               as.dist(ling.m)    pval
## Int               0.214632722 0.0740
## as.dist(cult.m)      0.266769243 0.0135
## as.dist(family.matrix) -0.233845007 0.1073
## as.dist(geoDist.m1)   0.002103012 0.9803
## as.dist(geoDist.m1^2)  0.016893496 0.7679
## as.dist(geoDist.m1^3)  0.002937588 0.8697
## as.dist(cc.m)         0.609370724 0.0001
##
## $r.squared
##      R2      pval
## 0.6107422 0.0001000
##
## $F.test
##      F    F.pval
## 191.9400  0.0001
```

Below, we run the same test, but using average string distances in basic vocabulary from the ASJP (Wichmann, Holman & Brown, 2018) as controls for history. We used the distances as calculated in Jäger (2018), which used them to construct historical phylogenies.

```
ecodist::MRM(as.dist(ling.m2) ~
as.dist(cult.m2) +
as.dist(asjp.m) +
as.dist(geoDist.m2) +
as.dist(cc.m2),nperm = 10000)
```

```
## $coef
##               as.dist(ling.m2)    pval
## Int               0.09389590 0.0004
## as.dist(cult.m2)   0.26068360 0.0226
## as.dist(asjp.m)    -0.25717809 0.0001
## as.dist(geoDist.m2) 0.03920662 0.6016
## as.dist(cc.m2)     0.61582319 0.0001
##
## $r.squared
##      R2      pval
## 0.6251321 0.0001000
##
## $F.test
##      F    F.pval
## 260.5635  0.0001
```



## Mantel tests

Read the historical distances for Indo-European, based on the phylogenetic distances.

### Data prep

The geographic distances are loaded above (from “../data/GeographicDistances.csv”).

Load historical distances:

```
hist = read.csv("../data/trees/IndoEuropean_historical_distances.csv", stringsAsFactors = F)
hist = hist[!duplicated(hist[,1]),!duplicated(hist[,1])]
rownames(hist) = hist[,1]
hist = hist[,2:ncol(hist)]
hist.m = as.matrix(hist)
colnames(hist.m) = rownames(hist.m)
hist.m = hist.m/max(hist.m)
```

Read the cultural distance as a matrix:

```
cult.m = read.csv("../results/EA_distances/CulturalDistances.csv", stringsAsFactors = F)
rownames(cult.m) = cult.m[,1]
cult.m = cult.m[,2:ncol(cult.m)]
```

Flip the cultural distance into a cultural similarity measure:

```
cult.m = 1-cult.m
```

Convert the linguistic similarities to a matrix. This uses `igraph` to make an undirected graph from the long format with `local_alignment` as the edge weights, then output a matrix of adjacencies.

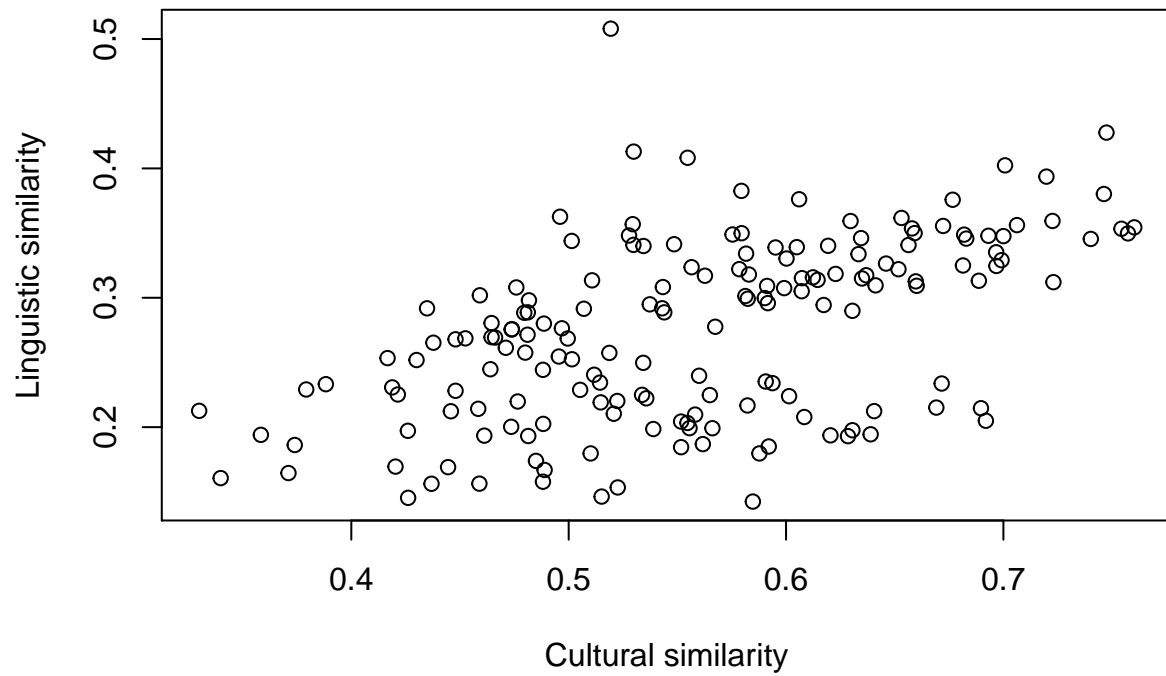
```
grph <- graph.data.frame(ling[,c("l1", "l2", "local_alignment")], directed=FALSE)
# add value as a weight attribute
ling.m = get.adjacency(grph, attr="local_alignment", sparse=FALSE)
rownames(ling.m) = 1[match(rownames(ling.m), l$iso2),]$Language2
colnames(ling.m) = 1[match(colnames(ling.m), l$iso2),]$Language2
```

Match the distance matrices

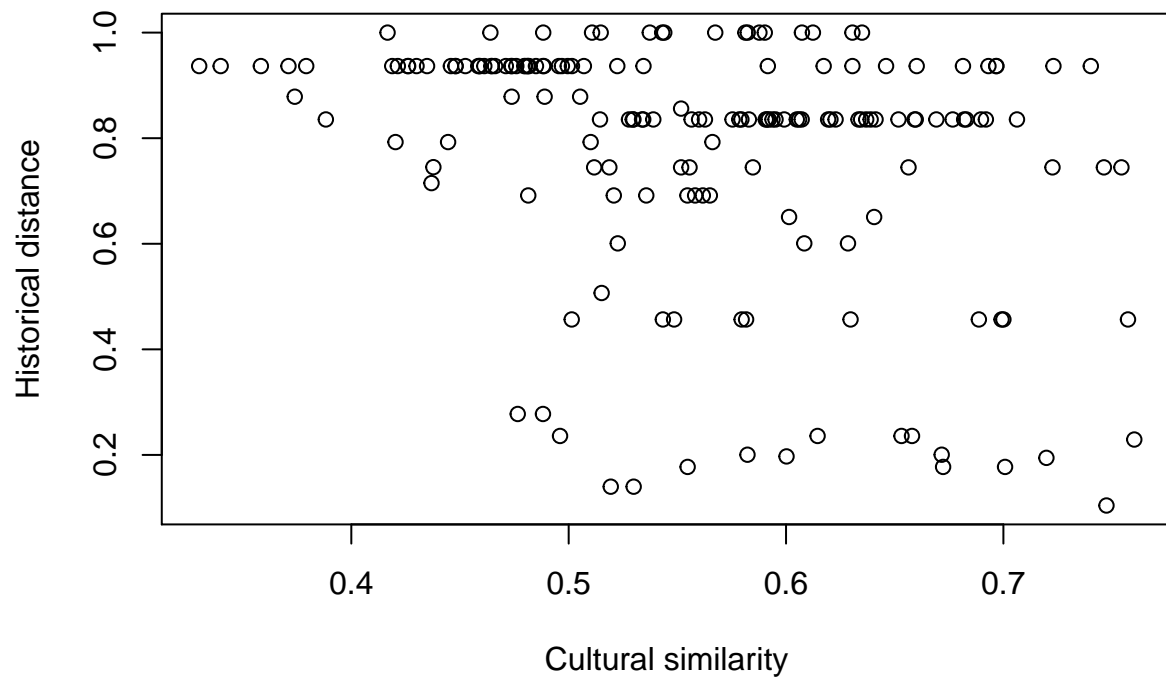
```
in.analysis = intersect(rownames(ling.m), rownames(cult.m))
in.analysis = intersect(in.analysis, rownames(hist.m))
cult.m2 = cult.m[in.analysis, in.analysis]
ling.m2 = ling.m[in.analysis, in.analysis]
hist.m2 = hist.m[in.analysis, in.analysis]
geo.m2 = geoDist.m[in.analysis, in.analysis]
```

Note that there are only 19 languages with data on linguistic, cultural and historical distance.

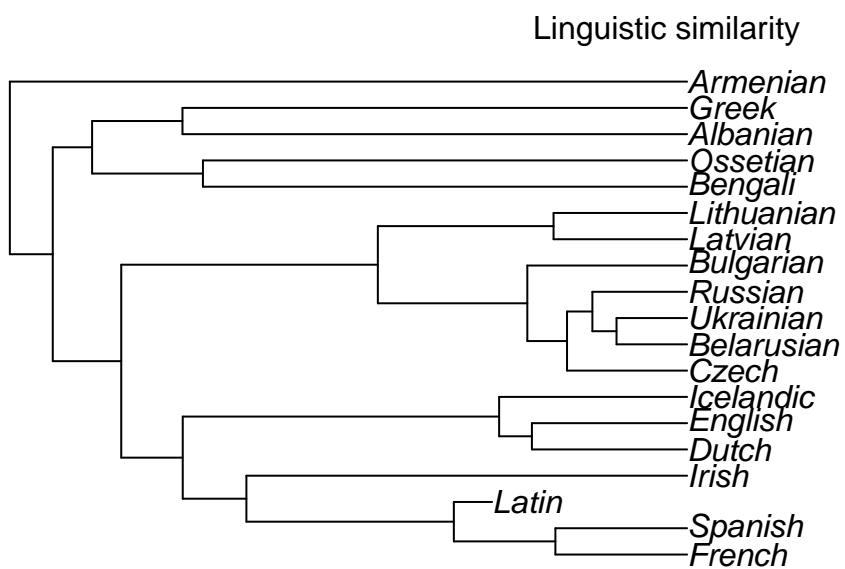
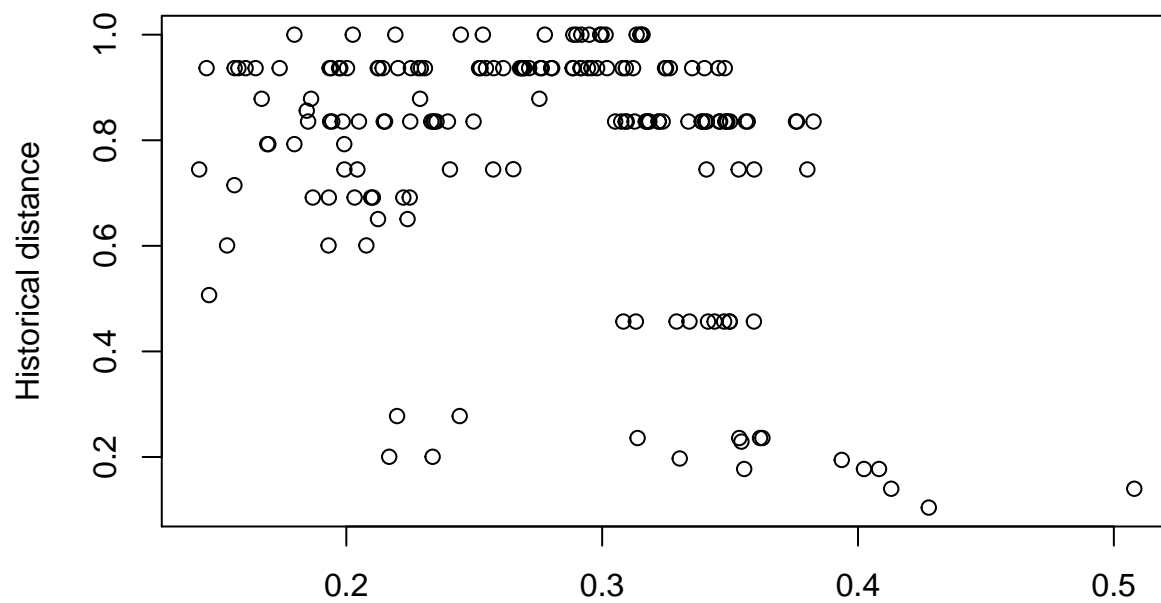
```
plot(as.dist(cult.m2), as.dist(ling.m2),
     xlab="Cultural similarity",
     ylab="Linguistic similarity")
```



```
plot(as.dist(cult.m2),as.dist(hist.m2),
     xlab="Cultural similarity",
     ylab="Historical distance")
```



```
plot(as.dist(ling.m2),as.dist(hist.m2),
     xlab="Linguistic similarity",
     ylab="Historical distance")
```



## Tests

The results of the test list the following measures:

- mantelr: Mantel correlation coefficient.
- pval1: one-tailed p-value (null hypothesis:  $r \leq 0$ ).
- pval2: one-tailed p-value (null hypothesis:  $r \geq 0$ ).
- pval3: two-tailed p-value (null hypothesis:  $r = 0$ ).
- llim: lower confidence limit for  $r$ .
- ulim: upper confidence limit for  $r$ .

```
set.seed(1498)
```

Run tests between each pair of measures.

```
distms = list("Cultrual"= cult.m2,
              "Linguistic" = ling.m2,
              "Historical" = hist.m2,
              "Geographic" = geo.m2)
for(i in 1:3){
  for(j in (i+1):4){
    var1 = names(distms)[i]
    var2 = names(distms)[j]
    print(paste("Correlation between",
                var1,"and",var2))
    stat = ecodist::mantel(as.dist(distms[[i]]) ~
                           as.dist(distms[[j]]),
                           nperm = 100000)
    print(stat)
    stat = round(stat,2)
    stat2 = sprintf("$r$ = %s[%s,%s], one-tailed $p$ = %s",
                    stat[1],
                    stat[5],
                    stat[6],
                    min(c(stat[2],stat[3])))
    cat(stat2,file=
        paste0("../results/stats/tex/Mantel",var1,"Vs",var2,"Distance.tex"))
  }
}
```

```
## [1] "Correlation between Cultrual and Linguistic"
##   mantelr      pval1      pval2      pval3  llim.2.5% ulim.97.5%
## 0.5243289 0.0050000 0.9950100 0.0050300 0.3796035 0.6586819
## [1] "Correlation between Cultrual and Historical"
##   mantelr      pval1      pval2      pval3  llim.2.5% ulim.97.5%
## -0.3243830 0.9871000 0.0129100 0.0138900 -0.4402666 -0.2385575
## [1] "Correlation between Cultrual and Geographic"
##   mantelr      pval1      pval2      pval3  llim.2.5% ulim.97.5%
## -0.4495398 0.9967200 0.0032900 0.0032900 -0.5754918 -0.3109193
## [1] "Correlation between Linguistic and Historical"
##   mantelr      pval1      pval2      pval3  llim.2.5% ulim.97.5%
## -0.3372882 0.9859600 0.0140500 0.0167300 -0.5019408 -0.1639425
## [1] "Correlation between Linguistic and Geographic"
##   mantelr      pval1      pval2      pval3  llim.2.5% ulim.97.5%
## -0.2594386 0.9182700 0.0817400 0.1195200 -0.3694719 -0.1840035
## [1] "Correlation between Historical and Geographic"
```

```
##      mantelr      pval1      pval2      pval3  llim.2.5% ulim.97.5%
## 0.4210629 0.0004100 0.9996000 0.0004100 0.3313578 0.5176683
```

Run a mantel test comparing the Linguistic alignment to the cultural similarity, controlling for the historical distance between languages:

```
ecodist::mantel(as.dist(ling.m2)~
               as.dist(cult.m2) +
               as.dist(hist.m2),
               nperm = 100000)
```

```
##      mantelr      pval1      pval2      pval3  llim.2.5% ulim.97.5%
## 0.4659407 0.0100000 0.9900100 0.0107800 0.3408500 0.5938397
```

*Main Test:* Run a mantel test comparing the Linguistic alignment to the cultural similarity, controlling for the historical distance and geographic distance between languages:

```
mainMantel = ecodist::mantel(as.dist(ling.m2)~
                           as.dist(cult.m2) +
                           as.dist(hist.m2) +
                           as.dist(geo.m2),
                           nperm = 100000)
```

```
mainMantel
```

```
##      mantelr      pval1      pval2      pval3  llim.2.5% ulim.97.5%
## 0.4508309 0.0114200 0.9885900 0.0119500 0.2962271 0.5993660
```

```
mainMantel = round(mainMantel,2)
mainMantel2 = sprintf("$r$ = %s[%s,%s], one-tailed $p$ = %s",
                      mainMantel[1],
                      mainMantel[5],
                      mainMantel[6],
                      mainMantel[2]
                      )
cat(mainMantel2,
    file="../results/stats/tex/MantelCultrualVsLinguisticDistance_Partial.tex")
```

## MRM

Perform the main test, but using multiple regression on distance matrices (MRM).

```
set.seed(21889)
mainMRM = ecodist::MRM(as.dist(ling.m2)~
                      as.dist(cult.m2) +
                      as.dist(hist.m2) +
                      as.dist(geo.m2), nperm=10000)
mainMRM
```

```
## $coef
##           as.dist(ling.m2)  pval
## Int           0.123122021 0.9147
## as.dist(cult.m2)  0.350192033 0.0108
## as.dist(hist.m2) -0.059044640 0.1623
## as.dist(geo.m2)  0.008177519 0.8212
##
## $r.squared
##      R2      pval
```

```
## 0.3072419 0.0073000
##
## $F.test
##      F      F.pval
## 24.68846 0.00730
```

```
mainMRM2 = sprintf("$\\beta= %s, $p=%s",
                    round(mainMRM$coef[2,1],2),
                    round(mainMRM$coef[2,2],2))
cat(mainMRM2,
    file="../results/stats/tex/MRMCulturalVsLinguisticDistance_Partial.tex")
```

## Analysis of filtered data

The analyses in this section use local alignment values based on (a) data that passes the wikipedia filter, and (b) data that passes the semantic filter.

### Wikipedia filter

```
ling.filtered = read.csv(
  "../data/FAIR/nel-wiki-k100-alignments-by-language-pair_Filtered.csv",
  stringsAsFactors = F)
```

Note that the semantic alignment for the filtered and unfiltered data are essentially exactly the same, but for fewer languages:

```
ling.filtered$unfiltered.rho =
  apply(ling.filtered[,
    c("iso2_l1", "iso2_l2")], 1,
  function(X){
    ling[(ling$l1==X[1] & ling$l2==X[2]) |
      (ling$l1==X[2] & ling$l2==X[1]),]$local_alignment[1]
  })
cor(ling.filtered$unfiltered.rho, ling.filtered$rho, use = "complete.obs")
```

```
## [1] 0.9999918
```

Continue to build data for replication:

```
ling.filtered$area1 = 1[match(ling.filtered$name_l1, 1$Language),]$autotyp.area
ling.filtered$area2 = 1[match(ling.filtered$name_l2, 1$Language),]$autotyp.area

fgroup = cbind(ling.filtered$family1, ling.filtered$family2)
fgroup = apply(fgroup, 1, sort)
ling.filtered$family.group = apply(fgroup, 2, paste, collapse=":")
agroup = cbind(ling.filtered$area1, ling.filtered$area2)
agroup = apply(agroup, 1, sort)
ling.filtered$area.group = apply(agroup, 2, paste, collapse=":")

ling.filtered$rho.center = scale(ling.filtered$rho)
ling.filtered$comparison_count.center = scale(ling.filtered$comparison_count)

matches = sapply(1:nrow(ling.filtered), function(i){
  x = which((cult$l1==ling.filtered$name_l1[i] &
    cult$l2==ling.filtered$name_l2[i]) |
    (cult$l2==ling.filtered$name_l1[i] &
    cult$l1==ling.filtered$name_l2[i]))
  x[1]
})

ling.filtered$cult.dist = cult[matches,]$cult.dist
# flip
ling.filtered$cult.dist = 1 - ling.filtered$cult.dist
ling.filtered = ling.filtered[!is.na(ling.filtered$cult.dist),]

ling.filtered$cult.dist.center = scale(ling.filtered$cult.dist)
```

```

m0F = lmer(
  rho.center ~ 1 +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = ling.filtered
)

## boundary (singular) fit: see ?isSingular

m0.5F = lmer(
  rho.center ~ 1 +
    comparison_count.center +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = ling.filtered
)

## boundary (singular) fit: see ?isSingular

m1F = lmer(
  rho.center ~ 1 +
    comparison_count.center +
    cult.dist.center +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = ling.filtered
)

an1F = anova(m0F, m0.5F, m1F)

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

an1F

## Data: ling.filtered
## Models:
## m0F: rho.center ~ 1 + (1 + cult.dist.center | family.group) + (1 +
## m0F:      cult.dist.center | area.group)
## m0.5F: rho.center ~ 1 + comparison_count.center + (1 + cult.dist.center |
## m0.5F:      family.group) + (1 + cult.dist.center | area.group)
## m1F: rho.center ~ 1 + comparison_count.center + cult.dist.center +
## m1F:      (1 + cult.dist.center | family.group) + (1 + cult.dist.center |
## m1F:      area.group)
##      Df    AIC    BIC logLik deviance   Chisq Chi Df Pr(>Chisq)
## m0F      8 446.96 473.74 -215.48   430.96
## m0.5F    9 428.63 458.76 -205.32   410.63 20.3271      1 6.527e-06 ***
## m1F    10 425.68 459.15 -202.84   405.68  4.9519      1  0.02606 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Cultural similarity is significantly correlated with Linguistic similarity, even in the filtered data. Here are the
model estimates:

summary(m1F)

## Linear mixed model fit by REML ['lmerMod']
## Formula: rho.center ~ 1 + comparison_count.center + cult.dist.center +
##      (1 + cult.dist.center | family.group) + (1 + cult.dist.center |
##      area.group)

```



```

## Data: ling.filtered
##
## REML criterion at convergence: 412.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.8211 -0.5105 -0.0662  0.4157  6.2698
##
## Random effects:
##      Groups      Name              Variance Std.Dev. Corr
## family.group (Intercept)          0.17449  0.4177
##               cult.dist.center 0.07149  0.2674  -0.21
## area.group   (Intercept)          0.64616  0.8038
##               cult.dist.center 0.02791  0.1670  1.00
## Residual                        0.26481  0.5146
## Number of obs: 210, groups: family.group, 31; area.group, 19
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    -0.82996    0.21638  -3.836
## comparison_count.center 0.41070    0.08668   4.738
## cult.dist.center    0.29681    0.11189   2.653
##
## Correlation of Fixed Effects:
##              (Intr) cmpr_
## cmprsn_cnt.   0.133
## clt.dst.cnt   0.387 -0.054

```

## Semantic filter

```
ling.semFiltered = read.csv(
  "../data/FAIR/nel-wiki-k100-alignments-by-language-pair_SemanticFiltered.csv",
  stringsAsFactors = F)

ling.semFiltered$area1 = 1[match(ling.semFiltered$name_l1,1$Language),]$autotyp.area
ling.semFiltered$area2 = 1[match(ling.semFiltered$name_l2,1$Language),]$autotyp.area

fgroup = cbind(ling.semFiltered$family1,ling.semFiltered$family2)
fgroup = apply(fgroup,1,sort)
ling.semFiltered$family.group = apply(fgroup,2,paste,collapse=":")
agroup = cbind(ling.semFiltered$area1,ling.semFiltered$area2)
agroup = apply(agroup,1,sort)
ling.semFiltered$area.group = apply(agroup,2,paste,collapse=":")

ling.semFiltered$rho.center = scale(ling.semFiltered$rho)
ling.semFiltered$comparison_count.center = scale(ling.semFiltered$comparison_count)

matches = sapply(1:nrow(ling.semFiltered), function(i){
  x = which((cult$l1==ling.semFiltered$name_l1[i] &
    cult$l2==ling.semFiltered$name_l2[i]) |
    (cult$l2==ling.semFiltered$name_l1[i] &
    cult$l1==ling.semFiltered$name_l2[i]))
  x[1]
})

ling.semFiltered$cult.dist = cult[matches,]$cult.dist
# flip
ling.semFiltered$cult.dist = 1 - ling.semFiltered$cult.dist
ling.semFiltered = ling.semFiltered[!is.na(ling.semFiltered$cult.dist),]

ling.semFiltered$cult.dist.center = scale(ling.semFiltered$cult.dist)

m0F = lmer(
  rho.center ~ 1 +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = ling.semFiltered
)

## boundary (singular) fit: see ?isSingular

m0.5F = lmer(
  rho.center ~ 1 +
    comparison_count.center +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = ling.semFiltered
)

## boundary (singular) fit: see ?isSingular

m1F = lmer(
  rho.center ~ 1 +
```

```

    comparison_count.center +
    cult.dist.center +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
    data = ling.semFiltered
)

## boundary (singular) fit: see ?isSingular
an1F = anova(m0F,m0.5F,m1F)

## refitting model(s) with ML (instead of REML)
an1F

## Data: ling.semFiltered
## Models:
## m0F: rho.center ~ 1 + (1 + cult.dist.center | family.group) + (1 +
## m0F:      cult.dist.center | area.group)
## m0.5F: rho.center ~ 1 + comparison_count.center + (1 + cult.dist.center |
## m0.5F:      family.group) + (1 + cult.dist.center | area.group)
## m1F: rho.center ~ 1 + comparison_count.center + cult.dist.center +
## m1F:      (1 + cult.dist.center | family.group) + (1 + cult.dist.center |
## m1F:      area.group)
##      Df    AIC    BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0F    8 1660.3 1697.1 -822.17  1644.3
## m0.5F  9 1300.8 1342.1 -641.39  1282.8 361.576      1 < 2.2e-16 ***
## m1F   10 1286.2 1332.1 -633.09  1266.2  16.595      1 4.627e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Cultural similarity is significantly correlated with Linguistic similarity, even in the semantic filtered data.
Here are the model estimates:

summary(m1F)

## Linear mixed model fit by REML ['lmerMod']
## Formula: rho.center ~ 1 + comparison_count.center + cult.dist.center +
##      (1 + cult.dist.center | family.group) + (1 + cult.dist.center |
##      area.group)
## Data: ling.semFiltered
##
## REML criterion at convergence: 1279.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6257 -0.6155  0.1002  0.6528  4.7581
##
## Random effects:
## Groups      Name                Variance Std.Dev. Corr
## family.group (Intercept)         0.1627947 0.40348
##              cult.dist.center 0.0001944 0.01394  1.00
## area.group   (Intercept)         0.0515199 0.22698
##              cult.dist.center 0.0037519 0.06125 -1.00
## Residual                        0.2916401 0.54004
## Number of obs: 731, groups: family.group, 48; area.group, 20
##

```

```

## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)    -0.39039   0.09111  -4.285
## comparison_count.center  0.62768   0.02766  22.696
## cult.dist.center     0.19836   0.03301   6.009
##
## Correlation of Fixed Effects:
##           (Intr) cmpr_
## cmprsn_cnt.  0.083
## clt.dst.cnt -0.192 -0.200
## convergence code: 0
## boundary (singular) fit: see ?isSingular

```

## Both filters

Main test on data where both the wikipedia and semantic filter are on.

```
ling.bothFiltered = read.csv(
  "../data/FAIR/nel-wiki-k100-alignments-by-language-pair_BothFiltered.csv",
  stringsAsFactors = F)

ling.bothFiltered$area1 = 1[match(ling.bothFiltered$name_11,1$Language),]$autotyp.area
ling.bothFiltered$area2 = 1[match(ling.bothFiltered$name_12,1$Language),]$autotyp.area

fgroup = cbind(ling.bothFiltered$family1,ling.bothFiltered$family2)
fgroup = apply(fgroup,1,sort)
ling.bothFiltered$family.group = apply(fgroup,2,paste,collapse=":")
agroup = cbind(ling.bothFiltered$area1,ling.bothFiltered$area2)
agroup = apply(agroup,1,sort)
ling.bothFiltered$area.group = apply(agroup,2,paste,collapse=":")

ling.bothFiltered$rho.center = scale(ling.bothFiltered$rho)
ling.bothFiltered$comparison_count.center = scale(ling.bothFiltered$comparison_count)

matches = sapply(1:nrow(ling.bothFiltered), function(i){
  x = which((cult$l1==ling.bothFiltered$name_11[i] &
    cult$l2==ling.bothFiltered$name_12[i]) |
    (cult$l2==ling.bothFiltered$name_11[i] &
    cult$l1==ling.bothFiltered$name_12[i]))
  x[1]
})

ling.bothFiltered$cult.dist = cult[matches,]$cult.dist
# flip
ling.bothFiltered$cult.dist = 1 - ling.bothFiltered$cult.dist
ling.bothFiltered = ling.bothFiltered[!is.na(ling.bothFiltered$cult.dist),]

ling.bothFiltered$cult.dist.center = scale(ling.bothFiltered$cult.dist)

m0F = lmer(
  rho.center ~ 1 +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = ling.bothFiltered
)

## boundary (singular) fit: see ?isSingular

m0.5F = lmer(
  rho.center ~ 1 +
    comparison_count.center +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = ling.bothFiltered
)

## boundary (singular) fit: see ?isSingular
```

```

m1F = lmer(
  rho.center ~ 1 +
    comparison_count.center +
    cult.dist.center +
    (1 + cult.dist.center | family.group) +
    (1 + cult.dist.center | area.group),
  data = ling.bothFiltered
)
an1F = anova(m0F,m0.5F,m1F)

## refitting model(s) with ML (instead of REML)
an1F

## Data: ling.bothFiltered
## Models:
## m0F: rho.center ~ 1 + (1 + cult.dist.center | family.group) + (1 +
## m0F:      cult.dist.center | area.group)
## m0.5F: rho.center ~ 1 + comparison_count.center + (1 + cult.dist.center |
## m0.5F:      family.group) + (1 + cult.dist.center | area.group)
## m1F: rho.center ~ 1 + comparison_count.center + cult.dist.center +
## m1F:      (1 + cult.dist.center | family.group) + (1 + cult.dist.center |
## m1F:      area.group)
##      Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0F    8 447.24 474.02 -215.62  431.24
## m0.5F  9 429.45 459.58 -205.73  411.45 19.7903      1 8.642e-06 ***
## m1F   10 426.47 459.95 -203.24  406.47  4.9762      1  0.0257 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Cultural similarity is significantly correlated with Linguistic similarity, even in the fully filtered data. Here are the model estimates:

```

summary(m1F)

## Linear mixed model fit by REML ['lmerMod']
## Formula: rho.center ~ 1 + comparison_count.center + cult.dist.center +
##      (1 + cult.dist.center | family.group) + (1 + cult.dist.center |
##      area.group)
## Data: ling.bothFiltered
##
## REML criterion at convergence: 413.6
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -1.8275 -0.5144 -0.0659  0.4117  6.2874
##
## Random effects:
##      Groups      Name      Variance Std.Dev. Corr
## family.group (Intercept)  0.17288  0.4158
##      cult.dist.center 0.07138  0.2672  -0.21
## area.group   (Intercept)  0.64816  0.8051
##      cult.dist.center 0.02802  0.1674   1.00
## Residual                0.26612  0.5159
## Number of obs: 210, groups: family.group, 31; area.group, 19
##

```

```

## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)    -0.8297    0.2166  -3.831
## comparison_count.center  0.4075    0.0872   4.673
## cult.dist.center      0.2976    0.1119   2.659
##
## Correlation of Fixed Effects:
##          (Intr) cmpr_
## cmprsn_cnt.  0.135
## clt.dst.cnt  0.387 -0.053

```

## Comparison between domains

The code that produce the results of this section can be found in `analysis/compareDomains.R`.

### Part 1: Compare each linguistic domain to the overall cultural similarity

We fit a mixed effects model to compare the linguistic similarity in a given domain to the overall cultural distance. The linguistic similarity for the given domain is the dependent variable. There are random intercepts for language family and area pairs, and random slopes for overall cultural similarity by language family and by area. The `comparison_count` variable is added as a fixed effect. This null model is compared to a model with an additional fixed effect for the overall cultural similarity.

There are 21 linguistic domains with enough data. All correlations are positive and 11 are significant at the 0.05 level (adjusted for multiple comparisons).

The full results are in the file:

```
../results/stats/wikipedia-main/Cor_LingAlignmentByDomains_vs_OverallCulturalSimilarity.csv
```

Summary:

p1res

##	Domain	Beta	p	Adjusted p	sig
## 2	Food and drink	0.29039152	3.842274e-08	8.068775e-07	*
## 6	Miscellaneous function words	0.31349670	9.672370e-08	2.031198e-06	*
## 9	The body	0.23183657	8.711593e-07	1.829434e-05	*
## 13	Animals	0.26483784	4.281952e-06	8.992099e-05	*
## 21	Time	0.26708073	3.341177e-05	7.016471e-04	*
## 3	Agriculture and vegetation	0.21319270	4.954909e-05	1.040531e-03	*
## 16	Modern world	0.15392213	2.860946e-04	6.007988e-03	*
## 14	The physical world	0.15530592	6.771587e-04	1.422033e-02	*
## 11	Spatial relations	0.11188738	1.323355e-03	2.779045e-02	*
## 20	Kinship	0.25408132	1.332699e-03	2.798669e-02	*
## 7	Clothing and grooming	0.16478921	2.245060e-03	4.714625e-02	*
## 10	Sense perception	0.11168260	2.806430e-03	5.893504e-02	
## 15	Social and political relations	0.10210872	6.603817e-03	1.386802e-01	
## 1	The house	0.10743767	1.485121e-02	3.118755e-01	
## 18	Quantity	0.13804241	1.691864e-02	3.552914e-01	
## 8	Speech and language	0.11367507	3.209804e-02	6.740588e-01	
## 19	Basic actions and technology	0.06996793	7.317704e-02	1.000000e+00	
## 17	Cognition	0.06413968	9.294337e-02	1.000000e+00	
## 12	Emotions and values	0.06324463	9.437249e-02	1.000000e+00	
## 5	Possession	0.07833831	1.102507e-01	1.000000e+00	
## 4	Motion	0.05544251	2.537090e-01	1.000000e+00	



## Part 2: Compare each linguistic domain to the cultural similarity of each original D-PLACE domain

The method is the same as for part 1, except the cultural distance for a particular cultural domain is used instead of the overall cultural distance.

The full results are in the file:

`../results/stats/wikipedia-main/Cor_LingAlignmentByDomains_vs_DPlaceCulturalDomains.csv`

The graph below shows the mixed effects model coefficient estimate for the relationship between each linguistic domain and each cultural domain. Pink colours indicate positive correlations and blue colours indicate negative correlations. Stronger colours indicate stronger correlations. An asterisk indicates that the correlation is stronger than would be expected by chance, when adjusting the p-value for multiple comparisons.

The insert in the top left shows the distribution of Beta values.

The domains are clustered using higherarchical clustering. This is for visualisaiton and reflects similarity in the numeric relations, not history or conceptual hierarchies.

List of significant correlations (after adjusting p-value for multiple comparisons):

##	Ling Domain	Cult Domain	Beta	Adjusted p
## 68	The body	Politics	0.2139638	1.292033e-03
## 155	Kinship	Settlement	0.2785591	8.766279e-03
## 43	Miscellaneous function words	Settlement	0.2899807	7.022120e-07
## 83	Spatial relations	Settlement	0.1122428	1.431007e-03
## 59	Speech and language	Settlement	0.1915031	3.729177e-05
## 107	The physical world	Settlement	0.1321783	4.102261e-02
## 17	Agriculture and vegetation	Subsistence	0.2513632	2.887202e-05
## 97	Animals	Subsistence	0.2942266	7.865336e-06
## 49	Clothing and grooming	Subsistence	0.2484714	1.338589e-04
## 89	Emotions and values	Subsistence	0.1524638	7.946118e-04
## 9	Food and drink	Subsistence	0.3005301	1.084517e-06
## 153	Kinship	Subsistence	0.2346825	4.160376e-03
## 41	Miscellaneous function words	Subsistence	0.3353616	2.648483e-05
## 121	Modern world	Subsistence	0.1851981	7.434982e-06
## 137	Quantity	Subsistence	0.2454534	7.092645e-03
## 73	Sense perception	Subsistence	0.1850017	6.280926e-04
## 113	Social and political relations	Subsistence	0.1544007	3.637901e-05
## 81	Spatial relations	Subsistence	0.1504141	6.897505e-04
## 57	Speech and language	Subsistence	0.1991926	2.699664e-04
## 65	The body	Subsistence	0.2764446	5.291731e-08
## 105	The physical world	Subsistence	0.2221189	1.157346e-04
## 161	Time	Subsistence	0.2921557	1.640226e-05

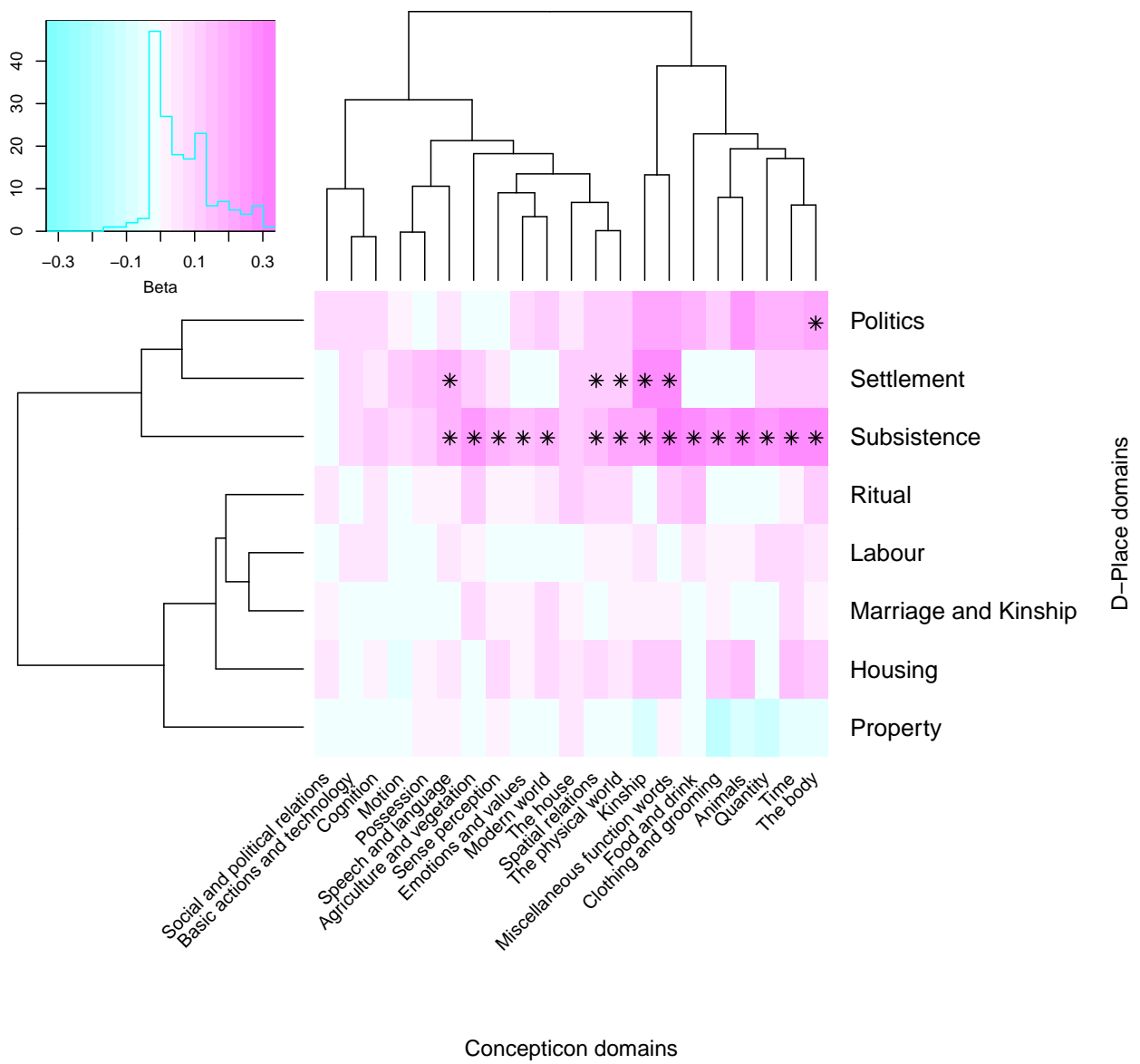


Figure 1:

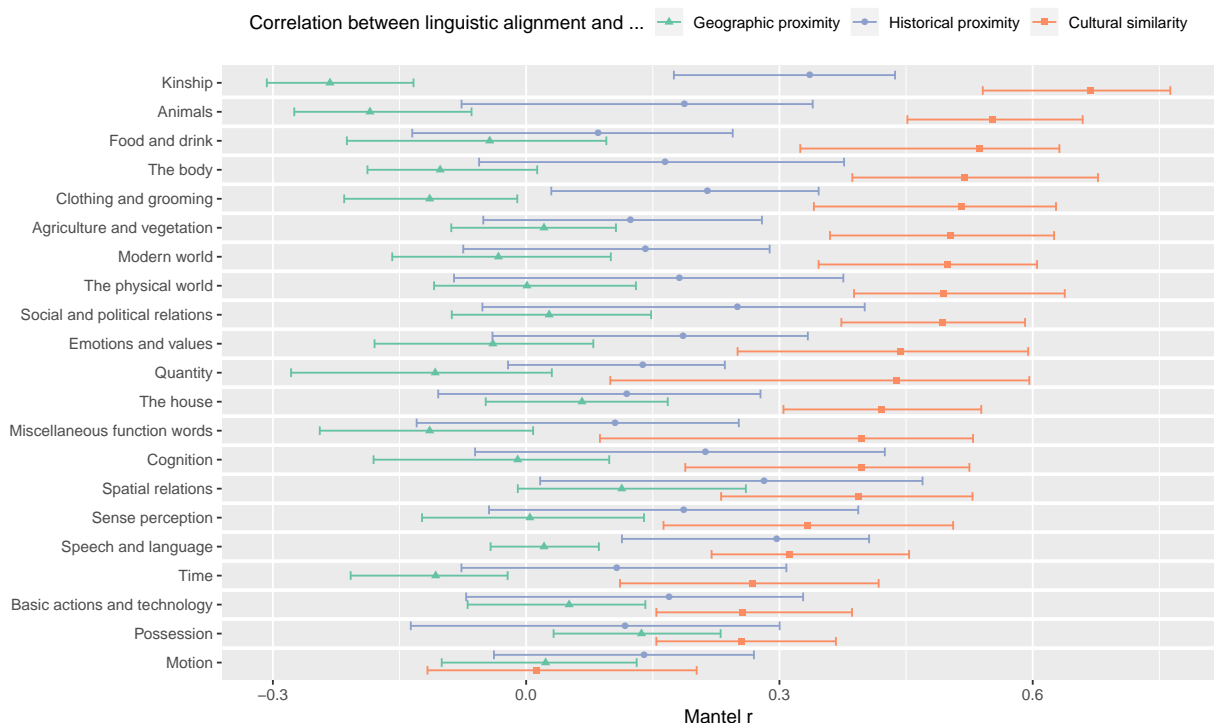


Figure 2:

### Part 3: Compare each linguistic domain to the phylogenetic and geographic distance

This test compares each linguistic similarity scores to each of three target distances: the cultural distance, the historical distance and the geographic distance. We use a partial Mantel test (from the package `ecodist`) to estimate the strength of the relationship between the linguistic domain and the target distance, while controlling for the other two distances. The test uses 100,000 permutations.

The full results are in the file:

`Cor_LingAlignmentByDomains_vs_HistoricalAndGeographicalDistance.csv`

The graph below shows the results. Point estimates are the estimated Mantel R. The error bars show the 95% confidence intervals from the permutation test.

There appears to be a trade-off: The stronger the relationship with geographic distance, the weaker the relationship with cultural distance ( $r = -0.529$ ,  $t = -2.72$ ,  $df=19$ ,  $p = 0.014$ ). This does not hold for historical and cultural distance ( $r = 0.27$ ,  $t = 1.22$ ,  $df=19$ ,  $p = 0.24$ ).

Note that, after controlling for multiple comparisons, only 2 domains are significant:

```
##      domain comparison  mantelr    lower    upper  pval3 p.adjusted
## 37 Animals  lingVCult 0.5518312 0.4515039 0.6591382 0.00129    0.02709
## 58 Kinship  lingVCult 0.6687835 0.5407906 0.7629987 0.00012    0.00252
```

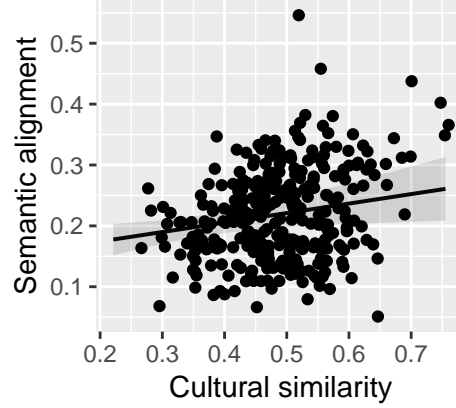


Figure 3: Semantic alignment and cultural similarity for data using the Common Crawl alignments

## Summary of alternative data sources

The github repository also includes the main tests in this document, but applied to data where the alignments are done according to the Common Crawl or Subtitles databases.

### Common Crawl

Mixed effects model: The correlation between semantic alignment and cultural similarity was significant ( $\beta=0.182$ ,  $\chi^2(1)=4.94$ ,  $p=0.026$ ). See figure 4.

MRM results:

	Estimate	p-value
Intercept	0.011	0.84
Cultural distance	0.086	0.172
Language family	0.001	0.987
Geographic distance	0.043	0.318
Comparison count	0.871	0.0001

Table 1: MRM analysis predicting semantic alignment (Common Crawl), with family control.  $R^2=0.761$

	Estimate	p-value
Intercept	0.034	0.0311
Cultural distance	0.072	0.315
ASJP	-0.168	0.0009
Geographic distance	0.075	0.108
Comparison count	0.841	0.0001

Table 2: MRM analysis predicting semantic alignment (Common Crawl), with ASJP control.  $R^2=0.744$

Mantel tests:

	Var1	Var2	r	llim	ulim	p
2	Cultural	Linguistic	-0.084	-0.201	0.000885	0.277
3	Cultural	Historical	-0.315	-0.447	-0.204	0.0211
4	Cultural	Geographic	-0.461	-0.586	-0.312	0.00295
5	Linguistic	Historical	-0.25	-0.357	-0.114	0.015
6	Linguistic	Geographic	0.136	-0.0134	0.235	0.121
7	Historical	Geographic	0.405	0.31	0.519	0.00101
71	Linguistic	Cultural **	-0.0831	-0.152	-0.00152	0.27

Table 3: Mantel tests (Common Crawl). \*\* = partial Mantel test, controlling for historical and geographical distance.

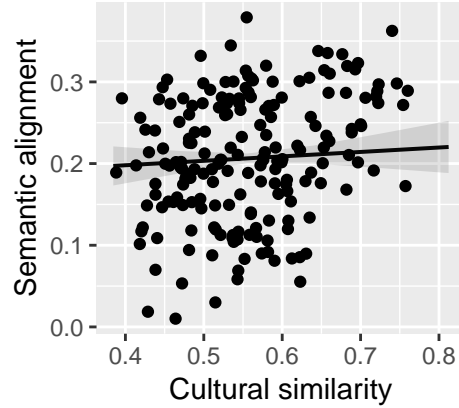


Figure 4: Semantic alignment and cultural similarity for data using the Subtitles alignments

## Subtitles

Mixed effects model: The correlation between semantic alignment and cultural similarity was not significant ( $\beta = 0.0606$ ,  $\chi^2(1) = 0.74$ ,  $p = 0.39$ ). See figure 5

MRM results:

	Estimate	p-value
Intercept	0.073	0.517
Cultural distance	0.125	0.413
Language family	-0.041	0.838
Geographic distance	-0.013	0.887
Comparison count	0.806	0.0002

Table 4: MRM analysis predicting semantic alignment (Subtitles), with family control.  $R^2 = 0.744$

Mantel tests:

	Estimate	p-value
Intercept	0.083	0.297
Cultural distance	-0.023	0.884
ASJP	-0.282	0.0083
Geographic distance	0.019	0.854
Comparison count	0.831	0.0003

Table 5: MRM analysis predicting semantic alignment (Subtitles), with ASJP control.  $R^2=0.803$

	Var1	Var2	r	llim	ulim	p
2	Cultural	Linguistic	0.351	0.241	0.538	0.0884
3	Cultural	Historical	-0.17	-0.286	-0.0153	0.155
4	Cultural	Geographic	-0.34	-0.57	-0.172	0.0276
5	Linguistic	Historical	-0.352	-0.503	-0.0822	0.0301
6	Linguistic	Geographic	-0.273	-0.462	-0.0818	0.0806
7	Historical	Geographic	0.346	0.181	0.522	0.01
71	Linguistic	Cultural **	0.281	0.129	0.466	0.135

Table 6: Mantel tests (Subtitles). \*\* = partial Mantel test, controlling for historical and geographical distance.

## References

- Bouckaert, Remco, Philippe Lemey, Michael Dunn, Simon J. Greenhill, Alexander V. Alekseyenko, Alexei J. Drummond, Russell D. Gray, Marc A. Suchard, and Quentin D. Atkinson (2012). Mapping the origins and expansion of the Indo-European language family. *Science*, 337(6097), 957-960.
- Lichstein, J. W. (2007). Multiple regression on distance matrices: a multivariate spatial analysis tool. *Plant Ecology*, 188(2), 117-131.
- Jäger, G. (2018). Global-scale phylogenetic linguistic inference from lexical resources. *Scientific data*, 5, 180189.
- Wichmann, Søren, Eric W. Holman, and Cecil H. Brown (eds.). 2018. The ASJP Database (version 17).