Supporting Materials for *The differential coding of perception in the world's languages*

Asifa Majid, Seán G. Roberts, Ludy Cilissen, Karen Emmorey, Brenda Nicodemus, Lucinda O'Grady, Bencie Woll, Barbara LeLan, Hilário de Sousa, Brian L. Cansler, Shakila Shayan, Connie de Vos, Gunter Senft, N. J. Enfield, Rogayah A. Razak, Sebastian Fedden, Sylvia Tufvesson, Mark Dingemanse, Ozge Ozturk, Penelope Brown, Clair Hill, Olivier Le Guen, Vincent Hirtzel, Rik van Gijn, Mark A. Sicoli, & Stephen C. Levinson

All data, processing code and analysis scripts are available in an online GitHub repository:
`https://github.com/seannyD/LoP_Codability_Public`.

Contents

www.pnas.org/cgi/doi/10.1073/pnas.1720419115

S1: Coding guidelines

Language of perception: Coding guidelines

Asifa Majid

The sections following detail how your data should be coded. Consult the sample table on the last page as you read through these instructions—this will make it easier to follow the formatting guidelines outlined below.

1. The main response

We are interested in the main *semantic* response, not the *syntactic* head. Although there may be fascinating questions to be explored about the linguistic classes, and their constituency, which are used to describe the stimuli we are not comparing these across languages. We want to know whether speakers agreed in the semantic category they used to describe the response.

In the head column:

- code the main semantic response – this should be in a consistent citation format (e.g. singular, without TAM-marking, the underived root-form if it is derived in various ways, etc.)
- code the first "weighty" response (i.e. if the person begins by saying "don't know" but then carries on and gives a description of the stimulus, code the first response counting from the description)
- code all responses thereafter (including "don't know" responses): if there are multiple responses, add rows which are clearly labeled for number of response, stimulus number and ID (if there are a succession of "don't know responses" then code each as a separate response if it appears in its own intonation unit)
- code responses even if they are repeated (e.g. *red, pink, really red* –> head: response 1: red; response 2: pink; response 3: red).
- if a coordinated phrase is used (e.g. *red and pink*) code as two responses (head: response 1: red; response 2: pink).
- if the response is a reduplication (e.g. *green green*) code as a single response (head: green; modifier: REDUP)
- every response must have a head response, modifiers should not be stranded
- if there is no "weighty" response code as, i.e. when a consultant didn't know how to describe an item (e.g. *don't know*, *not sure*, *nothing*, or non-target stimuli related response such as *two black thingo* for the shape task or *square* for the color task), this should be coded as head: no description. On the other hand, if a stimulus item was missed because of experimental error then code as head: n/a.

Tricky cases:

- code for the root (e.g. *fur* and *furry* would both be coded as *fur* – see section on SAE-coding)
- there may be clausal/phrasal expressions that are difficult to parse into main description and modifier columns (e.g. Umpila: *some, you know, hardwood that the old men might cut for a bed* for a shape descriptor). If these are not

relevant to cross-speaker consistency (it's a one-off response) then you can code them as the main response. If it is a more frequently occurring strategy, then consult with Asifa.

- in the case of complex expressions let the semantic category guide your coding (e.g. *teddy bear* should be coded as head for texture, rather than just *bear*; as should *shoe polish* for a smell response, rather than just *polish*; or *driehoek* for shape rather than *hoek*. The whole phrase picks out the relevant reference. On the other hand *fire, forest fire, camp fire* can all be counted as *fire* for a smell response since these are not distinct types.)
- in most cases it is easy to identify the semantic head, but occasionally, in some languages, there can be compounds that cannot be distinguished (equipotent). These should be coded as a unit (e.g. blue-green); if they can be distinguished at all then code as any other head modifier response.
- negated responses should be coded in the head column (e.g. *not green* -> head: NEG-green – see section on Modifier-coding)

2. Modifier coding

Use of modifiers or hedging can indicate lack of codability. Thus we are interested in how much modification a response gets. To help you with coding of modifiers here is a non-exhaustive list of English modifiers: *could be, really, like, very, probably, most, maybe, sorta, kind-of, dark, light, forest, swamp, fluorescent, etc.*

- Each modifier should be put in a separate cell. For each additional modifier, add a column, which should be labeled clearly (modifier 1, modifier 2, modifier 3, etc).
- If the head response is reduplicated (e.g. *green green*) code as REDUP in the modifier column (with *green* in the head column).
- If a modifier is reduplicated, there is no need to do any further decomposition (e.g. *very very green* -> head: green; modifier 1: very; modifier 2: very)
- If the modifier is a compound (e.g. *Florida-swamp green*), where the pieces cannot function alone then keep the modifier in one column -> head: green, modifier: Florida-swamp
- In the case of negation with a modifier, be sensitive to the scope of the negation. For example, in English *not exactly green* -> head: green; modifier: NEG-*exactly*.
- The use of the domain term is not a modifier (e.g. *green colour, round shape, banana smell*) – colour, shape, smell, etc are not modifiers. Nor are generic terms such as *thing* modifiers.
- Numerals should not be counted as modifiers, since number isn't the target domain.

- Be sure to code for hedges (e.g. *sort-of, maybe, kind-of*) as separate modifiers too. We are only interested in conventionalized linguistic hedges, not disfluencies or floor-holders (e.g. *um, weeellll...* etc.)

- Non-lexical modification – where there is conventionalised use of non-lexical modification (as with expressives or with sign languages) then code for non-lexical modifiers.

3. SAE coding

For each main response (head), we want to know whether the response was Source-based, Abstract or Evaluative.

- Abstract = descriptive response that captures the domain-property (e.g. colour: *red, green, blue;* smell: *musty, fragrant*; texture: *furry, silky, hard*)
- Source-based = refers to a specific object/source (e.g. colour: *gold, silver, ash;* smell: *vanilla, banana*; texture: *fur, silk, beads*)
- Evaluative = gives a subjective response to the stimulus (e.g. *nice, horrible, lovely, yummy*)

Tricky cases:

- Following Berlin & Kay (1969), if a colour term is also the name of an object also characteristically having that colour, then code as Source-based (e.g. *orange, olive, fuschia, lilac*). The same applies to the other domains (e.g. *star*).
- If a term is domain-specific but carries an evaluative component, then code as ABSTRACT. This would apply to terms such as "stinky". Although it could be argued that these are strongly evaluative, they nevertheless seem to be quite different in their behaviour and distribution from domain-general evaluative terms, such as "good", "bad", "weird", etc.

4. General info

Other issues:

- Please make sure that you retain the original whole description from each consultant in your excel sheet. This enables us to check your coding decisions, and if there is a challenge of our coding in the future, we can alter coding more easily.
- Possible notes and comments on coding should never be in the results sheet. They should be listed in the “general info” sheet.
- You should have the protocol for how you ran the experiment in a separate sheet, including the exact questions asked of participants.
- You should include all demographic information about your participants.

Response	Stimulus number	Munsell code	consultant 1 full response	consultant 1 head	consultant 1 modifier 1	consultant 1 modifier 2	consultant 1 modifier 3	consultant 1 SAE
1	1	10G 4/10	not red	NEG-red				A
1	2	5Y 4/6	green	green				A
2	2	5Y 4/6	kind of a swampish green	green	swampish	kind of		A
3	2	5Y 4/6	reminds me of the ponds of Florida	pond	Florida			S
1	3	10P 4/12	purple	purple				A
2	3	10P 4/12	deep dark purple	purple	deep	dark		A
1	4	5P 8/4	light green	green	light			A
1	5	10Y 8/12	slightly yellow	yellow	slightly			A
1	6	5BG 8/4	the colour blue	blue				A
2	6	5BG 8/4	sky-coloured	sky				S
3	6	5BG 8/4	kind of blue	blue	kind-of			A
1	7	10RP 6/12	pinkish red	red	pinkish			A
2	7	10RP 6/12	pinkish	pink	ish			A
1	8	5GY 4/8	yellowed	yellow				A
1	9	10B 2/6	brown, it looks brown, dark brown	brown				A
2	9	10B 2/6		brown				A
3	9	10B 2/6		brown	dark			A
1	10	10YR 2/2	call that one a darker sky blue	blue	sky	darker	call-that	A
1	11	5G 6/10		N/A				

S2: Ethnographic background questionnaire

Language of perception: Ethnographic background

Stephen Levinson and Asifa Majid

In order to understand better the cultural practices in each community that might predict differential codability, we have some questions. We have tried to make these as simple as possible, so most should be answerable by a simple yes or no. If you have more information, we would be delighted to learn more too!

Since we are interested in the long-term cultural background, these questions should be interpreted as pertaining to the indigenous culture/technology, prior to the recent massive globalization (say prior to 1990). We are interested in the traditional division of labour, the background of traditional crafts, traditional cuisine, traditional aesthetics.

Please add any notes about other cultural practices that may be relevant for 'language of perception' (e.g. elaborate terminologies for patterns, classifications of birdsongs, i.e., quacks/shrieks/hoots…, etc.).

Language name: Researcher(s):

1. Is the environment open (fields, savanna) or closed (jungle, forest)?

Open or closed: Can you give more details: Any other comments:

2. Is settlement nucleated (large villages/towns) or dispersed (small family compounds)?

Nucleated or dispersed: Any other comments:

3. Were there traditional markets with a market economy and trade?

Market economy or trade: Any other comments:

4. Beyond male/female tasks, is there any elaborate division of labour (e.g. specialist makers of things used in the society)?

Yes or no: Any other comments:

5. Are there traditional paints (applied to surface of objects, or the body)?

Yes or no: If yes, what colours are they? Any other comments:

6. Are there dyes (for colouring fabrics, for example)?

Yes or no: If yes, what colours are they? Any other comments:

7. Are there colours with specialised ritual uses (e.g. white or black worn by widows)?

Yes or no: If yes, what colours are they? Any other comments:

8. Are there professional colour experts (e.g., painters, dyers)?

Yes or no: Any other comments:

9. Do members of the society make pottery?

Yes or no: If yes, is it coloured? Is it patterned? Any other comments:

10. Do they make containers (e.g. of wood)?

Yes or no: If yes, what shapes (e.g. round, square)? Any other comments:

11. Are houses round or square?

Round, square, or other: Any other comments:

12. Are there professional builders?

Yes or no: Any other comments:

13. Do they make boats?

Yes or no: If yes, are there specialists? Any other comments:

14. Are there other specialist craftspeople? (e.g., makers of bags, nets, traps?)

Yes or no: If yes, are there specialists? Any other comments:

15. Is there spinning of thread in the culture?

Yes or no: If yes, is this a specialist activity? Any other comments:

16. Is there weaving in the culture?

Yes or no: If yes, is this a specialist activity? Any other comments:

17. Do they weave or dye patterns?

Yes or no: If yes, what patterns (e.g. curvilinear, rectilinear?) Any other comments:

18. Do they have fine leatherware?

Yes or no: If yes, is it decorated? If decorated, what patterns (e.g. curvilinear, rectilinear?) If yes, what patterns (e.g. curvilinear, rectilinear?) Any other comments:

19. Do they pulverise spices, grains or otherwise make powders?

Yes or no: Any other comments:

20. Are fine surfaces typical of house construction?

Yes or no: Any other comments:

21. Are there other crafts that may be relevant for texture?

Yes or no: If yes, what are they? Any other comments:

22. Are there professionals with interest in texture (e.g., weavers, crafts people)?

Yes or no: Any other comments:

23. Do people cook from scratch with primary ingredients?

Yes or no: Any other comments:

24. Is there an ideology of "cuisine" (e.g., set order of courses during the meal, hierarchies of meal types, etc)?

Yes or no: Any other comments:

25. Are there professional or specialist cooks/chefs?

Yes or no: Any other comments:

26. Do people value quantity or quality in food (in e.g. a feast)?

Quantity or quality: Any other comments:

27. Are spices/herbs used in cooking?

Yes or no: If yes, what are they? Any other comments:

28. Were there traditional sweet additives (e.g., sugar, honey)?

Yes or no: If yes, what are they? Any other comments:

29. Is salt added to cooking?

Yes or no: If yes, how was it traditionally obtained? Any other comments:

30. Were bitter additives used in food or medicine (e.g., quinine)?

Yes or no: If yes, what were they? Any other comments:

31. Were sour additives used (e.g., tamarind, lemon)?

Yes or no: If yes, what were they? Any other comments:

32. Is there access to umami additive (e.g., MSG)?

Yes or no: If yes, what were they? Any other comments:

33. Do people wash on a daily basis?

Yes or no: Any other comments:

34. Is there a traditional practice of applying smells to the body (e.g. perfumes, oils, flowers)?

Yes or no: If yes, what were they? Any other comments:

35. Do they apply smells elsewhere (e.g., air freshener)?

Yes or no: If yes, what were they? Any other comments:

36. Are smells used for ritual purposes (e.g. incense)?

Yes or no: If yes, what were they? Any other comments:

37. Is there a culture of fragrance in food (e.g. basmati rice, rose water)?

Yes or no: If yes, what were they? Any other comments:

38. Were there traditional musical instruments?

Yes or no: If yes, what were they? Any other comments:

39. Are there specialist musicians?

Yes or no: Any other comments:

40. Is there instruction/training for musical participation?

Yes or no: Any other comments:

41. Do children undergo musical instruction?

Yes or no: Any other comments:

42. Are birdsong or animal calls of cultural interest (e.g. imitated for hunting)?

Yes or no: Any other comments:

43. Any other observations?

Any other comments:

S3: Comparing diversity measures

Comparing diversity measures

Introduction

We are reccomending using Simpson's index where "no descriptions" are counted as unique responses. Simpson's index has the advantage of having a transparent definition: the probability that two observations taken at random from the sample are of the same type. Converting "no descriptions" to unique responses also means that Simpson's index and the Shannon index correlate very highly. It also has the advantage of producing numbers for stimuli where no participant provided a response.

Functions

```
di.shannon = function(labels){
  # counts for each label
  tx = table(labels)
  # convert to proportions
  tx = tx/sum(tx)
  -sum(tx * log(tx))
}
di.simpson = function(labels){
  # Full formula due to small datasets
  # (Hunter-Gaston index)
  n = table(labels)
  N = length(labels)
  sum(n * (n-1))/(N*(N-1))
}

di.BnL = function(labels){
  #CR-DR+20
  #where, DR is the number of different responses a stimulus item receives
  #and CR is the number of subjects who agree on the most common name
  DR = length(unique(labels))
  CR = max(table(labels))
  return(CR-DR+20)
}
```

Load data

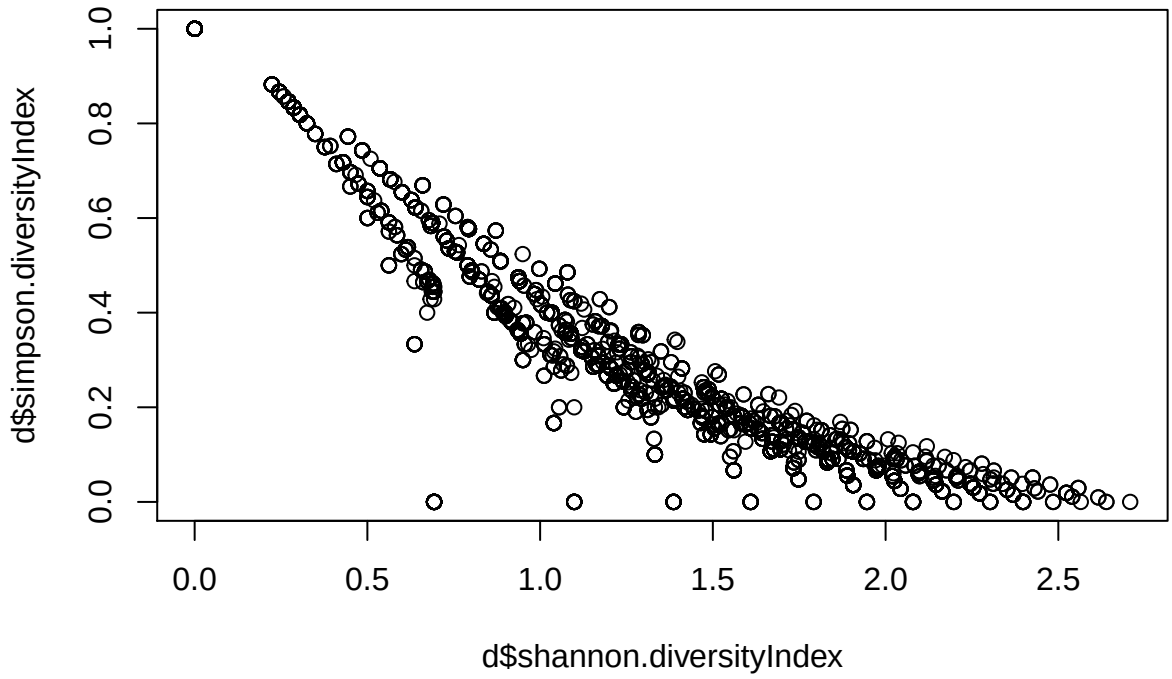
```
a = read.csv("../data/AllData_LoP.csv",stringsAsFactors = F)

d = read.csv("../data/DiversityIndices.csv", stringsAsFactors = F)

d = d[!is.na(d$simpson.diversityIndex),]
d$id = paste(d$Language,d$Stimulus.code)

d.nd = read.csv("../data/DiversityIndices_ND.csv", stringsAsFactors = F)
```

```
d.nd = d.nd[!is.na(d.nd$simpson.diversityIndex),]
d.nd$id = paste(d.nd$Language,d.nd$Stimulus.code)

l = read.delim("allCombs.txt", sep='', stringsAsFactors = F, header=F)
names(l) = c("N","shannon","simpson")
```

Compare measures

Plotting the Shannon index against Simpson's index, we see that there is a general correlation, but also several outliers.

```
plot(d$shannon.diversityIndex,d$simpson.diversityIndex)
```




```
cor.test(d$shannon.diversityIndex,d$simpson.diversityIndex)
```

```
##
##  Pearson's product-moment correlation
##
## data:  d$shannon.diversityIndex and d$simpson.diversityIndex
## t = -150.45, df = 2838, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.9466087 -0.9384030
## sample estimates:
##        cor
## -0.9426481
```

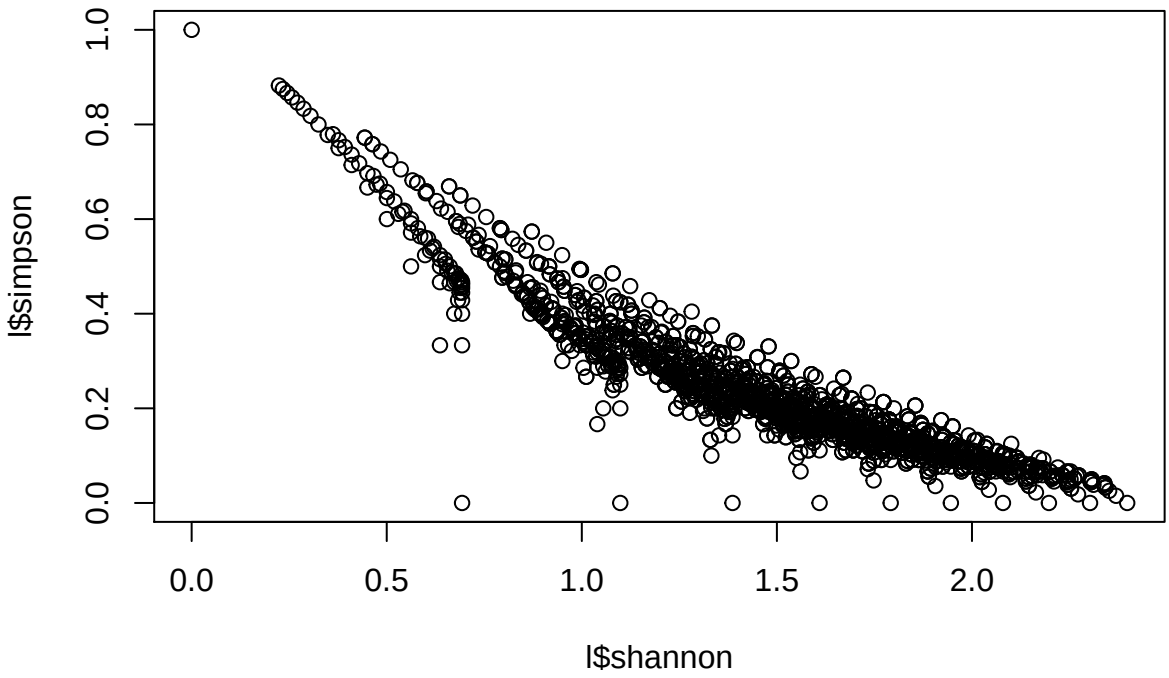
Taking into account the non-linear relationship, the variance explained in common is:

```
orig.cor = summary(lm(simpson.diversityIndex~
          shannon.diversityIndex +
          I(shannon.diversityIndex^2),
        data = d))
orig.cor$r.squared
```

```
## [1] 0.9442713
```

These outliers come close to covering the total space of possible relations between the two measures. The data from the plot below comes from `compareDiversityMeasures.py`, which generates all possible combinations of responses within the bounds of the experiment (between 2 and 14 categories, between 1 and 17 responses):

```
plot(l$shannon,l$simpson)
```



The outliers in the bottom left of the plot (where the two measures disagree) come from cases where there are many "no description" responses. e.g. colour 10G 8/6 for Umpila:

```
ax = a[a$Language=="Umpila" &          a$Stimulus.code=="colour.10G 8/6" &
         a$Response==1,]
table(ax$head)
```

```
##
##     kawithaman no description       paachala
##              1              9              1
```

```
tx = ax[ax$head!="no description",]$head
```

The original measures remove "no description" responses. That means that the example above above yeilds a Simpson index of 0 - there is no agreement between the two speakers who responded. The Shannon index is 0.6931472, since there are only two responses, and the Shannon index measures the information in that sequence. Had there been 14 completely different responses, then the Shannon index would be 2.64, which is closer to the simple relationship.

One solution is to count "no description" responses as unique labels. So in the example above, the table of responses would be:

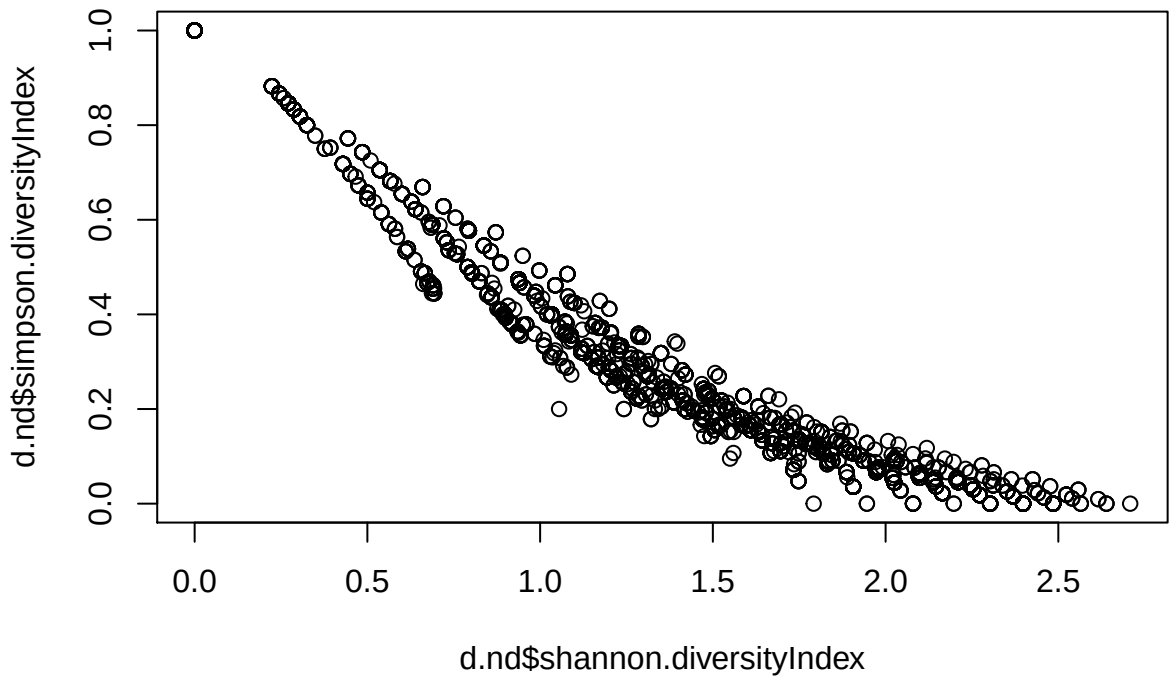
```
tx.nd = ax$head
tx.nd[tx.nd=='no description'] =
  paste0("R",1:sum(tx.nd=="no description"))
tx.nd
```

```
##  [1] "R1"         "R2"         "paachala"   "R3"         "R4"
##  [6] "R5"         "R6"         "kawithaman" "R7"         "R8"
## [11] "R9"
```

This does not affect the Simpson index, but raises the Shannon index to 2.4. It also has the advantage of producing a defined index for cases where no participants produced a label.

If we calculate all indices while counting "no description" responses as unique responses, then we get the following relationship:

```
plot(d.nd$shannon.diversityIndex,
     d.nd$simpson.diversityIndex)
```




```
cor.test(d.nd$shannon.diversityIndex,
     d.nd$simpson.diversityIndex)
```

```
##
##  Pearson's product-moment correlation
##
## data:  d.nd$shannon.diversityIndex and d.nd$simpson.diversityIndex
## t = -206.66, df = 2848, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.9704554 -0.9658590
## sample estimates:
##        cor
## -0.9682389
```

```
# Proportion of values unchanged
pvu = sum(d$simpson.diversityIndex ==
     d.nd$simpson.diversityIndex[match(d$id, d.nd$id)]) / nrow(d)
```

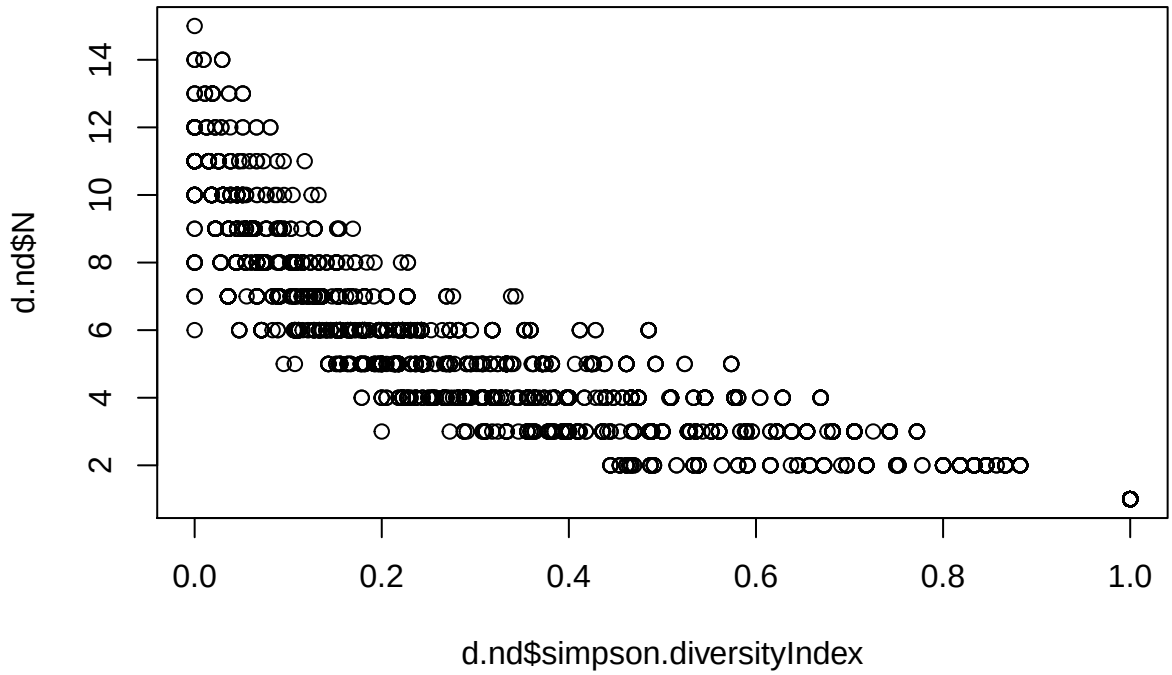
63.17% of values are unchanged. The new values are also more highly correlated:

```
nd.cor = summary(lm(simpson.diversityIndex~
          shannon.diversityIndex +
          I(shannon.diversityIndex^2),
        data = d.nd))
nd.cor$r.squared
```

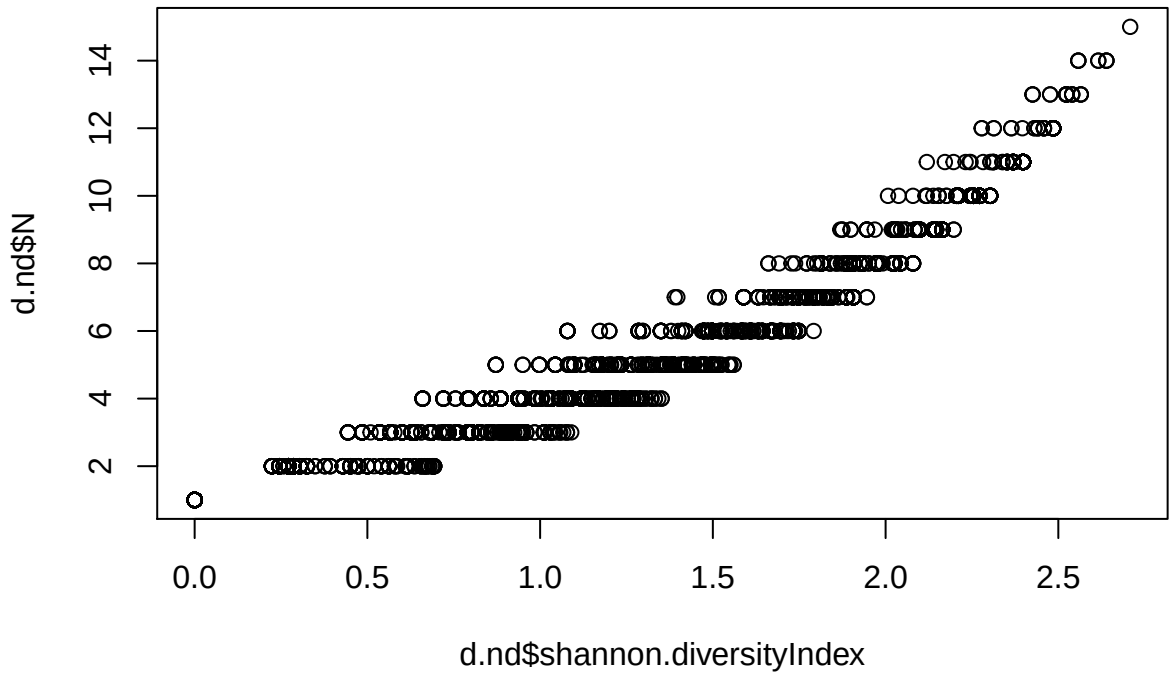
```
## [1] 0.9855785
```

Diversity and number of types

```
plot(d.nd$simpson.diversityIndex, d.nd$N)
```




```
plot(d.nd$shannon.diversityIndex, d.nd$N)
```



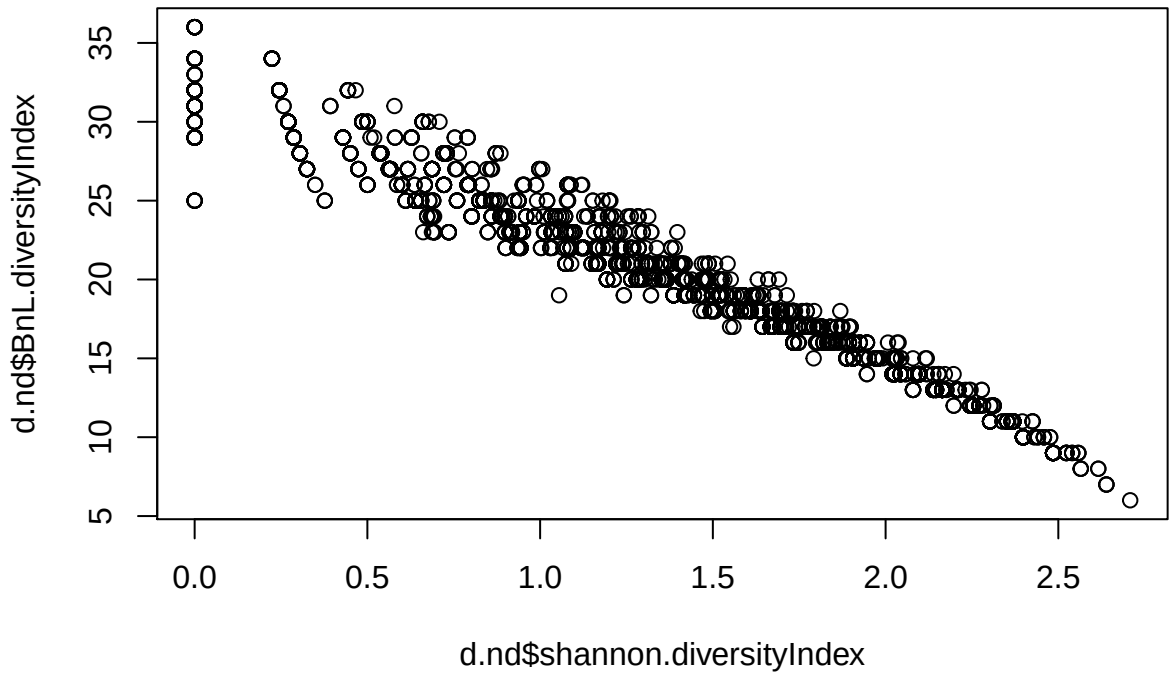
Brown and Lenneberg measure

The measure from Brown and Lenneberg (1954) of "interpersonal agreement" is caluclated as

CR-DR+20

Where, CR is the number of subjects who agree on the most common name and DR is the number of different responses a stimulus item receives (the +20 is so that the values remain positive). This does not adjust for the number of participants/responses. Still, the values are very highly correlated with both Simpson and Shannon indices, albeit non-linearly.

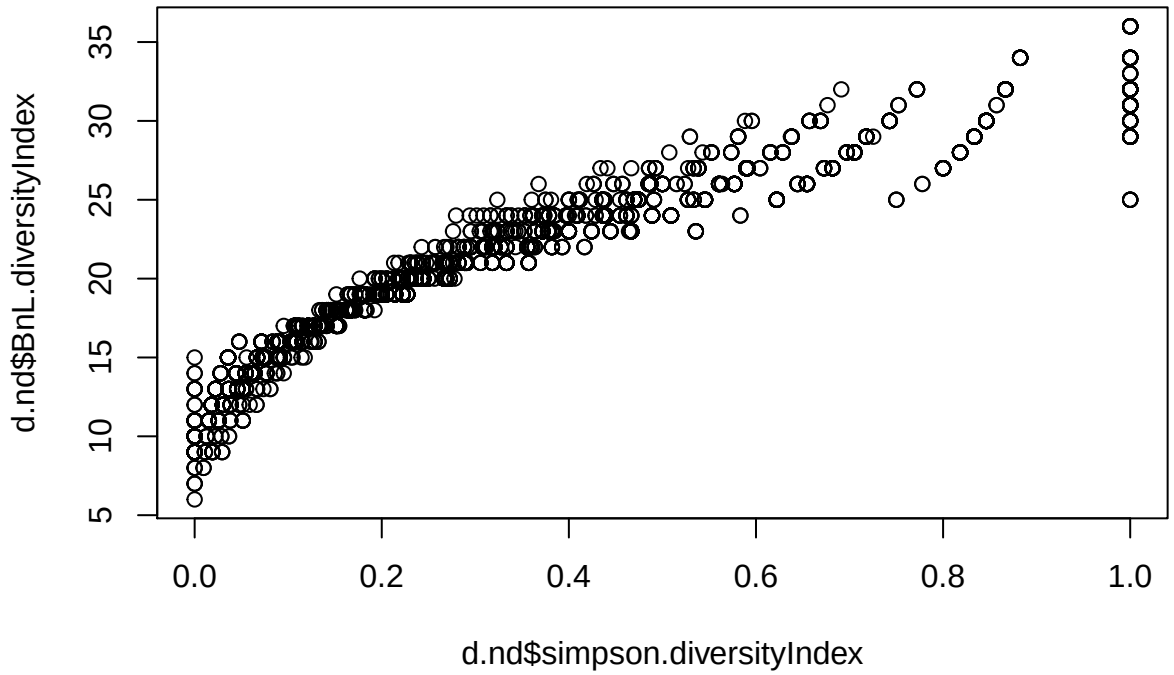
```
plot(d.nd$shannon.diversityIndex,
     d.nd$BnL.diversityIndex)
```




```
cor.test(d.nd$shannon.diversityIndex,
     d.nd$BnL.diversityIndex)
```

```
##
##  Pearson's product-moment correlation
##
## data:  d.nd$shannon.diversityIndex and d.nd$BnL.diversityIndex
## t = -272.42, df = 2848, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.9826563 -0.9799387
## sample estimates:
##        cor
## -0.9813465
```

```
plot(d.nd$simpson.diversityIndex,
     d.nd$BnL.diversityIndex)
```




```
cor.test(d.nd$simpson.diversityIndex,
     d.nd$BnL.diversityIndex)
```

```
##
##  Pearson's product-moment correlation
##
## data:  d.nd$simpson.diversityIndex and d.nd$BnL.diversityIndex
## t = 166.92, df = 2848, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.9489745 0.9557929
## sample estimates:
##       cor
## 0.9525029
```

In particular, the correlation with the Shannon index makes sense, because it is related to the 'surprisal' of encountering a label that is not your own. However, this measure is not theoretically motivated, so the other two are preferred.

S4: Codability across languages and domains

Codability across languages and domains

Contents

Introduction

This document provides R code for reproducing the test of the relative codability of the senses. We use mixed effects modelling to test the influence of language and domain. The full model included random intercepts for stimulus, domain, language, and the interaction between language and domain. Log-likelihood comparison was used to compare the full model to a model without one of those intercepts

Data

The main data comes from `../data/DiversityIndices_ND.csv`, which includes the Simpson's diversity index, counting no-responses as unique responses. Each row lists the codability of a particular stimulus for a particular community. The variables are:

- `Language`: Language/Community name
- `domain`: Sense domain
- `Stimulus.code`: Identity of the stimulus
- `simpson.diversityIndex`: Simpson's diversity index
- `shannon.diversityIndex`: Shannon diversity index
- `N`: Number of responses
- `BnL.diversityIndex`: Brown & Lenneberg diversity index
- `mean.number.of.words`: Mean number of words in full response

Load libraries

```
library(lme4)
library(sjPlot)
library(REEMtree)
library(ggplot2)
library(party)
library(reshape2)
library(rpart.plot)
library(lattice)
library(dplyr)
library(mgcv)
library(lmtest)
library(itsadug)
```

Load data

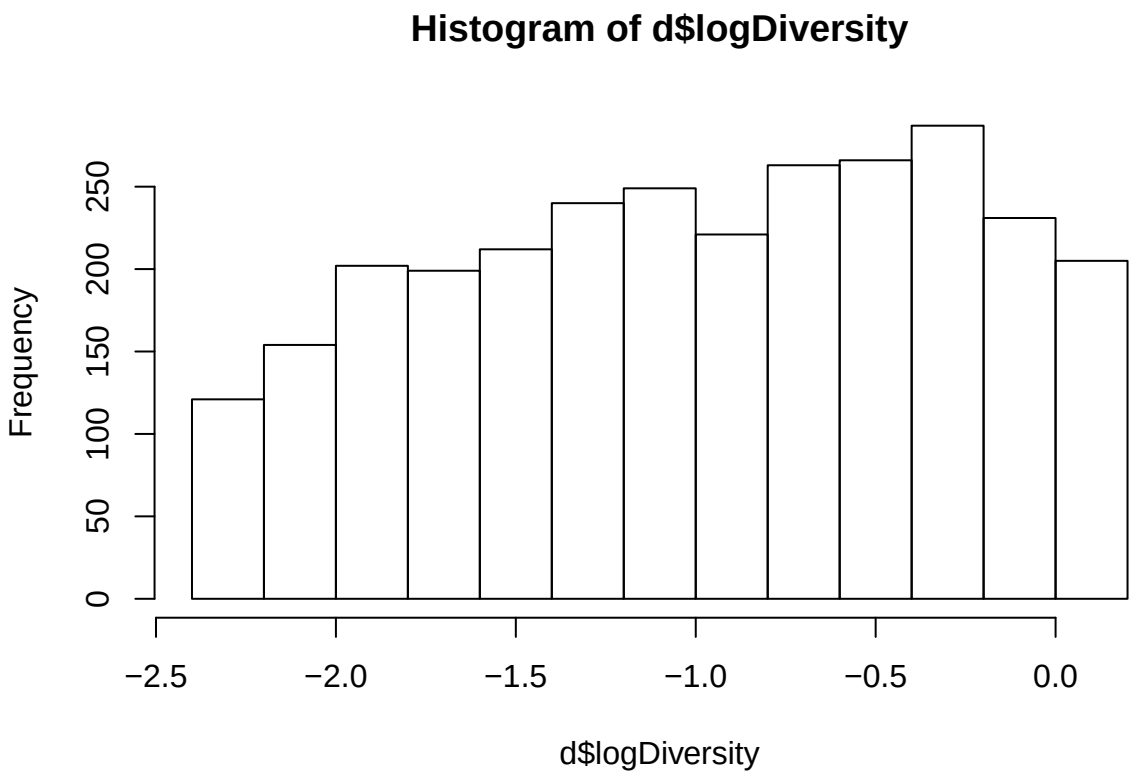
```
d = read.csv("../data/DiversityIndices_ND.csv", stringsAsFactors = F)

d = d[!is.na(d$simpson.diversityIndex),]

d$Language= as.factor(d$Language)
d$domain = factor(d$domain, levels=c("colour",'shape','sound','touch','taste','smell'))
```

Get log of diversity index, (add 0.1 to avoid infinite values)

```
d$logDiversity = log(d$simpson.diversityIndex+0.1)
```

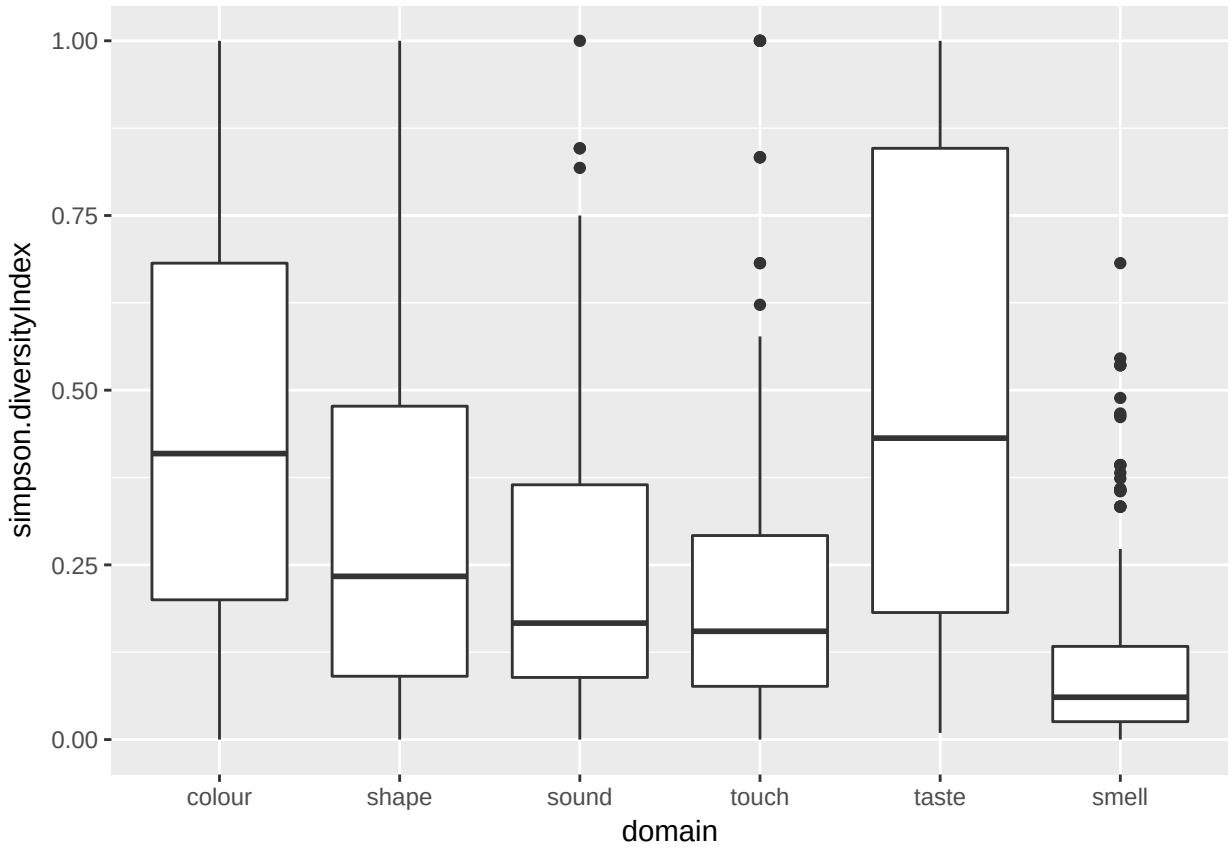
Distribution is not very normal, but it's difficult to approximate this distribution anyway.

```
hist(d$logDiversity)
```

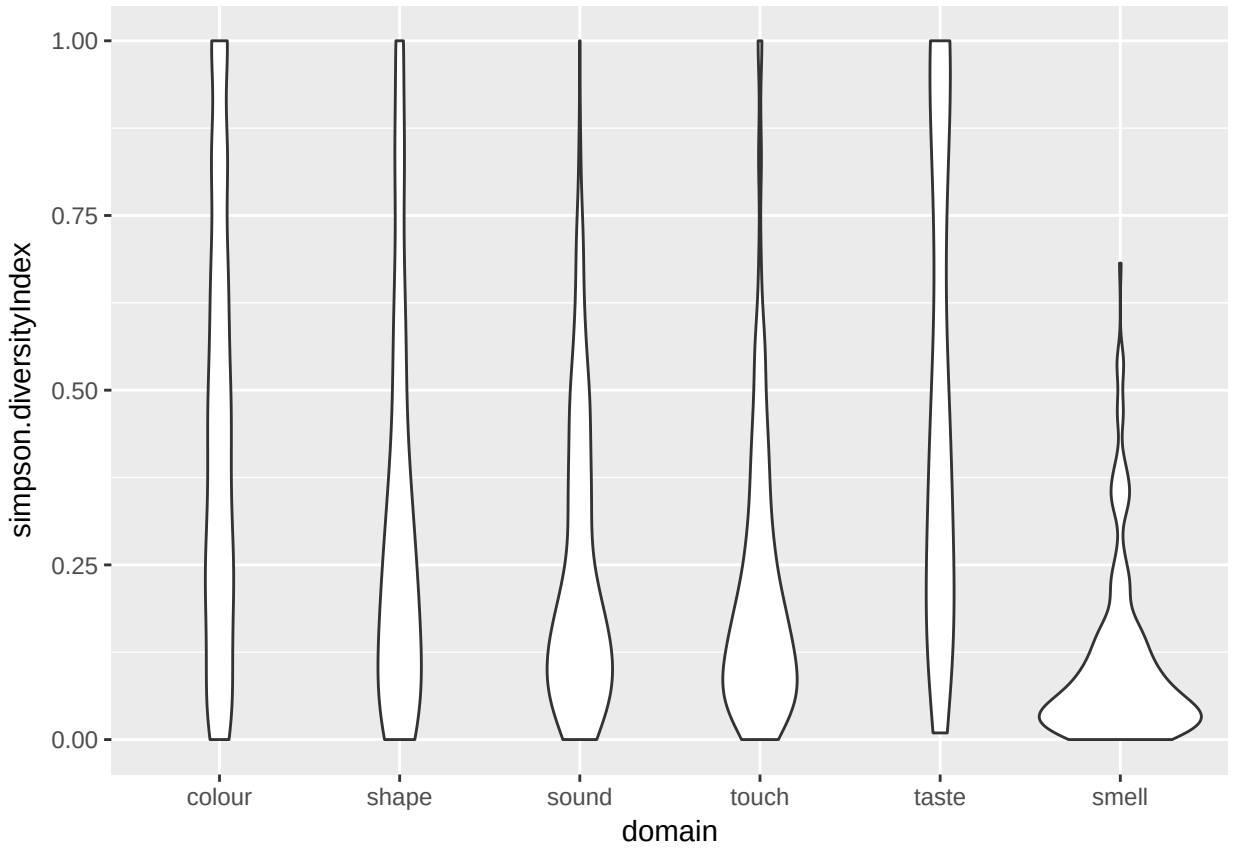


Plot data

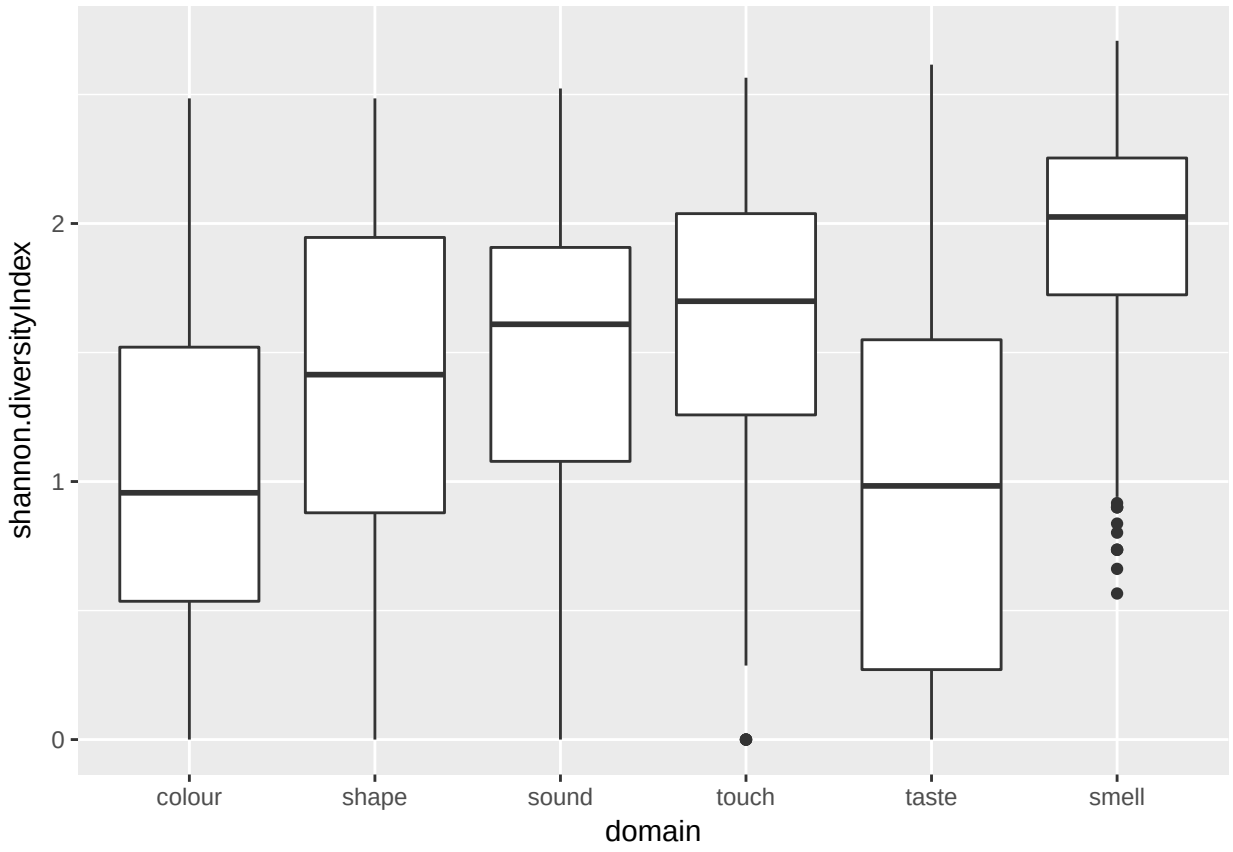
```
g = ggplot(d, aes(y=simpson.diversityIndex, x=domain))
g + geom_boxplot()
```



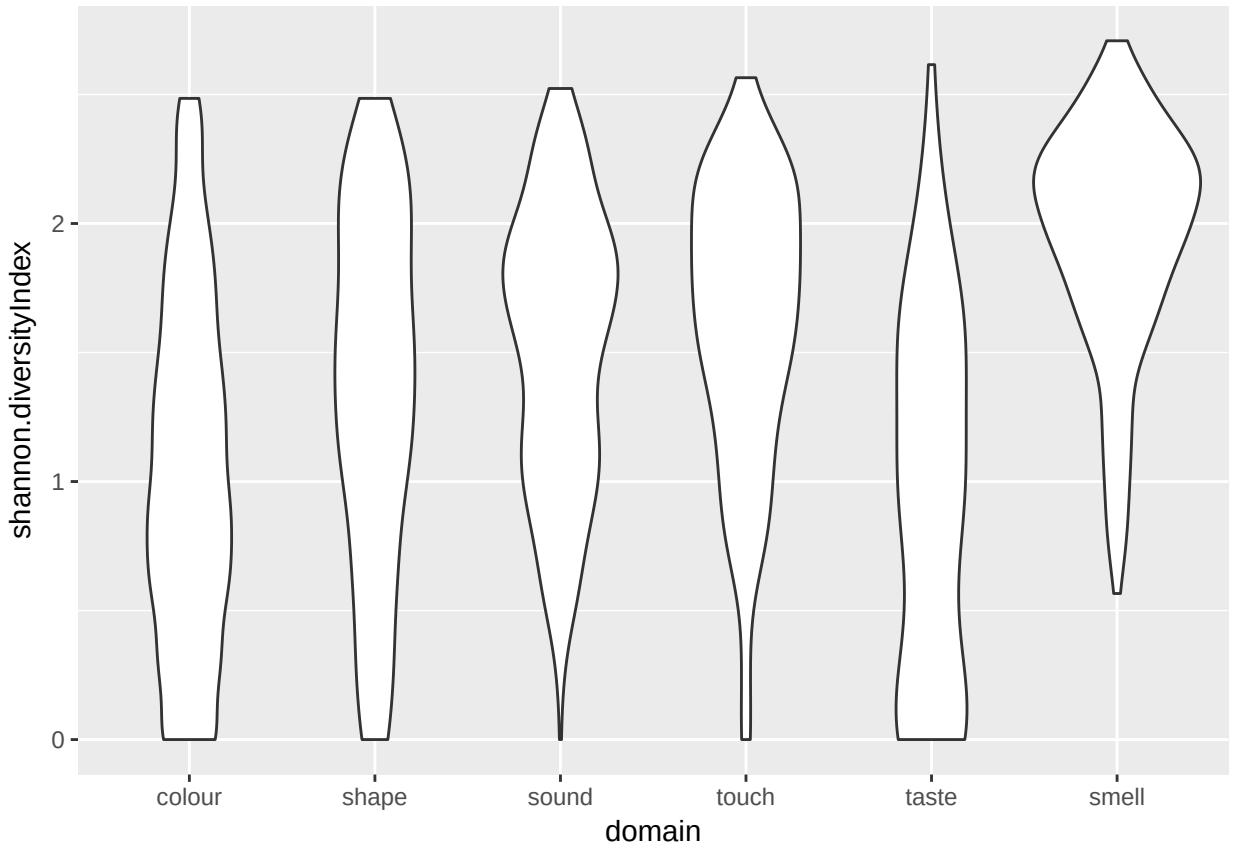

```
g + geom_violin()
```




```
g = ggplot(d, aes(y=shannon.diversityIndex, x=domain))
g + geom_boxplot()
```




```
g + geom_violin()
```



Run models

```
m.full = lmer( logDiversity ~ 1 +
               (1|Language) +
               (1|domain/Stimulus.code) +
               (1|Language:domain),
             data=d)

m.noL = lmer( logDiversity ~ 1 +
               (1|domain/Stimulus.code) +
               (1|Language:domain),
             data=d)

m.noDom = lmer( logDiversity ~ 1 +
               (1|Language) +
               (1|Stimulus.code) +
               (1|Language:domain),
             data=d)

m.noStim = lmer( logDiversity ~ 1 +
               (1|Language) +
               (1|domain) +
               (1|Language:domain),
             data=d)
```

```
m.noLxD = lmer( logDiversity ~ 1 +
              (1|Language) +
              (1|domain/Stimulus.code),
            data=d)
```

Test models:

```
anova(m.full, m.noL)
```

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

```
## Data: d
## Models:
## m.noL: logDiversity ~ 1 + (1 | domain/Stimulus.code) + (1 | Language:domain)
## m.full: logDiversity ~ 1 + (1 | Language) + (1 | domain/Stimulus.code) +
## m.full:     (1 | Language:domain)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m.noL   5 3941.9 3971.6 -1965.9   3931.9
## m.full  6 3939.3 3975.0 -1963.7   3927.3 4.5491      1    0.03294 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(m.full, m.noDom)
```

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

```
## Data: d
## Models:
## m.noDom: logDiversity ~ 1 + (1 | Language) + (1 | Stimulus.code) + (1 |
## m.noDom:     Language:domain)
## m.full: logDiversity ~ 1 + (1 | Language) + (1 | domain/Stimulus.code) +
## m.full:     (1 | Language:domain)
##         Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m.noDom  5 3965.1 3994.9 -1977.6   3955.1
## m.full   6 3939.3 3975.0 -1963.7   3927.3 27.827      1  1.326e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(m.full, m.noStim)
```

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

```
## Data: d
## Models:
## m.noStim: logDiversity ~ 1 + (1 | Language) + (1 | domain) + (1 | Language:domain)
## m.full: logDiversity ~ 1 + (1 | Language) + (1 | domain/Stimulus.code) +
## m.full:     (1 | Language:domain)
##          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m.noStim  5 4452.1 4481.9 -2221.1   4442.1
## m.full    6 3939.3 3975.0 -1963.7   3927.3 514.81      1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(m.full, m.noLxD)
```

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

```
## Data: d
## Models:
```

```
## m.noLxD: logDiversity ~ 1 + (1 | Language) + (1 | domain/Stimulus.code)
## m.full: logDiversity ~ 1 + (1 | Language) + (1 | domain/Stimulus.code) +
## m.full:     (1 | Language:domain)
##         Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m.noLxD  5 4637.3 4667.1 -2313.7   4627.3
## m.full   6 3939.3 3975.0 -1963.7   3927.3 700.03      1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Details:

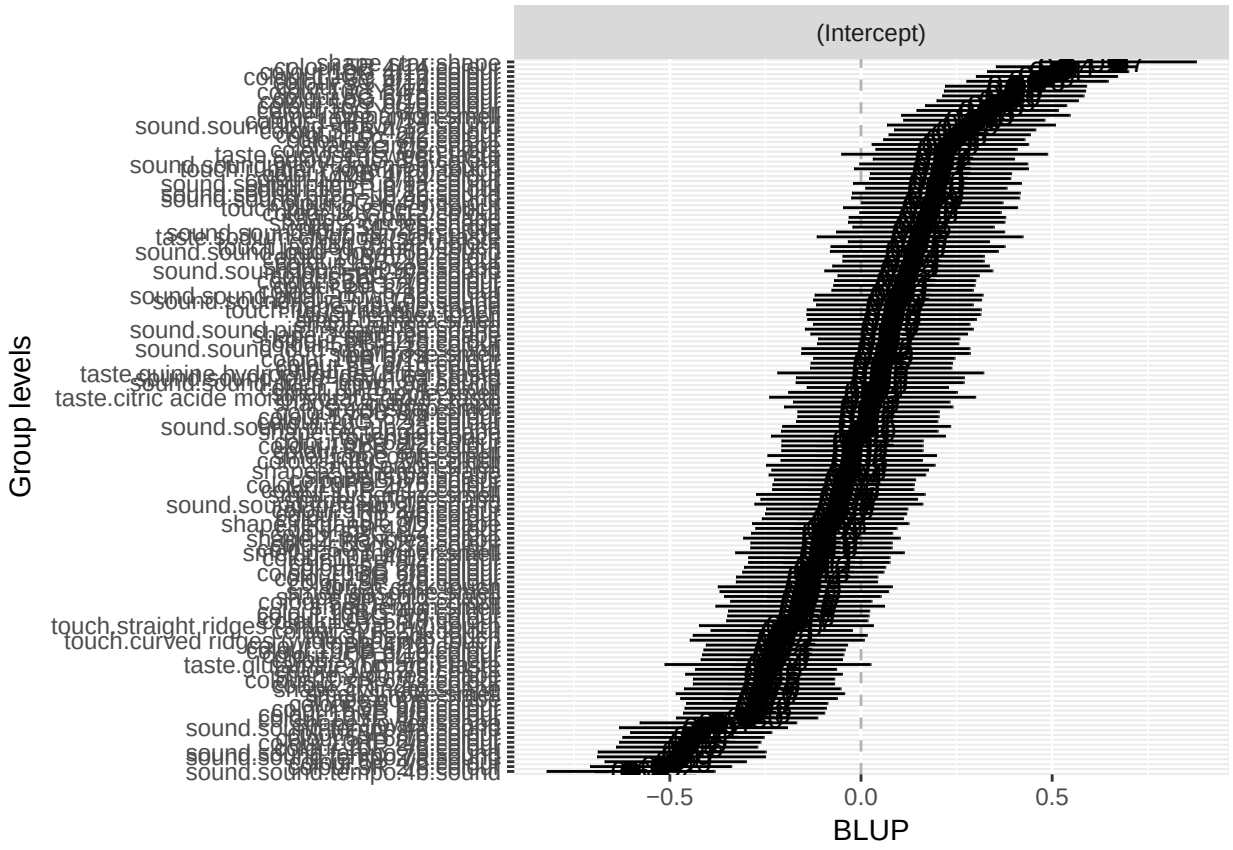
```
summary(m.full)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: logDiversity ~ 1 + (1 | Language) + (1 | domain/Stimulus.code) +
##     (1 | Language:domain)
##    Data: d
##
## REML criterion at convergence: 3929.3
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.0123 -0.6368  0.0153  0.6567  3.7445
##
## Random effects:
##  Groups               Name        Variance Std.Dev.
##  Stimulus.code:domain (Intercept) 0.06416  0.2533
##  Language:domain      (Intercept) 0.13367  0.3656
##  Language             (Intercept) 0.02731  0.1653
##  domain               (Intercept) 0.12029  0.3468
##  Residual                         0.18754  0.4331
## Number of obs: 2850, groups:
## Stimulus.code:domain, 147; Language:domain, 114; Language, 20; domain, 6
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  -1.1423     0.1536  -7.436
```

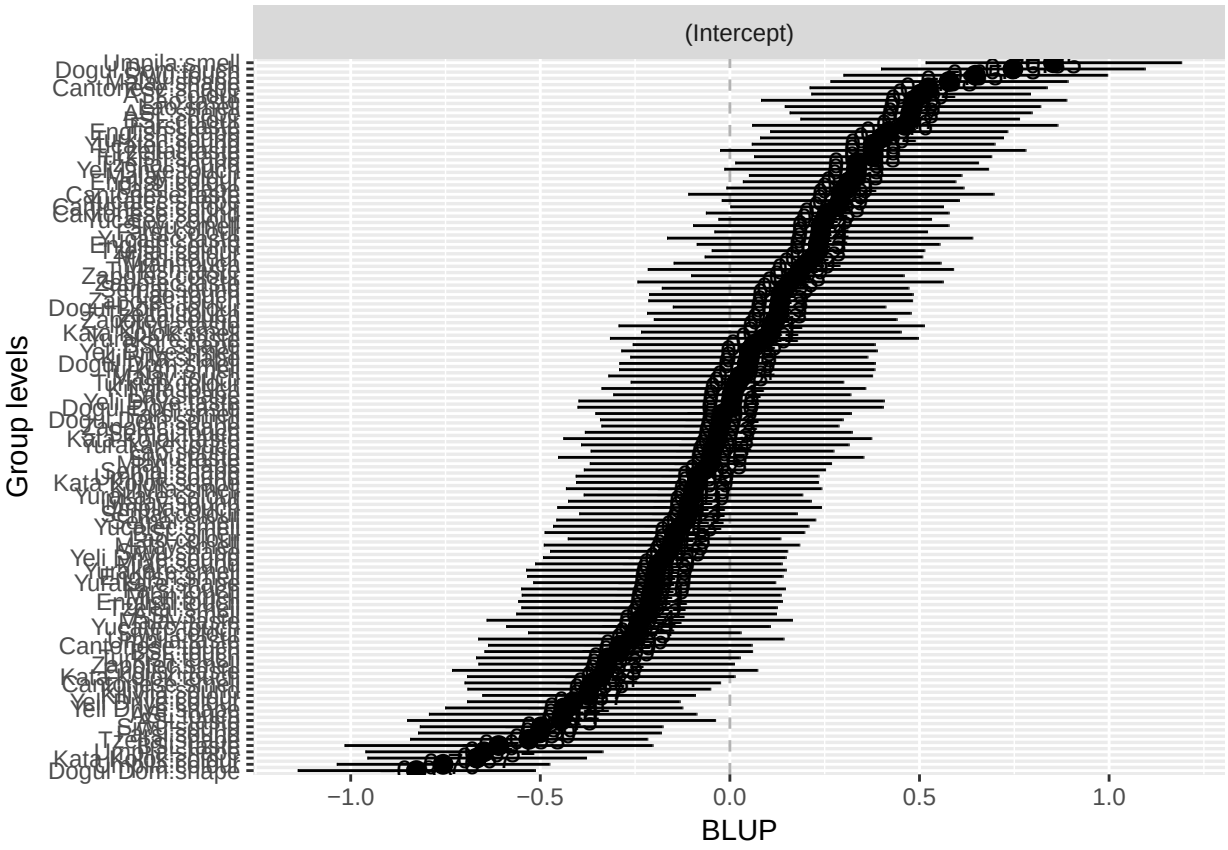
Random effects:

```
sjp.lmer(m.full, 're', sort.est = T, geom.colors=c(1,1))
```

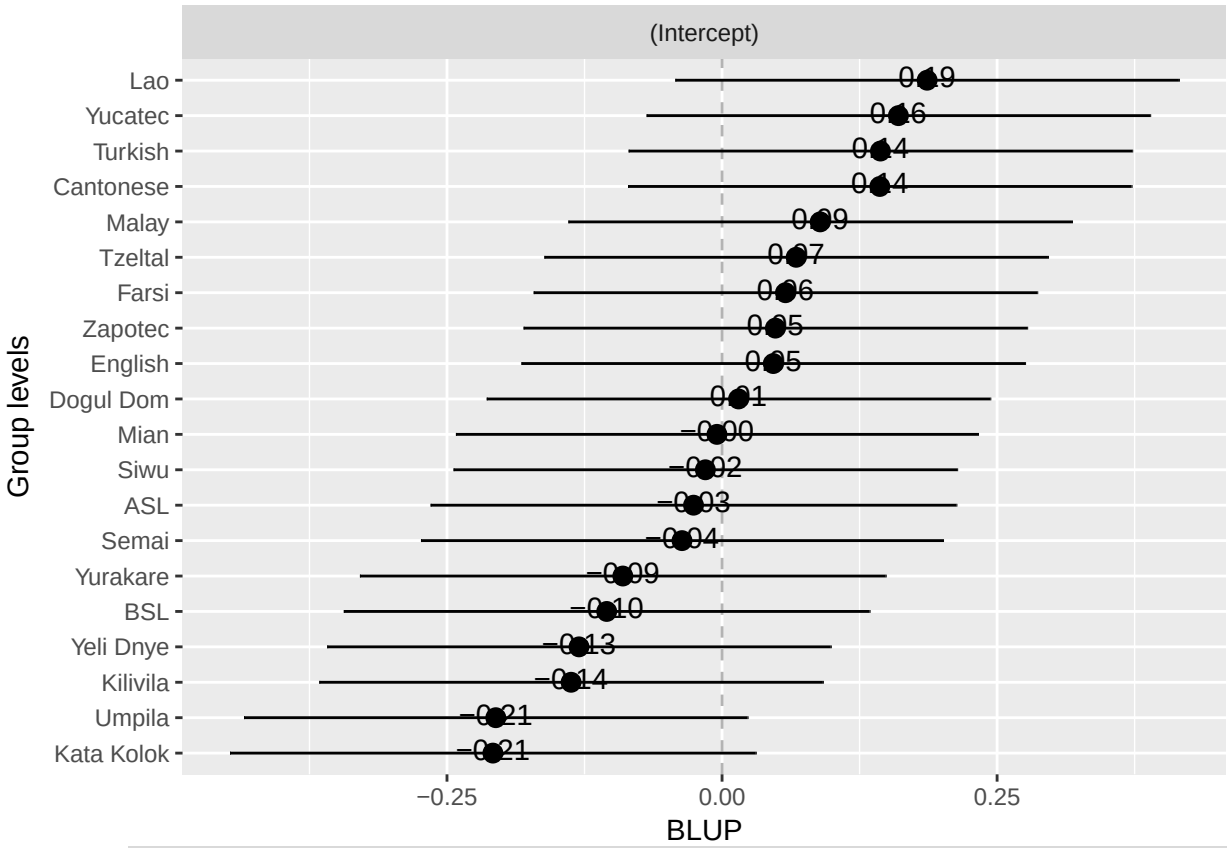
```
## Plotting random effects...
## Plotting random effects...
```

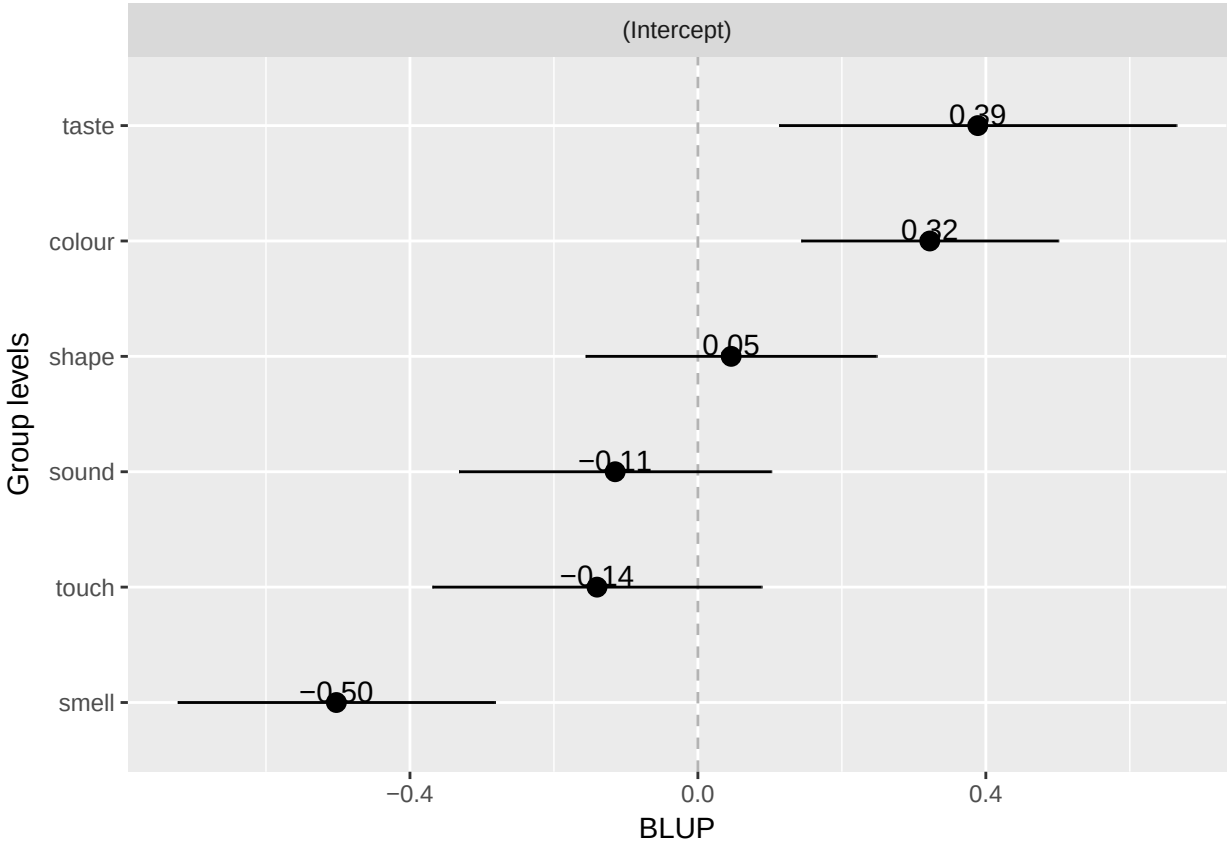



```
## Plotting random effects...
```

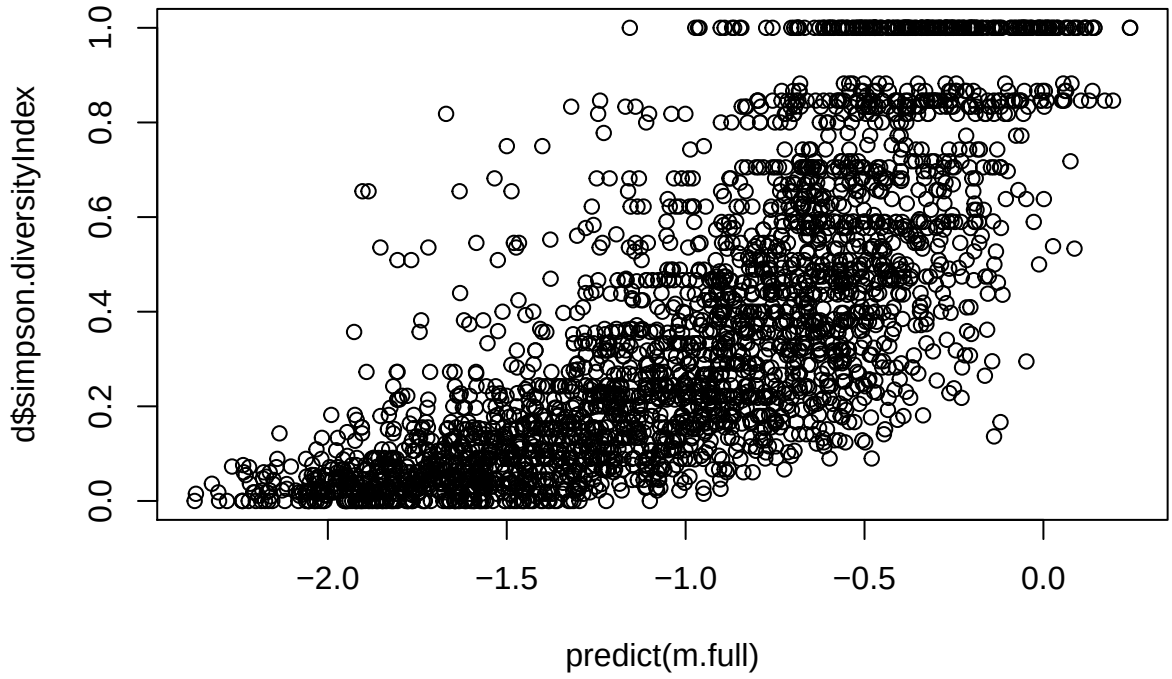



```
## Plotting random effects...
```


(Intercept)
Lao
Yucatec
Turkish
Cantonese
Malay
Tzeltal
Farsi
Zapotec
English
Dogul Dom
Mian
Siwu
ASL
Semai
Yurakare
BSL
Yeli Dnye
Kilivila
Umpila
Kata Kolok
Group levels
−0.25
0.00
0.25
BLUP


(Intercept)
taste
0.39
colour
0.32
shape
0.05
sound
−0.11
touch
−0.14
smell
−0.50
Group levels
−0.4
0.0
0.4
BLUP

```
plot(predict(m.full), d$simpson.diversityIndex)
```



Summary

The influence of each of the following random effects was tested:

- Language
- Domain
- Stimulus item (nested within domains)
- Domains within languages (interaction)

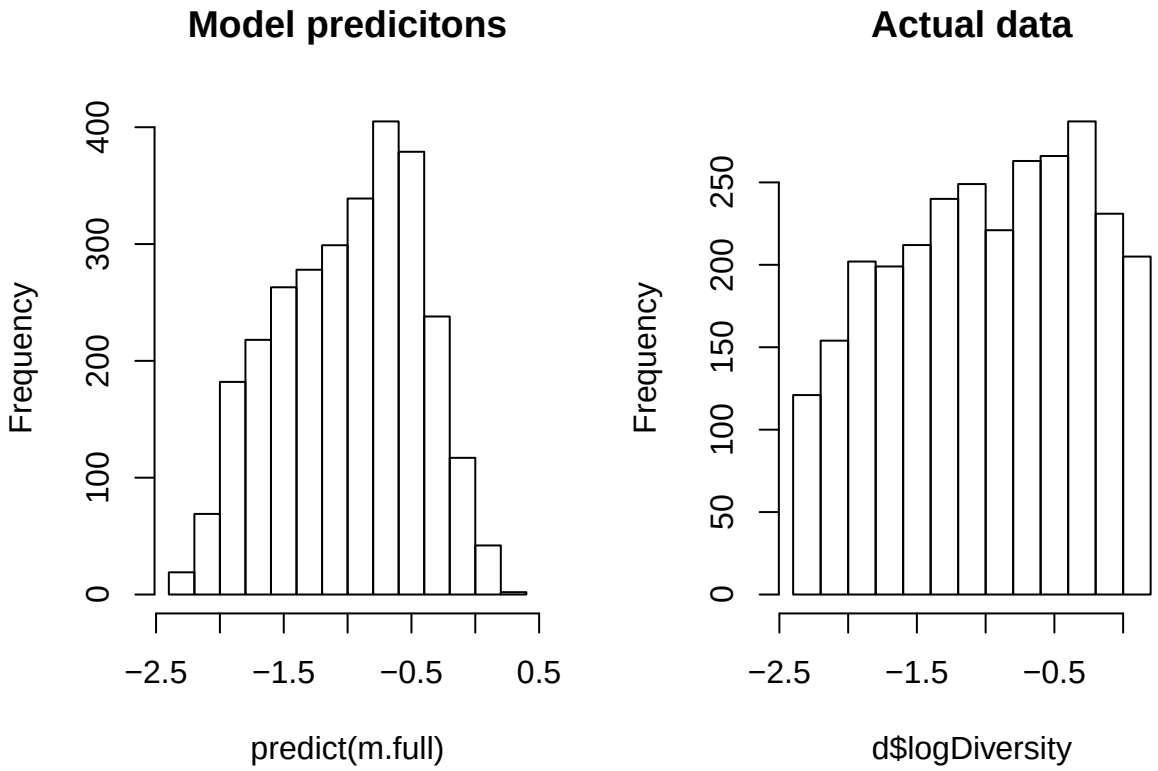
The influence of each was tested by comparing a full model with all random effects to one where the given random effect was removed.

There was a significant random effect for language (log likelihood difference = 2.3 , df = 1 , Chi Squared = 4.55 , p = 0.033). There was a significant random effect for domain (log likelihood difference = 14 , df = 1 , Chi Squared = 27.83 , p = 1.3e-07). There was a significant random effect for stimulus item (within domain) (log likelihood difference = 260 , df = 1 , Chi Squared = 514.81 , p = 5.7e-114). There was a significant random effect for the interaction between language and domain (log likelihood difference = 350 , df = 1 , Chi Squared = 700.03 , p = 3e-154).

Distribution assumpsions

The fit of the model distributions is reasonable:

```
par(mfrow=c(1,2))
hist(predict(m.full), main="Model predicitons")
hist(d$logDiversity, main="Actual data")
```



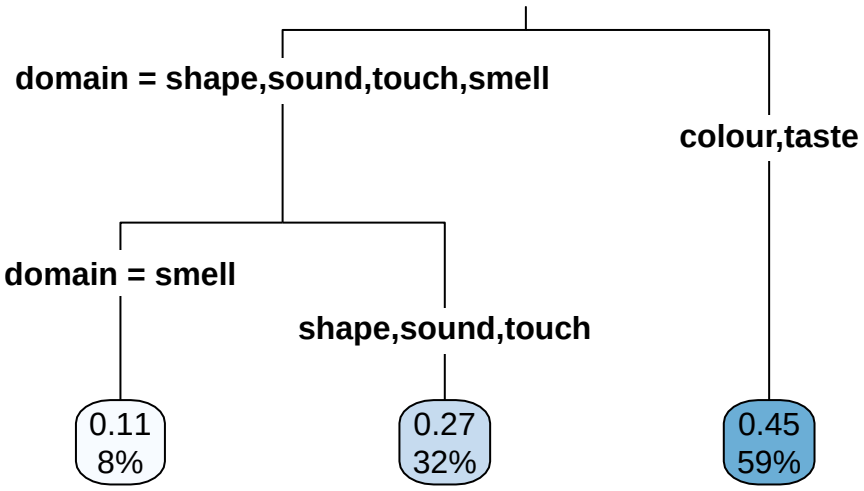
We can try fitting the data with different distributions (Gamma, inverse gaussian):

The gaussian model is the best fit by AIC.

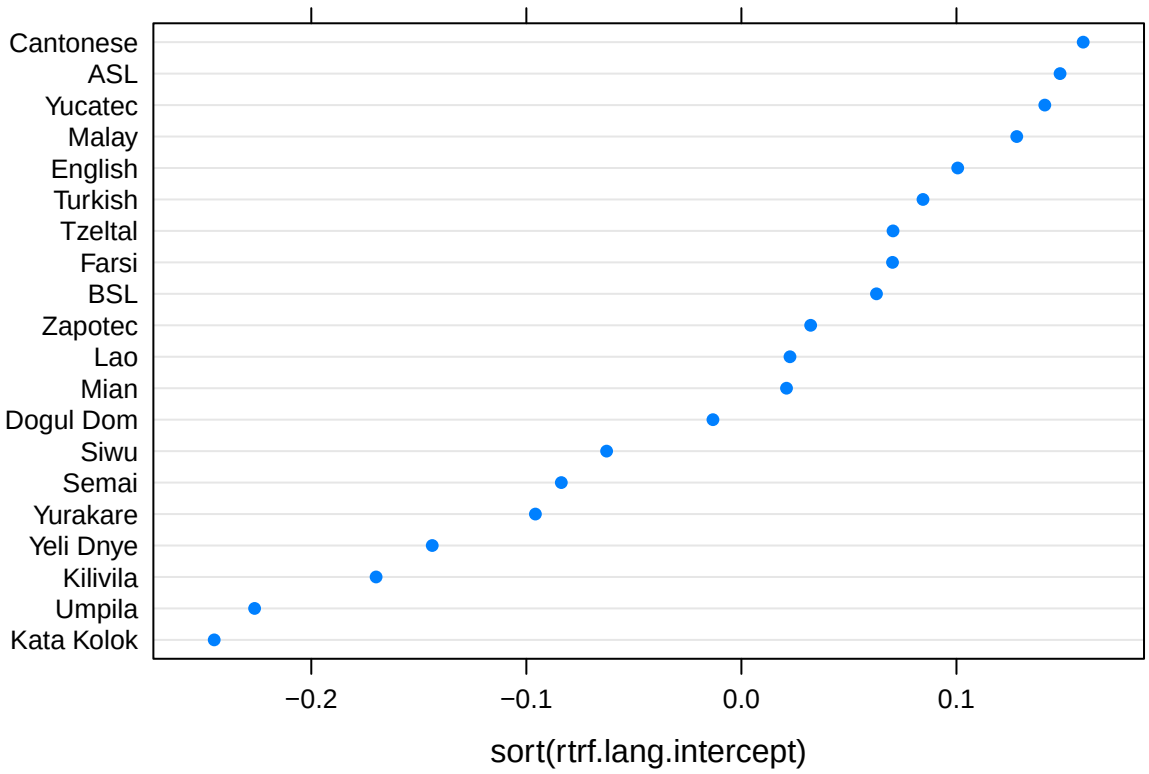
Differences between domains

How do the different domains cluster according to codability? We can use REEMtree which allows random effects for Language and Stimulus:

```
REEMresult<-REEMtree(simpson.diversityIndex~ domain,
                     data=d,
                     random= list(~ 1|Language,~1|Stimulus.code),
                     MaxIterations = 100000)
rpart.plot(tree(REEMresult), type=3)
```




```
rtrf.lang = REEMresult$RandomEffects$Language
rtrf.lang.intercept = rtrf.lang[,1]
names(rtrf.lang.intercept) = rownames(rtrf.lang)
dotplot(sort(rtrf.lang.intercept))
```



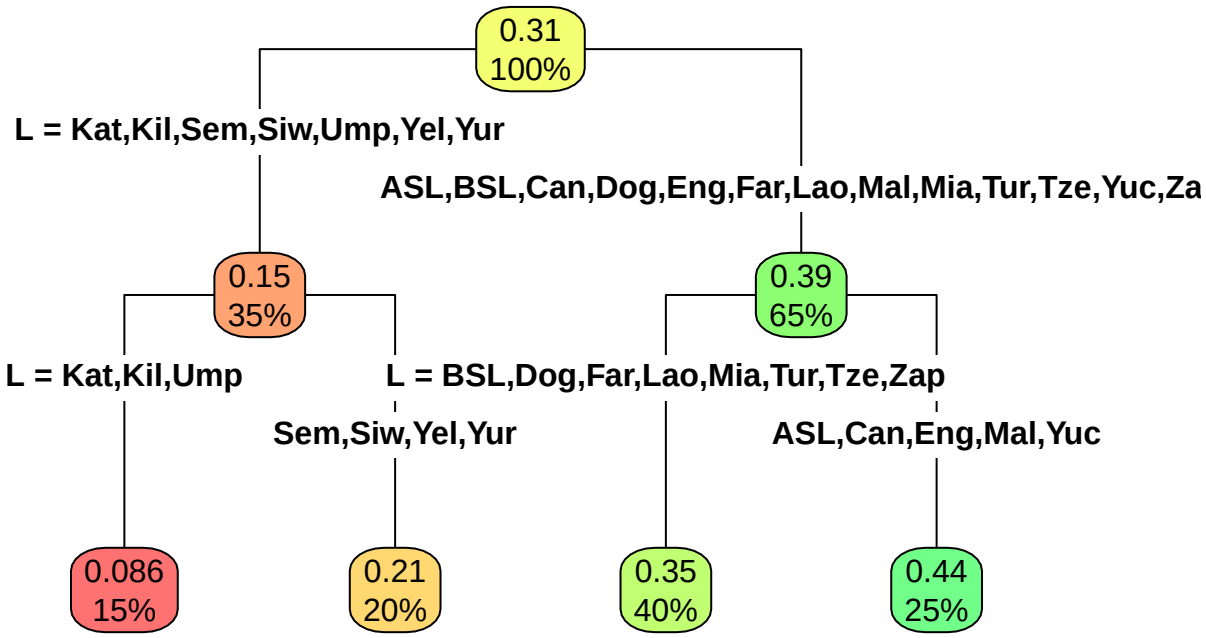
According to the decision tree results, the hierarchy of codability is:

[Colour, Taste] > [Shape, Sound, Touch] > Smell

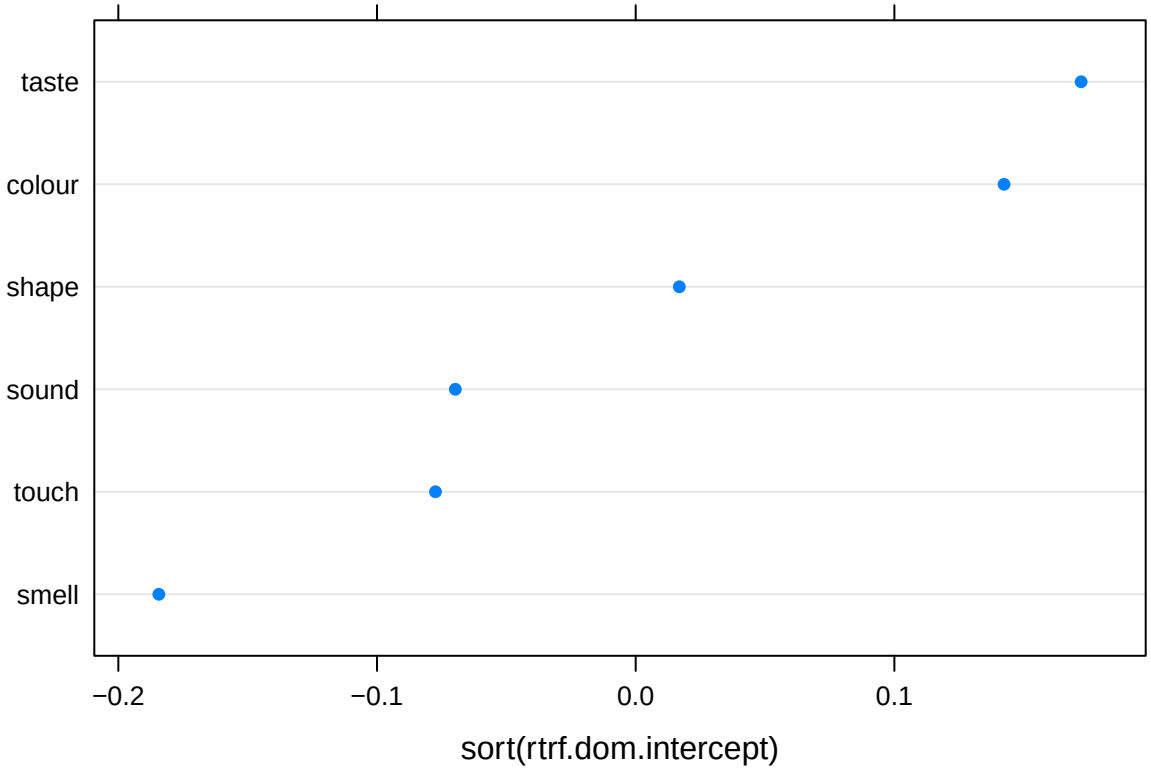
Differences between langauges

We can also ask which languages cluster together:

```
d$L = substr(d$Language,1,3)
REEMresult.lang<-REEMtree(simpson.diversityIndex~ L,
                      data=d,
                      random= c(~ 1|domain,~1|Stimulus.code),
                      MaxIterations = 100000)
rpart.plot(tree(REEMresult.lang), type=4, extra=100,
           box.palette="RdYlGn")
```

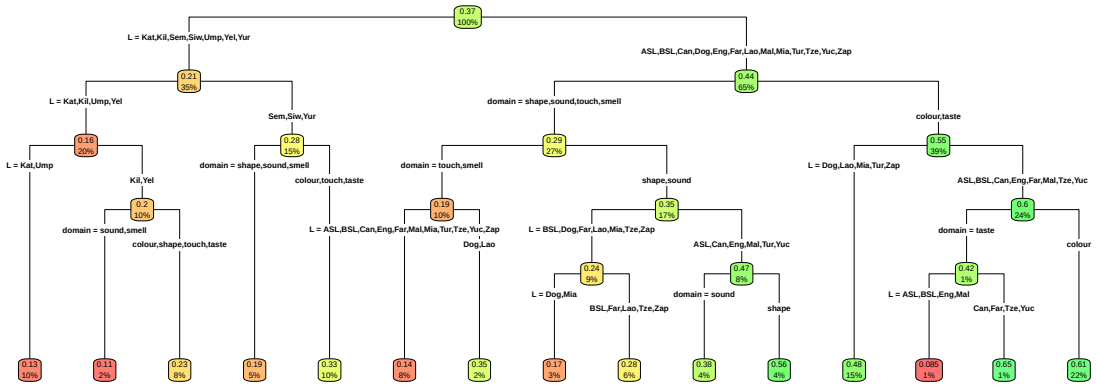



```
rtrf.dom = REEMresult.lang$RandomEffects$domain
rtrf.dom.intercept = rtrf.dom[,1]
names(rtrf.dom.intercept) = rownames(rtrf.dom)
dotplot(sort(rtrf.dom.intercept))
```



Here's a decision tree splitting the data by domain and language. It is harder to understand the splits here, which is to say that it is not easy to make a generalisation about the differences. The main point is that there are many interactions between langauge and domain, not just one big difference.

```
REEMresult.both<-REEMtree(simpson.diversityIndex~ L+domain,
                      data=d,
                      random= ~ 1|Stimulus.code,
                      MaxIterations = 100000)
rpart.plot(tree(REEMresult.both), type=4, extra=100,
           box.palette="RdYlGn")
```




```
pdf("../results/graphs/DecisionTree_LanguagesAndDomains.pdf",
    width=15, height=10)
rpart.plot(tree(REEMresult.both), type=4, extra=100,
           box.palette="RdYlGn")
dev.off()
```

```
## pdf
```

```
##   2
```

```
tree(REEMresult.both)$variable.importance
```

```
##        L   domain
## 53.49488 40.98518
```

We were also interested in whether languages differ by modality:

```
d$L = substr(d$Language,1,3)
d$modality = "Spoken"
d$modality[d$Language %in% c("ASL", "BSL", "Kata Kolok")] = "Signed"
REEMresult.mod<-REEMtree(simpson.diversityIndex~ L + domain + modality,
                     data=d,
                     random= c(~1|Stimulus.code),
                     MaxIterations = 100000)
tree(REEMresult.mod)$variable.importance
```

```
##         L    domain  modality
## 56.952422 42.103148  2.010103
```

Modality is not used in the tree (not shown), and is not used if it is the only variable in available to the tree (not shown). The importance measure for modality is 20 times lower than for language and domain. That is, languages do not cluster by modality.

Description types and codability

Is there better codability for more abstract terms?

```
sae = read.csv("../data/AllData_LoP.csv", stringsAsFactors = F)
sae = sae[!is.na(sae$head),]
sae = sae[!sae$head %in% c("n/a","no description"),]
sae = sae[!is.na(sae$SAE),]
sae = sae[sae$Response==1,]
prop.sae = sae %>% group_by(Language,domain,SAE) %>%
  summarise (n = n()) %>%
  mutate(prop = n / sum(n))
```

```
## Warning: package 'bindrcpp' was built under R version 3.3.2
```

```
d$Abstract = NA
# Match up each diversity measure with the proportion of
#  abstract terms used
for(lang in unique(d$Language)){
  for(dom in unique(d$domain)){
    propx = prop.sae[prop.sae$Language==lang & prop.sae$domain==dom & prop.sae$SAE=="A",]$prop
    if(length(propx)==0){
      propx = 0
    }
    sel = d$Language==lang & d$domain==dom
    if(sum(sel)!=0){
      d[sel,]$Abstract = propx
    }
  }
}
d$Abstract.scaled = scale(d$Abstract^2)
abs.scale = attr(d$Abstract.scaled,"scaled:scale")
abs.center = attr(d$Abstract.scaled,"scaled:center")
d$Abstract.scaled = as.numeric(d$Abstract.scaled)
```

Plot raw data:

```
rawgx  = ggplot(d, aes(Abstract, simpson.diversityIndex)) +
  geom_point(alpha=0.2) +
  stat_smooth(method = 'gam') +
  xlab("Proportion of abstract terms") +
  ylab("Codability")
pdf("../results/graphs/Codability_by_AbstractUse_Raw.pdf", width=4, height=4)
rawgx
dev.off()
```

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

Raw correlation:

```
cor(d$Abstract,d$simpson.diversityIndex)
```

```
## [1] 0.3416066
```

Compare models with and without the main effect of abstract types.

```
m0.sae = lmer( logDiversity ~ 1 +
               (1+Abstract.scaled|Language) +
               (1+Abstract.scaled|domain/Stimulus.code) +
               (1|Language:domain),
             data=d)

m1.sae = update(m0.sae, ~.+Abstract.scaled)
anova(m0.sae,m1.sae)
```

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

```
## Data: d
## Models:
## m0.sae: logDiversity ~ 1 + (1 + Abstract.scaled | Language) + (1 + Abstract.scaled |
## m0.sae:     domain/Stimulus.code) + (1 | Language:domain)
## m1.sae: logDiversity ~ (1 + Abstract.scaled | Language) + (1 + Abstract.scaled |
## m1.sae:     domain/Stimulus.code) + (1 | Language:domain) + Abstract.scaled
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0.sae 12 3871.3 3942.8 -1923.7   3847.3
## m1.sae 13 3858.3 3935.7 -1916.1   3832.3 15.009      1   0.000107 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
px = sjp.lmer(m1.sae,'eff','Abstract.scaled', show.ci = T, prnt.plot = F)
px$plot$data$x = sqrt((px$plot$data$x  * abs.scale + abs.center))
px$plot$data$y = exp(px$plot$data$y) -0.1
px$plot$data$upper = exp(px$plot$data$upper) -0.1
px$plot$data$lower = exp(px$plot$data$lower) -0.1
px = px$plot+ xlab("Proportion of abstract terms") +
  ylab("Codability") +
  theme(strip.background = element_blank(),
        strip.text.y = element_blank(),
        plot.title = element_blank())
pdf("../results/graphs/Codability_by_AbstractUse.pdf", width=4, height=4)
px
dev.off()
```

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

```
save(px,file="../results/graphs/Codability_by_AbstractUse_ggplot.RDat")
```

Permutation test

We can use a permutation test to test pairs of domains against each other. We test whether the difference in mean diversity between each pair of domains is greater than would be expected by chance. For each possible pairing of domains, calculate the difference in means for codability. Then randomly swap observations between the two doamins (permutation) and calculate the mean again. The difference in the two means is an indication of the extent of the difference between domains. Arguably, the decision tree in the seciton above is a better way of doing this, because it takes into account random effects for language and stimulus. However, the permutation test makes fewer assumptions about the shape of the distribution.

```
# The distribution of the variable is not important
#  in permutaiton, so we just use the raw index:
d$diversity = d$simpson.diversityIndex

permuteX = function(d,fact,p){
  pDiff = tapply(d[d[,fact] %in% p,]$diversity,
                   sample(d[d[,fact] %in% p,fact]),
                   mean)
  pDiff = abs(diff(pDiff[!is.na(pDiff)]))
  return(pDiff)
}

compareWithPermutation = function(d,fact, numPerms = 1000){
  pairs = combn(unique(as.character(d[,fact])),2)
  set.seed(2387)
  permTests = apply(pairs,2, function(p){
    trueDiff = tapply(d[d[,fact] %in% p,]$diversity,
                      d[d[,fact] %in% p,fact],
                      mean)
    trueDiff = abs(diff(trueDiff[!is.na(trueDiff)]))
    permDiff = replicate(numPerms,permuteX(d,fact,p))
    z = (trueDiff -mean(permDiff))/sd(permDiff)
    p = sum(permDiff >= trueDiff)/length(permDiff)
    if(p==0){
      p = 1/length(permDiff)
    }
    return(c(z,p))
  })

  res = data.frame(
    pair = apply(pairs,2,paste,collapse=','),
    perm.z = permTests[1,],
    perm.p = permTests[2,],
    perm.p.adjusted =
      p.adjust(permTests[2,],'bonferroni'))

  res
}

compareWithPermutation(d,'domain')
```

```
##            pair    perm.z perm.p perm.p.adjusted
## 1  colour,shape 10.229982  0.001           0.015
## 2  colour,smell 23.346891  0.001           0.015
## 3  colour,taste  1.527214  0.081           1.000
```

```
## 4  colour,touch 14.925907  0.001           0.015
## 5  colour,sound 16.716660  0.001           0.015
## 6   shape,smell 15.457834  0.001           0.015
## 7   shape,taste  7.292646  0.001           0.015
## 8   shape,touch  6.009034  0.001           0.015
## 9   shape,sound  5.685990  0.001           0.015
## 10  smell,taste 17.711571  0.001           0.015
## 11  smell,touch  9.603543  0.001           0.015
## 12  smell,sound 12.351339  0.001           0.015
## 13  taste,touch 11.245055  0.001           0.015
## 14  taste,sound 12.567821  0.001           0.015
## 15  touch,sound  0.463503  0.288           1.000
```

The mean codability for all paris of domains are different, except for:

- Colour and Taste
- Touch and Sound

So, the hierarchy is:

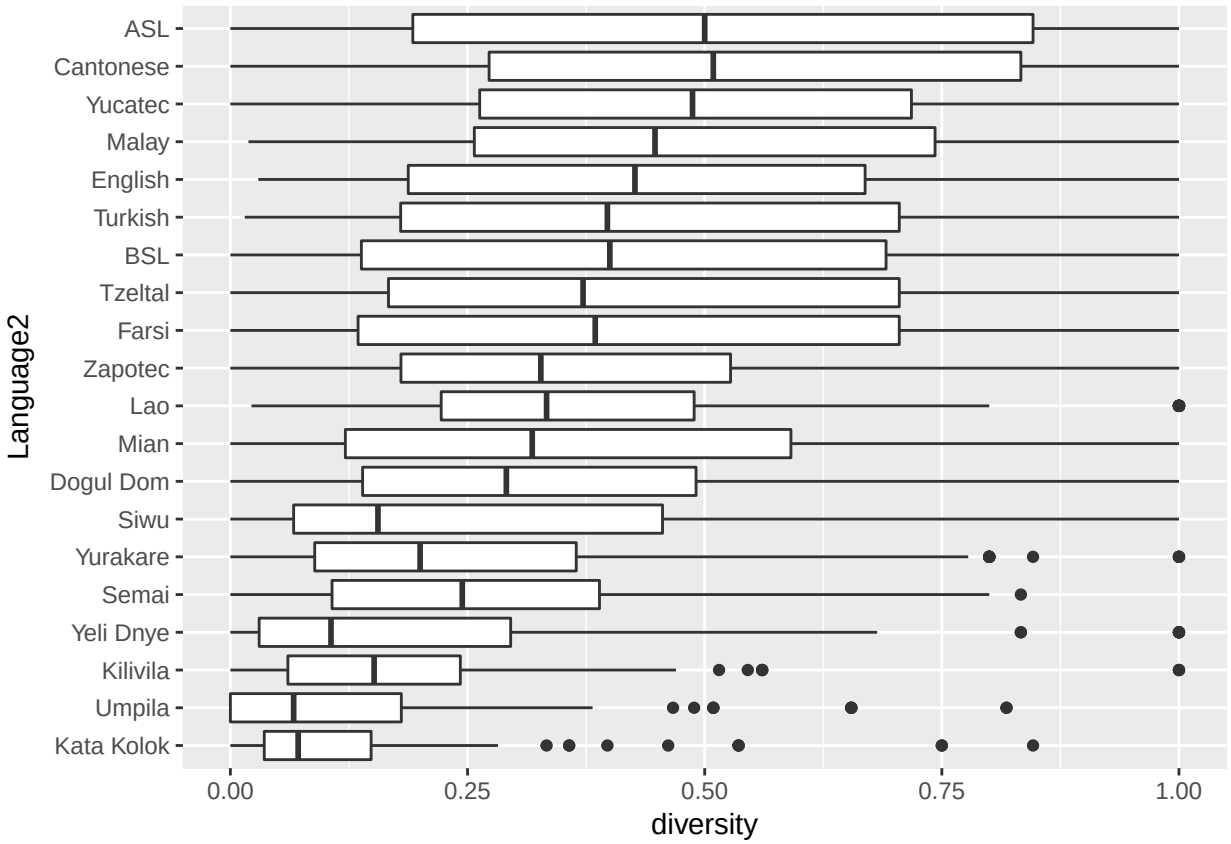
[Colour, Taste] > Shape > [Sound, Touch] > Smell

Which matches the decision tree hierarchy very well.

Permutation between languages

Test whether the mean diversity differs between each pair of languages. This is just to double-check that the results from the mixed effects model above are not artefacts of the shape of the codability distribution. A large number of permutations is needed so that the p-value remains significant when controlling for multiple comparisons.

```
d$Language2 = factor(d$Language,
                     levels =
                       names(sort(
                         tapply(d$simpson.diversityIndex,
                              d$Language,
                              mean))))

ggplot(d, aes(y=diversity,x=Language2)) +
  geom_boxplot() + coord_flip()
```




```
# (need 20000 permutations for Bonferroni correction)
langPerm = compareWithPermutation(d,'Language', numPerms = 20000)
```

List of significant differences:

```
langPerm[langPerm$perm.p.adjusted<0.01,]
```

```
##                      pair    perm.z perm.p perm.p.adjusted
## 3          ASL,Dogul Dom  6.386793  5e-05          0.0095
## 6         ASL,Kata Kolok 14.415690  5e-05          0.0095
## 7           ASL,Kilivila 13.020372  5e-05          0.0095
## 8                ASL,Lao  5.119374  5e-05          0.0095
## 10              ASL,Mian  4.755508  5e-05          0.0095
## 11             ASL,Semai 10.017882  5e-05          0.0095
## 12              ASL,Siwu  7.888725  5e-05          0.0095
## 15             ASL,Umpila 14.872409  5e-05          0.0095
## 16          ASL,Yeli Dnye 11.306146  5e-05          0.0095
## 18          ASL,Yurakare  8.723735  5e-05          0.0095
## 24        BSL,Kata Kolok 12.718123  5e-05          0.0095
## 25          BSL,Kilivila 10.739672  5e-05          0.0095
## 29             BSL,Semai  6.978705  5e-05          0.0095
## 30              BSL,Siwu  4.778091  5e-05          0.0095
## 33            BSL,Umpila 12.883928  5e-05          0.0095
## 34          BSL,Yeli Dnye  8.647660  5e-05          0.0095
## 36          BSL,Yurakare  5.794757  5e-05          0.0095
## 38   Cantonese,Dogul Dom  7.019165  5e-05          0.0095
## 41  Cantonese,Kata Kolok 15.741879  5e-05          0.0095
## 42    Cantonese,Kilivila 14.306751  5e-05          0.0095
```

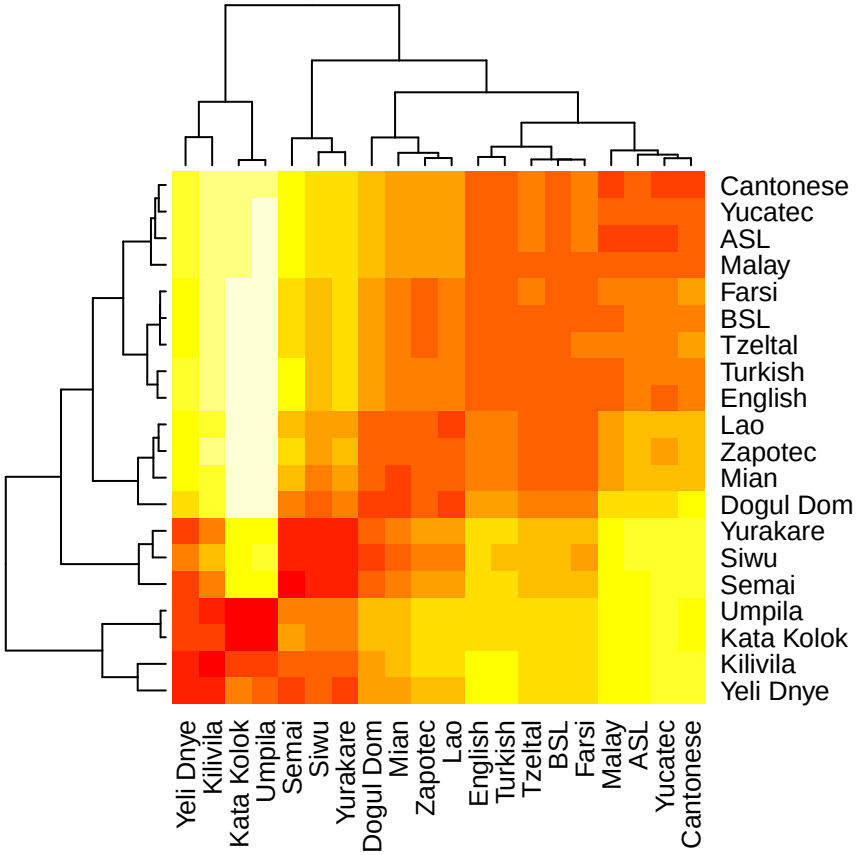
```
## 43         Cantonese,Lao  5.606992  5e-05          0.0095
## 45        Cantonese,Mian  5.207652  5e-05          0.0095
## 46       Cantonese,Semai 10.881228  5e-05          0.0095
## 47        Cantonese,Siwu  8.545814  5e-05          0.0095
## 50      Cantonese,Umpila 16.091613  5e-05          0.0095
## 51   Cantonese,Yeli Dnye 12.195978  5e-05          0.0095
## 53    Cantonese,Yurakare  9.526955  5e-05          0.0095
## 54     Cantonese,Zapotec  4.934960  5e-05          0.0095
## 57  Dogul Dom,Kata Kolok 11.168765  5e-05          0.0095
## 58    Dogul Dom,Kilivila  8.305659  5e-05          0.0095
## 60       Dogul Dom,Malay  5.805998  5e-05          0.0095
## 66      Dogul Dom,Umpila 11.144685  5e-05          0.0095
## 67   Dogul Dom,Yeli Dnye  5.845490  5e-05          0.0095
## 68     Dogul Dom,Yucatec  6.578805  5e-05          0.0095
## 72    English,Kata Kolok 14.261218  5e-05          0.0095
## 73      English,Kilivila 12.595069  5e-05          0.0095
## 77         English,Semai  8.608346  5e-05          0.0095
## 78          English,Siwu  6.186397  5e-05          0.0095
## 81        English,Umpila 14.512258  5e-05          0.0095
## 82     English,Yeli Dnye 10.281170  5e-05          0.0095
## 84      English,Yurakare  7.224110  5e-05          0.0095
## 86      Farsi,Kata Kolok 12.842217  5e-05          0.0095
## 87        Farsi,Kilivila 10.844462  5e-05          0.0095
## 91           Farsi,Semai  6.809733  5e-05          0.0095
## 95          Farsi,Umpila 13.043482  5e-05          0.0095
## 96       Farsi,Yeli Dnye  8.778286  5e-05          0.0095
## 98        Farsi,Yurakare  5.748382  5e-05          0.0095
## 101       Kata Kolok,Lao 13.387166  5e-05          0.0095
## 102     Kata Kolok,Malay 15.130729  5e-05          0.0095
## 103      Kata Kolok,Mian 11.453272  5e-05          0.0095
## 104     Kata Kolok,Semai  9.349440  5e-05          0.0095
## 105      Kata Kolok,Siwu  7.786608  5e-05          0.0095
## 106   Kata Kolok,Turkish 14.183490  5e-05          0.0095
## 107   Kata Kolok,Tzeltal 12.948404  5e-05          0.0095
## 110   Kata Kolok,Yucatec 16.100007  5e-05          0.0095
## 111  Kata Kolok,Yurakare  7.727963  5e-05          0.0095
## 112   Kata Kolok,Zapotec 12.986692  5e-05          0.0095
## 113         Kilivila,Lao 10.455641  5e-05          0.0095
## 114       Kilivila,Malay 13.540861  5e-05          0.0095
## 115        Kilivila,Mian  8.856748  5e-05          0.0095
## 116       Kilivila,Semai  4.971180  5e-05          0.0095
## 118     Kilivila,Turkish 12.264060  5e-05          0.0095
## 119     Kilivila,Tzeltal 11.005224  5e-05          0.0095
## 122     Kilivila,Yucatec 14.469779  5e-05          0.0095
## 124     Kilivila,Zapotec 10.455408  5e-05          0.0095
## 127            Lao,Semai  5.647939  5e-05          0.0095
## 131           Lao,Umpila 13.234881  5e-05          0.0095
## 132        Lao,Yeli Dnye  7.753110  5e-05          0.0095
## 133          Lao,Yucatec  5.017567  5e-05          0.0095
## 137          Malay,Semai  9.956038  5e-05          0.0095
## 138           Malay,Siwu  7.352764  5e-05          0.0095
## 141         Malay,Umpila 15.483867  5e-05          0.0095
## 142      Malay,Yeli Dnye 11.330134  5e-05          0.0095
## 144       Malay,Yurakare  8.461861  5e-05          0.0095
```

```
## 150          Mian,Umpila 11.574841  5e-05          0.0095
## 151       Mian,Yeli Dnye  6.770497  5e-05          0.0095
## 156        Semai,Turkish  8.180076  5e-05          0.0095
## 157        Semai,Tzeltal  7.038307  5e-05          0.0095
## 158         Semai,Umpila  8.942022  5e-05          0.0095
## 160        Semai,Yucatec 10.851852  5e-05          0.0095
## 162        Semai,Zapotec  5.921801  5e-05          0.0095
## 163         Siwu,Turkish  5.617457  5e-05          0.0095
## 165          Siwu,Umpila  7.902980  5e-05          0.0095
## 167         Siwu,Yucatec  8.138316  5e-05          0.0095
## 171       Turkish,Umpila 14.392934  5e-05          0.0095
## 172    Turkish,Yeli Dnye  9.926558  5e-05          0.0095
## 174     Turkish,Yurakare  6.823549  5e-05          0.0095
## 176       Tzeltal,Umpila 13.248762  5e-05          0.0095
## 177    Tzeltal,Yeli Dnye  8.751177  5e-05          0.0095
## 179     Tzeltal,Yurakare  5.780601  5e-05          0.0095
## 182       Umpila,Yucatec 16.471421  5e-05          0.0095
## 183      Umpila,Yurakare  7.599645  5e-05          0.0095
## 184       Umpila,Zapotec 13.166837  5e-05          0.0095
## 185    Yeli Dnye,Yucatec 12.207134  5e-05          0.0095
## 187    Yeli Dnye,Zapotec  8.009367  5e-05          0.0095
## 188     Yucatec,Yurakare  9.268163  5e-05          0.0095
```

Languages really are different, but some languages are closer than others. This heatmap gives an idea of which languages are similar to which.

```
d$Language2 = factor(d$Language, levels =
              names(sort(tapply(
                d$diversity,
                d$Language,
                mean))))

langPerm$l1 = sapply(as.character(langPerm$pair), function(X){strsplit(X,',')[[1]][1]})
langPerm$l2 = sapply(as.character(langPerm$pair), function(X){strsplit(X,',')[[1]][2]})

lxs = unique(d$Language)
langPerm2 = langPerm
langPerm2 = rbind(
  langPerm,
  data.frame(
    pair = paste(lxs,lxs,sep=','),
    perm.z = 0,
    perm.p = 1,
    perm.p.adjusted = 1,
    l1 = lxs,
    l2 = lxs
  )
)

langPerm2$perm.z = abs(langPerm2$perm.z)

langPermDist = acast(langPerm2, l1~l2, value.var="perm.z")

langPermDist[lower.tri(langPermDist)] = t(langPermDist)[lower.tri(langPermDist)]
```

```
heatmap(langPermDist)
```



Stimulus set size

A check that the size of the stimulus set does not predict the codability:

```
numStimuli = tapply(d$Stimulus.code,d$domain, function(X){length(unique(X))})

d$numStimuli = numStimuli[d$domain]

m.full = lmer( logDiversity ~ 1 +
                 (1|Language) +
                 (1|domain/Stimulus.code) +
                 (1|Language:domain),
               data=d)

m.ns = lmer( logDiversity ~ 1 +
               numStimuli +
                 (1|Language) +
                 (1|domain/Stimulus.code) +
                 (1|Language:domain),
               data=d)

anova(m.full, m.ns)
```

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

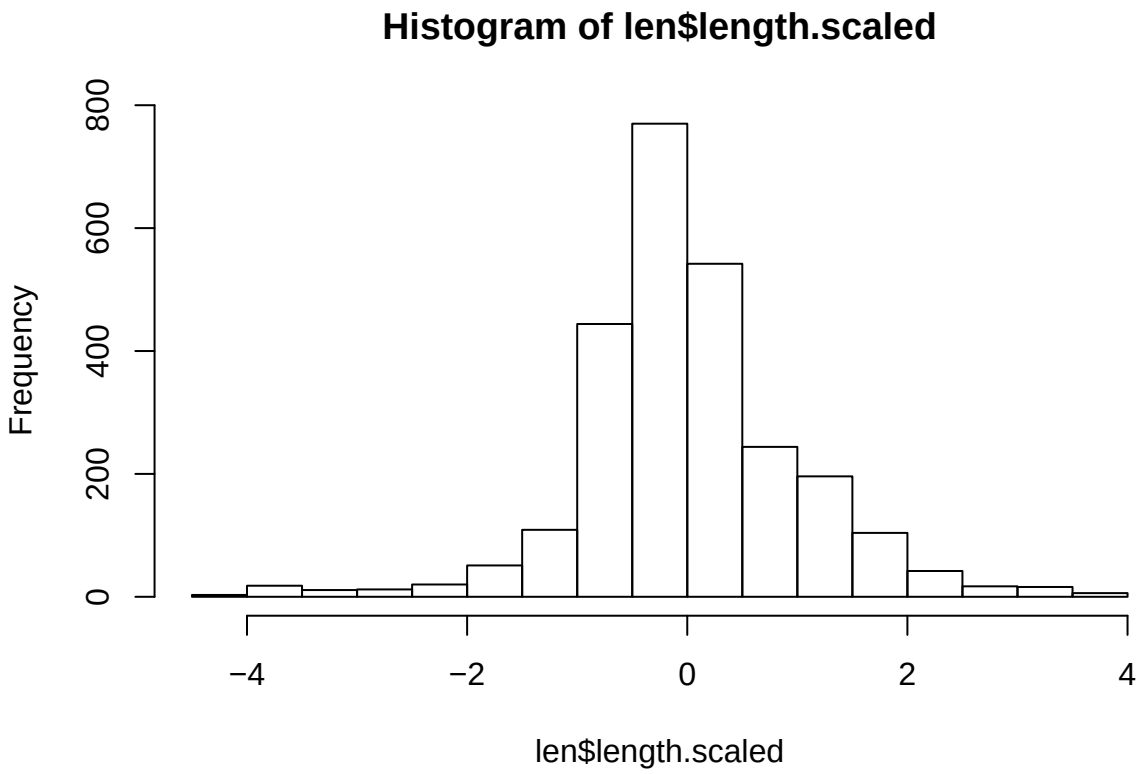
```
## Data: d
## Models:
## m.full: logDiversity ~ 1 + (1 | Language) + (1 | domain/Stimulus.code) +
## m.full:     (1 | Language:domain)
## m.ns: logDiversity ~ 1 + numStimuli + (1 | Language) + (1 | domain/Stimulus.code) +
## m.ns:     (1 | Language:domain)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m.full  6 3939.3 3975.0 -1963.7   3927.3
## m.ns    7 3940.2 3981.9 -1963.1   3926.2 1.1438      1     0.2848
```

No significant prediction. This is easy to see: Taste and Colour have roughly equal mean codability, but colour has the largest number of stimuli (80) and taste has the least (5).

Description lengths

Load the data. The column `mean` is the mean length, and `mean.log` is the mean of the log of the lengths.

```
len = read.csv("../data/DiversityIndices_ND_withLengths.csv",
               stringsAsFactors = F)
len = len[complete.cases(len),]

# Remove 2 outliers that had very few responses:
len = len[len$mean>=1,]

len$logDiversity = log(len$simpson.diversityIndex+0.1)
len$logDiversity.scaled = scale(len$logDiversity)
len$length.scaled = scale(len$mean.log)
len$Stimulus.code = factor(len$Stimulus.code)
len$Language = factor(len$Language)
len$domain = factor(len$domain)

hist(len$length.scaled)
```



Raw correlation:

```
cor(len$mean.log, len$simpson.diversityIndex)
```

```
## [1] -0.1942662
```

Linear model with random intercepts and slopes by language, domain and the interaction between language and domain:

```
mLenl0 = lmer( logDiversity.scaled ~ 1 +
                 (1+length.scaled|Language) +
                 (1+length.scaled|domain/Stimulus.code) +
                 (1+length.scaled|Language:domain),
               data=len)
mLenl1 = update(mLenl0, ~.+length.scaled)
mLenl2 = update(mLenl1, ~.+I(length.scaled^2))
anova(mLenl0,mLenl1,mLenl2)
```

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

```
## Data: len
## Models:
## mLenl0: logDiversity.scaled ~ 1 + (1 + length.scaled | Language) + (1 +
## mLenl0:     length.scaled | domain/Stimulus.code) + (1 + length.scaled |
## mLenl0:     Language:domain)
## mLenl1: logDiversity.scaled ~ (1 + length.scaled | Language) + (1 + length.scaled |
## mLenl1:     domain/Stimulus.code) + (1 + length.scaled | Language:domain) +
## mLenl1:     length.scaled
## mLenl2: logDiversity.scaled ~ (1 + length.scaled | Language) + (1 + length.scaled |
## mLenl2:     domain/Stimulus.code) + (1 + length.scaled | Language:domain) +
## mLenl2:     length.scaled + I(length.scaled^2)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
```

```
## mLenl0 14 5049.5 5131.6 -2510.8   5021.5
## mLenl1 15 5045.9 5133.9 -2508.0   5015.9 5.5888      1    0.01808 *
## mLenl2 16 5046.7 5140.5 -2507.3   5014.7 1.2463      1    0.26426
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

There is a significant effect, but no quadratic effect. Since extremely short responses are unlikely to be informative, we wondered if there were higher-level non-linear effects. We ran the same model as above, but as a generalised additive model (GAM):

```
library(mgcv)
library(itsadug)
library(lmtest)
mLen = bam(logDiversity.scaled ~
      s(length.scaled) +
      s(Language,bs='re')+
      s(domain,bs='re')+
      s(Stimulus.code,bs='re')+
      s(Language,domain,bs='re'), # interaction
    data = len)
```

Test for need for random slopes:

```
mLen2 = update(mLen, ~.+s(Language,length.scaled,bs='re'))
lrtest(mLen,mLen2)
```

```
## Likelihood ratio test
##
## Model 1: logDiversity.scaled ~ s(length.scaled) + s(Language, bs = "re") +
##     s(domain, bs = "re") + s(Stimulus.code, bs = "re") + s(Language,
##     domain, bs = "re")
## Model 2: logDiversity.scaled ~ s(length.scaled) + s(Language, bs = "re") +
##     s(domain, bs = "re") + s(Stimulus.code, bs = "re") + s(Language,
##     domain, bs = "re") + s(Language, length.scaled, bs = "re")
##      #Df  LogLik     Df  Chisq Pr(>Chisq)
## 1 214.93 -2192.5
## 2 232.94 -2103.9 18.008 177.13  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mLen3 = update(mLen2, ~.+s(domain,length.scaled,bs='re'))
lrtest(mLen2,mLen3)
```

```
## Likelihood ratio test
##
## Model 1: logDiversity.scaled ~ s(length.scaled) + s(Language, bs = "re") +
##     s(domain, bs = "re") + s(Stimulus.code, bs = "re") + s(Language,
##     domain, bs = "re") + s(Language, length.scaled, bs = "re")
## Model 2: logDiversity.scaled ~ s(length.scaled) + s(Language, bs = "re") +
##     s(domain, bs = "re") + s(Stimulus.code, bs = "re") + s(Language,
##     domain, bs = "re") + s(Language, length.scaled, bs = "re") +
##     s(domain, length.scaled, bs = "re")
##      #Df  LogLik     Df  Chisq Pr(>Chisq)
## 1 232.94 -2103.9
## 2 235.20 -2097.8 2.2673 12.354   0.002077 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mLen4 = update(mLen3, ~.+s(Stimulus.code,length.scaled,bs='re'))
lrtest(mLen3,mLen4)
```

```
## Likelihood ratio test
##
## Model 1: logDiversity.scaled ~ s(length.scaled) + s(Language, bs = "re") +
##     s(domain, bs = "re") + s(Stimulus.code, bs = "re") + s(Language,
##     domain, bs = "re") + s(Language, length.scaled, bs = "re") +
##     s(domain, length.scaled, bs = "re")
## Model 2: logDiversity.scaled ~ s(length.scaled) + s(Language, bs = "re") +
##     s(domain, bs = "re") + s(Stimulus.code, bs = "re") + s(Language,
##     domain, bs = "re") + s(Language, length.scaled, bs = "re") +
##     s(domain, length.scaled, bs = "re") + s(Stimulus.code, length.scaled,
##     bs = "re")
##     #Df  LogLik         Df Chisq Pr(>Chisq)
## 1 235.2 -2097.8
## 2 235.2 -2097.8 0.00010188 2e-04  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mLen5 = update(mLen4, ~.+s(Language,domain,length.scaled,bs='re'))
lrtest(mLen4,mLen5)
```

```
## Likelihood ratio test
##
## Model 1: logDiversity.scaled ~ s(length.scaled) + s(Language, bs = "re") +
##     s(domain, bs = "re") + s(Stimulus.code, bs = "re") + s(Language,
##     domain, bs = "re") + s(Language, length.scaled, bs = "re") +
##     s(domain, length.scaled, bs = "re") + s(Stimulus.code, length.scaled,
##     bs = "re")
## Model 2: logDiversity.scaled ~ s(length.scaled) + s(Language, bs = "re") +
##     s(domain, bs = "re") + s(Stimulus.code, bs = "re") + s(Language,
##     domain, bs = "re") + s(Language, length.scaled, bs = "re") +
##     s(domain, length.scaled, bs = "re") + s(Stimulus.code, length.scaled,
##     bs = "re") + s(Language, domain, length.scaled, bs = "re")
##      #Df  LogLik    Df  Chisq Pr(>Chisq)
## 1 235.20 -2097.8
## 2 261.83 -2029.0 26.63 137.43  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

All random slopes improve the model. Final model:

```
summary(mLen5)
```

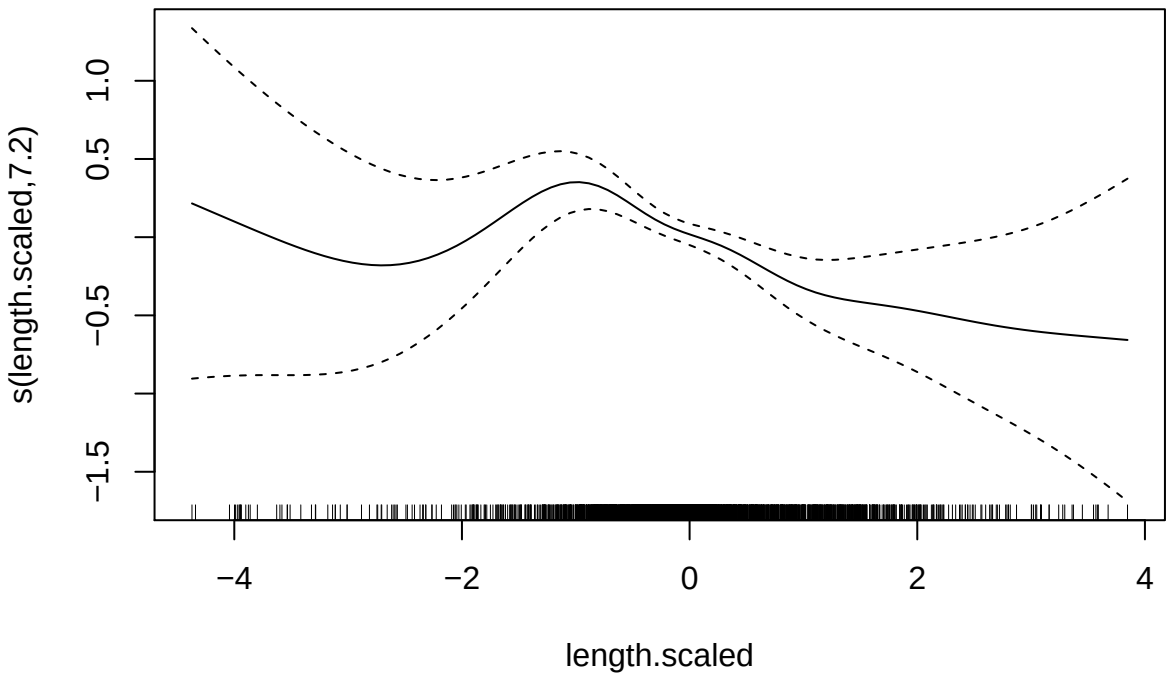
```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## logDiversity.scaled ~ s(length.scaled) + s(Language, bs = "re") +
##     s(domain, bs = "re") + s(Stimulus.code, bs = "re") + s(Language,
##     domain, bs = "re") + s(Language, length.scaled, bs = "re") +
##     s(domain, length.scaled, bs = "re") + s(Stimulus.code, length.scaled,
##     bs = "re") + s(Language, domain, length.scaled, bs = "re")
##
```

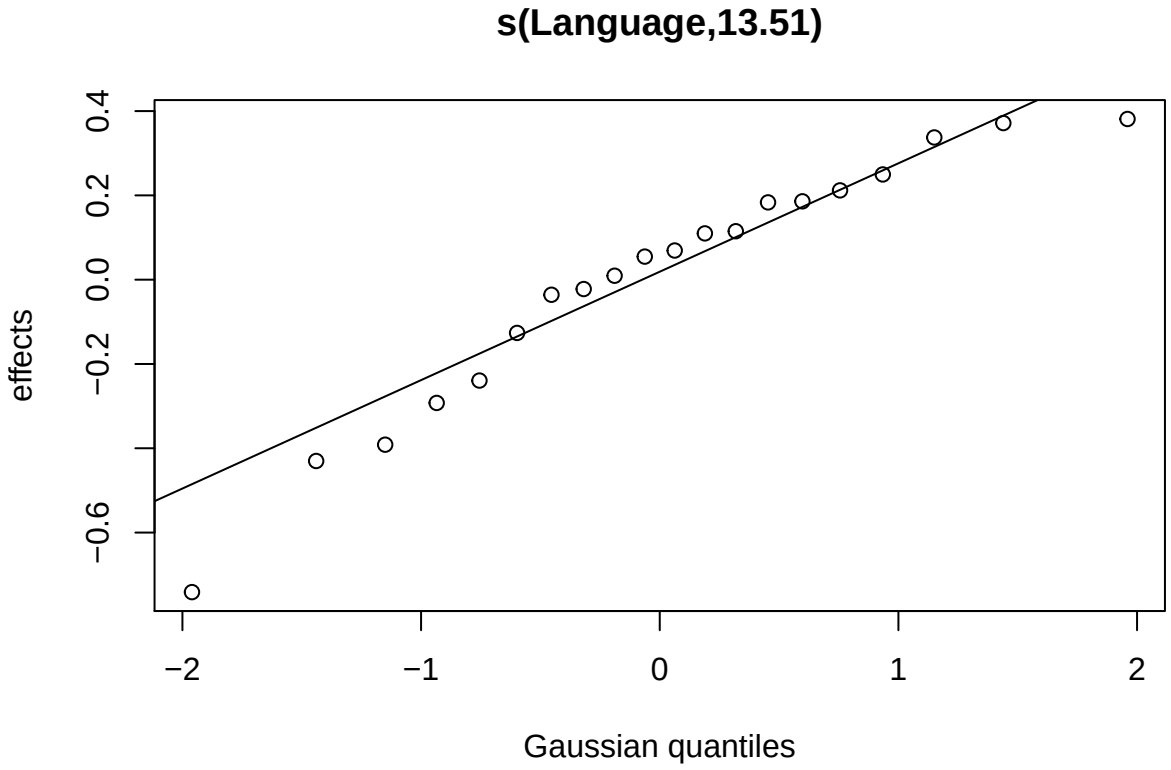
```
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.1470     0.2136  -0.688    0.491
##
## Approximate significance of smooth terms:
##                                        edf Ref.df        F  p-value
## s(length.scaled)                 7.202e+00   8.23    5.177 1.29e-06 ***
## s(Language)                      1.351e+01  19.00 1565.987 3.54e-07 ***
## s(domain)                        4.489e+00   5.00 4818.072 2.96e-07 ***
## s(Stimulus.code)                 1.063e+02 131.00    8.931 6.37e-09 ***
## s(Language,domain)               6.323e+01 113.00  279.468 3.16e-13 ***
## s(Language,length.scaled)        1.081e+01  19.00  702.913  0.00188 **
## s(domain,length.scaled)          1.507e+00   5.00  116.030  0.29047
## s(Stimulus.code,length.scaled)   1.998e-05 131.00    0.000  0.99332
## s(Language,domain,length.scaled) 5.003e+01 113.00  115.193  0.00236 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.691   Deviance explained = 72.2%
## fREML =   2504  Scale est. = 0.30859   n = 2605
```

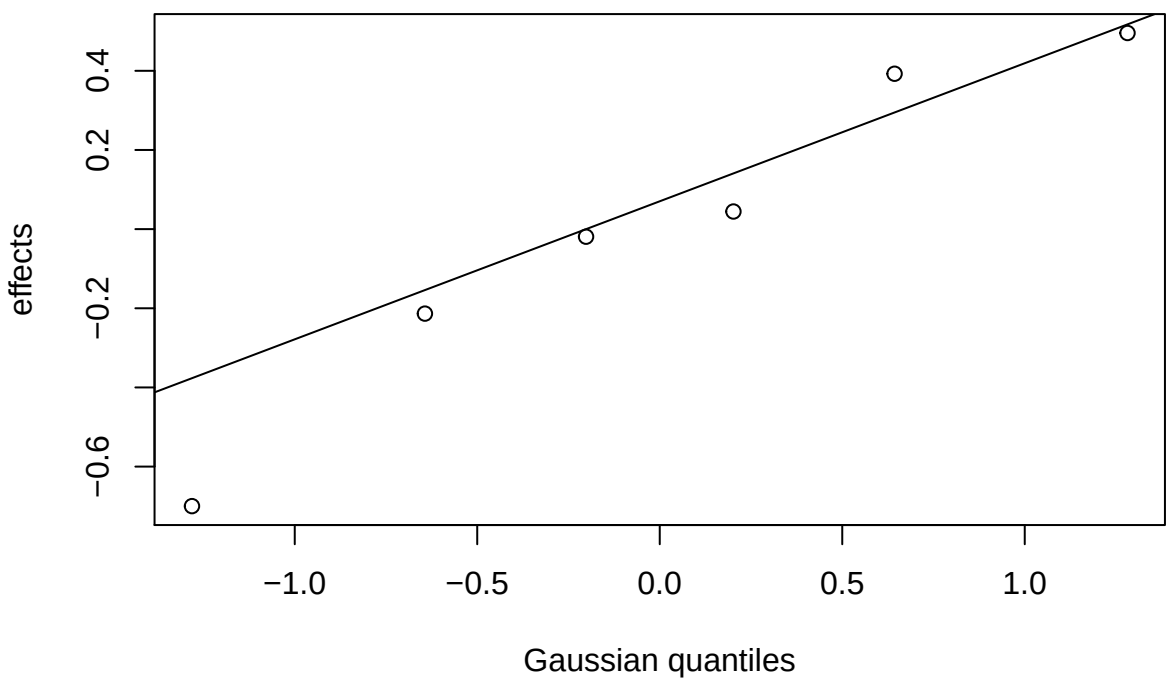
Note that there are significant random slopes for length by Language x domain and by Language, indicating that the stength of the length effect differes across cultures.

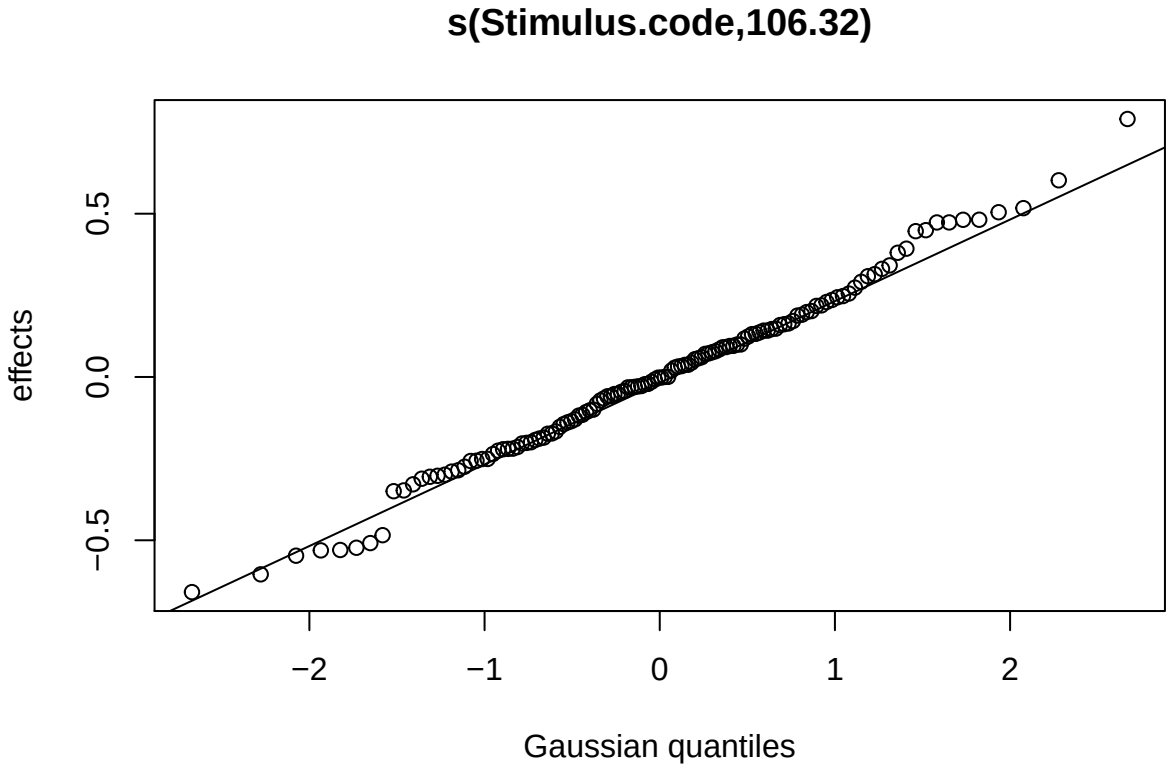
We can plot the model smooths.

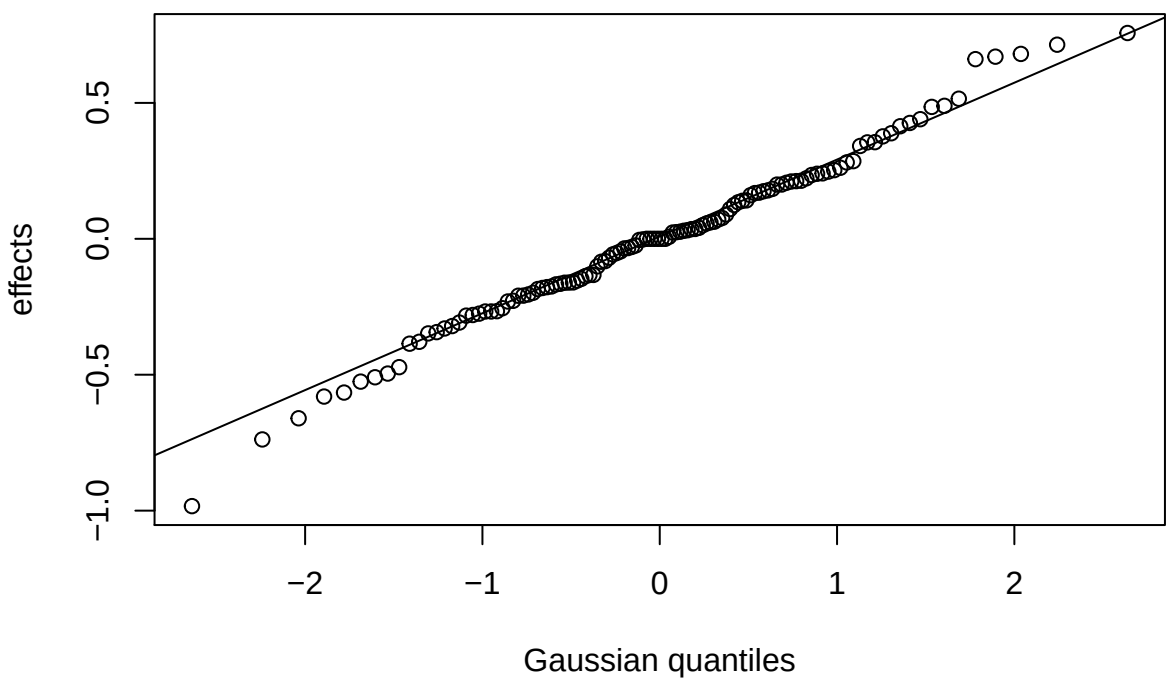
```
plot(mLen5)
```

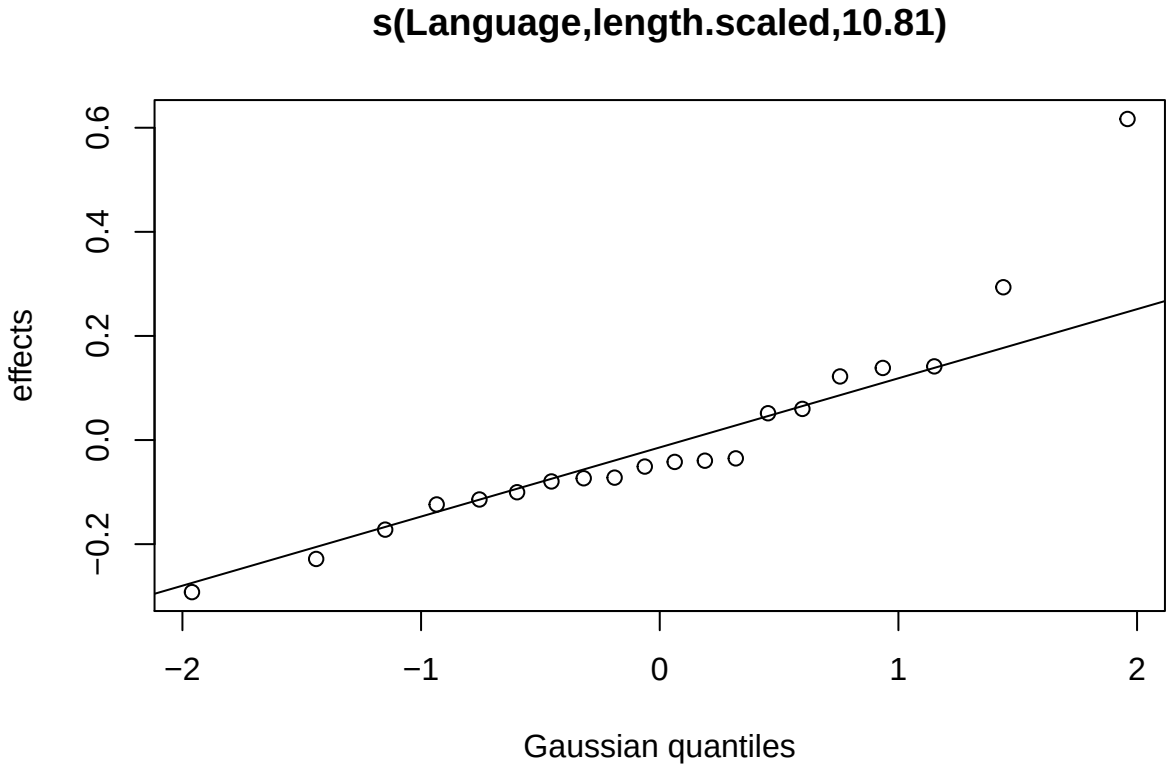


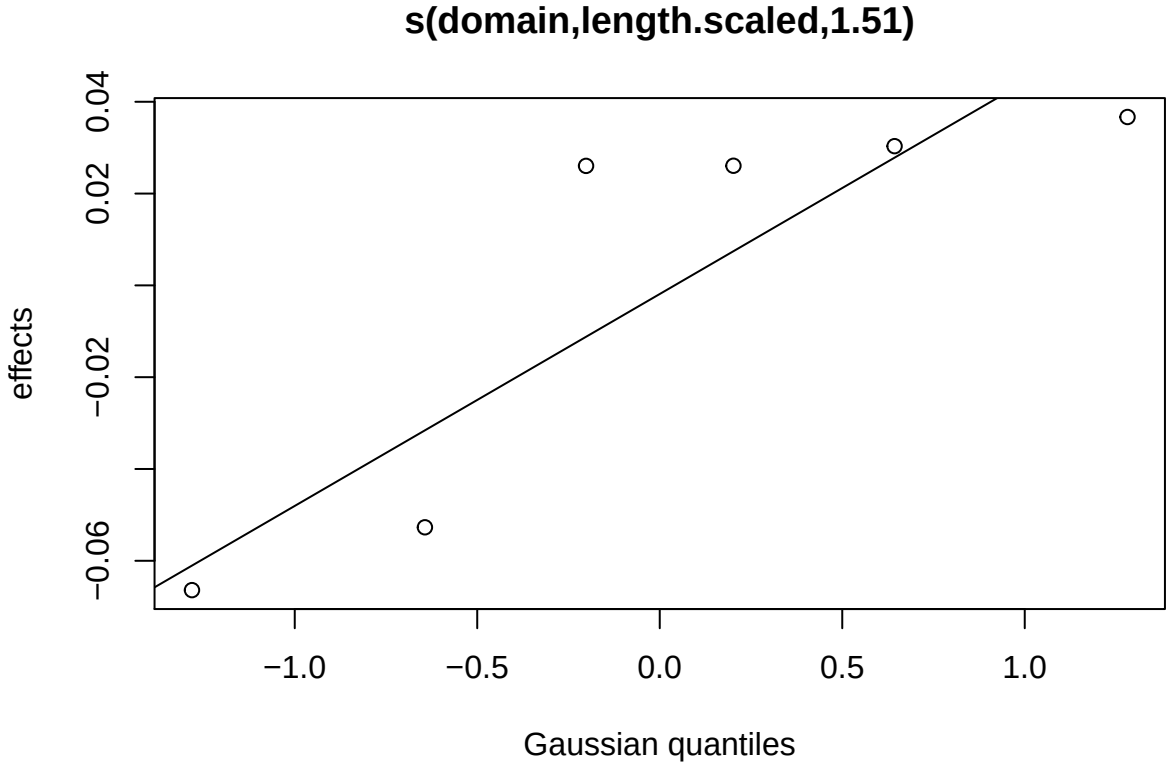

s(Language,13.51)
effects
0.4
0.2
0.0
−0.2
−0.6
−2
−1
0
1
2
Gaussian quantiles

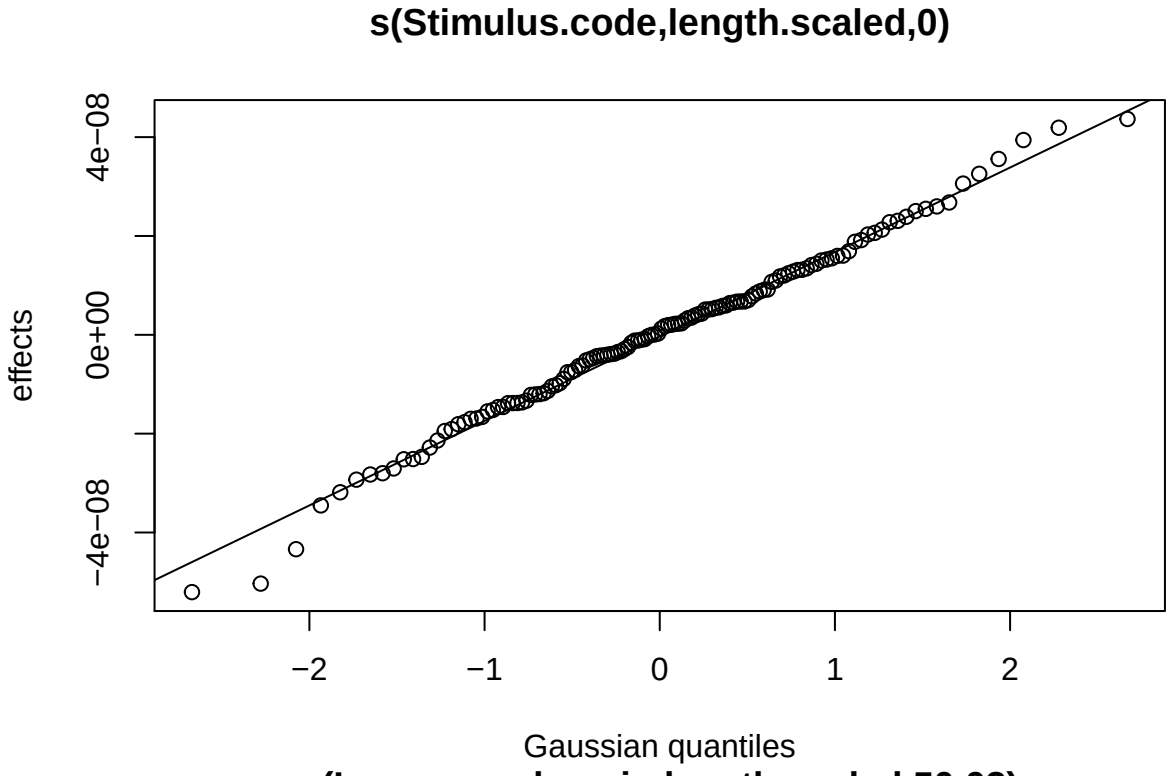

s(domain,4.49)
effects
0.4
0.2
−0.2
−0.6
−1.0
−0.5
0.0
0.5
1.0
Gaussian quantiles

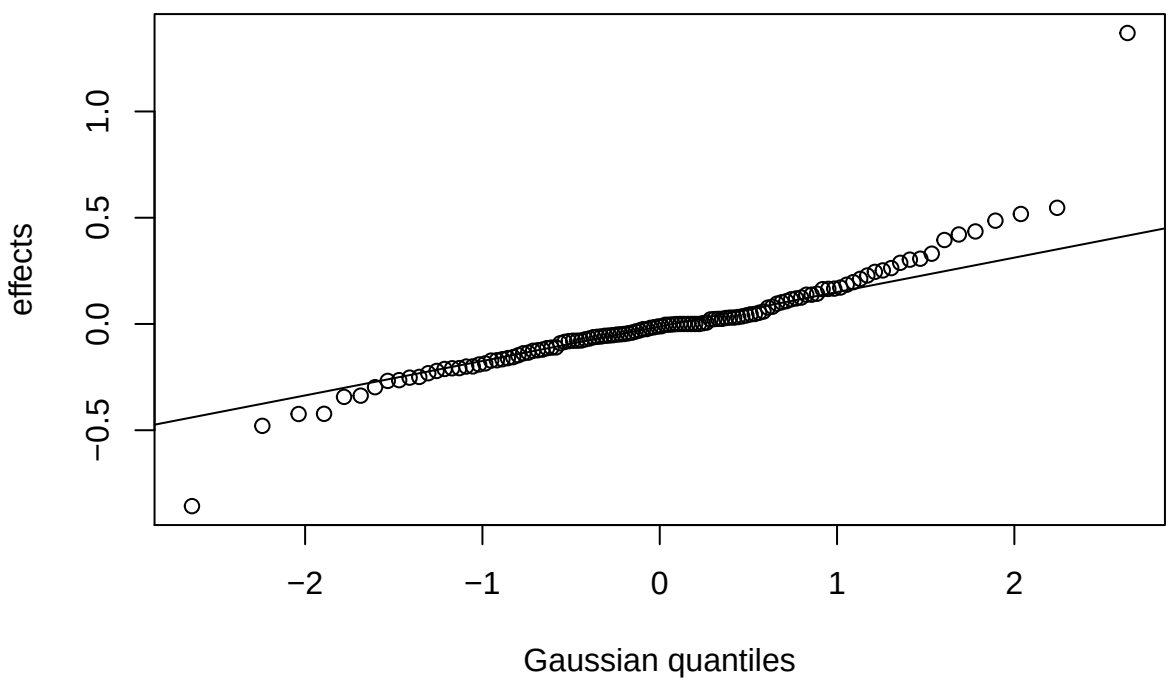

s(Stimulus.code,106.32)
effects
0.5
0.0
−0.5
−2
−1
0
1
2
Gaussian quantiles


s(Language,domain,63.23)
effects
0.5
0.0
−0.5
−1.0
−2
−1
0
1
2
Gaussian quantiles


s(Language,length.scaled,10.81)
effects
0.6
0.4
0.2
0.0
−0.2
−2
−1
0
1
2
Gaussian quantiles


s(domain,length.scaled,1.51)
effects
0.04
0.02
−0.02
−0.06
−1.0
−0.5
0.0
0.5
1.0
Gaussian quantiles





Look at the variation between domains (random slopes). These show the difference in how sensitive domains are to length. For example, the effect of length is less pronounced for smell and more pronounced for touch (though this differs between languages).

```
mDom = mLen5$coefficients
mDom = mDom[grepl("s\\(domain,length.scaled\\)",names(mDom))]
```

```
names(mDom) = as.character(levels(len$domain))
t(t(sort(mDom)))
```

```
##               [,1]
## touch  -0.06639260
## taste  -0.05270594
## colour  0.02603199
## sound   0.02606074
## shape   0.03032637
## smell   0.03667944
```

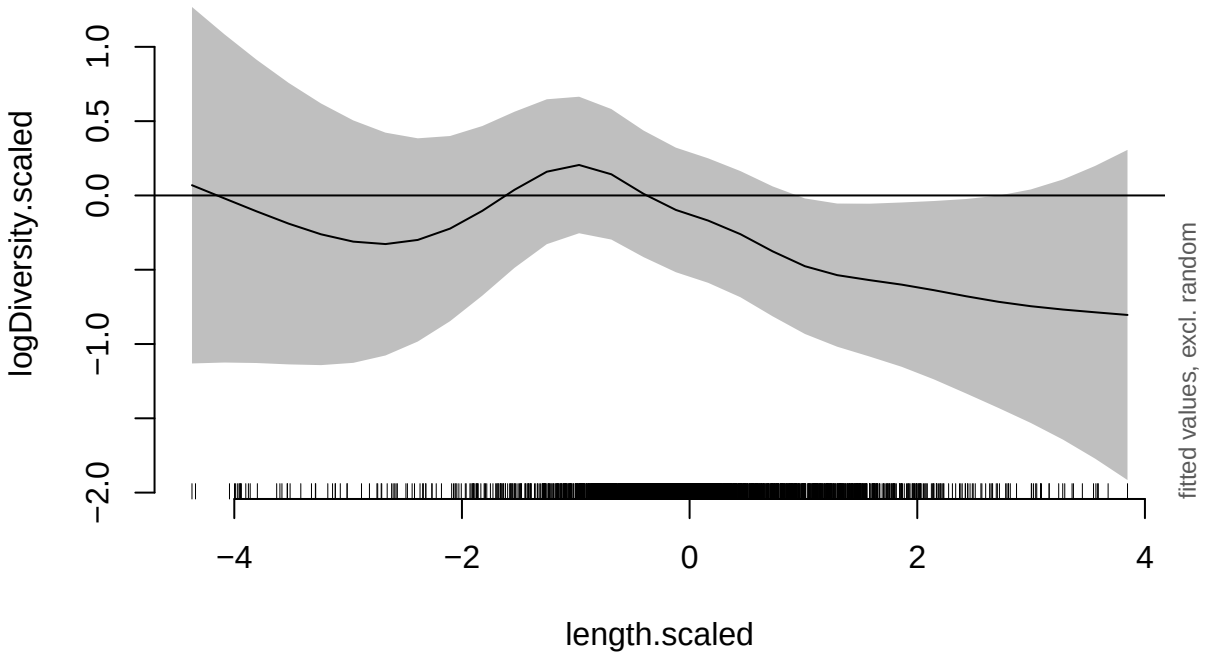
And between languages:

```
mLang = mLen5$coefficients
mLang = mLang[grepl("s\\(Language,length.scaled\\)",names(mLang))]
names(mLang) = as.character(levels(len$Language))
t(t(sort(mLang)))
```

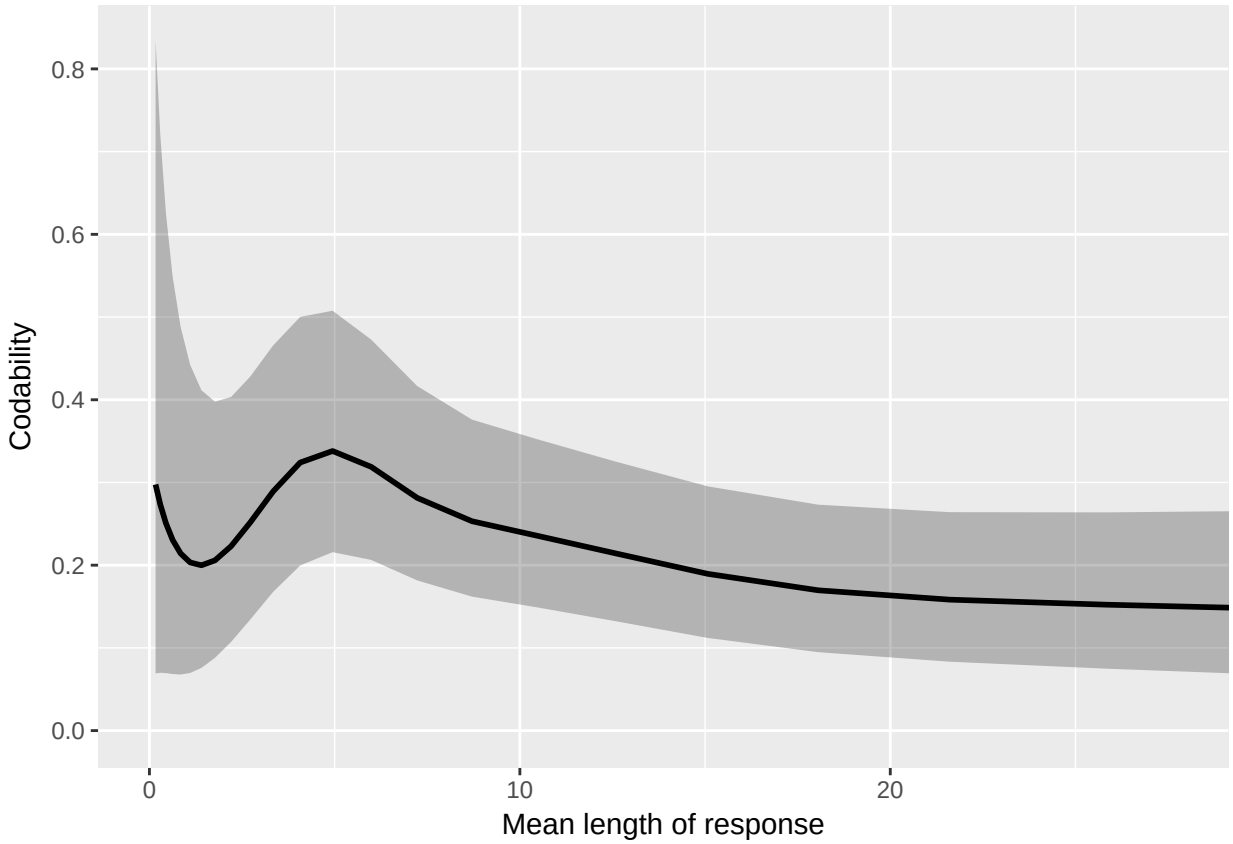
```
##                   [,1]
## Yurakare   -0.29214367
## Dogul Dom  -0.22843955
## Tzeltal    -0.17213762
## BSL        -0.12373691
## Kilivila   -0.11421187
## Turkish    -0.10026139
## Kata Kolok -0.07953295
## Semai      -0.07343907
## ASL        -0.07220170
## English    -0.05093427
## Farsi      -0.04204591
## Lao        -0.03968849
## Zapotec    -0.03518524
## Cantonese   0.05152590
## Malay       0.05983917
## Yucatec     0.12218071
## Siwu        0.13851096
## Mian        0.14155083
## Yeli Dnye   0.29353532
## Umpila      0.61681574
```

We can also use the `itsadug` library to plot the effect of length independent of the random effects. This also scales everything back into the original units, but cuts the length range to show 90% of the data (to hide the long tail)

```
convertLogDiversity = function(X){
  # Convert the scaled diversity measure
  #  back to the original units
  exp(X * attr(len$logDiversity.scaled,"scaled:scale") +
        attr(len$logDiversity.scaled,"scaled:center"))-0.1
}

px = plot_smooth(mLen5,view="length.scaled", rm.ranef = T, print.summary=F)
```




```
px$fv$fit = convertLogDiversity(px$fv$fit)
px$fv$ul = convertLogDiversity(px$fv$ul)
px$fv$ll = convertLogDiversity(px$fv$ll)
px$fv$length.scaled = exp(px$fv$length.scaled *
                            attr(len$length.scaled,"scaled:scale") +
                            attr(len$length.scaled,"scaled:center"))-0.5

gLen = ggplot(px$fv, aes(x=length.scaled,y=fit)) +
  geom_ribbon(aes(ymin=ll,ymax=ul), alpha=0.3) +
  geom_line(size=1) +
  ylab("Codability") +
  xlab("Mean length of response") +
  coord_cartesian(xlim=c(0,quantile(len$mean, 0.90)))
gLen
```




```
pdf("../results/graphs/Codability_by_Length.pdf",
    width = 4, height = 4)
gLen
dev.off()
```

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

S5: Test hierarchy of the senses

Test hierarchy

Load libraries

```
library(dplyr)
library(Skillings.Mack)
library(PMCMR)
library(ggplot2)
library(DyaDA)
library(stringdist)
```

Note that the package `DyaDA` is still in development, and will need to be installed from github:

```
#install.packages("devtools")
#library(devtools)
#install_github("DLEIVA/DyaDA")
#library(DyaDA)
```

Load data

```
d = read.csv("../data/DiversityIndices_ND.csv", stringsAsFactors = F)

domain.order = c("colour","shape",'sound','touch','taste','smell')

d$domain = factor(d$domain, levels=domain.order, labels=c("Color","Shape","Sound","Touch","Taste","Smel

# Note spellingo f Yucatec / Yucatek
d$Language = factor(d$Language,
                    levels =
   rev(c("English", "Farsi", "Turkish",
         "Dogul Dom", "Siwu", "Cantonese", "Lao",
         "Malay", "Semai", "Kilivila", "Mian",
         "Yeli Dnye", "Umpila", "Tzeltal",
         "Yucatec", "Zapotec", "Yurakare",
         "ASL", "BSL", "Kata Kolok")),
                    labels =
   rev(c("English", "Farsi", "Turkish",
         "Dogul Dom", "Siwu", "Cantonese", "Lao",
         "Malay", "Semai", "Kilivila", "Mian",
         "Yélî Dnye", "Umpila", "Tzeltal",
         "Yucatec", "Zapotec", "Yurakare",
         "ASL", "BSL", "Kata Kolok")))

labels= data.frame(Language=as.character(levels(d$Language)))
labels$x = 1:nrow(labels)
```

Summarise diversity index by domain and language:

```
d2 = d %>% group_by(Language,domain) %>%
  summarise(m=mean(simpson.diversityIndex, na.rm=T),
```

```
            upper=mean(simpson.diversityIndex)+sd(simpson.diversityIndex),
            lower=mean(simpson.diversityIndex)-sd(simpson.diversityIndex))
```

```
## Warning: package 'bindrcpp' was built under R version 3.3.2
```

```
d2$rank = unlist(tapply(d2$m,d2$Language,rank))
```

Analyse hierarchy

There's clearly no strict hierarchy. here is a table each domain's rank number within each language. If there as a strict hierarchy, then each domain would have a single rank number:

```
table(d2$domain,d2$rank)
```

```
##
##          1  2  3  4  5  6
##   Color  0  0  1  7 11  1
##   Shape  2  1  5  8  3  1
##   Sound  3  4  6  3  0  0
##   Touch  2  9  5  1  1  2
##   Taste  0  0  3  1  5  9
##   Smell 13  6  0  0  0  1
```

Calculate median codability.

```
meanCodability = sapply(rev(as.character(unique(d2$Language))),function(l){
  d2x = d2[as.character(d2$Language)==l,]
  mx = d2x$m
  names(mx) = as.character(d2x$domain)
  mx[as.character(unique(d2$domain))]
})
meanCodability = t(meanCodability)
```

Number of unique rank orders

Some languages have no data for some domains, so need to check whether each language is consistent with every other language. The functions below calculate the number of unique compatible rank orders.

```
matchCompatibleij = function(i,j,data){
  # Take two row indices and check if the
  # ranks of the vectors of the rows in data
  # are in a compatible order.
  # Rows can include missing data.
  ix = data[i,]
  jx = data[j,]
  complete = !(is.na(ix)|is.na(jx))
  all(order(ix[complete])==order(jx[complete]))
}
matchCompatible <- Vectorize(matchCompatibleij, vectorize.args=list("i","j"))

compatibleMatches = function(data){
  # Compare all individuals to all others,
  # checking if each is compatible
  m = outer(1:nrow(data),1:nrow(data),matchCompatible,data=data)
  rownames(m) = rownames(data)
  colnames(m) = rownames(data)
  return(m)
}

matches = compatibleMatches(meanCodability)
```

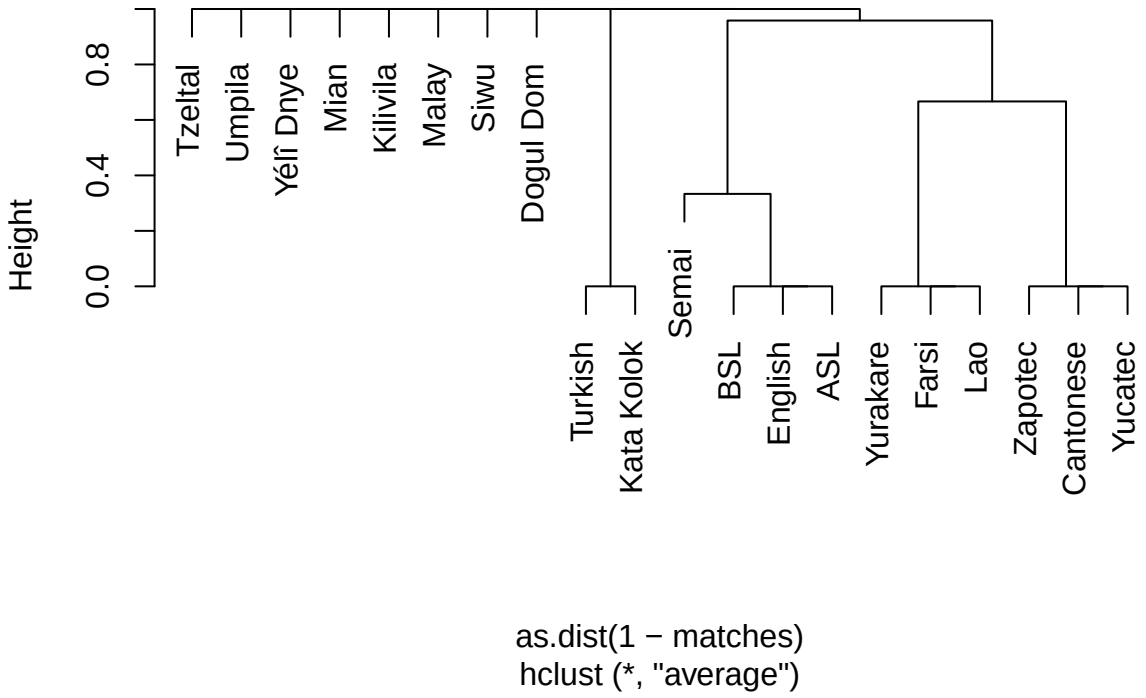
Languages with unique rankings:

```
names(which(rowSums(matches)==1))
```

```
## [1] "Dogul Dom" "Siwu"      "Malay"     "Kilivila"  "Mian"      "Yélî Dnye"
## [7] "Umpila"    "Tzeltal"
```

Use hierarchical clustering to identify unique rankings:

```
hc = hclust(as.dist(1-matches),method = "average")
plot(hc)
```



Number of unique rankings:

```
trueUniqueRanks = length(unique(cutree(hc,h = 0)))
```

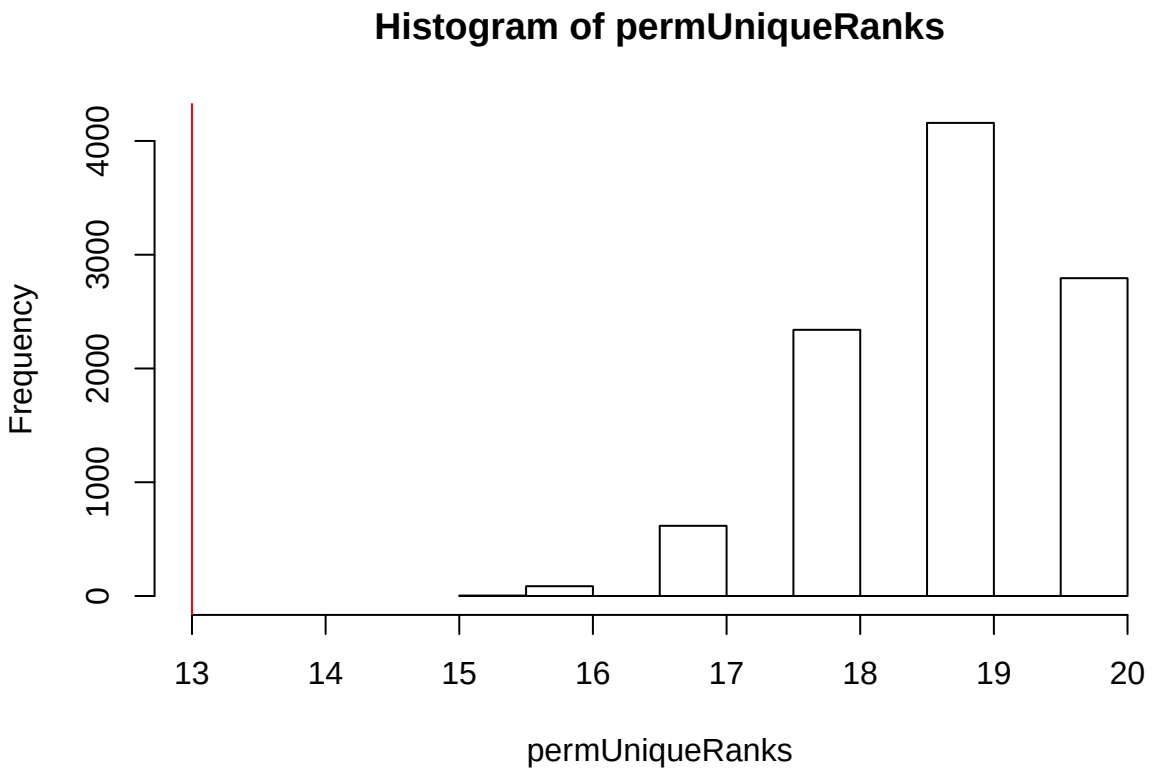
There are 13 unique rankings. We can calculate the probability of seeing this many rankings due to chance. However, an exact solution is difficult because of the missing data. Instead, we can just use permutation to sample the space of possibilities.

```
permWithinRows = function(m){
  # Permute values within rows,
  # keeping NAs in place
  n = colnames(m)
  m = t(apply(m,1,function(X){
    if(sum(is.na(X))>0){
      return(append(sample(X[!is.na(X)]),
                    NA,which(is.na(X))-1))
    } else{
      return(sample(X))
    }
  }))
  colnames(m) = n
  return(m)
}

permRanks = function(){
  matches = compatibleMatches(permWithinRows(meanCodability))
  hc = hclust(as.dist(1-matches),method = "average")
  length(unique(cutree(hc,h = 0)))
}
```

```
permUniqueRanks = replicate(10000,permRanks())
```

Compare true number of unique ranks to the permuted distribution:

```
hist(permUniqueRanks,
     xlim=range(c(permUniqueRanks,trueUniqueRanks)))
abline(v=trueUniqueRanks,col=2)
```




```
p = sum(permUniqueRanks<=trueUniqueRanks)/length(permUniqueRanks)
z = (trueUniqueRanks-mean(permUniqueRanks))/sd(permUniqueRanks)
```

The observed number of unique compatible ranks is less than would be expected by chance (z = -6.4586029, $p < 0.001$).

Aristotelian hierarchy

How compatible are the rank orderings with the Aristotelian hierarchy? This question is complicated by the fact that some languages do not have data for some domains, so each langauge needs to be assessed only comparing to those domains where data is available. The domains of colour and shape are also collapsed under the category of "Sight".

We're using Spearman's footrule to measure distance between rankings.

```
aristotelian.order =
c("Sight","Sight", "Sound", "Touch","Taste","Smell")

# Convert domains to senses (collapse colour and shape to sight)
meanCodability.Senses = meanCodability
colnames(meanCodability.Senses) = c("Sight","Sight","Touch",'Taste',"Smell","Sound")


spearmanFootrule = function(v1,v2){
  # Version of Spearmans' footrule that can handle
  # Multiple tied ranks
  sum(sapply(seq_along(v1), function(i) min(abs(i - (which(v2 == v1[i])))))
}

spearmanFootruleFromAristotelanOrder = function(X){
  rk = names(sort(X,decreasing = T,na.last = NA))
  # filter aristotelian.order list
  ao = aristotelian.order[aristotelian.order %in% rk]
  rk.rank = as.numeric(factor(rk,levels=unique(ao)))
  ao.rank = as.numeric(factor(ao,levels=unique(ao)))
  spearmanFootrule(rk.rank,ao.rank)
}

# Compare each language to the Aristotelian hierarchy
trueNumEdits = apply(meanCodability.Senses,1,spearmanFootruleFromAristotelanOrder)
t(t(trueNumEdits))
```

```
##            [,1]
## English       2
## Farsi         9
## Turkish       9
## Dogul Dom    13
## Siwu         13
## Cantonese     7
## Lao           9
## Malay         4
## Semai         2
## Kilivila      7
## Mian          4
## Yélî Dnye    11
## Umpila       15
## Tzeltal       7
## Yucatec       7
## Zapotec       7
## Yurakare      5
## ASL           2
```

```
## BSL           2
## Kata Kolok    7
```

```
mean(trueNumEdits)
```

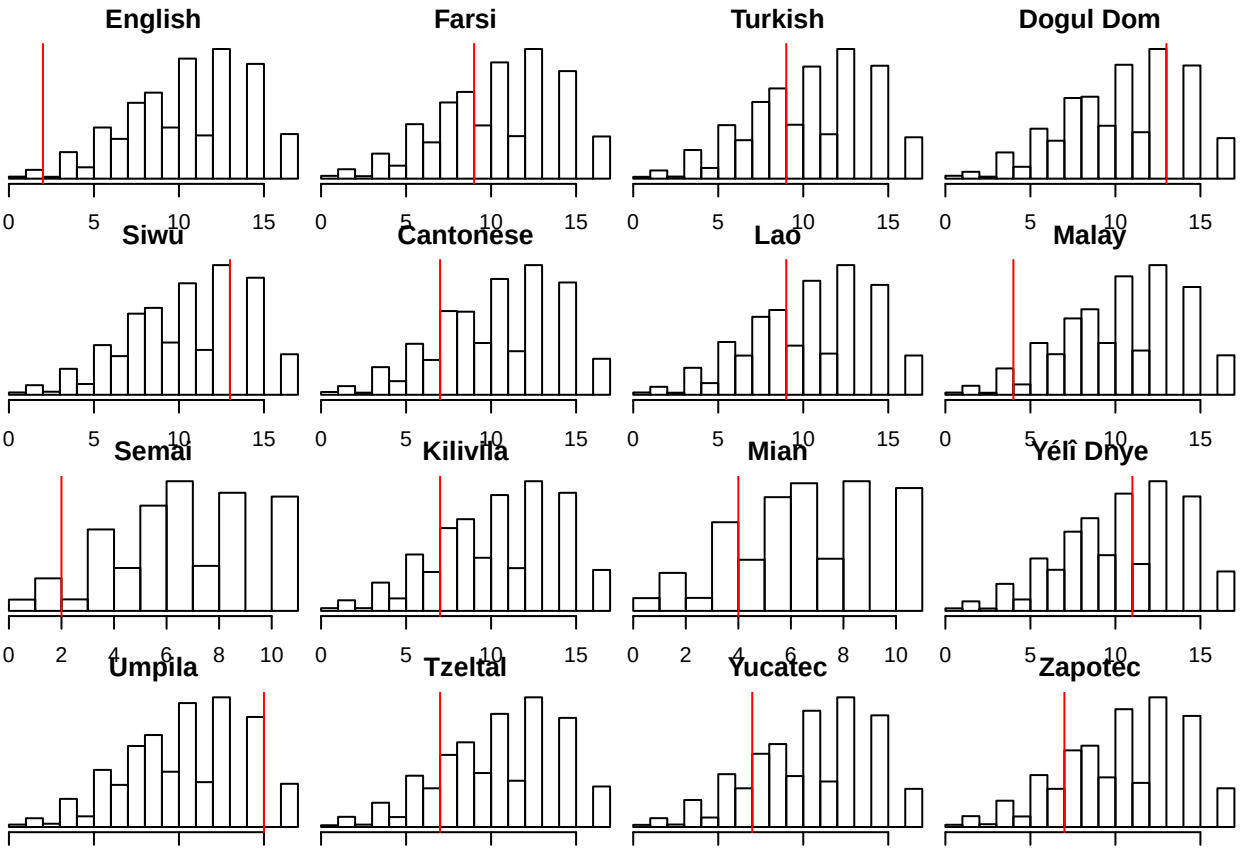
```
## [1] 7.1
```

Get expected Spearman's footrule for each langage when permuting codability scores within languages (maintaining missing domain data).

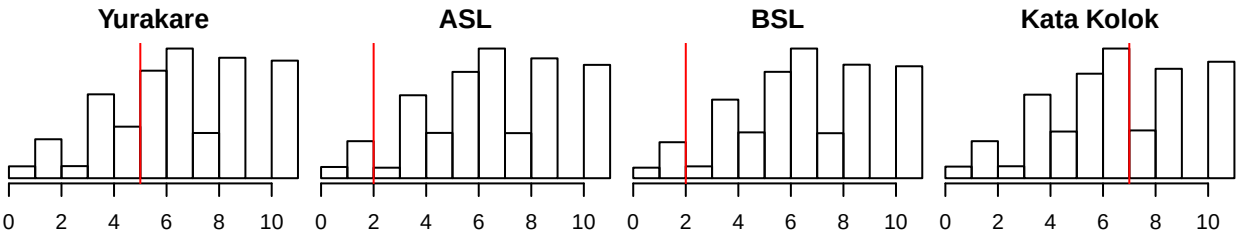
```
set.seed(1290)
permutedNumEdits = replicate(10000,
    apply(permWithinRows(meanCodability.Senses),1,
      spearmanFootruleFromAristotelanOrder))
```

Analyse the difference:

```
par(mfrow=c(4,4),mar=c(1,0,2,0))
for(i in 1:length(trueNumEdits)){
  hist(permutedNumEdits[i,],
     xlim=range(c(permutedNumEdits[i,],trueNumEdits[i])),
     main=names(trueNumEdits)[i],
     yaxt='n')
abline(v=trueNumEdits[i],col=2)
}
```



```
par(mfrow=c(1,1))
```




```
p = sapply(1:length(trueNumEdits), function(i){
  sum(permutedNumEdits[i,]<=trueNumEdits[i])/ncol(permutedNumEdits)
})
names(p) = names(trueNumEdits)
```

Table of p-values of each language, showing the probaility of the permuted distances being smaller or equal to the true distance:

```
t(t(sort(p)))
```

```
##               [,1]
## English     0.0134
## Malay       0.0497
## Semai       0.0633
## BSL         0.0675
## ASL         0.0688
## Tzeltal     0.1757
## Cantonese   0.1765
## Yucatec     0.1791
## Zapotec     0.1803
## Kilivila    0.1839
## Mian        0.2033
## Yurakare    0.2759
## Farsi       0.3841
## Turkish     0.3857
## Lao         0.3875
## Yélî Dnye   0.5979
## Kata Kolok  0.6083
## Siwu        0.8040
## Dogul Dom   0.8071
## Umpila      0.9481
```

Note that these p-values do not ajust for multiple comparisons.

Skillings Mack test

This is similar to the Friedman test, but allows missing data.

```
# Add the missing data back in
d4 = as.data.frame(d2[,c("Language",'domain','m')])
missing_data= rbind(
           c(Language="Yurakare",domain="Sound",m=NA),
           c("ASL","Sound",NA),
           c("BSL","Sound",NA),
           c("Kata Kolok","Sound",NA),
           c("Semai","Taste",NA),
           c("Mian","Taste",NA))
d4 = rbind(d4, missing_data)
d4$m = as.numeric(d4$m)

sm = capture.output(Ski.Mack(y = d4$m,
         groups = d4$domain,
         blocks = d4$Language,
         simulate.p.value = T,
         B = 10000))

print(sm[1:4])
```

```
## [1] ""
## [2] "Skillings-Mack Statistic =  32.927402 , p-value =  4e-06 "
## [3] "Note: the p-value is based on the chi-squared distribution with d.f. =  5 "
## [4] "Based on B =  10000 , Simulated p-value =  0.000000 "
```

The p-value is small, so we can reject the null hypothesis that the distribution of mean codability of domains are is the same across langauges. That is, there are some statistical hierarchies in the data.

We can now run post-hoc tests on pairs of domains to discover the hierarchies. I'm using the Nemenyi test, following Demšar (2006).

Demšar, J. (2006). Statistical comparisons of classifiers over multiple data sets. Journal of Machine learning research, 7(Jan), 1-30.

```
ph = posthoc.friedman.nemenyi.test(
      y = d4$m,
      groups = d4$domain,
      blocks = d4$Language)
ph
```

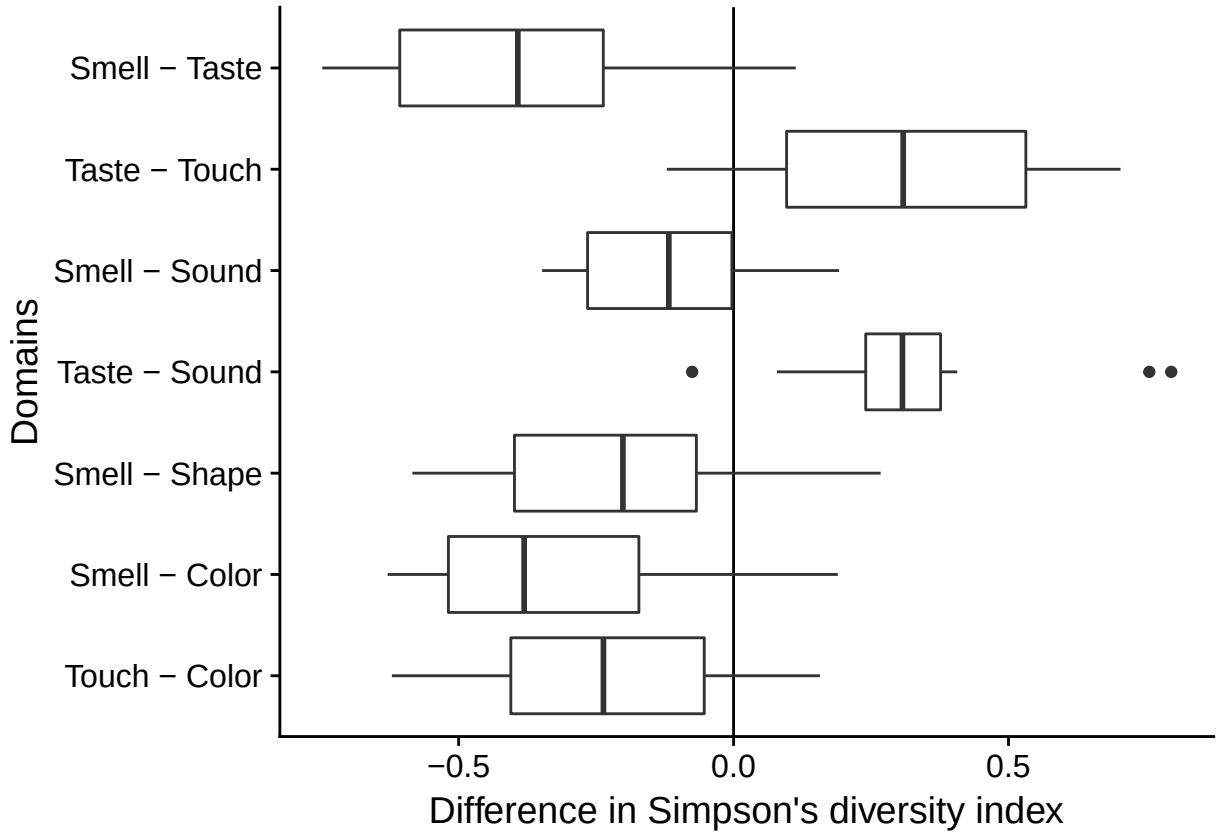
```
##
##  Pairwise comparisons using Nemenyi multiple comparison test
##              with q approximation for unreplicated blocked data
##
## data:  d4$m , d4$domain and d4$Language
##
##       Color   Shape   Sound   Touch   Taste
## Shape 0.53819 -       -       -       -
## Sound 0.20136 0.99163 -       -       -
## Touch 0.02837 0.75555 0.97398 -       -
## Taste 0.91341 0.07430 0.01258 0.00071 -
## Smell 3.8e-06 0.00702 0.04674 0.28044 1.0e-08
##
```

```
## P value adjustment method: none
```

Significant pairs:

```
sig.threshold = 0.05

sig = which(ph$p.value<sig.threshold,arr.ind = T, useNames = F)
sig[,1] = rownames(ph$p.value)[sig[,1]]
sig[,2] = colnames(ph$p.value)[as.numeric(sig[,2])]
```

```
diff = sapply(1:nrow(sig), function(i){
  meanCodability[,sig[i,1]] -
    meanCodability[,sig[i,2]]
})

cnt = sapply(1:nrow(sig), function(i){
  max(sum(meanCodability[,sig[i,1]] >
        meanCodability[,sig[i,2]],na.rm=T) ,
      sum(meanCodability[,sig[i,1]] <
        meanCodability[,sig[i,2]],na.rm=T))
})
cnt.poss = apply(meanCodability,2,function(X){sum(!is.na(X))})

colnames(diff) = paste(sig[,1],"-",sig[,2])

ggplot(as.data.frame.table(diff),
       aes(x=Var2,y=Freq)) +
  geom_hline(yintercept = 0) +
  geom_boxplot() +
  ylab("Difference in Simpson's diversity index") +
  xlab("Domains") +
  coord_flip()
```



Summarise the patterns alongside the statistics:

```
mdiff = colMeans(diff,na.rm = T)
direction = c(">","<")[1+(mdiff>0)]
ruleLables = sapply(1:nrow(sig), function(i){
  if(mdiff[i]>0){
    return(paste(sig[i,2],"<",sig[i,1]))
  } else{
    return(paste(sig[i,1],"<",sig[i,2]))
  }})
ruleP = ph$p.value[ph$p.value<sig.threshold & !is.na(ph$p.value)]
ruleP = signif(ruleP,2)
ruleP[ruleP<0.001] = "< 0.001"
paste(ruleLables,"(p =",ruleP,",",
      cnt,"/",cnt.poss,"languages)")
```

```
## [1] "Touch < Color (p = 0.028 , 17 / 20 languages)"
## [2] "Smell < Color (p = < 0.001 , 19 / 20 languages)"
## [3] "Smell < Shape (p = 0.007 , 18 / 20 languages)"
## [4] "Sound < Taste (p = 0.013 , 13 / 18 languages)"
## [5] "Smell < Sound (p = 0.047 , 12 / 20 languages)"
## [6] "Touch < Taste (p = < 0.001 , 16 / 16 languages)"
## [7] "Smell < Taste (p = < 0.001 , 17 / 20 languages)"
```

Linearity test

We use algorithms from ethology for converting a matrix of wins and losses in dyadic interactions into a consistent linear hierarchy. That is, we treat domains as "individuals" and see in how many languages a domain "dominantes" (more codable than) another.

Build a dominance matrix:

```
domain.labels = c("Color","Shape","Sound","Touch","Taste","Smell")

m = apply(expand.grid(domain.labels,domain.labels),1, function(X){
  #gt = d2[d2$domain==X[1],]$m > d2[d2$domain==X[2],]$m
  gt = meanCodability[,X[1]]>meanCodability[,X[2]]
  sum(gt,na.rm=T)
})
m = matrix(m,nrow=length(domain.labels), ncol=length(domain.labels))
rownames(m) = domain.labels
colnames(m) = domain.labels
m
```

```
##       Color Shape Sound Touch Taste Smell
## Color     0    16    16    17     4    19
## Shape     4     0    12    14     4    18
## Sound     0     4     0     8     1    12
## Touch     3     6     8     0     2    17
## Taste    14    14    13    16     0    17
## Smell     1     2     4     3     1     0
```

In the table above, e.g. Colour is more codable than Smell in 19 languages.

Run the linearity test:

```
set.seed(3298)
linear.hierarchy.test(m)
```

```
##
## Linearity test: Landau's h
## ==========================
##
##
##  Number of individuals: 6  ( 15 dyads)
##  Total number of interactions: 270
##
##  Descriptive table of dyadic relationships:
##             Frequency Percentage
## Unknown             0    0.00000
## Tied                1    6.66667
## One-way             1    6.66667
## Two-way            14   93.33333
## Significant        11   73.33333
##
##  Landau's h index: 0.971429
##  E(h): 0.428571
##  Var(h): 0.083333
##  Improved Landau's h: 0.971429
##  Number of randomizations: 9999
##  P-value (right): 0.0229
```

```
##  P-value (left): 0.9772
##
##
## Linearity test: Kendall's rho
## ============================
##
##  Number of circular dyads: 0.25
##  Expected number of circular dyads: 5
##  Maximum number of circular dyads: 8
##  Kendall's rho index: 0.96875
## Cannot computed since n<10.
```

The statistic is significant, suggesting that there is some consistency to the dominance ranking. Remember, this is just based on 'wins' being bigger than 'losses', it doesn't take into account the significance of the differences.

Find the most consistent order using the I&SI algorithm:

```
# Needed to fix one of the methods
source("DyaDA_ISIMethod2.R")
isi = ISI.method2(m,names = rownames(m))
isi
```

```
##
## Ordering a dominance matrix: I&SI Method
##
##  Call:
##  ISI.method2(X = m, names = rownames(m))
##
##  Initial order:  Color Shape Sound Touch Taste Smell
##
##       Color Shape Sound Touch Taste Smell
## Color     .    16    16    17     4    19
## Shape     4     .    12    14     4    18
## Sound     .     4     .     8     1    12
## Touch     3     6     8     .     2    17
## Taste    14    14    13    16     .    17
## Smell     1     2     4     3     1     .
##
##  Initial number of inconsistencies:  4
##  Initial strength of incosistencies:  4
##
##  Inconsistent dyads and strength of inconsistencies:
##   Individual.i Individual.j Strength.Inconsistency
## 1       Ind. 1       Ind. 5                     4
## 2       Ind. 2       Ind. 5                     3
## 3       Ind. 3       Ind. 5                     2
## 4       Ind. 4       Ind. 5                     1
##
## ***********************************************************
##  Final order:  Taste Color Shape Touch Sound Smell
##
##       Taste Color Shape Touch Sound Smell
## Taste     .    14    14    16    13    17
## Color     4     .    16    17    16    19
## Shape     4     4     .    14    12    18
```

```
## Touch     2     3     6     .     8    17
## Sound     1     .     4     8     .    12
## Smell     1     1     2     3     4     .
##
##  Final number of inconsistencies:  0
##  Final strength of inconsistencies:  0
##
##  Inconsistent dyads and strength of inconsistencies:
## [1] NA
```

The linear order most consistent with the domain ranking within languages is (according to the I&SI algorithm):

```
best.order= rownames(isi$dataFinal)
paste(best.order,collapse =">")
```

```
## [1] "Taste>Color>Shape>Touch>Sound>Smell"
```

Again, you can't interpret this as "Touch is significantly more codable than sound", it's just an order that is consistent with each domain being more codable in more languages than the last.

```
actual.orders = apply(meanCodability,1,function(X){
  x = rev(colnames(meanCodability)[order(X)])
  all(x == best.order[best.order %in% x])
          })
sum(actual.orders)
```

```
## [1] 0
```

```
which(actual.orders)
```

```
## named integer(0)
```

There are no languages that are compatible with this order, so it's a poor approximation.

S6: Explaining Codability

Explaining codability

Contents

Introduction

This set of analyses tries to explain the codability scores according to non-linguistic factors. A list of a-priori hypotheses about external factors that could influence agreement in each domain was compiled. The analysis of agreement across domains used a linear mixed effects model with random effects for domains nested within languages and for stimuli nested within domains. Predictor variables were added to the model as fixed effects and remained if they significantly improved the model according to log likelihood comparison.

The factors that were predicted to explain general levels of codability within a population are:

- Number of speakers of the language (from Ethnologue or field linguist's estimate)
- Formal schooling (low, medium, high)
- Subsistance type (hunter-gatherer, horticultural, stable agriculture, industrial, post-industrial)
- Environment type (closed, open, both)
- Environment subtype (urban, jungle, fields, rocky plateau, forest, forest & sea)
- Settlement type (nucleated, dispersed)
- Society has a market (yes, no)

- Society supports specialists (yes, no)

The Environment subtype variable was too varied to provide meaningful explanation in such a small sample, so is left out of this analysis.

For domains where predictor variables were highly co-linear, a two-step approach was taken. A random forests regression with random intercepts for languages was used to predict variation in agreement according to all a-priori predictor variables. Variable importance measures were used to identify key variables. The effect of these variables was tested with a full mixed effects model with random intercepts for language and stimulus.

The hypotheses for each domain were as follows:

Colour

- Presence of paints
- Number of paints (none, few, many)
- Presence of dyes
- Number of dyes (none, few, many)
- Ritual use of colour (yes, no)
- Professional colour (yes, no)
- Coloured (yes, no)
- Weaving patterns (yes, no)

Shape

- formal schooling (low, medium, high)
- pottery (yes, no)
- patterned pottery (yes, no)
- containers (yes, no)
- number of abstract shape categories (none, one, many)
- professional builders (yes, no)
- society makes boats (yes, no)
- boat specialists (yes, no)
- craft specialists (yes, no)
- spinning thread (yes, no)
- weaving (yes, no)
- weaving specialists (yes, no)
- weave patterns (yes, no)
- what weave patterns (none < simple < angular < complex)
- leatherware (yes, no)
- decorated.leatherware (yes, no)

In addition, it is predicted that communities living in round houses will have lower codability for angular shapes than those living in angular (square or rectangular) houses.

Sound

- musical instrument (yes, no)
- specialist musician (yes, no)
- training music (yes, no)
- children music (yes, no)
- animal sounds (yes, no)

Touch

- pulverise spices (yes, no)
- fine surfaces on houses (yes, no)
- professional textures (yes, no)

Taste

- pulverise.spices (yes, no)
- spices herbs (yes, no)
- Number of additives (0-5)
- sweet additive (for sweet stimulus, yes, no)
- salt additive (for salty stimulus, yes, no)
- bitter additive (for bitter stimulus, yes, no)
- sour additive (for sour stimulus, yes, no)
- umami additive (for umami stimulus, yes, no)
- fragrant food (yes, no)

In addition, having particular additives is predicted to increase the codability for the particular taste stimuli.

Smell

- pulverise spices (yes, no)
- spices herbs (yes, no)
- fragrant food (yes, no)
- Subsistance type (particularly hunter-gratherers)
- latitude (proxy for humidity)

Colinearity

These pairs of variables that are co-linear in our sample, meaning that it is redundant to add them both:

- “market”, “spices/herbs”
- “pottery coloured”, “spinning specialists”
- “pottery coloured”, “leatherware”
- “spinning specialists”, “leatherware”
- “decorated leatherware”, “what leatherware patterns?”
- “pulverise spices”, “sweet additive”
- “pulverise spices”, “sour additive”
- “sweet additive”, “sour additive”

Load libraries

```
library(party)
library(rpart.plot)
library(XLConnect)
library(reshape2)
library(ggplot2)
library(usdm)
library(REEMtree)
library(lme4)
library(sjPlot)
library(gridExtra)
```

Load data

```
s = read.csv("../data/DiversityIndices_ND.csv")

ethnography = read.csv("../data/ethnography/LoP_ethnography_processed.csv")

v.with.variation = apply(ethnography,2,function(X){length(unique(X))>1})

ethnography = ethnography[,v.with.variation]

ethnography$paints.cat =
  factor(ethnography$paints.cat,
         levels=c("none",'few','many'),
         ordered = TRUE)
ethnography$dyes.cat =
  factor(ethnography$dyes.cat,
         levels=c("none",'few','many'),
         ordered = TRUE)

ethnography$ritual.colour.cat =
  factor(ethnography$dyes.cat,
         levels=c("none",'few','many'),
         ordered = TRUE)

ethnography$environment =
  factor(ethnography$environment,
         levels = c("closed",'both','open'))

ethnography$subsistance =
  factor(ethnography$subsistance,
         levels = c("hunter-gatherer","horticultural",
                    'stable agriculture','industrial',
                    "post-industrial"), ordered = T)

ethnography$formal.schooling =
  factor(ethnography$formal.schooling,
         levels = c("low",'medium','high'), ordered = T)
```

```
ethnography$num.additives.scaled = scale(ethnography$num.additives)

ethnography$what.weave.patterns2 =
  factor(ethnography$what.weave.patterns2,
         levels=c("no",'simple','angular','complex'),
         ordered = T)

ethnography$shape2 = "many"
ethnography$shape2[ethnography$shape =="no"] = "none"
ethnography$shape2[ethnography$shape %in% c("oblong",'cylinderical','round')] = "one"
ethnography$shape2 = factor(ethnography$shape2,
                            levels=c("none",'one','many'),
                            ordered = T)

# Add ethnography data to diversity scores
s = cbind(s,
          ethnography[
            match(s$Language,ethnography$Language),
            !names(ethnography) %in%
              c("Language","Language.orig")])

s$pop.logcenter = scale(log(s$pop))

# Cut population into 3 categories
# (may not be used)
s$pop.cat = cut(s$pop.logcenter,
                quantile(s$pop.logcenter,
                         probs=seq(0,1,length.out=4)),
                include.lowest = T,
                labels = c("Low","Medium","High"))

# Transform the diversity index to log scale
# (note that this does not actually change the results much)
s$simpson.diversityIndex.log = log(0.1+s$simpson.diversityIndex)
# scale and center
s$simpson.diversityIndex.log = scale(s$simpson.diversityIndex.log)
```

Set random seed:

```
set.seed(9999)
```

General properties

Use a mixed effects model to test whether the overall codability is affected by general properties of the communities. We start with a null model and add variables if their inclusion significantly improves the fit of the model.

We are quite conservative here, and add random effects for domains within languages and also for stimuli within domains.

```
m0 = lmer(simpson.diversityIndex.log~
            1 +
            (1 | Language/domain) +
            (1|domain/Stimulus.code),data = s)
mPop = update(m0, ~.+pop.logcenter)
anova(m0,mPop)
```

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

```
## Data: s
## Models:
## m0: simpson.diversityIndex.log ~ 1 + (1 | Language/domain) + (1 |
## m0:     domain/Stimulus.code)
## mPop: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mPop:     pop.logcenter
##      Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0    6 5909.4 5945.1 -2948.7   5897.4
## mPop  7 5896.1 5937.7 -2941.0   5882.1 15.353      1  8.918e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mEnv = update(mPop, ~.+environment)
anova(mPop,mEnv)
```

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

```
## Data: s
## Models:
## mPop: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mPop:     pop.logcenter
## mEnv: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mEnv:     pop.logcenter + environment
##      Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mPop  7 5896.1 5937.7 -2941.0   5882.1
## mEnv  9 5897.2 5950.8 -2939.6   5879.2 2.8746      2     0.2376
```

```
mEnvD = update(mPop, ~.+environment.details)
anova(mPop,mEnvD)
```

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

```
## Data: s
## Models:
## mPop: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mPop:     pop.logcenter
## mEnvD: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mEnvD:     pop.logcenter + environment.details
##       Df    AIC    BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## mPop   7 5896.1 5937.7  -2941   5882.1
```

```
## mEnvD 12 5900.0 5971.5  -2938   5876.0 6.0605      5     0.3004
```

```
mSett = update(mPop, ~.+settlement)
anova(mPop, mSett)
```

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

```
## Data: s
## Models:
## mPop: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mPop:     pop.logcenter
## mSett: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mSett:     pop.logcenter + settlement
##       Df    AIC    BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## mPop   7 5896.1 5937.7  -2941   5882.1
## mSett  8 5898.0 5945.7  -2941   5882.0 0.0121      1     0.9125
```

```
mMark = update(mPop, ~.+market)
anova(mPop,mMark)
```

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

```
## Data: s
## Models:
## mPop: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mPop:     pop.logcenter
## mMark: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mMark:     pop.logcenter + market
##       Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mPop   7 5896.1 5937.7 -2941.0   5882.1
## mMark  8 5896.8 5944.5 -2940.4   5880.8 1.2432      1     0.2649
```

```
mSpec = update(mPop, ~.+specialists)
anova(mPop,mSpec)
```

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

```
## Data: s
## Models:
## mPop: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mPop:     pop.logcenter
## mSpec: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mSpec:     pop.logcenter + specialists
##       Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mPop   7 5896.1 5937.7 -2941.0   5882.1
## mSpec  8 5897.9 5945.5 -2940.9   5881.9 0.1514      1     0.6972
```

```
mSubs = update(mPop, ~.+subsistance)
anova(mPop,mSubs)
```

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

```
## Data: s
## Models:
## mPop: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mPop:     pop.logcenter
## mSubs: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mSubs:     pop.logcenter + subsistance
##       Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
```

```
## mPop   7 5896.1 5937.7 -2941.0   5882.1
## mSubs 11 5898.9 5964.4 -2938.4   5876.9 5.1745      4     0.2699
```

```
mScho = update(mPop, ~.+formal.schooling)
anova(mPop,mScho)
```

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

```
## Data: s
## Models:
## mPop: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mPop:     pop.logcenter
## mScho: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 | domain/Stimulus.code) +
## mScho:     pop.logcenter + formal.schooling
##       Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mPop   7 5896.1 5937.7 -2941.0   5882.1
## mScho  9 5894.3 5947.9 -2938.2   5876.3 5.7206      2    0.05725 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The only significant variable is population size. We can also test whether the relationship survives allowing for random slopes by domain (random slopes by language don't make sense because population doesn't vary by language).

```
m0.popSlope = lmer(simpson.diversityIndex.log~
                     1 +
                     (1 | Language/domain) +
                     (1 +pop.logcenter|domain/Stimulus.code),
                   data = s)
mPop2 = update(m0.popSlope, ~.+pop.logcenter)
anova(m0.popSlope,mPop2)
```

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

```
## Data: s
## Models:
## m0.popSlope: simpson.diversityIndex.log ~ 1 + (1 | Language/domain) + (1 +
## m0.popSlope:     pop.logcenter | domain/Stimulus.code)
## mPop2: simpson.diversityIndex.log ~ (1 | Language/domain) + (1 + pop.logcenter |
## mPop2:     domain/Stimulus.code) + pop.logcenter
##             Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0.popSlope 10 5751.5 5811.0 -2865.7   5731.5
## mPop2       11 5748.7 5814.2 -2863.3   5726.7 4.7884      1    0.02865 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mPop2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## simpson.diversityIndex.log ~ (1 | Language/domain) + (1 + pop.logcenter |
##     domain/Stimulus.code) + pop.logcenter
##    Data: s
##
## REML criterion at convergence: 5731.5
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
```

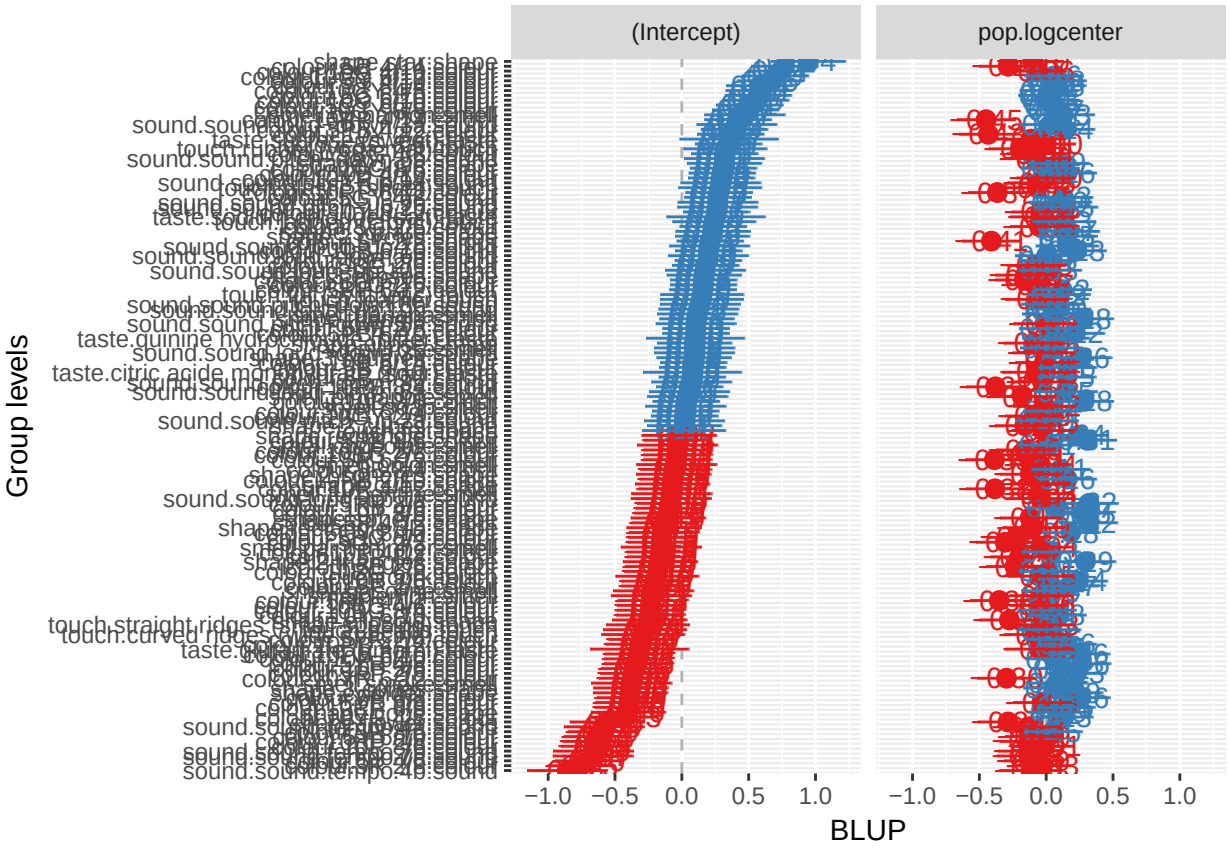
```
## -2.9443 -0.6193  0.0218  0.6113  3.6973
##
## Random effects:
##  Groups                Name          Variance Std.Dev. Corr
##  Stimulus.code:domain (Intercept)   0.129513 0.35988
##                       pop.logcenter 0.040504 0.20126  -0.01
##  domain:Language      (Intercept)   0.220798 0.46989
##  Language             (Intercept)   0.006338 0.07961
##  domain               (Intercept)   0.233937 0.48367
##                       pop.logcenter 0.039240 0.19809  0.80
##  Residual                           0.331665 0.57590
## Number of obs: 2850, groups:
## Stimulus.code:domain, 147; domain:Language, 114; Language, 20; domain, 6
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)   -0.21071    0.20785  -1.014
## pop.logcenter  0.24036    0.09763   2.462
##
## Correlation of Fixed Effects:
##             (Intr)
## pop.logcntr 0.633
```

Statistical summary: There was a significant main effect of population size predicting general agreement (log likelihood difference = 2.4 , df = 1 , Chi Squared = 4.79 , p = 0.029).

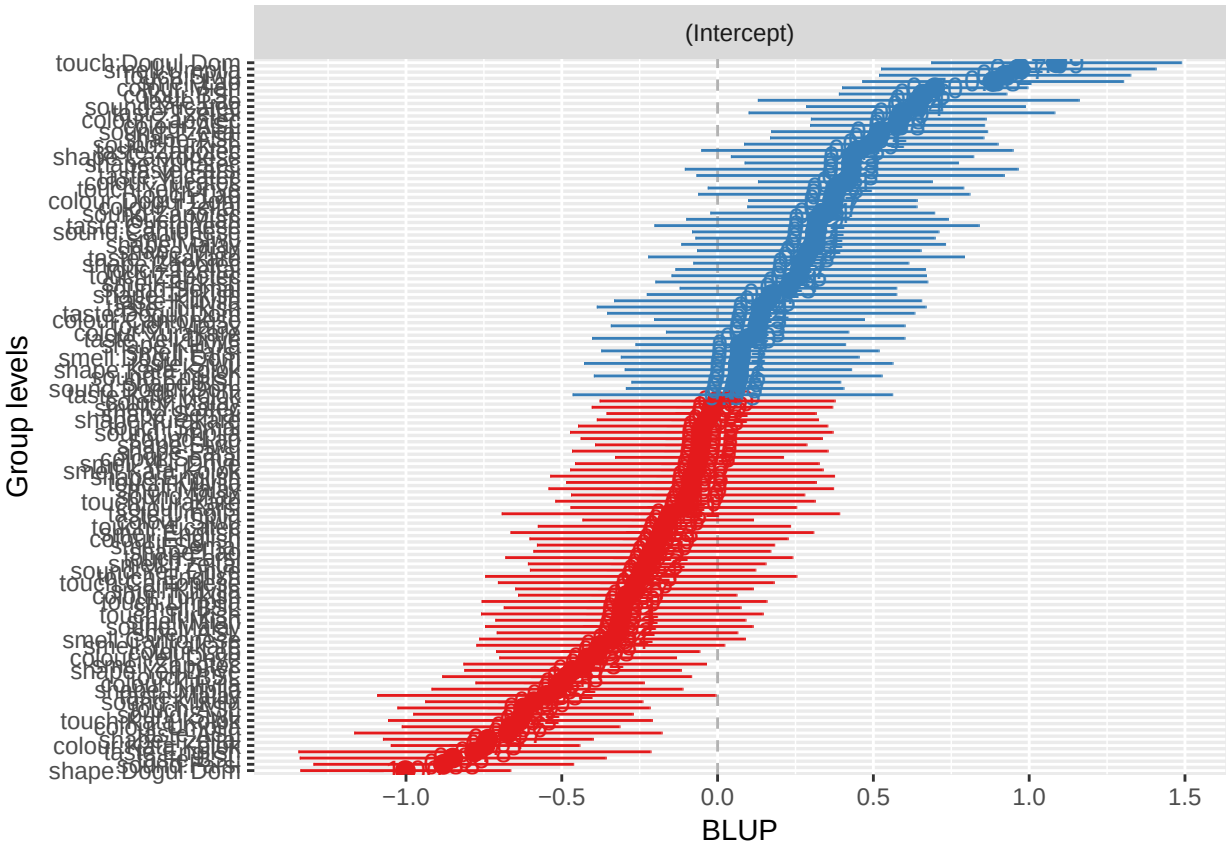
Plot the random effects:

```
sjp.lmer(mPop2, 're', sort.est = "(Intercept)")
```

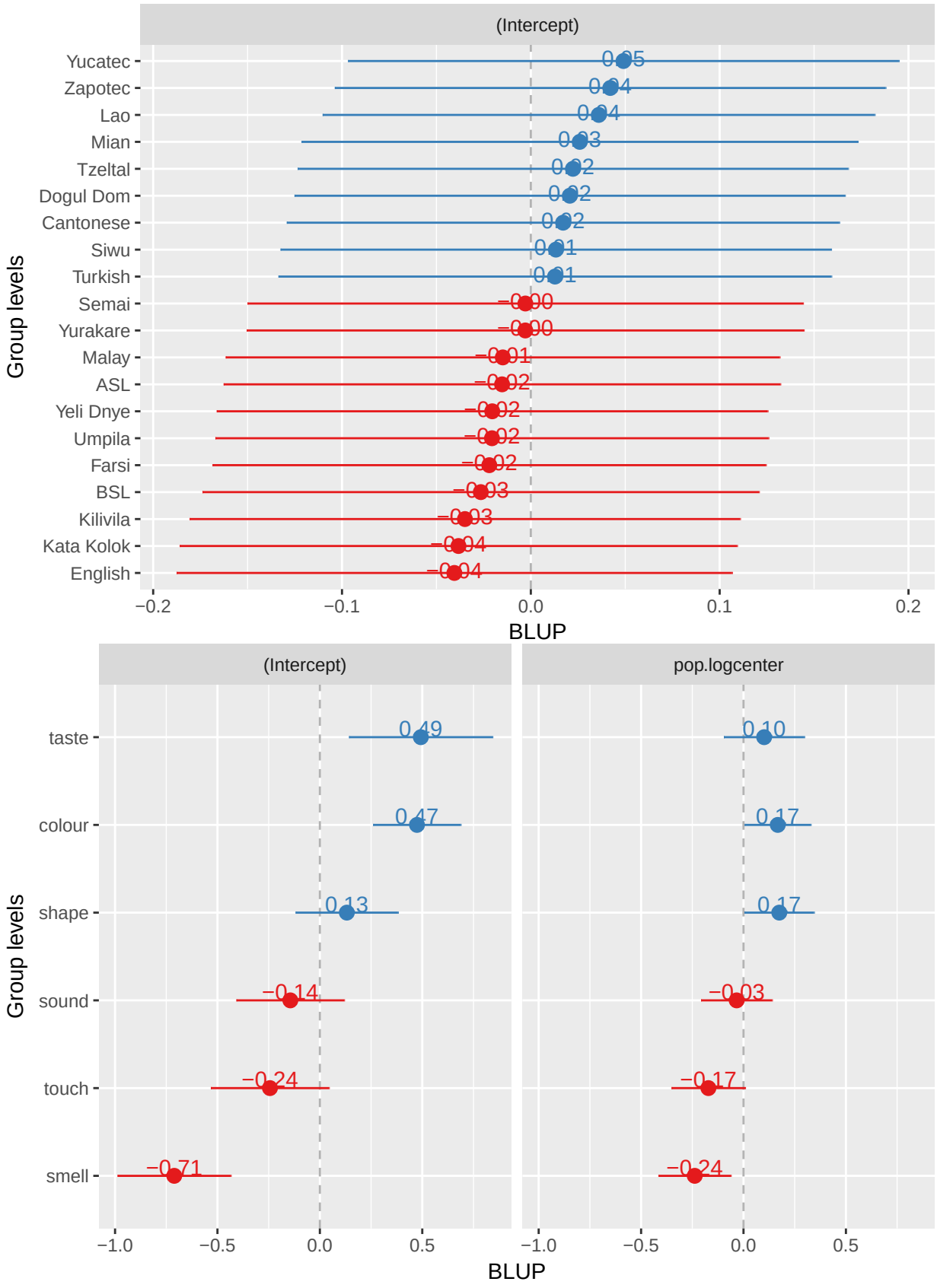
```
## Plotting random effects...
## Plotting random effects...
```




```
## Plotting random effects...
```




```
## Plotting random effects...
```

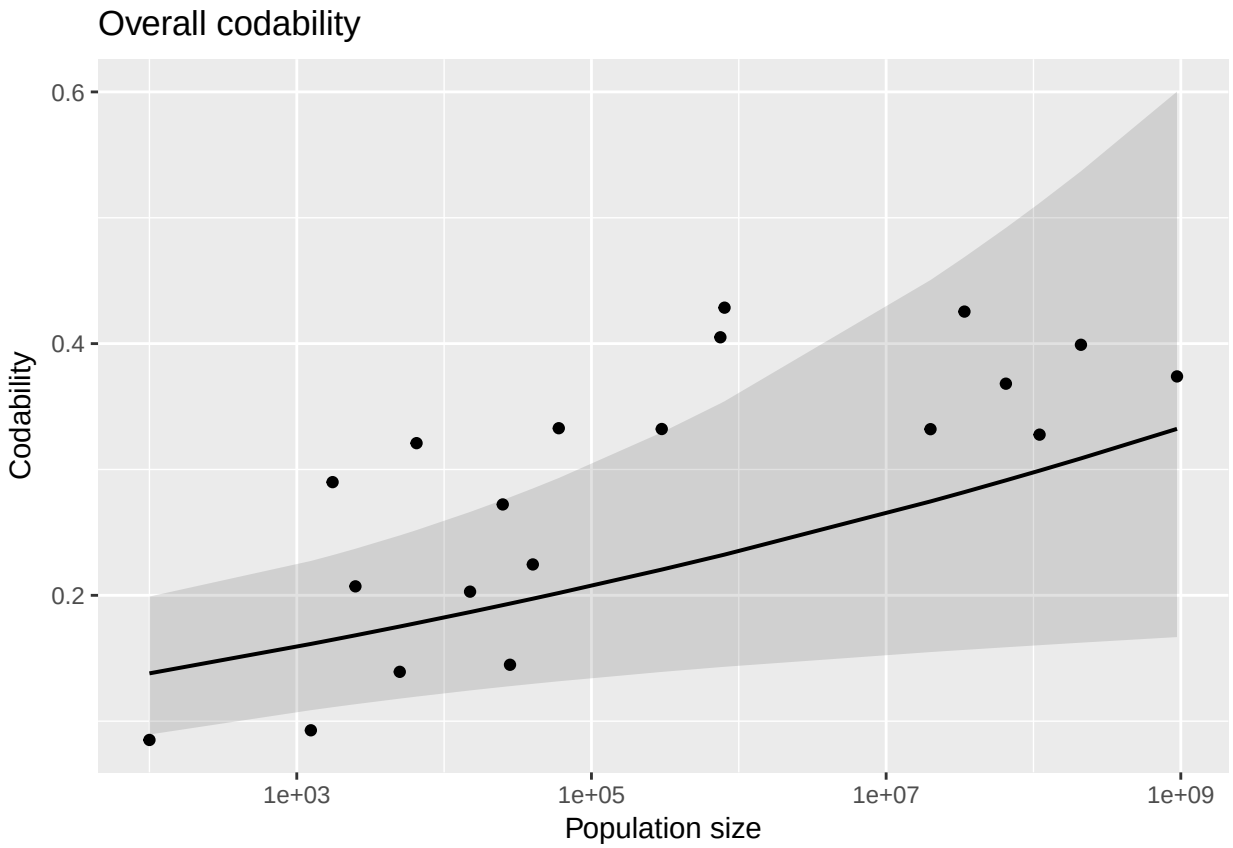


Plot the model effects for population size (extra code is to scale everything back into real numbers):

```
popxcod = data.frame(
  population=tapply(s$pop.logcenter,s$Language, mean),
  mean.codability =
    tapply(s$simpson.diversityIndex.log,s$Language,mean))

popxcod$population = exp((popxcod$population*
  attr(s$pop.logcenter,'scaled:scale')) +
    attr(s$pop.logcenter,'scaled:center'))

popxcod$mean.codability = exp(((popxcod$mean.codability*
  attr(s$simpson.diversityIndex.log,'scaled:scale')) +
    attr(s$simpson.diversityIndex.log,'scaled:center')))-0.1

plotsX = sjp.lmer(mPop2, "eff", show.ci = T,
         show.scatter = T,prnt.plot=F,facet.grid=F)
```

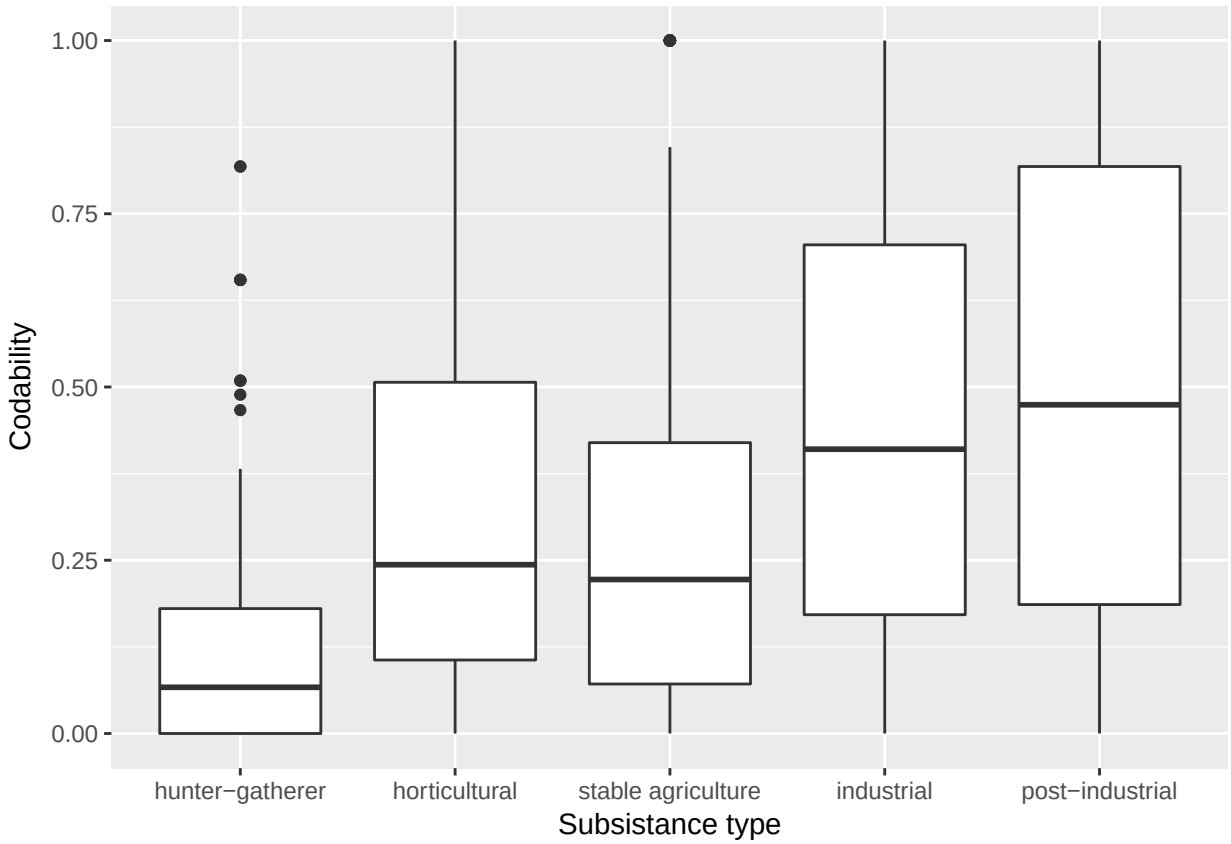
```
## Warning: package 'bindrcpp' was built under R version 3.3.2
```

```
plotsX$plot.list[[1]]$labels$title = ""

plotsX$plot.list[[1]]$data$x =
  exp((plotsX$plot.list[[1]]$data$x*
  attr(s$pop.logcenter,'scaled:scale')) +
    attr(s$pop.logcenter,'scaled:center'))

plotsX$plot.list[[1]]$data$y =
  exp(((plotsX$plot.list[[1]]$data$y*
  attr(s$simpson.diversityIndex.log,'scaled:scale')) +
    attr(s$simpson.diversityIndex.log,'scaled:center')))-0.1

plotsX$plot.list[[1]]$data$lower =
  exp(((plotsX$plot.list[[1]]$data$lower*
  attr(s$simpson.diversityIndex.log,'scaled:scale')) +
    attr(s$simpson.diversityIndex.log,'scaled:center')))-0.1

plotsX$plot.list[[1]]$data$upper =
  exp(((plotsX$plot.list[[1]]$data$upper*
  attr(s$simpson.diversityIndex.log,'scaled:scale')) +
    attr(s$simpson.diversityIndex.log,'scaled:center')))-0.1

gx.pop = plotsX$plot.list[[1]] +
  scale_x_log10() +
  xlab("Population size") +
  ylab("Codability") +
  ggtitle("Overall codability") +
  geom_point(data=popxcod, aes(population,mean.codability))

gx.pop
```

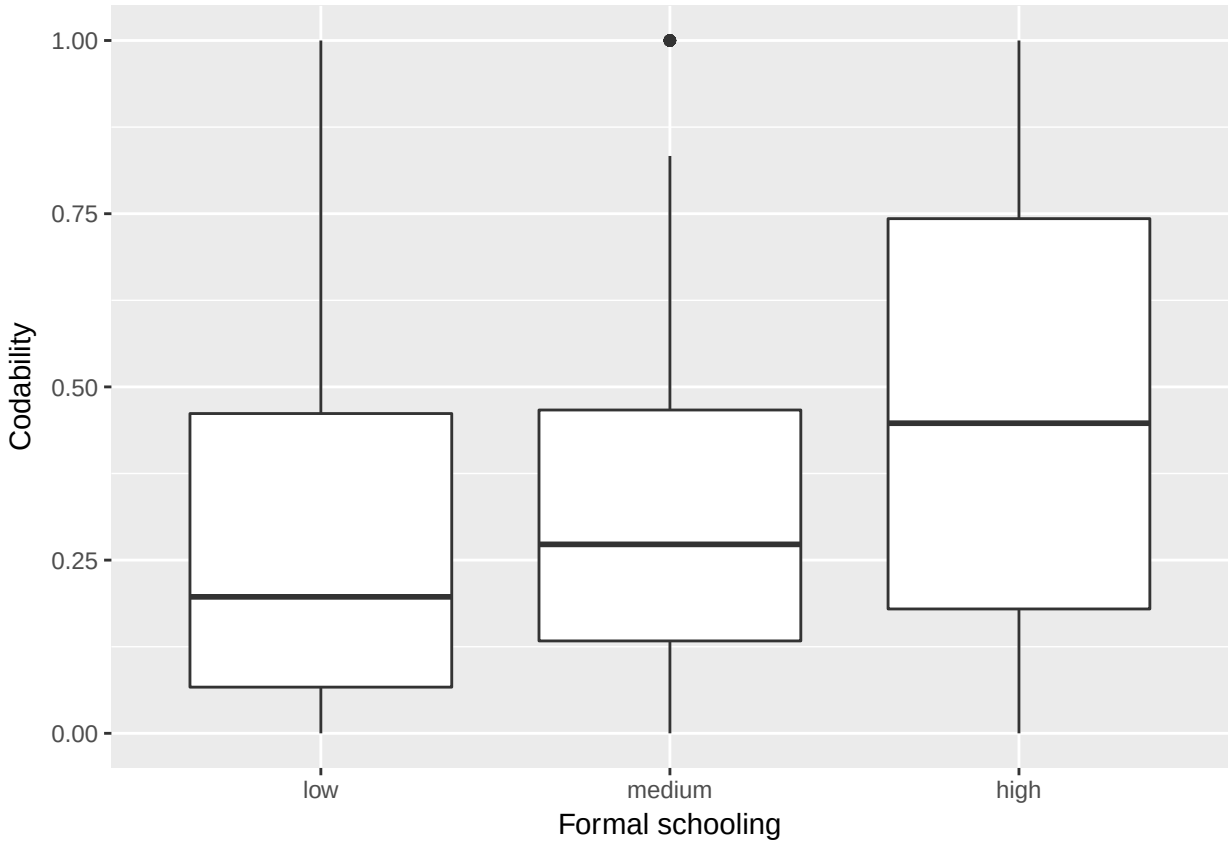


Plots for subsistance, formal schooling.

```
ggplot(s,
       aes(subsistance,simpson.diversityIndex)) +
  geom_boxplot() +
  xlab("Subsistance type") +
  ylab("Codability")
```




```
gg.formalschooling =
  ggplot(s,
       aes(formal.schooling,simpson.diversityIndex)) +
  geom_boxplot() +
  xlab("Formal schooling") +
  ylab("Codability")
gg.formalschooling
```



Correlation between population size and subsistance:

```
kruskal.test(ethnography$pop, ethnography$subsistance)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  ethnography$pop and ethnography$subsistance
## Kruskal-Wallis chi-squared = 12.004, df = 4, p-value = 0.01732
```

Specific domains

There are many more variables to consider for the individual domains. Many are highly correlated, and there are many missing combinations in the data. This makes a regression approach difficult. Instead, we can use a binary decision tree to find clusters in the data based on salient properties. The package `REEMtree` also allows an additional random effect for Language (crossed random effects for stimulus type are not permitted). So we use random forests to identify key variables (or exclude unimportant variables), then mixed effects modelling to determine significance of main effects.

Note that we're using a categorical version of the population variable that splits the data into "small","medium",'large'. This is because the raw population variable is a continuous variable that can be used by a decision tree to split the languages into many arbitrary categories, giving it an unfair advantage over the other variables and making it difficult to interpret the plot.

Colour

Calculate the optimal decision tree, given variables related to colour:

```
s.colour = s[s$domain=='colour',]
rt = REEMtree(simpson.diversityIndex~
          formal.schooling +
          paints.cat+
          dyes.cat+
          ritual.colour.cat+
          professional.colour+
          pottery.coloured+
          weave.patterns,
         random = ~1|Language,
         data = s.colour,
         MaxIterations=100000)
```

Colour Results

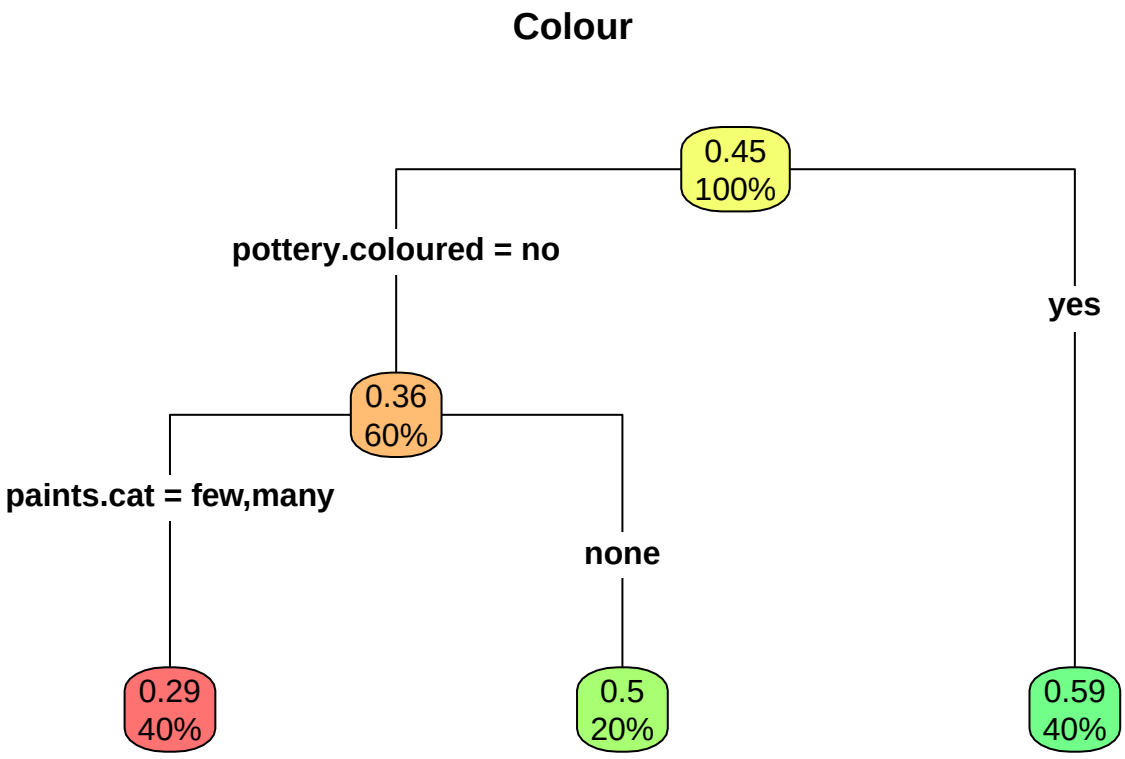
Proportion of variance explained:

```
# R squared
cor(predict.REEMtree(rt,s.colour,id=s.colour$Language,
  EstimateRandomEffects = T),
    s.colour$simpson.diversityIndex)^2
```

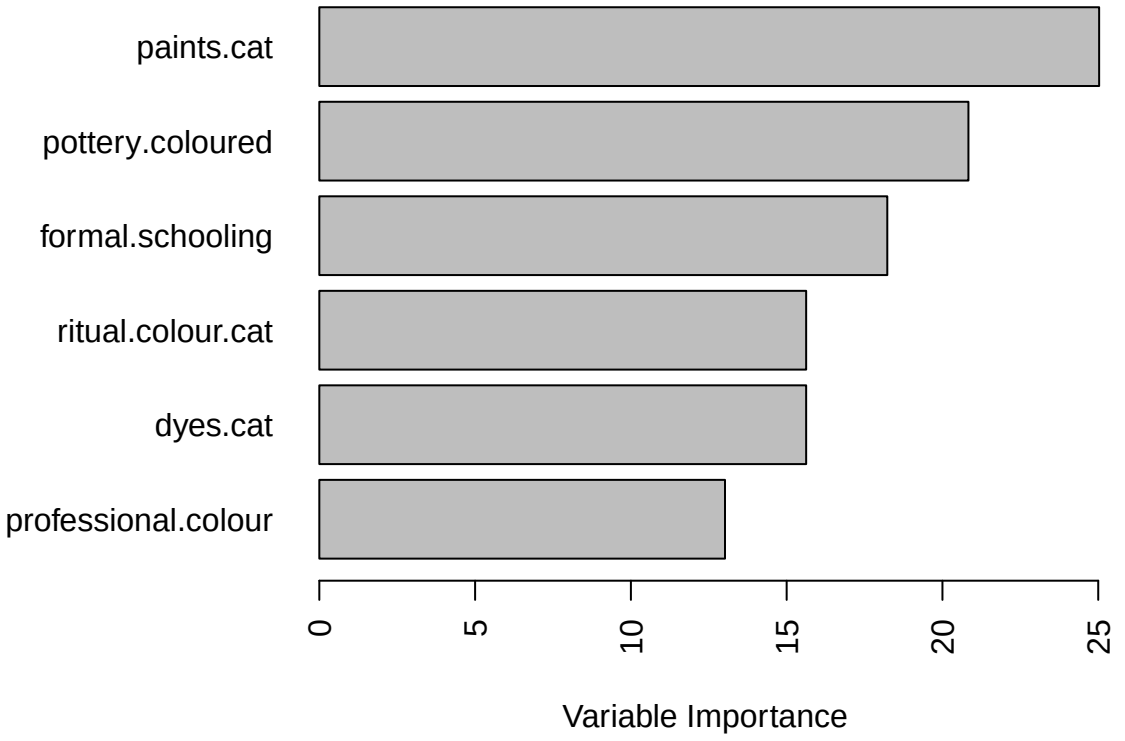
```
## [1] 0.3132261
```

Plot the tree and calculate variable importance:

```
rpart.plot(tree(rt), type=4,extra=100, branch.lty=1, box.palette="RdYlGn", main="Colour")
```



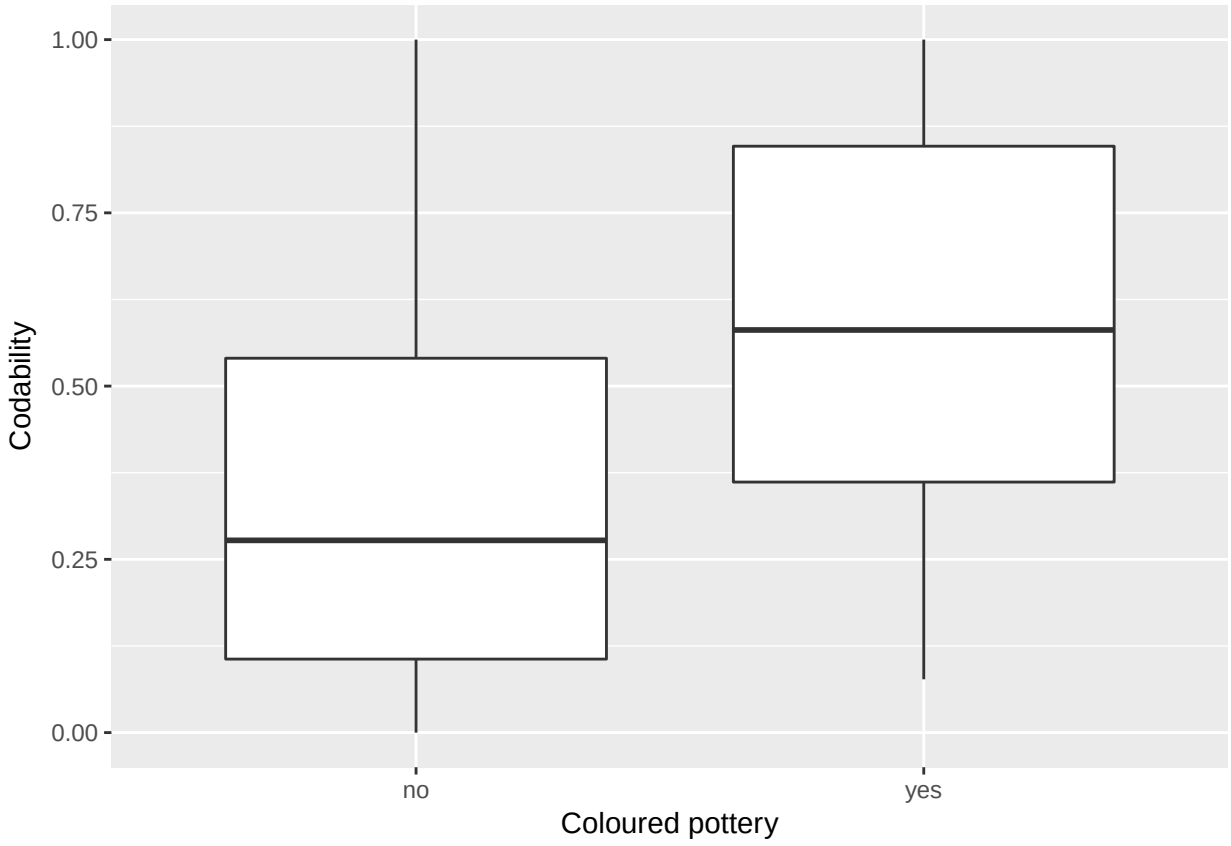

```
varimp = rt$Tree$variable.importance

par(mar=c(5,10,2,2))
barplot(sort(varimp), horiz=T, las=2,
        xlab="Variable Importance")
```



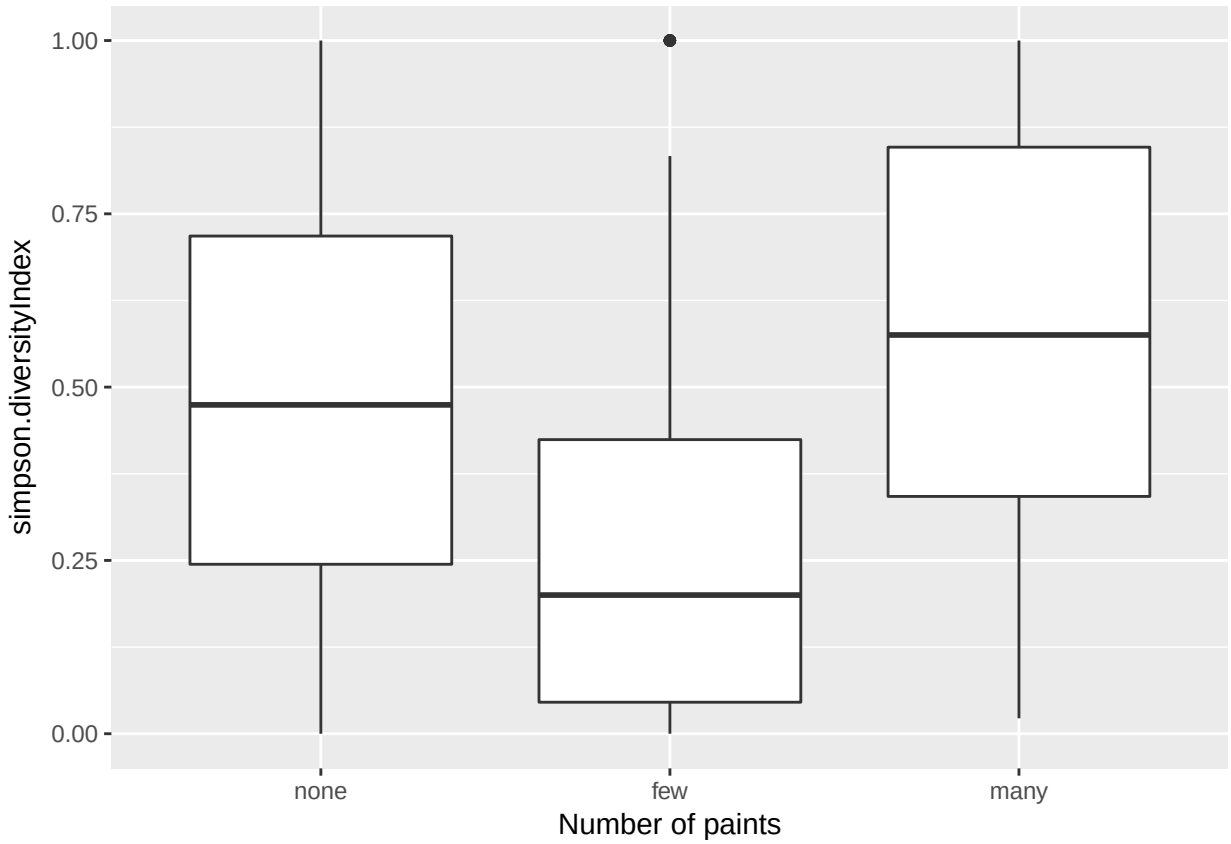
```
par(mar=c(5, 4, 4, 2) + 0.1)
```

Plot the relationships:

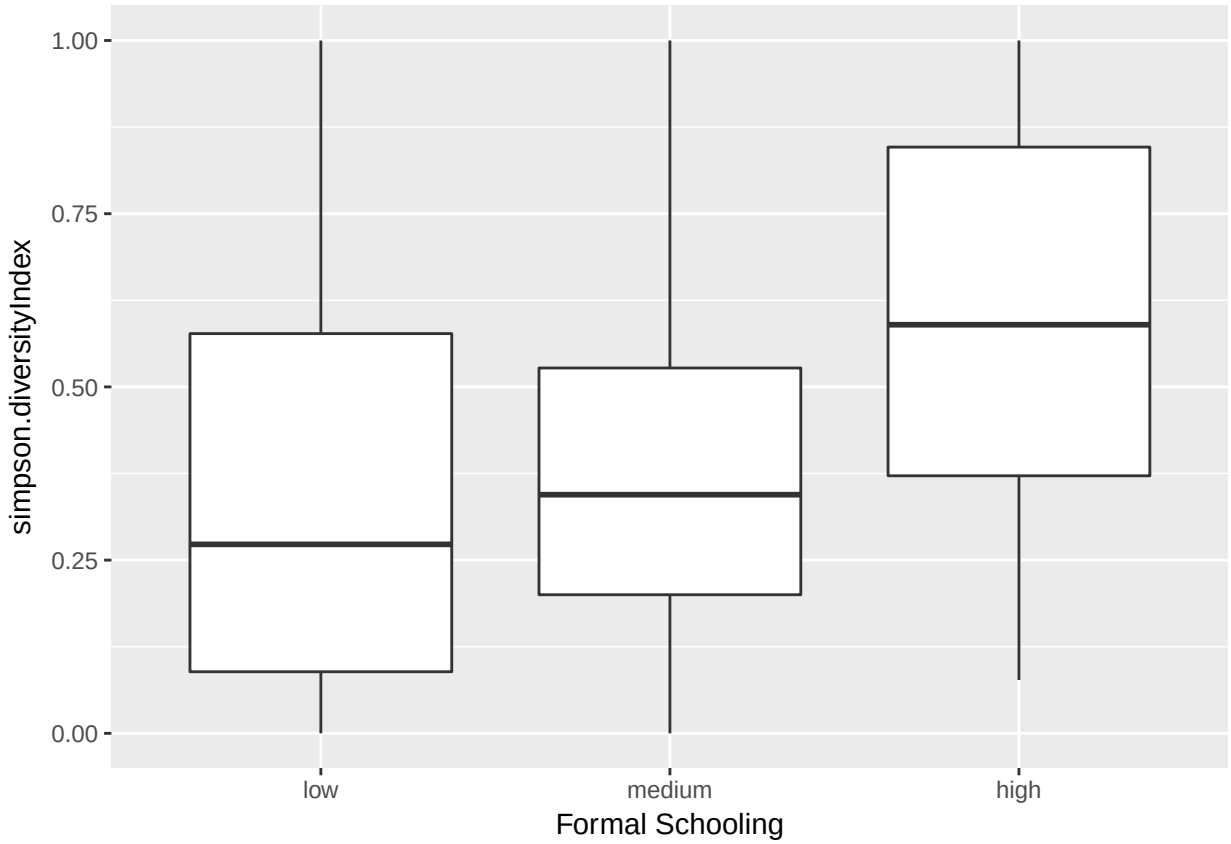
```
ggplot(s.colour,
       aes(pottery.coloured,simpson.diversityIndex)) +
  geom_boxplot() +
  xlab("Coloured pottery") +
  ylab("Codability")
```




```
ggplot(s.colour,
       aes(paints.cat,simpson.diversityIndex)) +
  geom_boxplot() +
  xlab("Number of paints")
```




```
ggplot(s.colour,
       aes(formal.schooling,simpson.diversityIndex)) +
  geom_boxplot() +
  xlab("Formal Schooling")
```



Test the most important variables with a mixed effects model:

```
mc.all = lmer(simpson.diversityIndex.log ~
        1 +
          paints.cat +
          pottery.coloured +
          formal.schooling +
        (1 | Language) +
        (1 | Stimulus.code),
     data = s.colour)

mc.noPaints = lmer(simpson.diversityIndex.log ~
        1 +
          pottery.coloured +
          formal.schooling +
        (1 | Language) +
        (1 | Stimulus.code),
     data = s.colour)

mc.noSchool = lmer(simpson.diversityIndex.log ~
        1 +
          pottery.coloured +
          paints.cat +
        (1 | Language) +
        (1 | Stimulus.code),
     data = s.colour)
```

```
mc.noPott = lmer(simpson.diversityIndex.log ~
        1 +
          paints.cat +
          formal.schooling +
        (1 | Language) +
        (1 | Stimulus.code),
     data = s.colour)

anova(mc.all, mc.noPaints)
```

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

```
## Data: s.colour
## Models:
## mc.noPaints: simpson.diversityIndex.log ~ 1 + pottery.coloured + formal.schooling +
## mc.noPaints:     (1 | Language) + (1 | Stimulus.code)
## mc.all: simpson.diversityIndex.log ~ 1 + paints.cat + pottery.coloured +
## mc.all:     formal.schooling + (1 | Language) + (1 | Stimulus.code)
##             Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## mc.noPaints  7 3396.1 3433.8 -1691.1   3382.1
## mc.all       9 3390.2 3438.6 -1686.1   3372.2 9.925      2   0.006996 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(mc.all, mc.noSchool)
```

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

```
## Data: s.colour
## Models:
## mc.noSchool: simpson.diversityIndex.log ~ 1 + pottery.coloured + paints.cat +
## mc.noSchool:     (1 | Language) + (1 | Stimulus.code)
## mc.all: simpson.diversityIndex.log ~ 1 + paints.cat + pottery.coloured +
## mc.all:     formal.schooling + (1 | Language) + (1 | Stimulus.code)
##             Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mc.noSchool  7 3386.7 3424.3 -1686.3   3372.7
## mc.all       9 3390.2 3438.6 -1686.1   3372.2 0.5037      2     0.7774
```

```
anova(mc.all, mc.noPott)
```

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

```
## Data: s.colour
## Models:
## mc.noPott: simpson.diversityIndex.log ~ 1 + paints.cat + formal.schooling +
## mc.noPott:     (1 | Language) + (1 | Stimulus.code)
## mc.all: simpson.diversityIndex.log ~ 1 + paints.cat + pottery.coloured +
## mc.all:     formal.schooling + (1 | Language) + (1 | Stimulus.code)
##           Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mc.noPott  8 3388.4 3431.4 -1686.2   3372.4
## mc.all     9 3390.2 3438.6 -1686.1   3372.2 0.1791      1     0.6721
```

There is only a contribution of number of paints beyond population size, but this goes in the opposite direction of the predicted one: societies with few paints have fewer categories than societies with none or many. There was a significant main effect of number of paints (log likelihood difference = 5 , df = 2 , Chi Squared = 9.92 , p = 0.007).

Shape

Calculate the optimal decision tree, given variables related to shape:

```
s.shape = s[s$domain=='shape',]

rt.shape = REEMtree(simpson.diversityIndex~
          formal.schooling +
          pottery +
          pottery.patterned +
          containers +
          shape2 +
          professional.builders +
          make.boats+
          boat.specialists+
          craft.specialists+
          spinning.thread+
          weaving+
          weaving.specialists+
          weave.patterns+
          what.weave.patterns2+
          leatherware+
          decorated.leatherware,
         random = ~1|Language,
         data = s.shape,
         MaxIterations=100000)
```

Shape Results

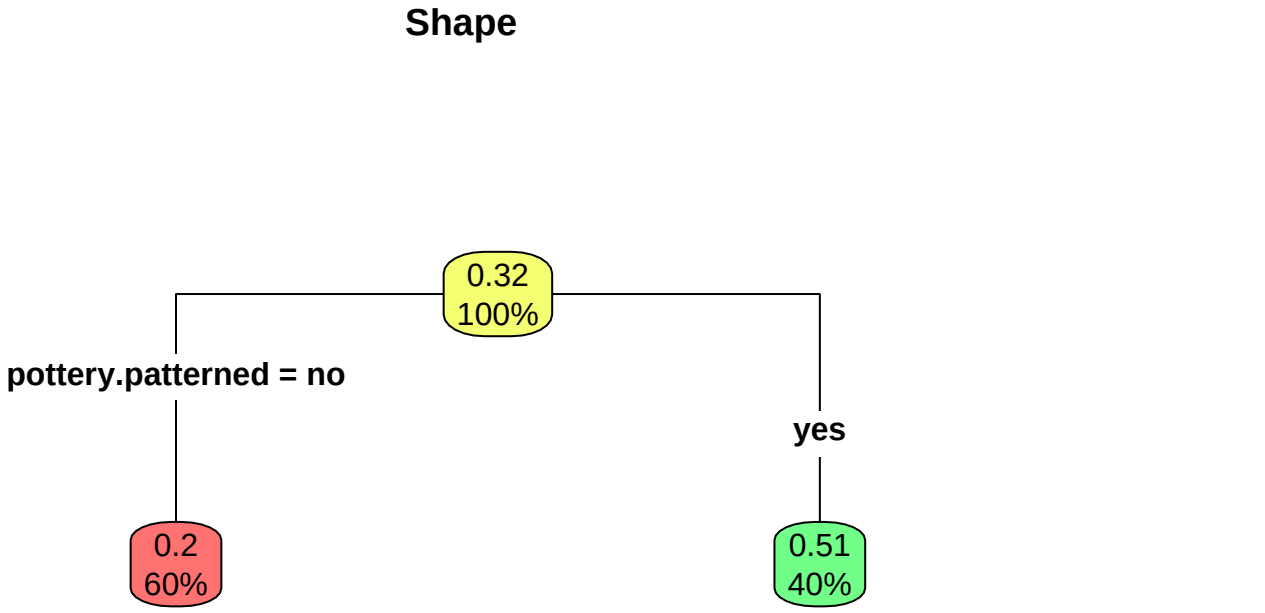
Proportion of variance explained:

```
# R squared
cor(predict.REEMtree(rt.shape,s.shape,id=s.shape$Language, EstimateRandomEffects = T),
    s.shape$simpson.diversityIndex)^2
```

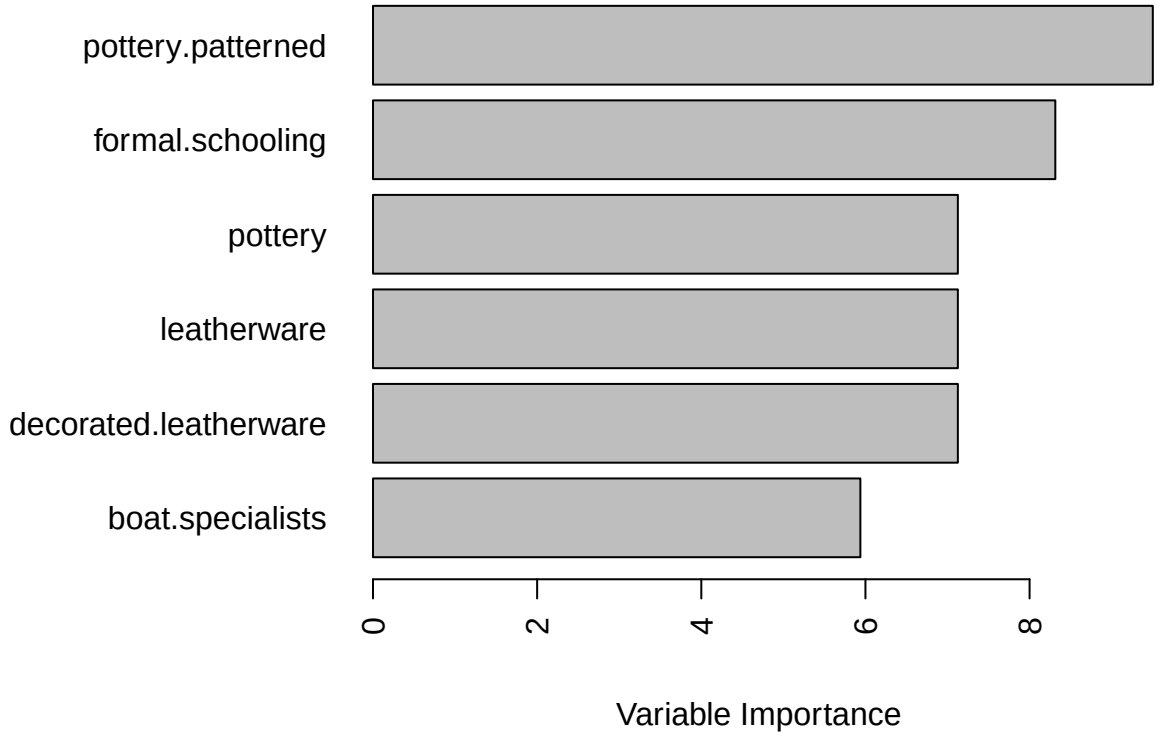
```
## [1] 0.4100091
```

Plot the tree and calculate variable importance:

```
rpart.plot(tree(rt.shape), type=4,extra=100, branch.lty=1, box.palette="RdYlGn", main="Shape")
```




```
varimp = rt.shape$Tree$variable.importance

par(mar=c(5,10,2,2))
barplot(sort(varimp), horiz=T, las=2,
        xlab="Variable Importance")
```




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

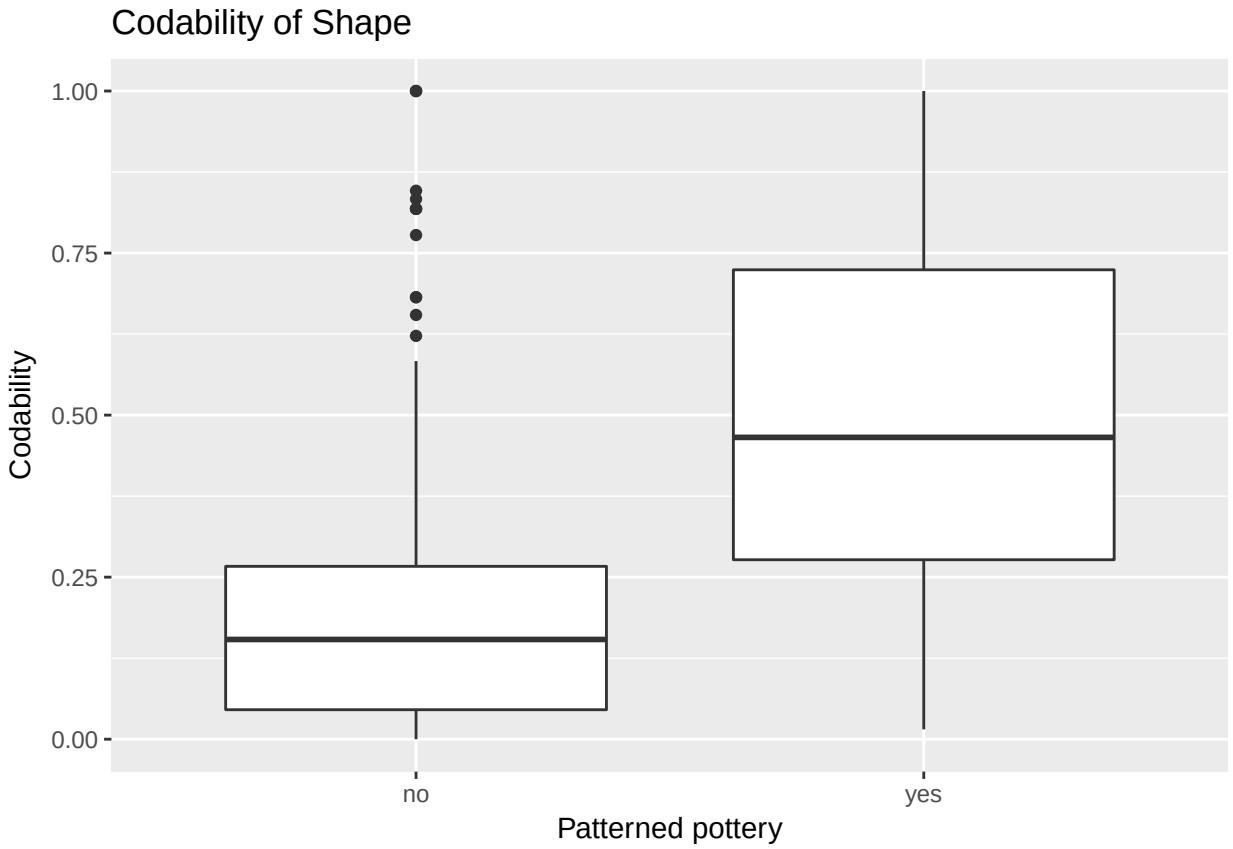
Both `pottery.patterned` and `formal.schooling` have high importance. The two variables are highly co-linear (there are no societies with 'high' formal schooling without patterned pottery):

```
table(s$formal.schooling, s$pottery.patterned)
```

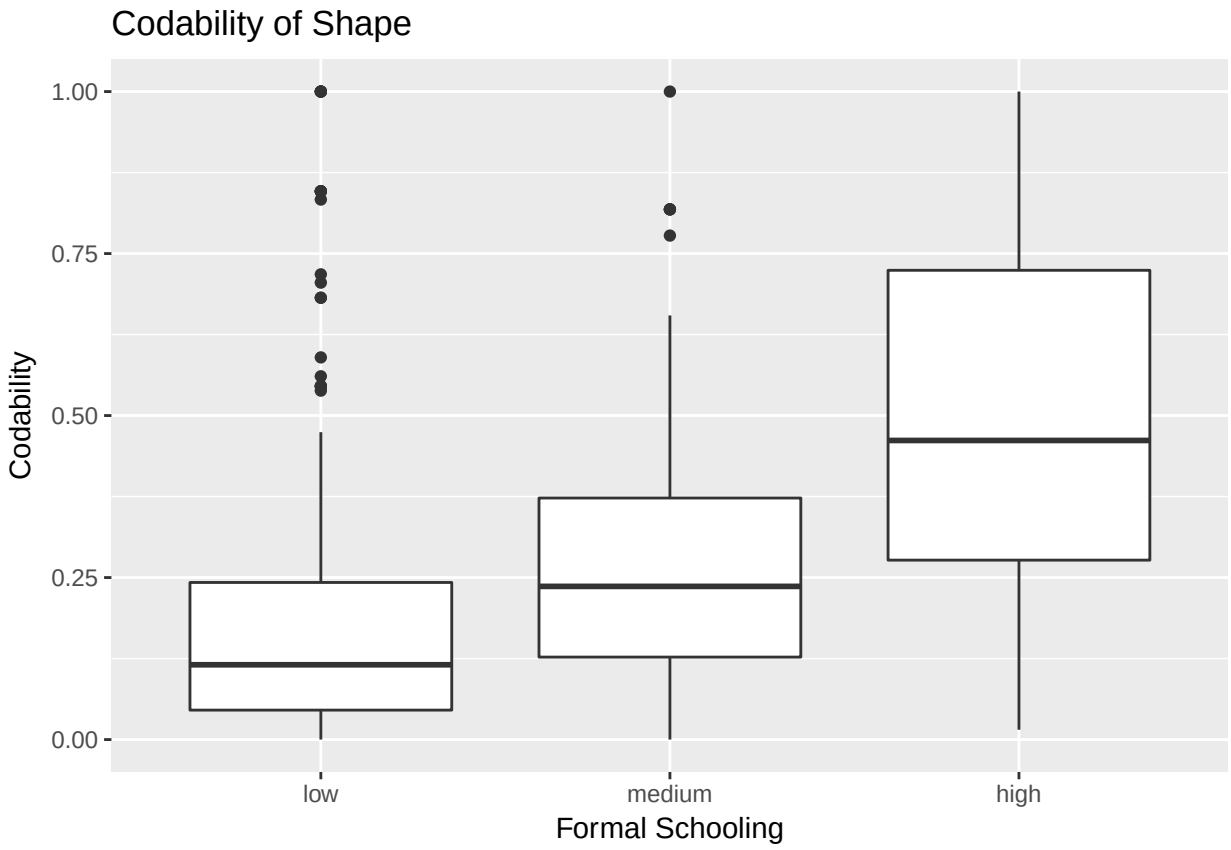
```
##
##            no  yes
##   low    1131  147
##   medium  583    0
##   high      0  989
```

So we can look at both:

```
gx.shape = ggplot(s.shape, aes(pottery.patterned, simpson.diversityIndex))+
  geom_boxplot() +
  xlab("Patterned pottery") +
  ylab("Codability")+
  ggtitle("Codability of Shape")

gx.shape
```




```
gx.shape2 = ggplot(s.shape, aes(formal.schooling, simpson.diversityIndex))+
  geom_boxplot() +
  xlab("Formal Schooling") +
  ylab("Codability") +
  ggtitle("Codability of Shape")

gx.shape2
```



And use a mixed effects model to test the contribuion of each:

```
m.both = lmer(simpson.diversityIndex.log ~
       pottery.patterned +
       formal.schooling +
        (1 | Language) +
        (1 | Stimulus.code),
     data = s.shape)

m.noSchool = lmer(simpson.diversityIndex.log ~
       pottery.patterned +
        (1 | Language) +
        (1 | Stimulus.code),
     data = s.shape)

m.noPPottery = lmer(simpson.diversityIndex.log ~
       formal.schooling +
        (1 | Language) +
        (1 | Stimulus.code),
     data = s.shape)

anova(m.both,m.noSchool)
```

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

```
## Data: s.shape
## Models:
## m.noSchool: simpson.diversityIndex.log ~ pottery.patterned + (1 | Language) +
```

```
## m.noSchool:     (1 | Stimulus.code)
## m.both: simpson.diversityIndex.log ~ pottery.patterned + formal.schooling +
## m.both:     (1 | Language) + (1 | Stimulus.code)
##            Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## m.noSchool  5 864.60 884.56 -427.30   854.60
## m.both      7 861.83 889.77 -423.92   847.83 6.771      2    0.03386 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(m.both,m.noPPottery)
```

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

```
## Data: s.shape
## Models:
## m.noPPottery: simpson.diversityIndex.log ~ formal.schooling + (1 | Language) +
## m.noPPottery:     (1 | Stimulus.code)
## m.both: simpson.diversityIndex.log ~ pottery.patterned + formal.schooling +
## m.both:     (1 | Language) + (1 | Stimulus.code)
##              Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m.noPPottery  6 869.44 893.39 -428.72   857.44
## m.both        7 861.83 889.77 -423.92   847.83 9.6056      1    0.00194 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(m.both)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## simpson.diversityIndex.log ~ pottery.patterned + formal.schooling +
##     (1 | Language) + (1 | Stimulus.code)
##    Data: s.shape
##
## REML criterion at convergence: 854.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.73983 -0.68983  0.02328  0.68054  2.88331
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  Language      (Intercept) 0.1292   0.3595
##  Stimulus.code (Intercept) 0.1163   0.3410
##  Residual                  0.4070   0.6380
## Number of obs: 400, groups:  Language, 20; Stimulus.code, 20
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)          -0.574896   0.193048  -2.978
## pottery.patternedyes  1.305659   0.410185   3.183
## formal.schooling.L   -0.003141   0.292338  -0.011
## formal.schooling.Q   -0.499201   0.256664  -1.945
##
## Correlation of Fixed Effects:
##             (Intr) pttry. frm..L
## pttry.pttrn -0.787
```

```
## frml.schl.L  0.714 -0.882
## frml.schl.Q  0.469 -0.725  0.658
```

```
# R squared:
cor(s.shape$simpson.diversityIndex.log,predict(m.both))^2
```

```
##           [,1]
## [1,] 0.6122963
```

```
# M
tapply(s.shape$simpson.diversityIndex,s.shape$formal.schooling,mean)
```

```
##       low    medium      high
## 0.1946866 0.2803914 0.5109820
```

There was a significant main effect of schooling (log likelihood difference = 3.4 , df = 2 , Chi Squared = 6.77 , p = 0.034).

There was a significant main effect of patterned pottery (log likelihood difference = 4.8 , df = 1 , Chi Squared = 9.61 , p = 0.0019).

Specific hypotheses about shape

Natural objects have (mostly) organic rounded shapes. Living in square/rectangular houses should give more names for angular shaped objects. We test whether living in rounded houses predicts codability for angular shapes. Note that there is only one community which lives in round houses (Umpila). Umpila are Hunter-gatherers, who are not necessarily low-codability across the board (they have very high codability for smell).

```
s.shape$angularShapes = s.shape$Stimulus.code %in%
              c("shape.2 cubes",
                "shape.3 squares",
                'shape.cube',
                'shape.square',
                'shape.rectangle',
                'shape.rectangle 3D')
# Null model
m0 = lmer(simpson.diversityIndex.log ~
            1 +
            (1 | Language) +
            (1 +I(houses=="round")| Stimulus.code),
          data = s.shape[s.shape$angularShapes,])
# Add fixed effect
m1 = lmer(simpson.diversityIndex.log ~
            1 +
            I(houses=="round") +
            (1 | Language) +
            (1 +I(houses=="round")| Stimulus.code),
          data = s.shape[s.shape$angularShapes,])
anova(m0,m1)
```

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

```
## Data: s.shape[s.shape$angularShapes, ]
## Models:
## m0: simpson.diversityIndex.log ~ 1 + (1 | Language) + (1 + I(houses ==
## m0:     "round") | Stimulus.code)
```

```
## m1: simpson.diversityIndex.log ~ 1 + I(houses == "round") + (1 |
## m1:     Language) + (1 + I(houses == "round") | Stimulus.code)
##    Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0  6 256.70 273.43 -122.35   244.70
## m1  7 254.77 274.29 -120.39   240.77 3.9308      1    0.04741 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(m1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: simpson.diversityIndex.log ~ 1 + I(houses == "round") + (1 |
##     Language) + (1 + I(houses == "round") | Stimulus.code)
##    Data: s.shape[s.shape$angularShapes, ]
##
## REML criterion at convergence: 240.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.87221 -0.58415 -0.00682  0.59798  2.95397
##
## Random effects:
##  Groups        Name                        Variance Std.Dev. Corr
##  Language      (Intercept)                 0.645532 0.80345
##  Stimulus.code (Intercept)                 0.009365 0.09677
##                I(houses == "round")TRUE    0.017855 0.13362  -1.00
##  Residual                                  0.276179 0.52553
## Number of obs: 120, groups:  Language, 20; Stimulus.code, 6
##
## Fixed effects:
##                            Estimate Std. Error t value
## (Intercept)                -0.01047    0.19483  -0.054
## I(houses == "round")TRUE -1.69196    0.85495  -1.979
##
## Correlation of Fixed Effects:
##             (Intr)
## I(==="")TRUE -0.231
```

Very weak significant effect for communities with rounded houses to have less agreement on angular shapes than those living in angular houses. Mean codability for angular houses = 0.35153; mean codability for round houses = 0.0121212

```
gx.shape.house = ggplot(s.shape[s.shape$angularShapes,],
       aes(houses!="round",simpson.diversityIndex)) +
  xlab("House shape") +
  scale_x_discrete(labels=c("Round","Angular")) +
  ylab("Codability") +
  geom_boxplot()
```

Sound

Calculate the optimal decision tree, given variables related to shape:

```
s.sound = s[s$domain=='sound',]

rt.sound = REEMtree(simpson.diversityIndex~
          musical.instrument +
          specialist.musician+
          training.music+
          children.music+
          animal.sounds,
         random = ~1|Language,
         data = s.sound,
         MaxIterations=100000,
         tree.control = rpart.control(maxdepth = 1))
```

Sound Results

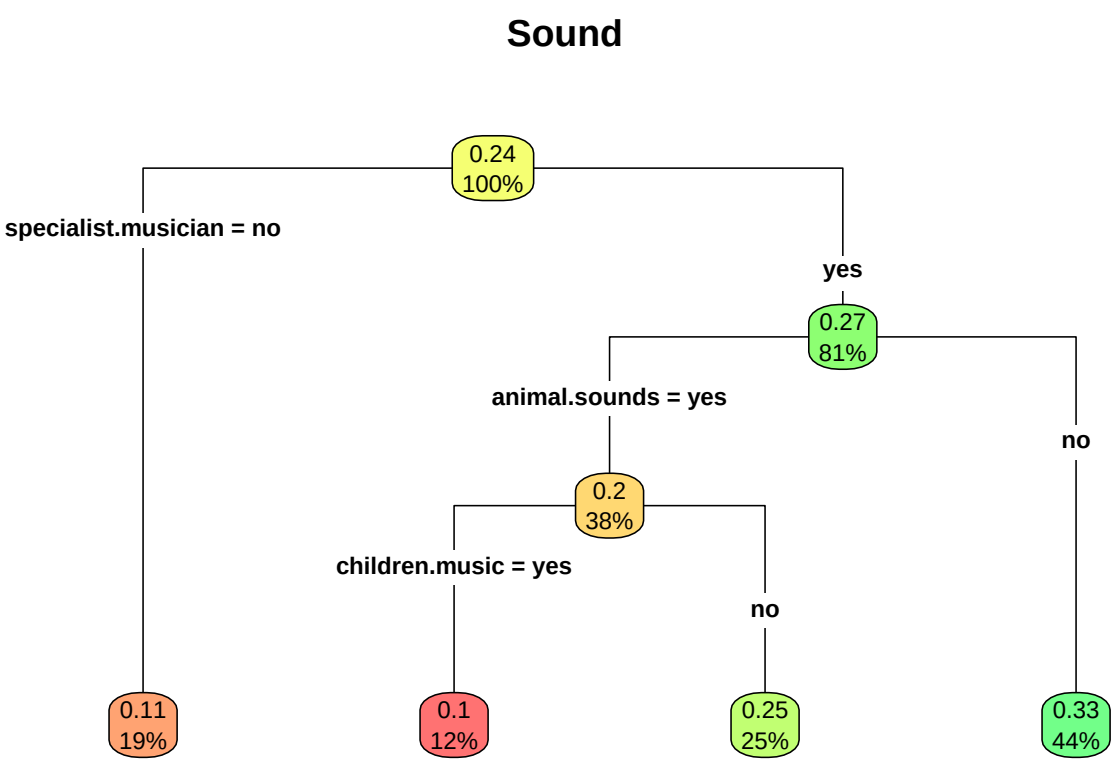
Proportion of variance explained:

```
# R squared
cor(predict.REEMtree(rt.sound,s.sound,id=s.sound$Language, EstimateRandomEffects = T),
    s.sound$simpson.diversityIndex)^2
```

```
## [1] 0.4052415
```

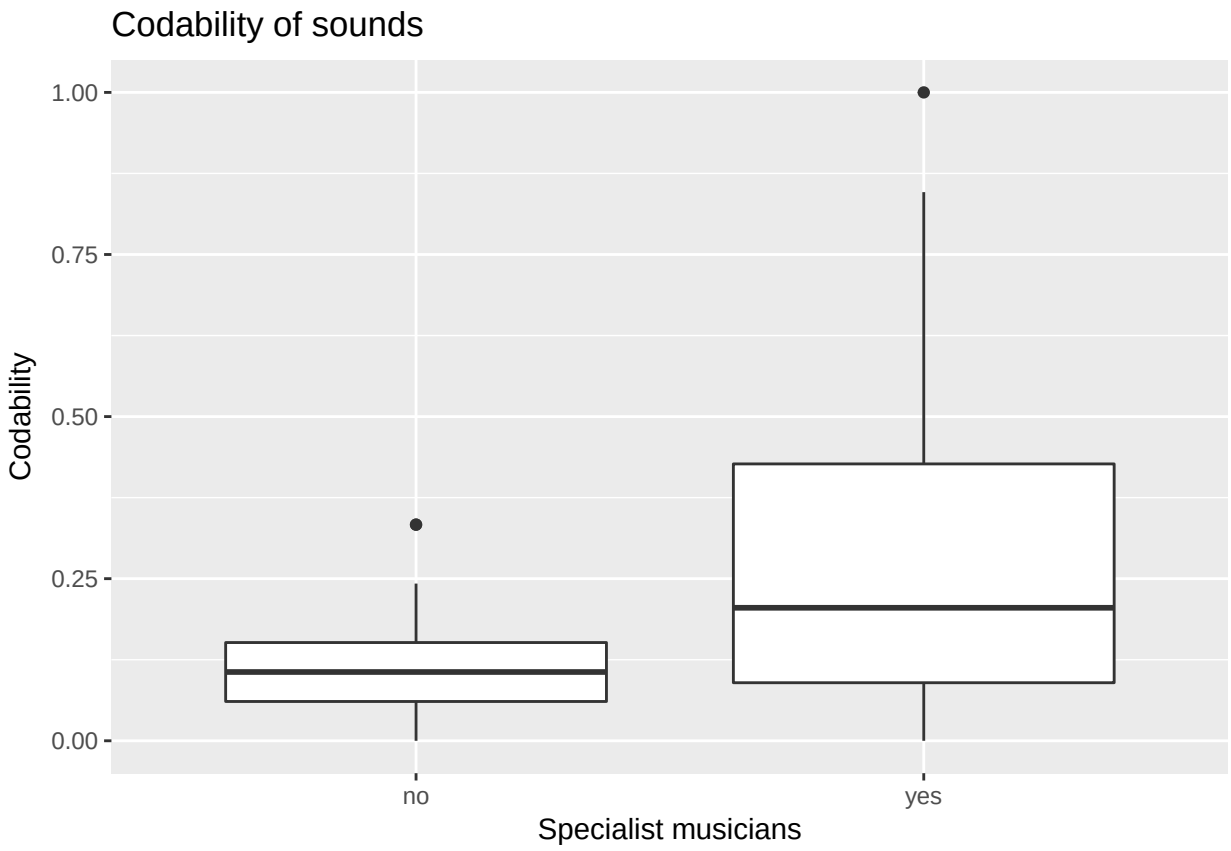
Plot the tree and calculate variable importance:

```
rpart.plot(tree(rt.sound), type=4,extra=100,
           branch.lty=1, box.palette="RdYlGn", main="Sound")
```



This suggests that the training of musicians and having specialist musicians is important. Training of musicians depends on having specialist musicians, so we concentrate on the latter.

```
gx.sound = ggplot(s.sound, aes(specialist.musician, simpson.diversityIndex))+
  geom_boxplot() +
  xlab("Specialist musicians") +
  ylab("Codability") +
  ggtitle("Codability of sounds")
gx.sound
```



Test with mixed effects modelling:

```
mSd.null = lmer(simpson.diversityIndex.log ~
       1 +
        (1 | Language) +
        (1 | Stimulus.code),
     data = s.sound)

mSd.music = lmer(simpson.diversityIndex.log ~
       1 +
         specialist.musician +
        (1 | Language) +
        (1 | Stimulus.code),
     data = s.sound)

anova(mSd.null, mSd.music)
```

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

```
## Data: s.sound
## Models:
## mSd.null: simpson.diversityIndex.log ~ 1 + (1 | Language) + (1 | Stimulus.code)
## mSd.music: simpson.diversityIndex.log ~ 1 + specialist.musician + (1 | Language) +
## mSd.music:     (1 | Stimulus.code)
##           Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mSd.null   4 540.57 555.64 -266.29   532.57
## mSd.music  5 538.47 557.31 -264.24   528.47 4.1008      1    0.04286 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#M
tapply(s.sound$simpson.diversityIndex,s.sound$specialist.musician,mean)
```

```
##        no       yes
## 0.1101010 0.2709464
```

Touch

Calculate the optimal decision tree, given variables related to shape:

```
s.touch = s[s$domain=='touch',]

rt.touch = REEMtree(simpson.diversityIndex~
          pulverise.spices +
          fine.surfaces.on.houses +
          professional.textures,
         random = ~1|Language,
         data = s.touch,
         MaxIterations=100000)
```

Touch Results

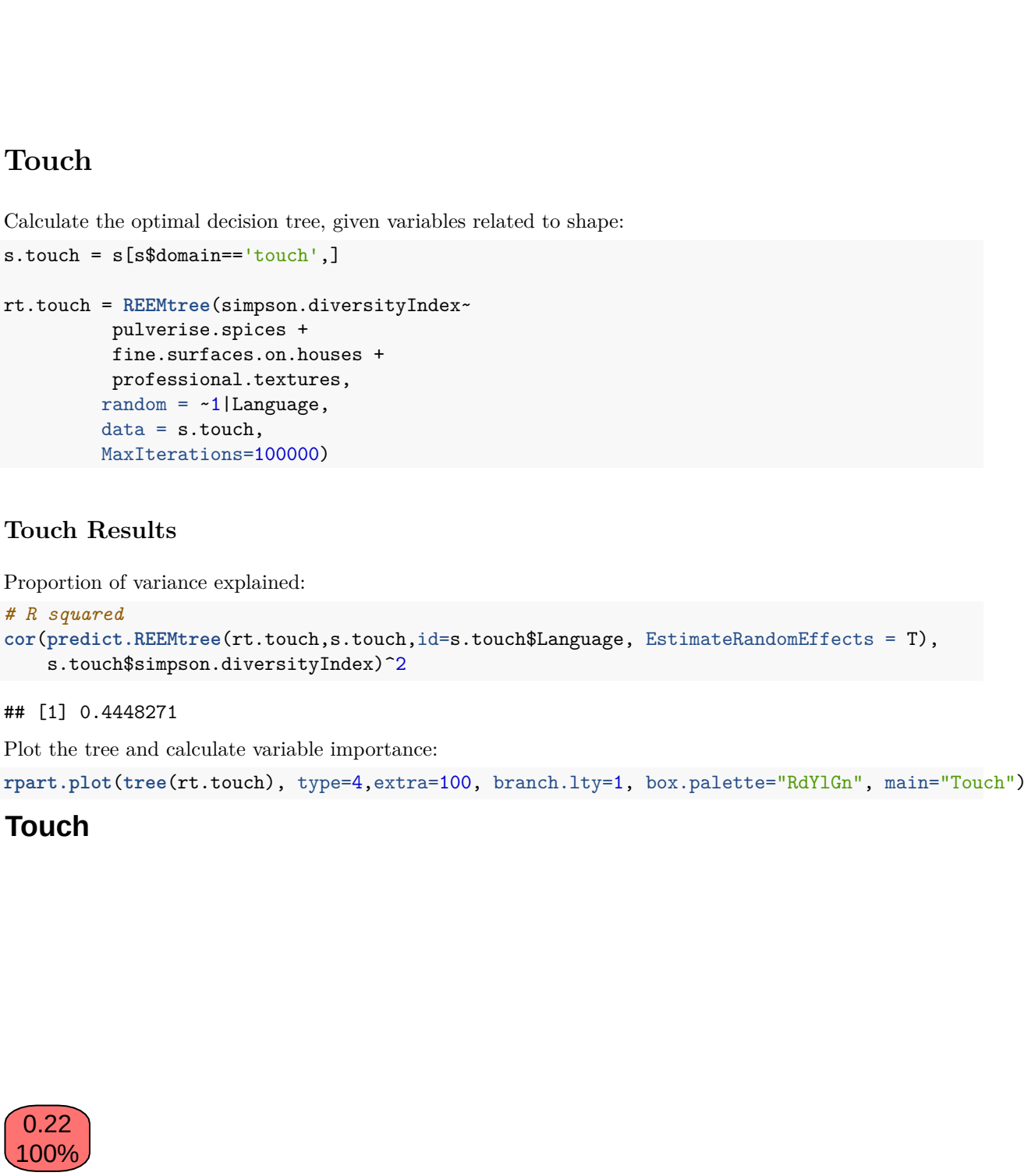
Proportion of variance explained:

```
# R squared
cor(predict.REEMtree(rt.touch,s.touch,id=s.touch$Language, EstimateRandomEffects = T),
    s.touch$simpson.diversityIndex)^2
```

```
## [1] 0.4448271
```

Plot the tree and calculate variable importance:

```
rpart.plot(tree(rt.touch), type=4,extra=100, branch.lty=1, box.palette="RdYlGn", main="Touch")
```




```
#varimp = rt.touch$Tree$variable.importance

#par(mar=c(5,10,2,2))
#barplot(sort(varimp), horiz=T, las=2,
#        xlab="Variable Importance")
#par(mar=c(5, 4, 4, 2) + 0.1)
```

There are no significant partitions for touch.

Taste

Calculate the optimal decision tree, given variables related to taste:

(some variables are co-linear, so we take out sweet.addivit ve and sour.additive)

```
s.taste = s[s$domain=='taste',]

rt.taste = REEMtree(simpson.diversityIndex~
         pulverise.spices+
         spices.herbs+
         num.additives.scaled +
         fragrant.food,
         random = ~1|Language,
         data = s.taste,
         MaxIterations=100000)
```

Taste Results

Proportion of variance explained:

```
# R squared
cor(predict.REEMtree(rt.taste,s.taste,id=s.taste$Language, EstimateRandomEffects = T),
    s.taste$simpson.diversityIndex)^2
```

```
## [1] 0.5397018
```

Plot the tree and calculate variable importance:

```
if(nrow(tree(rt.taste)$splits)>0){
  rpart.plot(tree(rt.taste), type=4,extra=100, branch.lty=1, box.palette="RdYlGn", main="Taste")
}

if(nrow(tree(rt.taste)$splits)>0){
  varimp = rt.taste$Tree$variable.importance

  par(mar=c(5,10,2,2))
  barplot(sort(varimp), horiz=T, las=2,
          xlab="Variable Importance")
  par(mar=c(5, 4, 4, 2) + 0.1)
}
```

No strong effect of number of additives in a full model:

```
mT.null = lmer(simpson.diversityIndex.log ~
       1 +
        (1 | Language) +
        (1 | Stimulus.code),
     data = s.taste)
mT.nA = lmer(simpson.diversityIndex.log ~
       1 + num.additives.scaled +
        (1 | Language) +
        (1 | Stimulus.code),
     data = s.taste)
anova(mT.null, mT.nA)
```

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

```
## Data: s.taste
## Models:
## mT.null: simpson.diversityIndex.log ~ 1 + (1 | Language) + (1 | Stimulus.code)
## mT.nA: simpson.diversityIndex.log ~ 1 + num.additives.scaled + (1 |
## mT.nA:     Language) + (1 | Stimulus.code)
##         Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mT.null  4 219.36 229.36 -105.68   211.36
## mT.nA    5 220.67 233.17 -105.33   210.67 0.6901      1     0.4061
```

Specific taste hypotheses

Does the codability of a specific taste correlate with having an additive for that taste?

```
tx = s.taste[s.taste$Stimulus.code=="taste.citric acide monohydrate (sour)",]
t.test(tx$simpson.diversityIndex ~ tx$sour.additive)
```

```
##
##  Welch Two Sample t-test
##
## data:  tx$simpson.diversityIndex by tx$sour.additive
## t = -1.3496, df = 15.841, p-value = 0.1961
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.30612907  0.06808546
## sample estimates:
##  mean in group no mean in group yes
##         0.3831169         0.5021387
```

```
tx = s.taste[s.taste$Stimulus.code=="taste.glutamate (umami)",]
t.test(tx$simpson.diversityIndex ~ tx$umami.additive)
```

```
##
##  Welch Two Sample t-test
##
## data:  tx$simpson.diversityIndex by tx$umami.additive
## t = -0.31073, df = 8.0573, p-value = 0.7639
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.4177380  0.3184188
## sample estimates:
##  mean in group no mean in group yes
##         0.3132727         0.3629323
```

```
tx = s.taste[s.taste$Stimulus.code=="taste.quinine hydrochloride (bitter)",]
t.test(tx$simpson.diversityIndex ~ tx$bitter.additive)
```

```
##
##  Welch Two Sample t-test
##
## data:  tx$simpson.diversityIndex by tx$bitter.additive
## t = -0.12993, df = 10.88, p-value = 0.899
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.4251373  0.3778017
## sample estimates:
```

```
##  mean in group no mean in group yes
##         0.5184787         0.5421466
```

```
tx = s.taste[s.taste$Stimulus.code=="taste.sodium chloride (salt)",]
t.test(tx$simpson.diversityIndex ~ tx$salt.additive)
```

```
##
##  Welch Two Sample t-test
##
## data:  tx$simpson.diversityIndex by tx$salt.additive
## t = -1.9499, df = 7.4425, p-value = 0.08972
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.45775223  0.04127946
## sample estimates:
##  mean in group no mean in group yes
##         0.3787879         0.5870242
```

```
tx = s.taste[s.taste$Stimulus.code=="taste.sucrose (sweet)",]
t.test(tx$simpson.diversityIndex ~ tx$sweet.additive)
```

```
##
##  Welch Two Sample t-test
##
## data:  tx$simpson.diversityIndex by tx$sweet.additive
## t = -1.3499, df = 1.7914, p-value = 0.3224
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -1.110774  0.624763
## sample estimates:
##  mean in group no mean in group yes
##         0.4053030         0.6483085
```

There are no specific taste effects.

Smell

```
s.smell = s[s$domain=='smell',]

rt.smell = REEMtree(simpson.diversityIndex~
          pulverise.spices+
          spices.herbs+
          fragrant.food +
          subsistance,
         random = ~1|Language,
         data = s.smell,
         MaxIterations=100000)
```

Smell Results

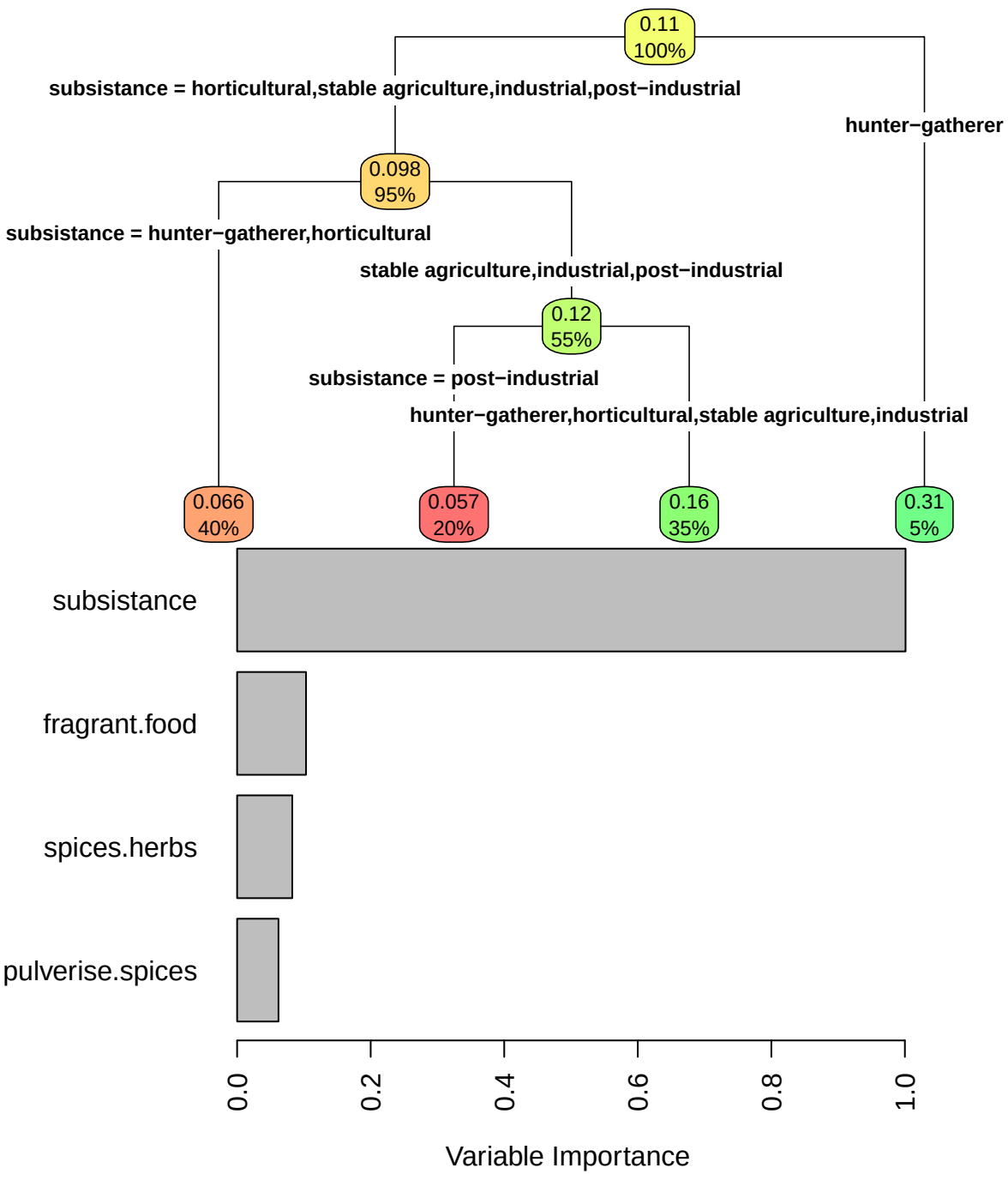
Proportion of variance explained:

```
# R squared
cor(predict.REEMtree(rt.smell,s.smell,id=s.smell$Language, EstimateRandomEffects = T),
    s.smell$simpson.diversityIndex)^2
```

```
## [1] 0.3861878
```

Plot the tree and calculate variable importance:

```
if(nrow(tree(rt.smell)$cptable)>1){
  rpart.plot(tree(rt.smell), type=4,extra=100, branch.lty=1, box.palette="RdYlGn", main="Smell")

  varimp = rt.smell$Tree$variable.importance

  par(mar=c(5,10,2,2))
  barplot(sort(varimp), horiz=T, las=2,
          xlab="Variable Importance")
  par(mar=c(5, 4, 4, 2) + 0.1)
}
```



Subsistance predicts codability. Particularly the hunter-gatherer langauge.

```
s.smell$subsistance = factor(s.smell$subsistance, levels=rev(levels(s.smell$subsistance)))
m0.smell = lmer(simpson.diversityIndex.log ~
        1 +
        (1 | Language) +
        (1 + subsistance | Stimulus.code),
```

```
    data = s.smell)

m1.smell = update(m0.smell, ~. + subsistance)
anova(m0.smell,m1.smell)
```

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

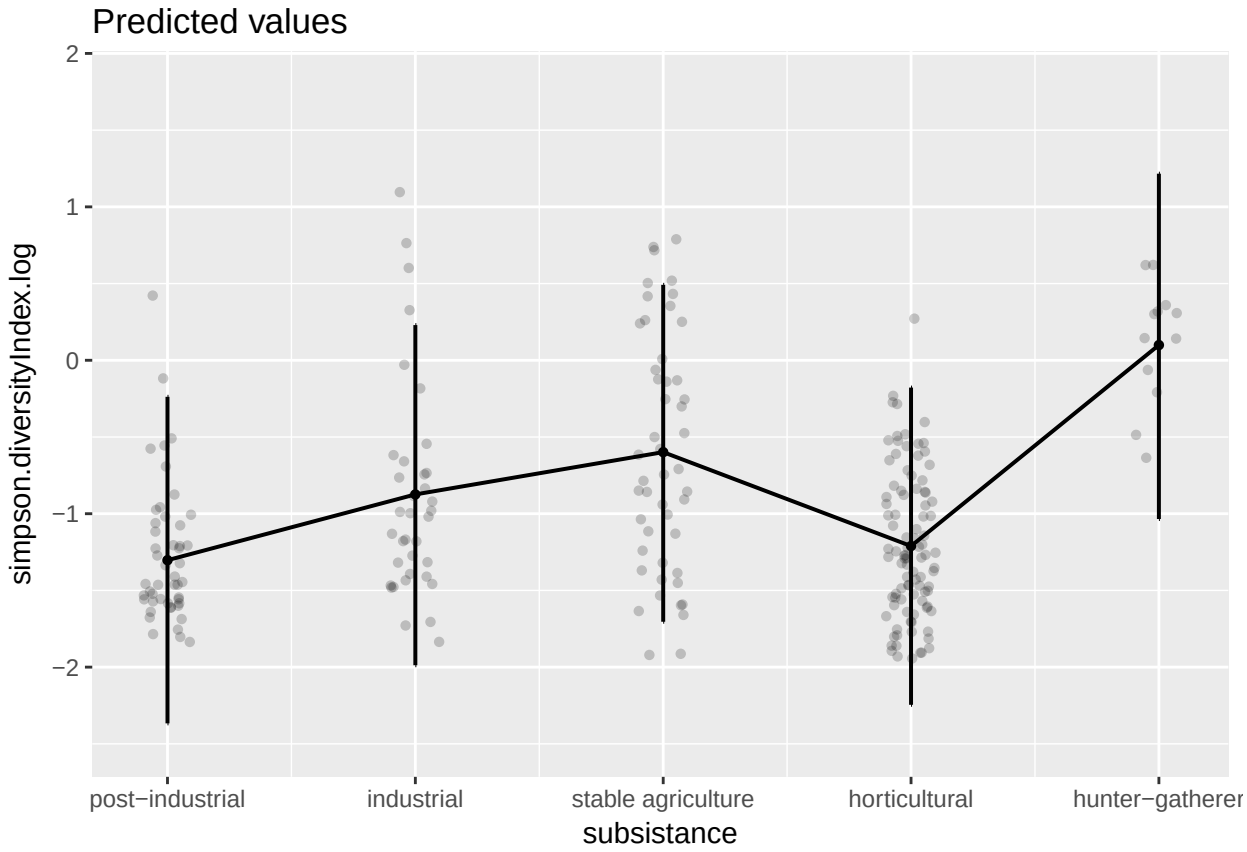
```
## Data: s.smell
## Models:
## m0.smell: simpson.diversityIndex.log ~ 1 + (1 | Language) + (1 + subsistance |
## m0.smell:     Stimulus.code)
## m1.smell: simpson.diversityIndex.log ~ (1 | Language) + (1 + subsistance |
## m1.smell:     Stimulus.code) + subsistance
##          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0.smell 18 432.62 495.27 -198.31   396.62
## m1.smell 22 416.96 493.53 -186.48   372.96 23.659      4  9.348e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(m1.smell)
```

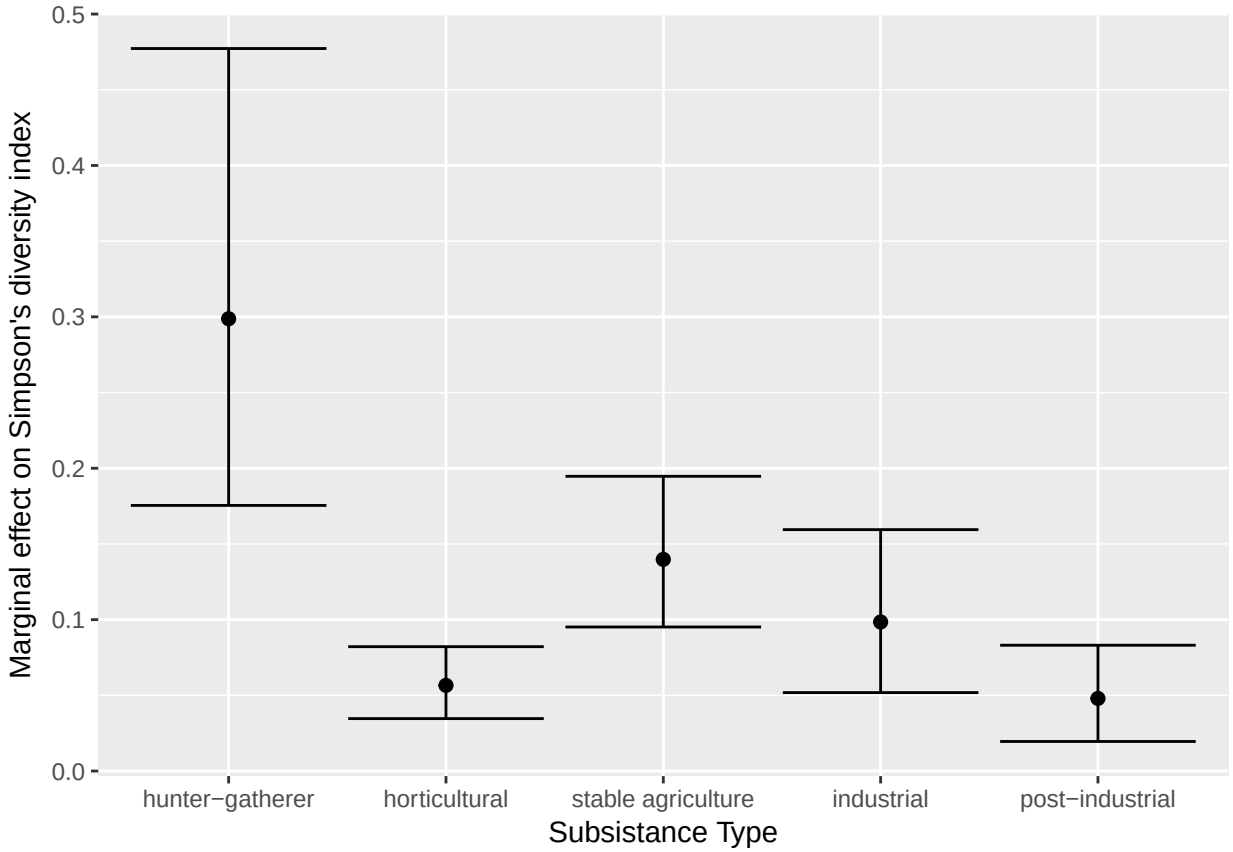
```
## Linear mixed model fit by REML ['lmerMod']
## Formula: simpson.diversityIndex.log ~ (1 | Language) + (1 + subsistance |
##     Stimulus.code) + subsistance
##    Data: s.smell
##
## REML criterion at convergence: 384.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3109 -0.6086 -0.1843  0.5665  2.7232
##
## Random effects:
##  Groups        Name          Variance Std.Dev. Corr
##  Language      (Intercept)   0.04893  0.2212
##  Stimulus.code (Intercept)   0.05062  0.2250
##                subsistance.L 0.02622  0.1619   -0.73
##                subsistance.Q 0.01212  0.1101    0.20 -0.82
##                subsistance.C 0.01019  0.1009    0.99 -0.81  0.32
##                subsistance^4 0.07803  0.2793   -0.57  0.98 -0.92 -0.67
##  Residual                    0.22559  0.4750
## Number of obs: 240, groups:  Language, 20; Stimulus.code, 12
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)   -0.77520    0.09759  -7.943
## subsistance.L  0.78019    0.19787   3.943
## subsistance.Q  0.25163    0.17959   1.401
## subsistance.C  0.65474    0.14742   4.441
## subsistance^4  0.42002    0.15335   2.739
##
## Correlation of Fixed Effects:
##             (Intr) sbss.L sbss.Q sbss.C
## subsistnc.L  0.172
## subsistnc.Q  0.342  0.483
```

```
## subsistnc.C  0.478  0.330  0.246
## subsistnc^4 -0.101  0.318  0.019 -0.174
```

```
sjp.lmer(m1.smell, 'pred', "subsistance", show.ci = T)
```




```
gx = sjp.lmer(m1.smell, 'eff', show.ci = T, prnt.plot = F)
subsd = gx$plot$data
subsd$`Subsistance Type` = factor(subsd$label,
          levels = c("hunter-gatherer","horticultural",
                     'stable agriculture','industrial',
                     "post-industrial"), ordered = T)

convertSimps = function(X){
  exp(X * attr(s$simpson.diversityIndex.log,'scaled:scale') +
    attr(s$simpson.diversityIndex.log,'scaled:center'))-0.1
}

subsd$y = convertSimps(subsd$y)
subsd$lower = convertSimps(subsd$lower)
subsd$upper = convertSimps(subsd$upper)

ggplot(subsd,
       aes(`Subsistance Type`, y)) +
  geom_point(size=2) +
  geom_errorbar(aes(ymin = lower, ymax = upper)) +
  ylab("Marginal effect on Simpson's diversity index")
```




```
# Raw data
gx.smell = ggplot(s[s$domain=="smell",],
       aes(subsistance=="hunter-gatherer", simpson.diversityIndex)) +
  geom_boxplot() +
  xlab("Subsistance Type") +
  ylab("Codability") +
  scale_x_discrete(labels=c("Other","Hunter-gatherer")) +
  coord_cartesian(ylim=c(0,1))
```

```
# M
tapply(s.smell$simpson.diversityIndex,s.smell$subsistance,mean)
```

```
##    post-industrial         industrial stable agriculture
##         0.05675500         0.12930588         0.17779720
##      horticultural    hunter-gatherer
##         0.06604194         0.31296296
```

```
tapply(s.smell$simpson.diversityIndex,s.smell$subsistance=='hunter-gatherer',mean)
```

```
##      FALSE       TRUE
## 0.09760326 0.31296296
```

Relationship with latitude:

```
m0.smell = lmer(simpson.diversityIndex.log ~
        1  +
        (1 | Language) +
        (1 + I(abs(latitude)) | Stimulus.code),
     data = s.smell)
```

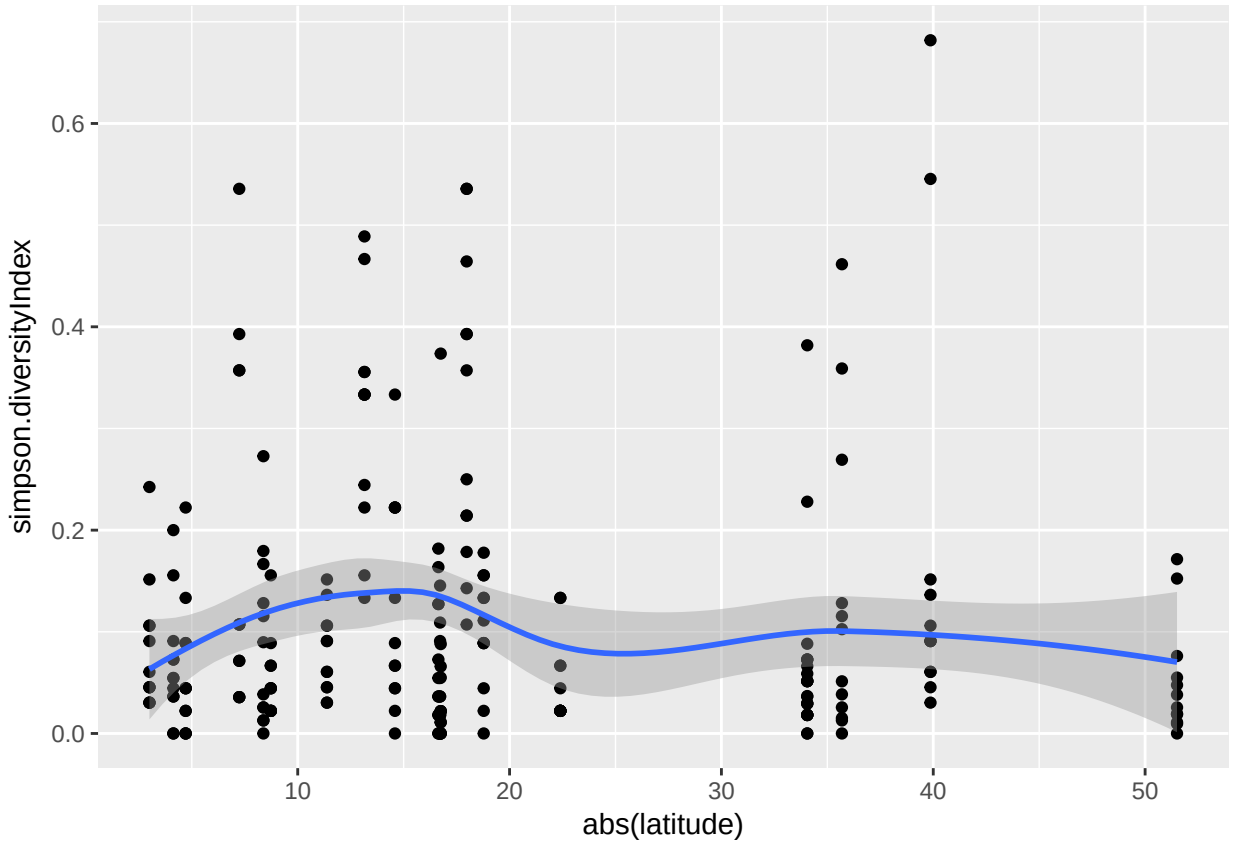
```
m1.smell = update(m0.smell, ~. +I(abs(latitude)))
m2.smell = update(m1.smell, ~. +I(abs(latitude)^2))

anova(m0.smell, m1.smell,m2.smell)
```

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

```
## Data: s.smell
## Models:
## m0.smell: simpson.diversityIndex.log ~ 1 + (1 | Language) + (1 + I(abs(latitude)) |
## m0.smell:     Stimulus.code)
## m1.smell: simpson.diversityIndex.log ~ (1 | Language) + (1 + I(abs(latitude)) |
## m1.smell:     Stimulus.code) + I(abs(latitude))
## m2.smell: simpson.diversityIndex.log ~ (1 | Language) + (1 + I(abs(latitude)) |
## m2.smell:     Stimulus.code) + I(abs(latitude)) + I(abs(latitude)^2)
##           Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0.smell   6 408.97 429.85 -198.48   396.97
## m1.smell   7 410.83 435.20 -198.42   396.83 0.1329      1     0.7155
## m2.smell   8 412.20 440.05 -198.10   396.20 0.6325      1     0.4264
```

```
ggplot(s.smell, aes(abs(latitude), simpson.diversityIndex)) +
  geom_point() + geom_smooth()
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



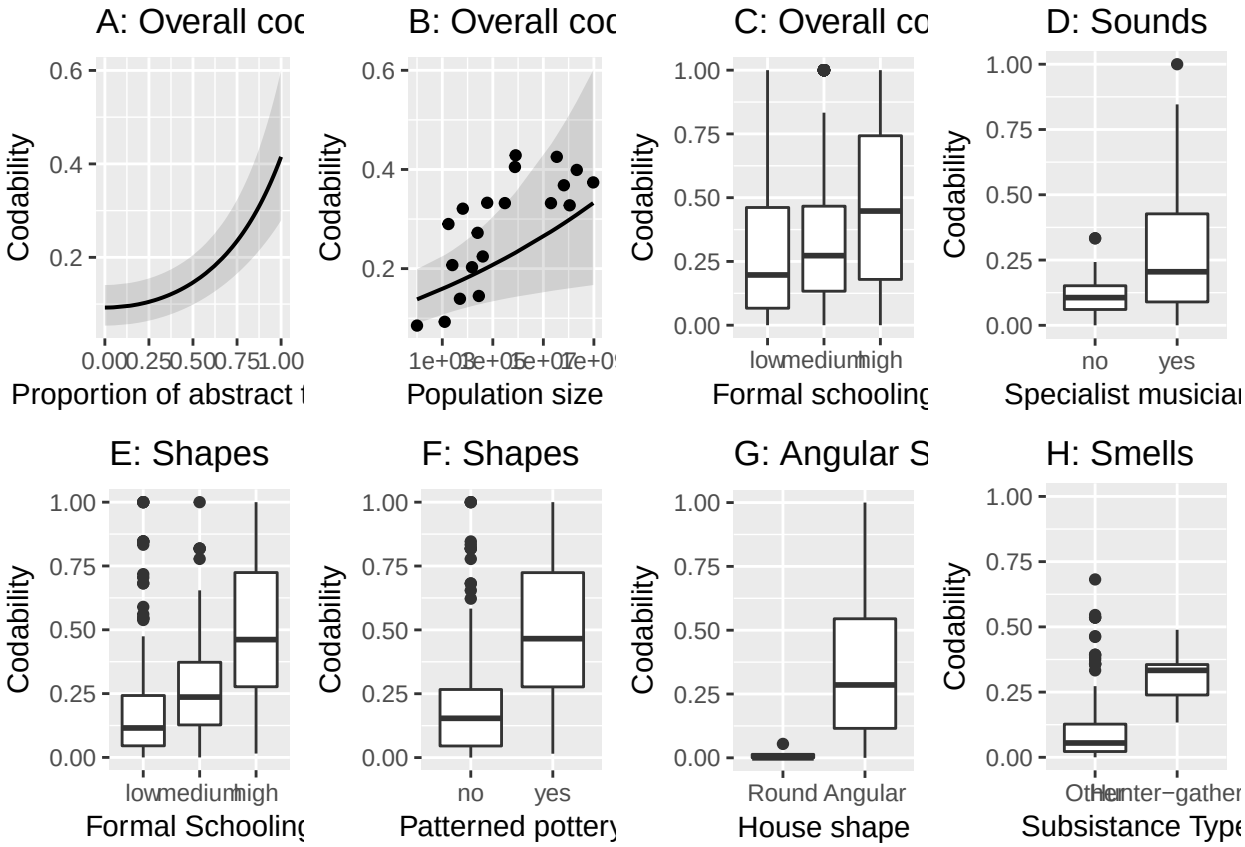
No significant relationship with latitude.

Extra Graphs

```
pdf("../results/graphs/Diversity_by_population.pdf", width=6, height=6)
gx.pop
dev.off()
```

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

```
load("../results/graphs/Codability_by_AbstractUse_ggplot.RDat")
gx.abstractTerms = px
gx.abstractTerms =  gx.abstractTerms+ theme(strip.text = element_blank())
gx.abstractTerms$theme$plot.title = gx.pop$theme$plot.title


gx2b = grid.arrange(
        gx.abstractTerms + ggtitle("A: Overall codability"),
        gx.pop + ggtitle("B: Overall codability"),
        gg.formalschooling + ggtitle("C: Overall codability"),
        gx.sound + ggtitle("D: Sounds"),
        gx.shape2 + ggtitle("E: Shapes"),
        gx.shape + ggtitle("F: Shapes"),
        gx.shape.house + ggtitle("G: Angular Shapes"),
        gx.smell +ggtitle("H: Smells"),
        layout_matrix = rbind(c(1,2,3,4),c(5,6,7,8)))
```



```
pdf("../results/graphs/Diversity_plots.pdf", width=10, height=6)
plot(gx2b)
dev.off()
```

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

```
setEPS()
postscript("../results/graphs/Diversity_plots.eps", width=10, height=6)
gx2b
```

```
## TableGrob (2 x 4) "arrange": 8 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (1-1,3-3) arrange gtable[layout]
## 4 4 (1-1,4-4) arrange gtable[layout]
## 5 5 (2-2,1-1) arrange gtable[layout]
## 6 6 (2-2,2-2) arrange gtable[layout]
## 7 7 (2-2,3-3) arrange gtable[layout]
## 8 8 (2-2,4-4) arrange gtable[layout]
```

```
dev.off()
```

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

S7: SAE tests

SAE tests

Contents

Load libraries

```
library(party)
library(rpart.plot)
library(MCMCglmm)
library(RColorBrewer)
library(ggplot2)
library(scales)
library(reshape2)
library(lme4)
library(MuMIn)
library(dplyr)
```

Load data

```
# Load data
d = read.csv("../data/AllData_LoP.csv", stringsAsFactors = F)

# Get rid of non-responses
d = d[!is.na(d$head),]
d = d[!d$head %in% c("n/a","no description"),]
d = d[!is.na(d$SAE),]

d.all = d
```

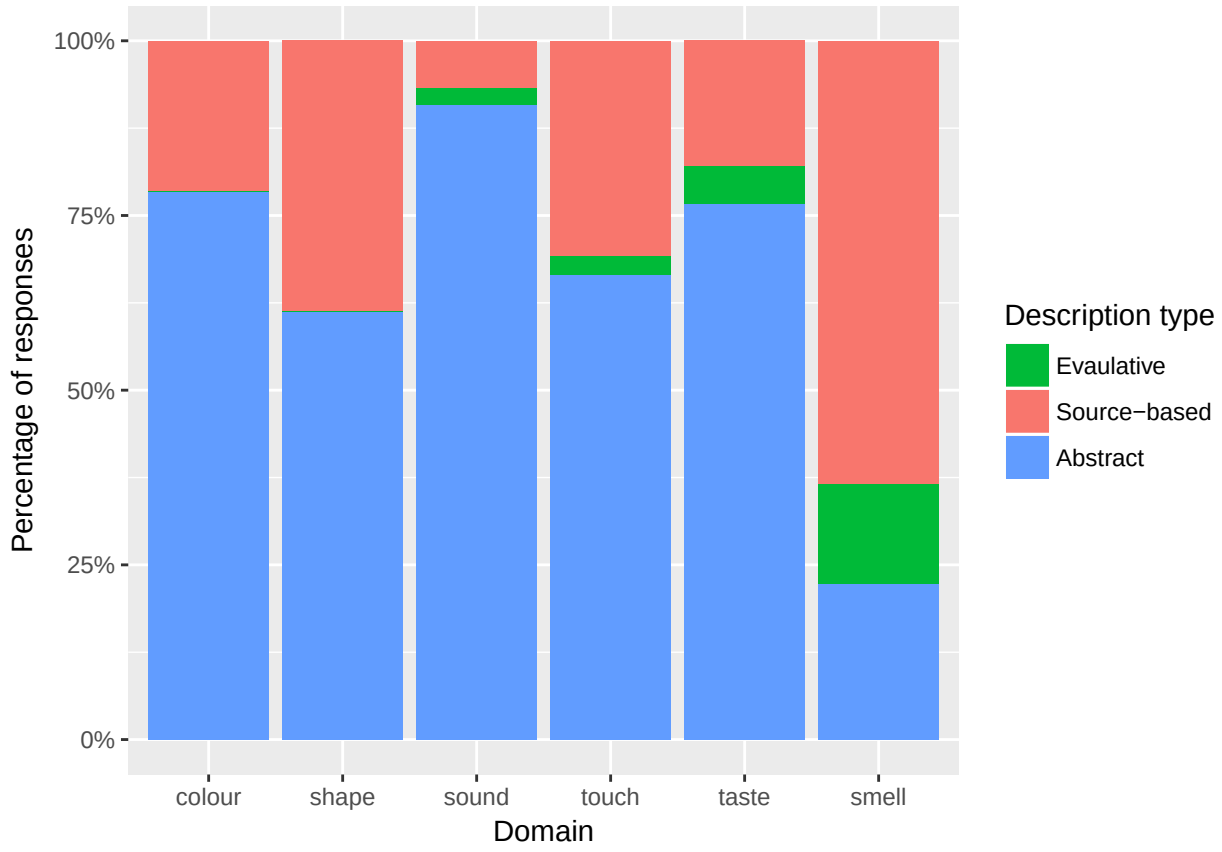
Are different kinds of responses more likely for different domains?

Different domains are more or less likely to use different types of description (look at first responses only):

```
d = d[d$Response==1,]

d$SAE = as.factor(d$SAE)

#sae.order = names(sort(tapply(d$SAE,d$domain, function(X){sum(X=="A")/length(X)}),decreasing = T))
# Make colour baseline
sae.order = c("colour","shape","sound","touch","taste","smell")

d$domain = factor(d$domain, levels = sae.order)

tx = table(d$SAE,d$domain)
tx2 =melt(prop.table(tx,margin = 2))
tx2$Var1 = factor(tx2$Var1, levels = c("S","E","A"))

gx = ggplot(tx2,aes(x = Var2, y = value,fill = Var1)) +
  geom_bar(position = "fill",stat = "identity") +
  scale_y_continuous(labels = percent_format()) +
  xlab("Domain") + ylab("Percentage of responses") +
  scale_fill_discrete(name = "Description type",
                      breaks = c("E","S", "A"),
                      labels=c("Evaulative","Source-based","Abstract"))

pdf("../results/graphs/SAE_RawProportions.pdf")
gx
dev.off()
```

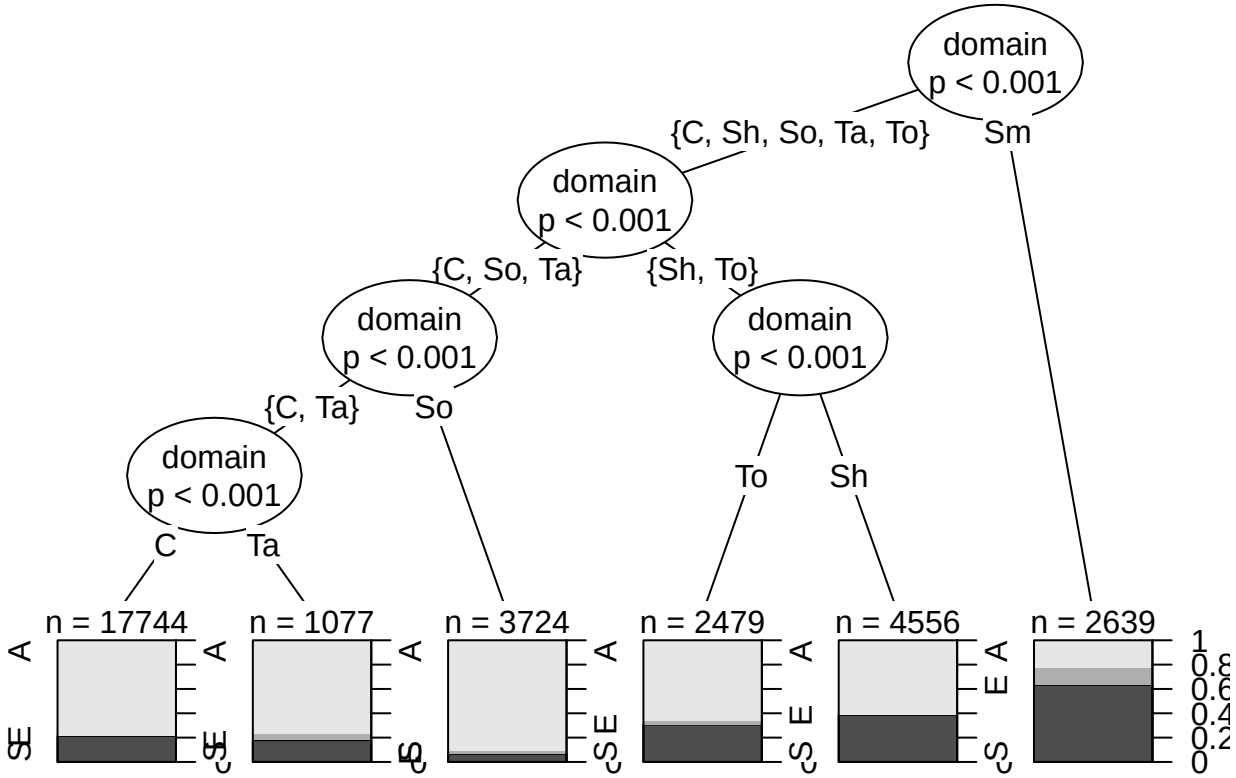
```
## pdf
##   2
```

```
gx
```



We can look for clusters using a simple decision tree (though this doesn't control for random effects):

```
d2 = d
d2$domain = factor(d2$domain,
  levels=c("colour","shape","smell","sound","taste",'touch'),
  labels=c("C","Sh","Sm","So","Ta","To"))
d2$SAE = as.factor(d2$SAE)
rt.sae = ctree(SAE~
          domain,
         data = d2)
plot(rt.sae,
  terminal_panel=node_barplot(rt.sae,
  beside = F,id=F, ylines=1),
  ip_args=list(cex=0.5),
  inner_panel = node_inner(rt.sae,id=F))
```

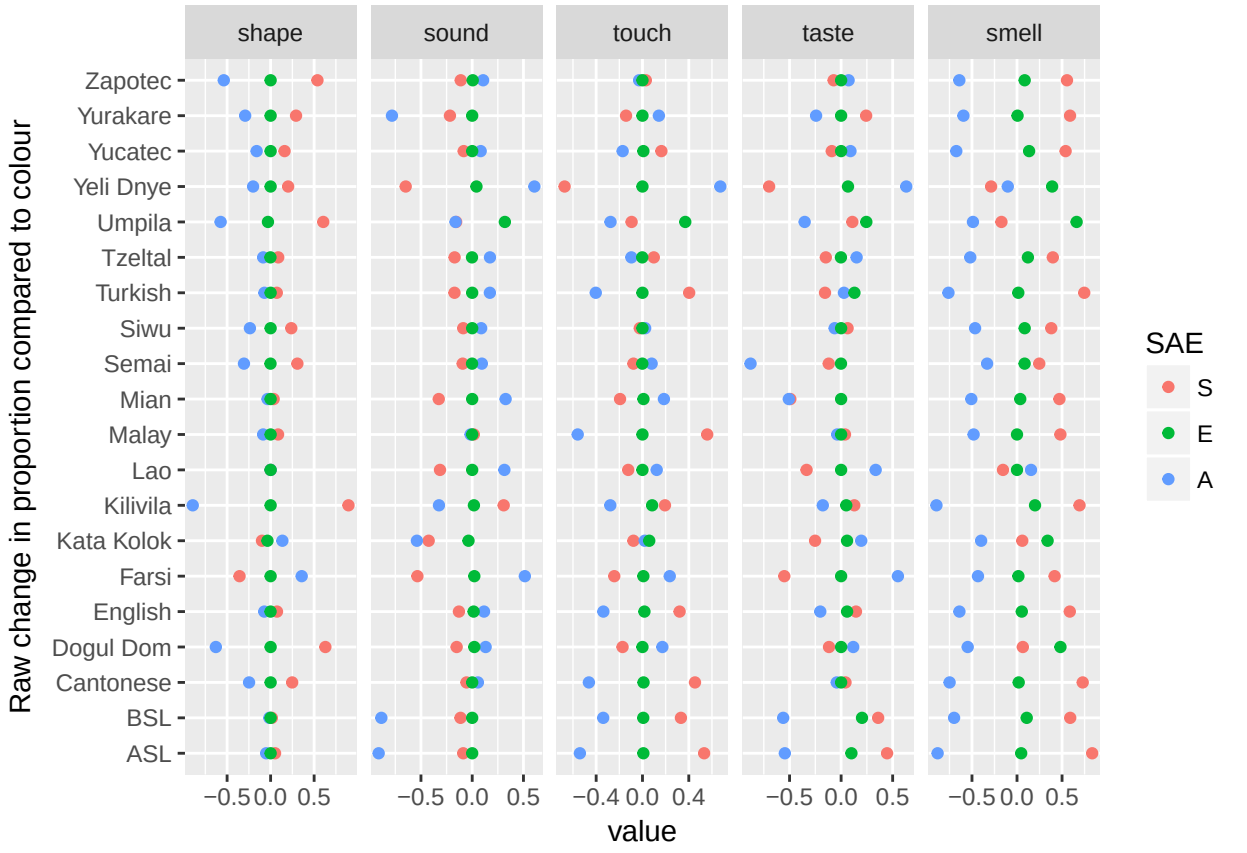



```
prop = d %>% group_by(Language,domain,SAE) %>%
  summarise (n = n()) %>%
  mutate(prop = n / sum(n))
```

```
## Warning: package 'bindrcpp' was built under R version 3.3.2
```

```
res = data.frame(Language=NA,SAE=NA,shape=0,sound=0,touch=0,taste=0,smell=0)

for(lang in unique(prop$Language)){
  for(saex in c("S","A","E")){
    dx = prop[prop$Language==lang & prop$SAE==saex,]
    px = dx$prop[match(c("colour","shape",'sound','touch','taste','smell'),dx$domain)]
    px[is.na(px)] = 0
    res = rbind(res,
                c(lang, saex,
                  (px[2:6] - px[1]) # difference between colour and other domains
                  ))
  }
}
res = res[2:nrow(res),]
for(i in 3:7){
  res[,i] = as.numeric(res[,i])
}

res2 = melt(res, id=c("Language","SAE"))

res2$SAE = factor(res2$SAE,levels=c("S","E",'A'))

gx = ggplot(res2,
            aes(x=Language, y=value, colour=SAE)) +
```

```
  geom_point() +
  coord_flip() +
  facet_grid(.~variable, scales = 'free_x') +
  xlab("Raw change in proportion compared to colour")

gx
```



MCMCglmm

Because there are three possible categories of response, a categorical model is needed. In addition, there are multiple random effects in the design. Therefore, we use the `MCMCglmm` package which can handle this situation. The framework is similar to an `lme4` mixed effects model, except that estimation is done using a Monte Carlo Markov Chain which converges on a good fit over a number of iterations.

Set the random seed for replicability:

```
set.seed(328)
```

(the code below is actually processed on a cluster computer, but shown here for posterity)

```
k <- length(levels(d$SAE))
I <- diag(k-1)
J <- matrix(rep(1, (k-1)^2), c(k-1, k-1))

prior.m <- list(
  R = list(fix=1, V=0.5 * (I + J), n = 2),
  G=list(
```

```
        #Language
        G1=list(V =diag(1),n=1),  # set to 2 for RSlope
        # Stimulus.code
        G2=list(V =diag(1),n=1),
        # consultant
        G3=list(V =diag(1),n=1)))

randomLang.model <- MCMCglmm(
  SAE ~ -1 + trait * domain,
  ~ us(1):Language +
    us(1):Stimulus.code +
    us(1):consultant,
  data   = d,
  rcov = ~ us(trait):units,
  family = "categorical",
  prior  = prior.m,
  thin   =      10,
  burnin =   10000,
  nitt   =  110000,
  verbose = F)

save(m.mcmcglmm, file="../results/SAE_mcmc_model.rdat")
```

Model with no random effect for language:

```
prior.m <- list(
  R = list(fix=1, V=0.5 * (I + J), n = 2),
  G=list(
    #Language
    #G1=list(V =diag(1),n=1),
    # Stimulus.code
    G1=list(V =diag(1),n=1),
    # consultant
    G2=list(V =diag(1),n=1)))
m.mcmcglmm <- MCMCglmm(
  SAE ~ -1 + trait * domain,
  ~ us(1):Stimulus.code +
    us(1):consultant,
  data   = d,
  rcov = ~ us(trait):units,
  family = "categorical",
  prior  = prior.m,
  thin   =  10,
  burnin =   10000,
  nitt   =  510000,
  verbose = T)

save(m.mcmcglmm, file="../results/SAE_mcmc_model_full_long_noLanguage.rdat")
```

Model with interaction between langauge and domain (random slopes for domain by language):

```
prior.m <- list(
  R = list(fix=1, V=0.5 * (I + J), n = 2),
  G=list(
    #Language
```

```
    G1=list(V =diag(6),n=6),  # One level for each domain
    # Stimulus.code
    G2=list(V =diag(1),n=1),
    # consultant
    G3=list(V =diag(1),n=1)))

m.mcmcglmm <- MCMCglmm(
  SAE ~ -1 + trait * domain,
  ~ us(1+domain):Language +
    us(1):Stimulus.code +
    us(1):consultant,
  data   = d,
  rcov = ~ us(trait):units,
  family = "categorical",
  prior  = prior.m,
  thin   =      100,
  burnin =   600000,
  nitt   =  5600000,
  verbose = T)
save(m.mcmcglmm, file="../results/SAE_mcmc_model_full_long_RSlope.rdat")
```

Compare models

We ran three models: With no random effect for language, with a random intercept for language and with a random slope for domain by language (interaction).

Load the models:

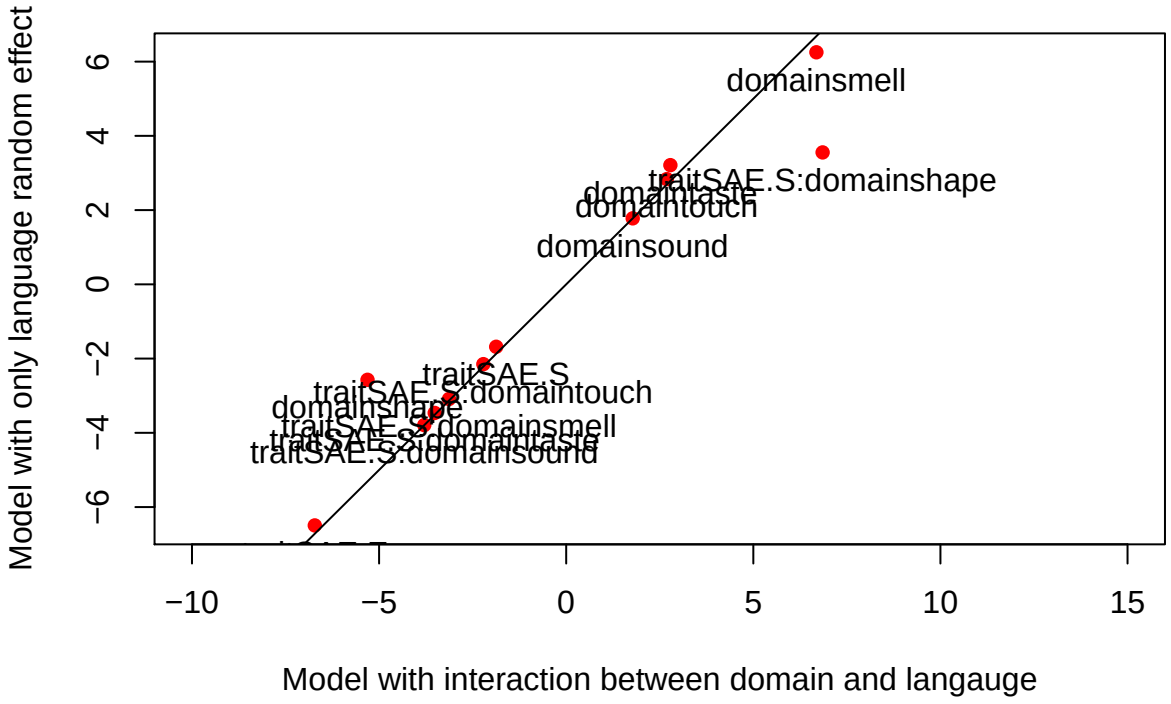
```
load("../results/SAE_mcmc_model_full.rdat")
randomLang.model = m.mcmcglmm
load("../results/SAE_mcmc_model_full_long_noLanguage.rdat")
noLang.model = m.mcmcglmm
load("../results/SAE_mcmc_model_full_long_RSlope_longBurnin_2.rdat")
interaction.model = m.mcmcglmm
```

```
model.sel(randomLang.model,noLang.model,interaction.model, rank="DIC")
```

```
## Model selection table
##                   dmn trt dmn:trt                      random df    logLik
## interaction.model   +   +       + u(1+d):L+u(1):S.cd+u(1):cn 22 -12470.50
## noLang.model        +   +       +          u(1):S.cd+u(1):cn 16 -13887.10
## randomLang.model    +   +       +   u(1):L+u(1):S.cd+u(1):cn 17 -13901.22
##                       DIC   delta weight
## interaction.model 28597.4    0.00      1
## noLang.model      31811.4 3214.06      0
## randomLang.model  31835.8 3238.39      0
## Models ranked by DIC(x)
## Random terms:
## u(1+d):L+u(1):S.cd+u(1):cn = '~us(1 + domain):Language + us(1):Stimulus.code + us(1):consultant'
## u(1):S.cd+u(1):cn = '~us(1):Stimulus.code + us(1):consultant'
## u(1):L+u(1):S.cd+u(1):cn = '~us(1):Language + us(1):Stimulus.code + us(1):consultant'
```

The model with a random slope for domain by language is the best. It's a considerable jump in log likelihood. However, looking at the fixed effects estimates, they are very similar between the model with and without random slopes for languages. The main difference is for shape:

```
interaction.model.coef = as.data.frame(summary(interaction.model)$solutions)
randomLang.model.coef = as.data.frame(summary(randomLang.model)$solutions)

plot(interaction.model.coef$post.mean,
     randomLang.model.coef[rownames(interaction.model.coef),]$post.mean,
     xlim=c(-10,15), col=2, pch=16,
     xlab="Model with interaction between domain and langauge",
     ylab="Model with only language random effect")
text(interaction.model.coef$post.mean,
     randomLang.model.coef[rownames(interaction.model.coef),]$post.mean,
      rownames(interaction.model.coef),
     pos=1)
abline(0,1)
```



Final model:

```
final.model = interaction.model
```

Plot the model convergence traces (Render as png to save space):

```
# Fixed effects:
for(i in seq(1,12,by=4)){
  png(paste0("../results/MCMCConvergence_",i,".png"))
  plot(final.model$Sol[,i:min((i+3),12)])
  dev.off()
}
# Some selected random slopes
c1 = c("(Intercept):(Intercept).Language",
  "(Intercept):(Intercept).Stimulus.code",
  "(Intercept):(Intercept).consultant")

c2a = c("(Intercept):domainshape.Language",
  "(Intercept):domainsound.Language",
  "(Intercept):domaintouch.Language")
c2b = c("(Intercept):domaintaste.Language",
  "(Intercept):domainsmell.Language")

png("../results/MCMCConvergence1.png")
plot(final.model$VCV[,c1])
dev.off()
```

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

```
png("../results/MCMCConvergence2a.png")
plot(final.model$VCV[,c2a])
dev.off()
```

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

```
png("../results/MCMCConvergence2b.png")
plot(final.model$VCV[,c2b])
dev.off()
```

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

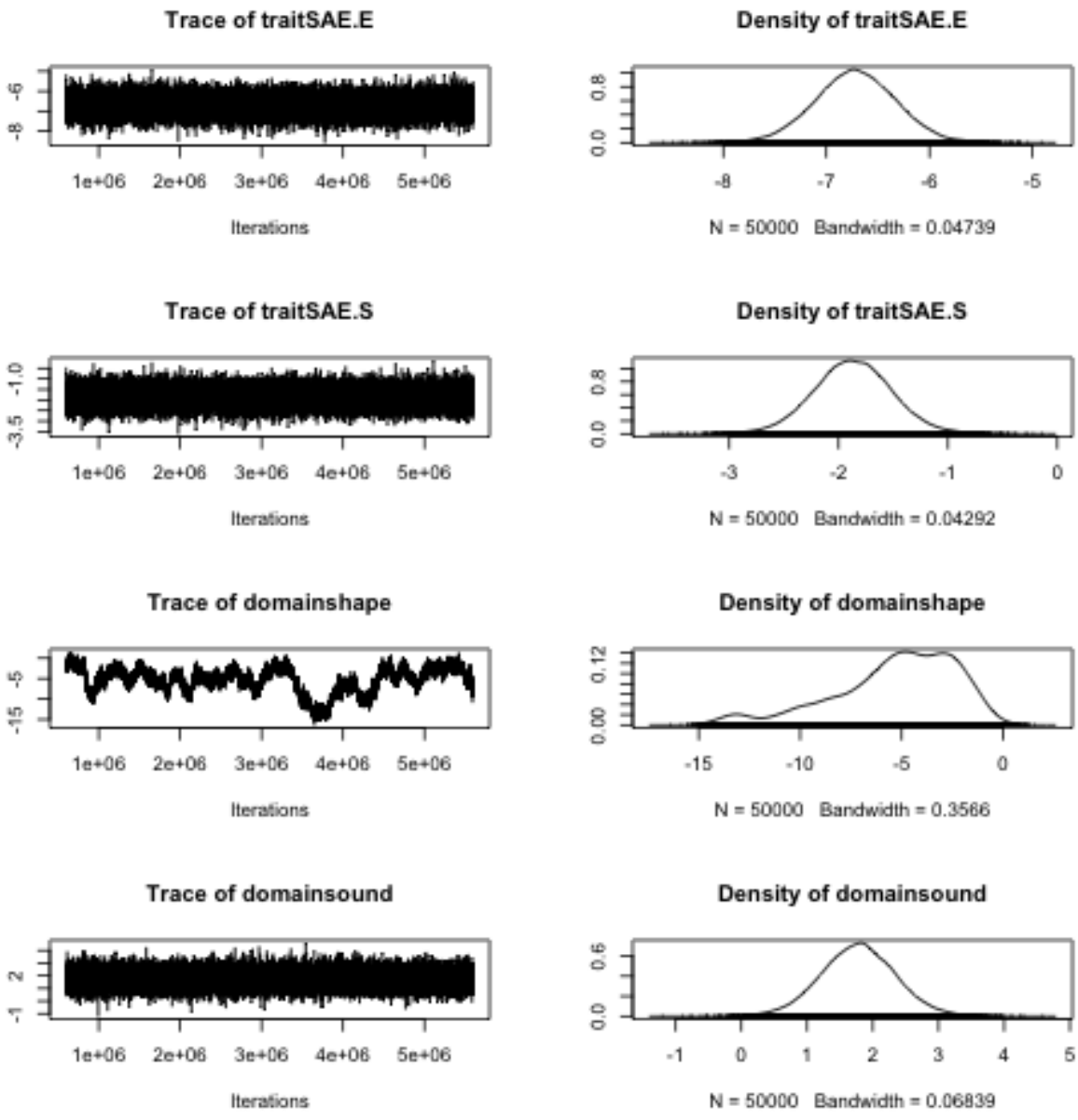


Figure 1:

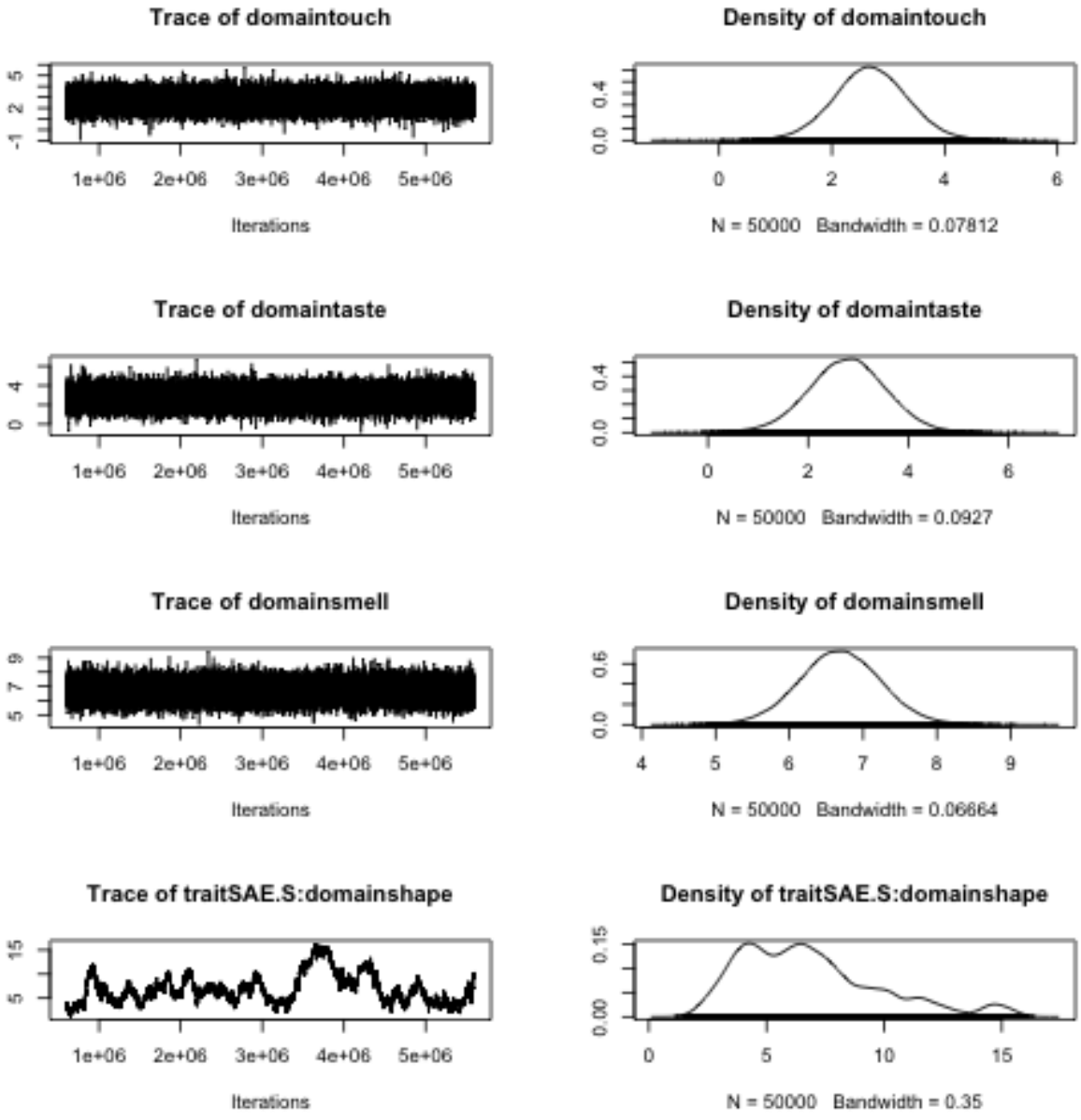

Trace of domaintouch
Density of domaintouch
Iterations
N = 50000 Bandwidth = 0.07812
Trace of domaintaste
Density of domaintaste
Iterations
N = 50000 Bandwidth = 0.0927
Trace of domainsmell
Density of domainsmell
Iterations
N = 50000 Bandwidth = 0.06664
Trace of traitSAE.S:domainshape
Density of traitSAE.S:domainshape
Iterations
N = 50000 Bandwidth = 0.35

Figure 2:

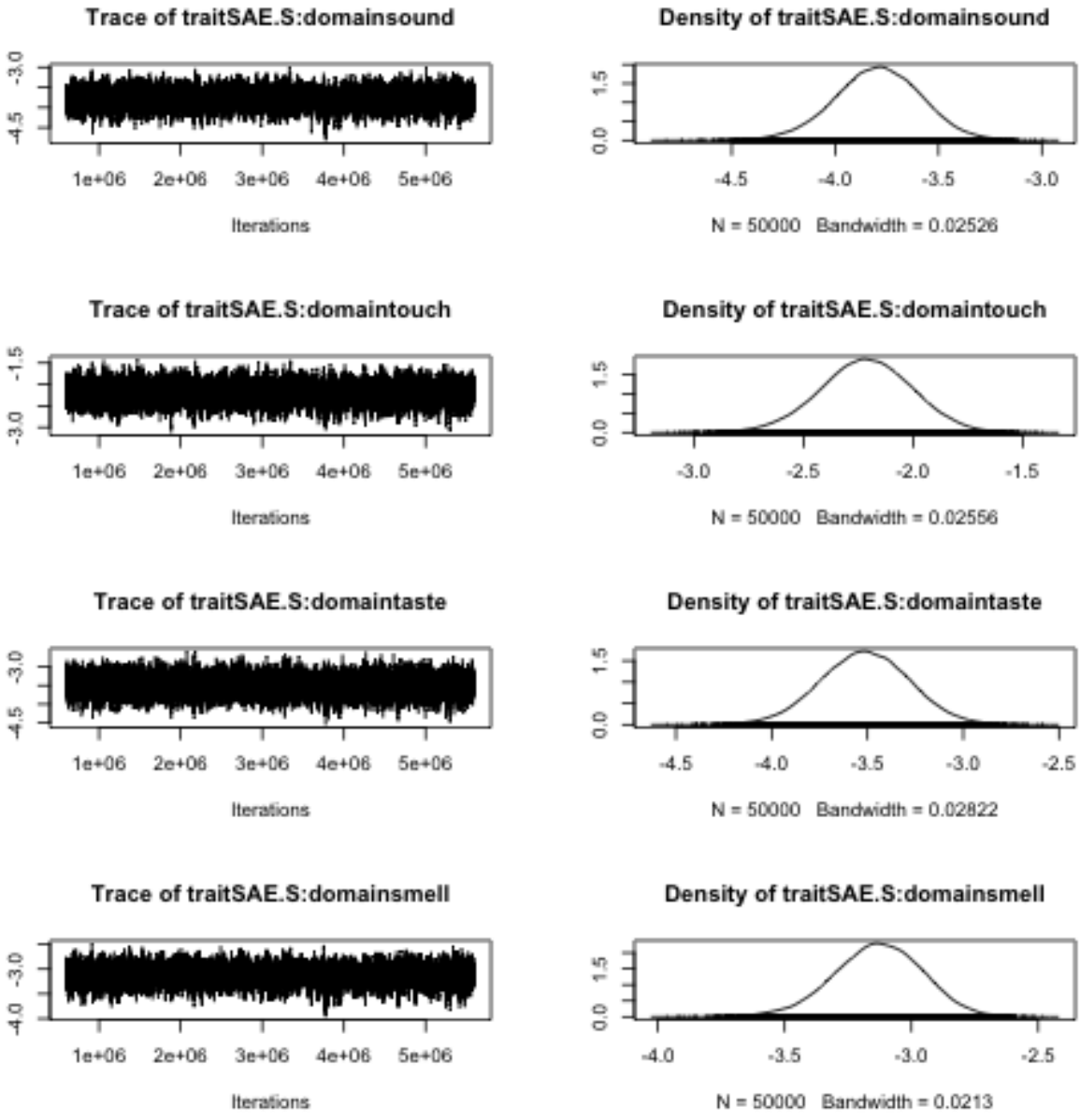

Trace of traitSAE.S:domainsound
Density of traitSAE.S:domainsound
Iterations
N = 50000 Bandwidth = 0.02526
Trace of traitSAE.S:domaintouch
Density of traitSAE.S:domaintouch
Iterations
N = 50000 Bandwidth = 0.02556
Trace of traitSAE.S:domaintaste
Density of traitSAE.S:domaintaste
Iterations
N = 50000 Bandwidth = 0.02822
Trace of traitSAE.S:domainsmell
Density of traitSAE.S:domainsmell
Iterations
N = 50000 Bandwidth = 0.0213

Figure 3:

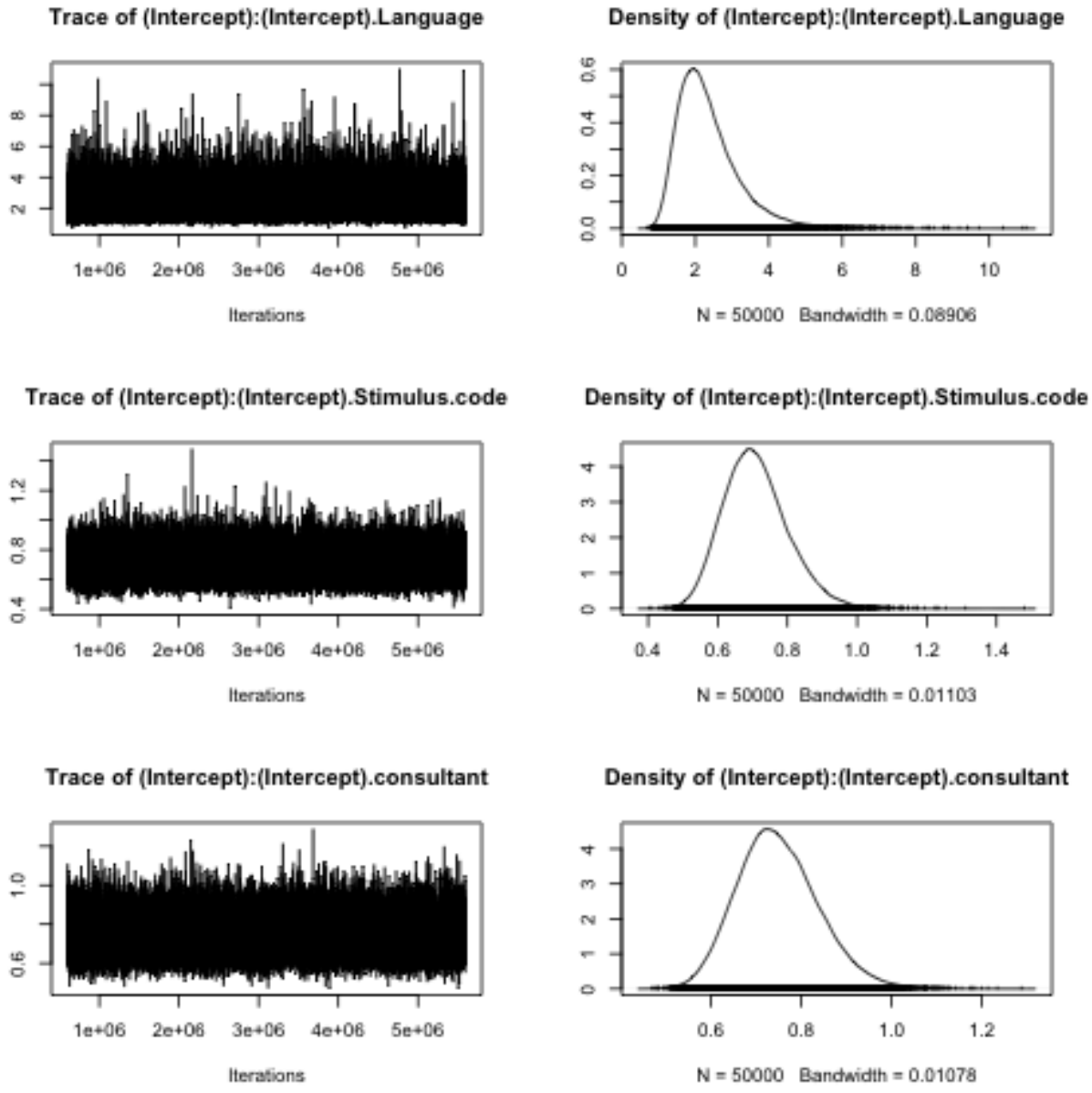

Trace of (Intercept):(Intercept).Language
Density of (Intercept):(Intercept).Language
Iterations
N = 50000 Bandwidth = 0.08906
Trace of (Intercept):(Intercept).Stimulus.code
Density of (Intercept):(Intercept).Stimulus.code
Iterations
N = 50000 Bandwidth = 0.01103
Trace of (Intercept):(Intercept).consultant
Density of (Intercept):(Intercept).consultant
Iterations
N = 50000 Bandwidth = 0.01078

Figure 4:

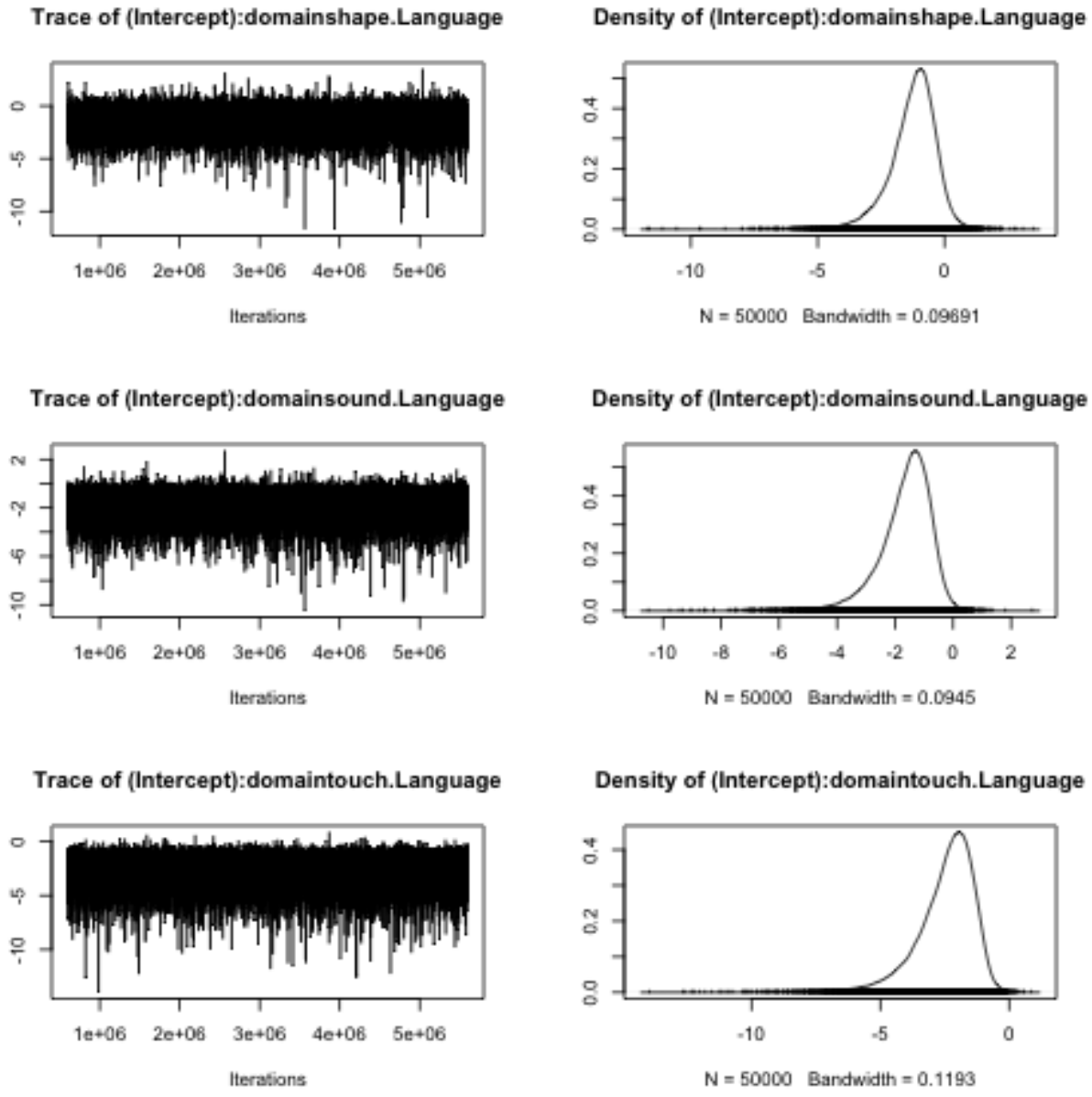
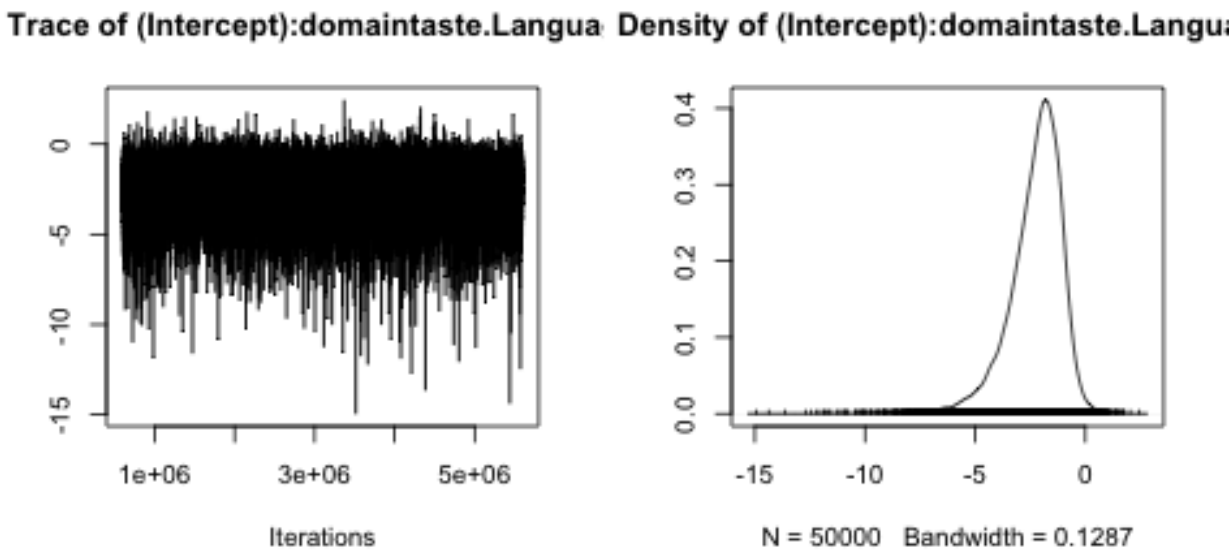

Trace of (Intercept):domainshape.Language
Density of (Intercept):domainshape.Language
Iterations
N = 50000 Bandwidth = 0.09691
Trace of (Intercept):domainsound.Language
Density of (Intercept):domainsound.Language
Iterations
N = 50000 Bandwidth = 0.0945
Trace of (Intercept):domaintouch.Language
Density of (Intercept):domaintouch.Language
Iterations
N = 50000 Bandwidth = 0.1193

Figure 5:


Trace of (Intercept):domaintaste.Langua
Density of (Intercept):domaintaste.Langu
0
-5
-10
-15
1e+06
3e+06
5e+06
Iterations
0.0
0.1
0.2
0.3
0.4
-15
-10
-5
0
N = 50000 Bandwidth = 0.1287

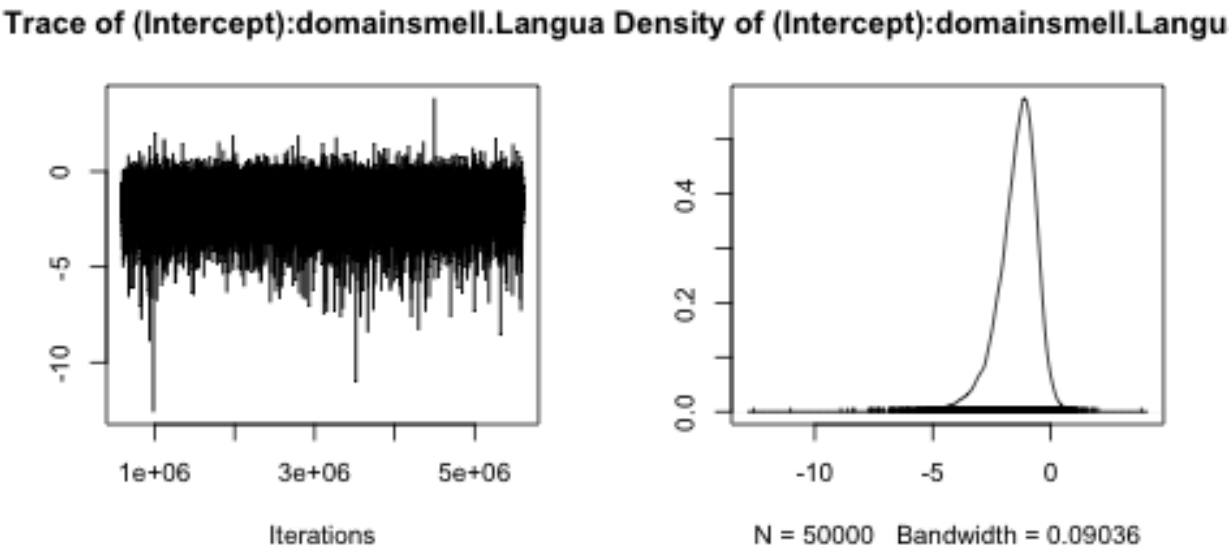

Trace of (Intercept):domainsmell.Langua
Density of (Intercept):domainsmell.Langu
0
-5
-10
1e+06
3e+06
5e+06
Iterations
0.0
0.2
0.4
-10
-5
0
N = 50000 Bandwidth = 0.09036

Figure 6:

Interpreting the results

Fixed effects estimates:

```
sx.all = as.data.frame(summary(final.model)$solutions)
apply(sx.all,2,signif,digits=3)
```

```
##                         post.mean l-95% CI u-95% CI eff.samp   pMCMC
## traitSAE.E                  -6.72   -7.490   -5.950   5200.0 0.00002
## traitSAE.S                  -1.87   -2.590   -1.160  50000.0 0.00002
## domainshape                 -5.31  -11.800   -0.189     15.6 0.00688
## domainsound                  1.78    0.639    2.880   9440.0 0.00264
## domaintouch                  2.69    1.370    3.940  12300.0 0.00024
## domaintaste                  2.78    1.270    4.310  15100.0 0.00080
## domainsmell                  6.69    5.570    7.750  10100.0 0.00002
## traitSAE.S:domainshape       6.85    1.880   12.900     14.3 0.00002
## traitSAE.S:domainsound      -3.79   -4.200   -3.380   1460.0 0.00002
## traitSAE.S:domaintouch      -2.21   -2.630   -1.810   1460.0 0.00002
## traitSAE.S:domaintaste      -3.51   -3.970   -3.060   1910.0 0.00002
## traitSAE.S:domainsmell      -3.13   -3.460   -2.780   1140.0 0.00002
```

The results show that, across the board, abstract descriptions are more likely than source-based descriptions, which are more likely than evaluative descriptions. Compared to the colour domains, other domains are more likely to use evaluative descriptions, except for shape which is more likely to use source-based descriptions. The estimates for source-based descriptions of smell, sound, taste and touch are very similar, as are the estimates for evaluative descriptions for sound, taste and touch. However, the estimate for evaluative descriptions for smell is much higher, suggesting that evaluative descriptions are more likely for the smell domain.

The graph below shows how the probaility of using Evaluative and Source-based descriptions differs from the baseline condition, which is the sound domain. The vertical axis is in log probability, so above 0 means more likely and below zero means less likely. If the 95% confidence intervals are different from 0, then there is a significant effect. The difference in proportion of abstract responses for each domain (compared to colour) is implied by the difference between the evaluative and source-based, and is plotted for ease of reference, but no confidence intervals are given.

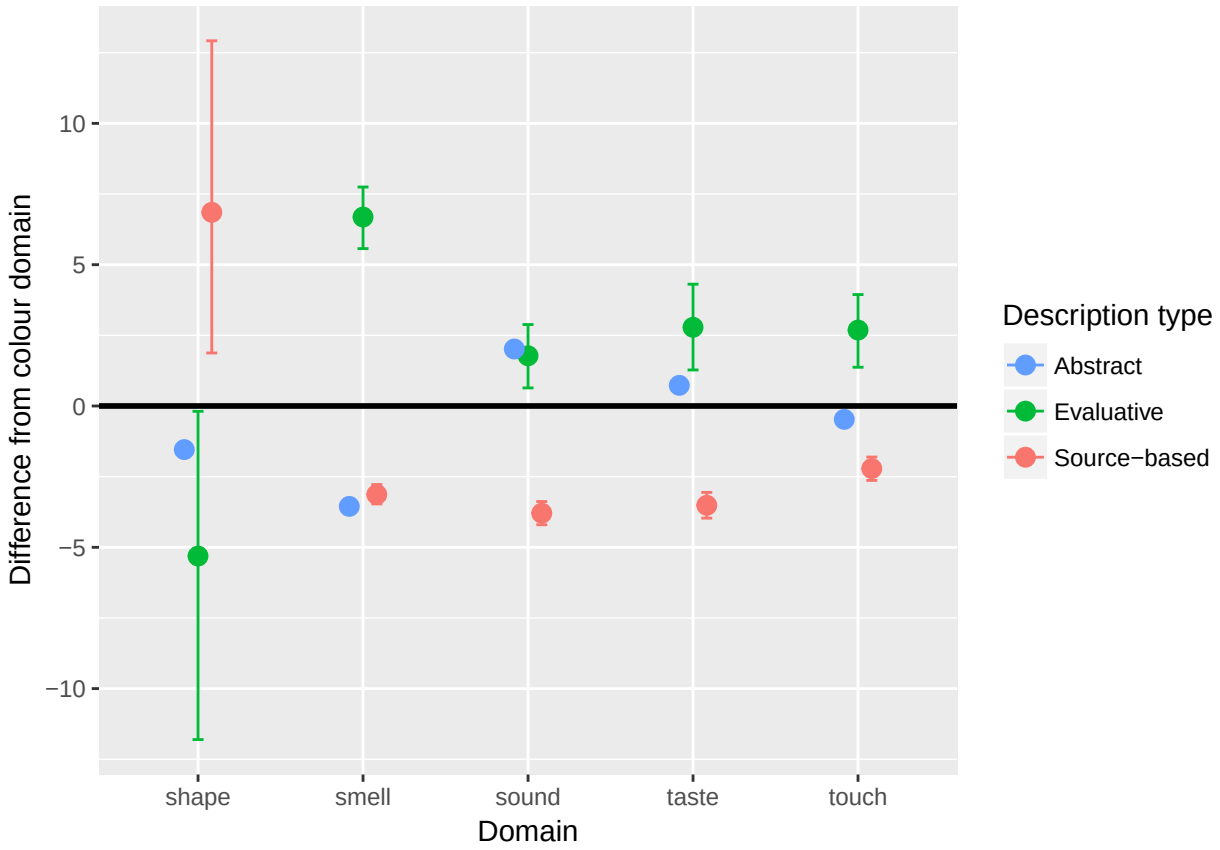
See the file results/SAE_interpretation.pdf for a fuller explanation of the results.

Note that the effective sample size (eff.samp) for two of the parameters is very low (< 100). These results come from increasing the number of iterations by an order of magnitude compared to the other models (to roughly two weeks processing time on a cluster computer). These increases made little difference to the effective sample size, but did make the estimate distributions less bimodal. It is likely that a different prior would help. However, the estimates are still significant, the outlying estimates suggest a greater effect size (not closer to zero) and the model fits the data well. We suggest that the differences are still significant. Also note that the model selection test preferred the interaction model even when all models were run for the same number of iterations.

```
plotModelEstimates = function(sx,ylab){

  sx$var = rownames(sx)
  sx = sx[grepl("domain",sx$var),]
  sx$grp = "Evaluative"
  sx$grp[grepl("traitSAE\\.S",sx$var)] = "Source-based"

  sx$domain = gsub("domain","",sx$var)
  sx$domain = gsub("traitSAE\\.S\\:","",sx$domain)

  sx$var = substr(sx$var, 7,nchar(sx$var))
```

```
  sx$var = factor(sx$var,levels = sae.order)
  names(sx)[names(sx)=="l-95% CI"] = 'lower'
  names(sx)[names(sx)=="u-95% CI"] = 'upper'

  # add logical estimate of change for abstract
  sx = rbind(sx,
    data.frame(
      post.mean = -(sx[1:5,1] + sx[6:10,1]),
      lower = rep(NA,5),
      upper = rep(NA,5),
      eff.samp = rep(NA,5),
      pMCMC = rep(NA,5),
      var = sx[1:5,]$var,
      grp = rep("Abstract",5),
      domain = sx[1:5,]$var
  ))

  gx = ggplot(sx, aes(y=post.mean,x=domain, colour=grp)) +
    geom_hline(yintercept=0, color="black", size=1) +
    geom_point(size=3, position = position_dodge(width = 0.25)) +
    geom_errorbar(aes(ymax=upper,
                      ymin=lower),width=0.2,
                  position = position_dodge(width=0.25))+
    xlab("Domain")+
    ylab(ylab) +
    scale_color_manual(values=c("#619CFF", "#00BA38", "#F8766D"),name = "Description type")
  return(gx)
}

gx = plotModelEstimates(sx.all,"Difference from colour domain")
gx
```

```
## Warning: Removed 5 rows containing missing values (geom_errorbar).
```




```
pdf("../results/graphs/SAE_Results.pdf", height = 5)
gx
```

```
## Warning: Removed 5 rows containing missing values (geom_errorbar).
```

```
dev.off()
```

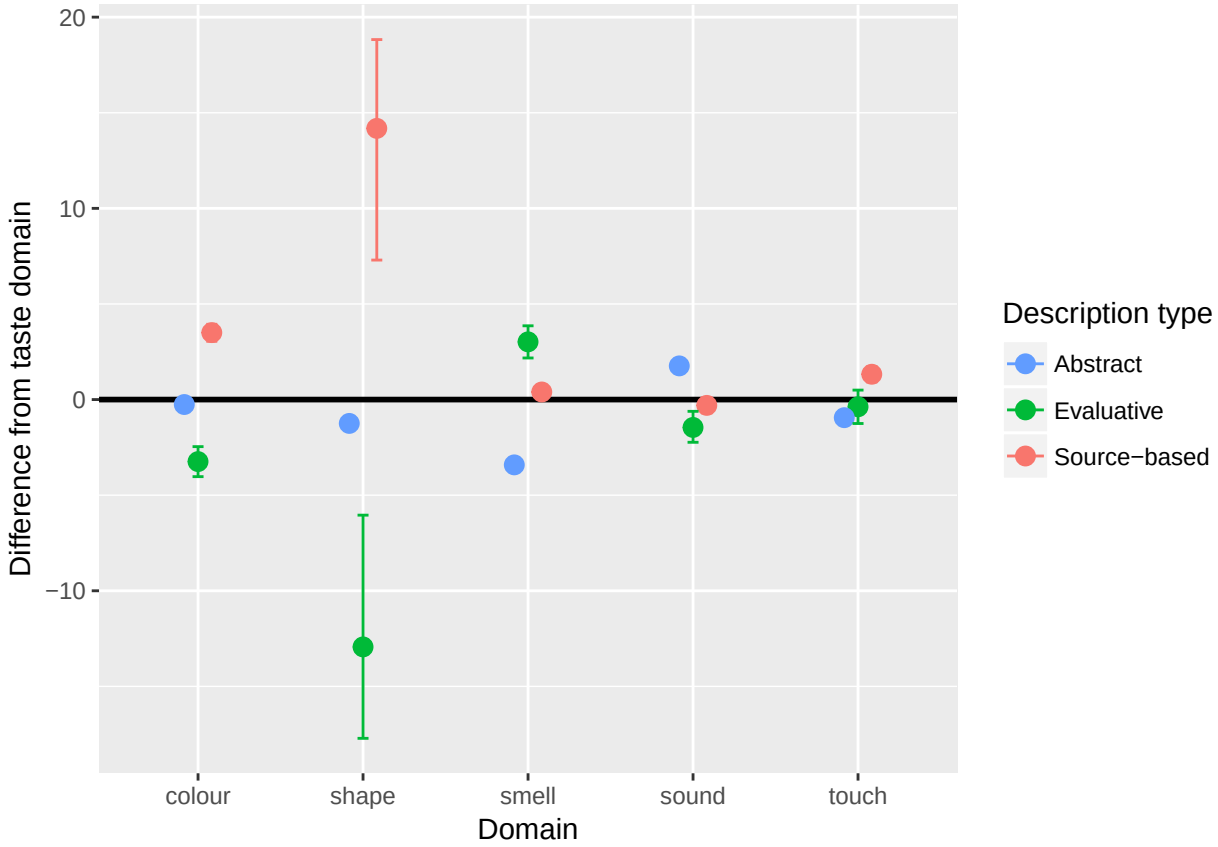
```
## pdf
##   2
```

SAE model with alternative intercept

A model where the intercept is taste gives equivalent results:

```
load("../results/SAE_mcmc_model_full_long_InterceptIsTaste.rdat")
taste.model = m.mcmcglmm
gx.taste = plotModelEstimates(as.data.frame(summary(taste.model)$solutions),
                              "Difference from taste domain")
gx.taste
```

```
## Warning: Removed 5 rows containing missing values (geom_errorbar).
```




```
pdf("../results/graphs/SAE_Results_InterceptIsTaste.pdf", height = 5)
gx.taste
```

```
## Warning: Removed 5 rows containing missing values (geom_errorbar).
```

```
dev.off()
```

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

Test differences between modalities

Are signed languages more likely to use particular types of response? Use a mixed effects model, predicting likelihood of an abstract response, with random effects for language, consultant, domain, stimulus and the interaction between language and domain. Then add a random effect for modality by domain, and a fixed effect of modality

```
d$modality = "Spoken"
d$modality[d$Language %in% c("ASL", "BSL", "Kata Kolok")] = "Signed"
d$modality = factor(d$modality, levels=c("Spoken",'Signed'))
dSignTest = d[d$domain!='sound',]
dSignTest$domain = factor(dSignTest$domain)
dSignTest$Language = factor(dSignTest$Language)
dSignTest$Stimulus.code = factor(dSignTest$Stimulus.code)
dSignTest$consultant = factor(dSignTest$consultant)
dSignTest = dSignTest[complete.cases(dSignTest[,c("Language",'domain','SAE','consultant','Stimulus.code
dSignTest$Abstract = dSignTest$SAE == "A"
m0 = glmer(Abstract ~
             1 +
             (1|Language/consultant) +
             (1|domain/Stimulus.code) +
             (1|Language:domain),
           data = dSignTest,
           family = binomial)
m1 = update(m0,~.+(0 + modality|domain))
m2 = update(m1,~.+modality)
anova(m0,m1,m2)
```

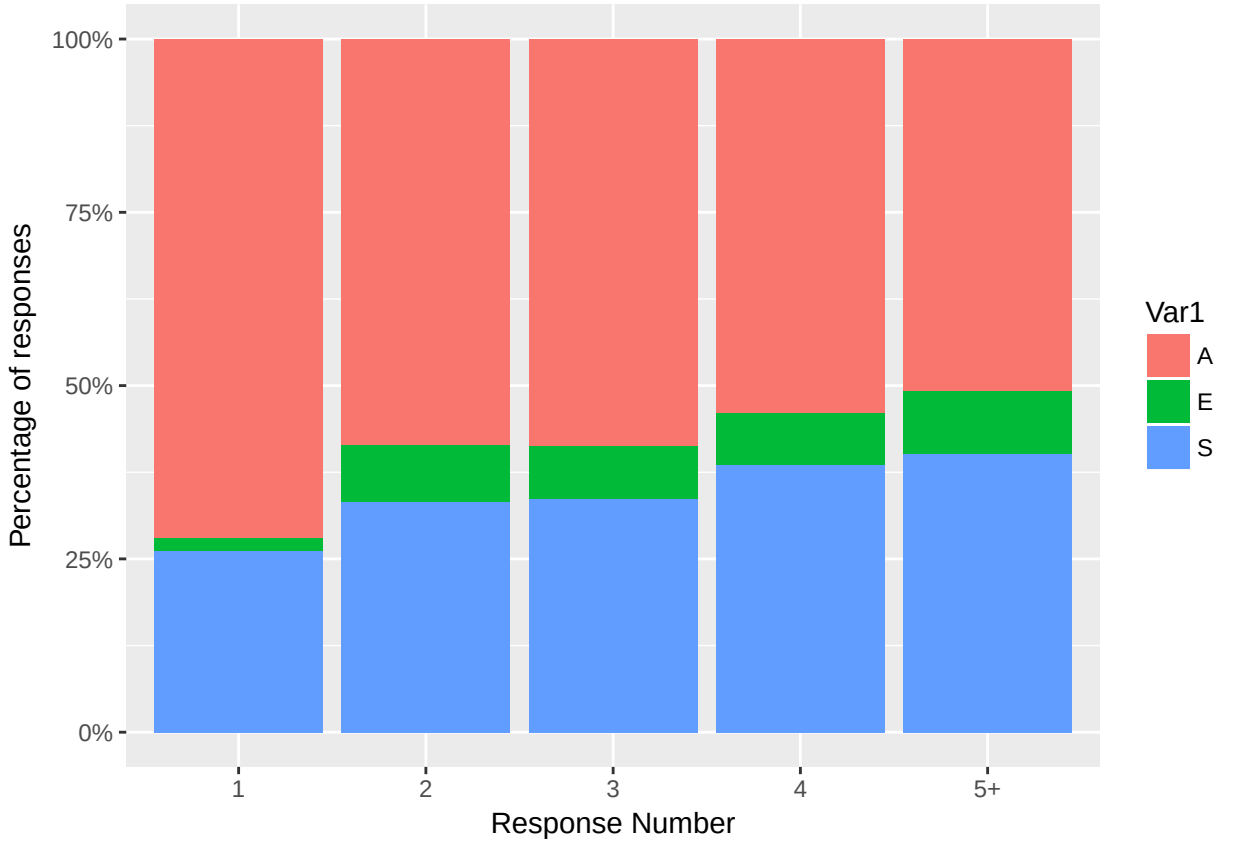
```
## Data: dSignTest
## Models:
## m0: Abstract ~ 1 + (1 | Language/consultant) + (1 | domain/Stimulus.code) +
## m0:     (1 | Language:domain)
## m1: Abstract ~ (1 | Language/consultant) + (1 | domain/Stimulus.code) +
## m1:     (1 | Language:domain) + (0 + modality | domain)
## m2: Abstract ~ (1 | Language/consultant) + (1 | domain/Stimulus.code) +
## m2:     (1 | Language:domain) + (0 + modality | domain) + modality
##    Df   AIC   BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## m0  6 24556 24606 -12272    24544
## m1  9 24558 24633 -12270    24540 3.9828      3     0.2633
## m2 10 24560 24642 -12270    24540 0.4999      1     0.4796
```

Neither the fixed effect of modality nor the random effect of modality by domain improves the model. That is, signed languages are not a distinct group.

Test if abstract responses are less likely in later descriptions.

Respondents could produce multiple responses. In conversational interaction, participants tend to move towards more specific information when converging on a referent of a description (Dingemanse et al., 2015). Abstract responses are proportionately less likely in later descriptions:

```
d = d.all # switch back to all responses
# Recode categories to plot
d$Response.cat = "1"
d[d$Response==2,]$Response.cat = "2"
d[d$Response==3,]$Response.cat = "3"
d[d$Response==4,]$Response.cat = "4"
d[d$Response>4,]$Response.cat = "5+"

txR = melt(prop.table(table(d$SAE,d$Response.cat),2))

ggplot(txR,aes(x = Var2, y = value,fill = Var1)) +
  geom_bar(position = "fill",stat = "identity") +
  scale_y_continuous(labels = percent_format()) +
  xlab("Response Number") + ylab("Percentage of responses")
```



We test whether the probability of using an abstract description varies according to the number of times that stimuli had been named by the respondent previously. Response numbers range from 1 to 15, but 99% are 5 or lower. We set all response numbers of 5 or more to be equal to 5. We used a linear mixed effects model with random intercepts for respondent within languages and stimuli within domains, with a random slope for response number by domain.

We compare a model with random intercepts for consultants within languages and stimuli within domain.

Then a third model adds the main effect for response number.

```
logit2prob=function(X){
    exp(X)/(1+exp(X))
}

d$SAE.abstract = d$SAE=="A"
d$Response2 = d$Response
d$Response2[d$Response>5]=5
d$Response2 = d$Response2-1

m0 = glmer(SAE.abstract~ 1 +
             (1|Language/consultant) +
             (1|domain/Stimulus.code),
           data = d,
           family='binomial')

mR = glmer(SAE.abstract~ 1 +
       (1|Language/consultant) +
       (1|domain/Stimulus.code) +
       (0+Response2|domain),
       data = d,
       family='binomial')

mRD = glmer(SAE.abstract~ Response2 +
       (1|Language/consultant) +
       (1|domain/Stimulus.code) +
       (0+Response2|domain),
       data = d,
       family='binomial')

ax = anova(m0,mR,mRD)
ax
```

```
## Data: d
## Models:
## m0: SAE.abstract ~ 1 + (1 | Language/consultant) + (1 | domain/Stimulus.code)
## mR: SAE.abstract ~ 1 + (1 | Language/consultant) + (1 | domain/Stimulus.code) +
## mR:     (0 + Response2 | domain)
## mRD: SAE.abstract ~ Response2 + (1 | Language/consultant) + (1 | domain/Stimulus.code) +
## mRD:     (0 + Response2 | domain)
##     Df   AIC   BIC logLik deviance   Chisq Chi Df Pr(>Chisq)
## m0   5 40039 40083 -20015    40029
## mR   6 39820 39872 -19904    39808 221.076      1     <2e-16 ***
## mRD  7 39821 39881 -19904    39807   1.408      1     0.2354
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(mRD)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## SAE.abstract ~ Response2 + (1 | Language/consultant) + (1 | domain/Stimulus.code) +
##     (0 + Response2 | domain)
```

```
##    Data: d
##
##      AIC      BIC   logLik deviance df.resid
##  39820.9  39881.4 -19903.5  39806.9    41592
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -9.5246 -0.5257  0.3216  0.5305  7.3251
##
## Random effects:
##  Groups               Name        Variance Std.Dev.
##  consultant.Language  (Intercept) 0.65725  0.8107
##  Stimulus.code.domain (Intercept) 0.32418  0.5694
##  Language             (Intercept) 0.55582  0.7455
##  domain               Response2   0.05305  0.2303
##  domain.1             (Intercept) 1.62350  1.2742
## Number of obs: 41599, groups:
## consultant:Language, 313; Stimulus.code:domain, 147; Language, 20; domain, 6
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.84131    0.55340   1.520    0.128
## Response2   -0.12239    0.09648  -1.269    0.205
##
## Correlation of Fixed Effects:
##           (Intr)
## Response2 -0.003
```

```
# estimated probability at first response:
pA.R1 = logit2prob(fixef(mRD)[1])
# probability decrease with each response:
pA.Rplus = pA.R1 - logit2prob(sum(fixef(mRD)))

#The probability of producing an abstract response in the first turn is
round(pA.R1*100,1)
```

```
## (Intercept)
##        69.9
```

```
# % .  This decreases by
round(pA.Rplus*100,1)
```

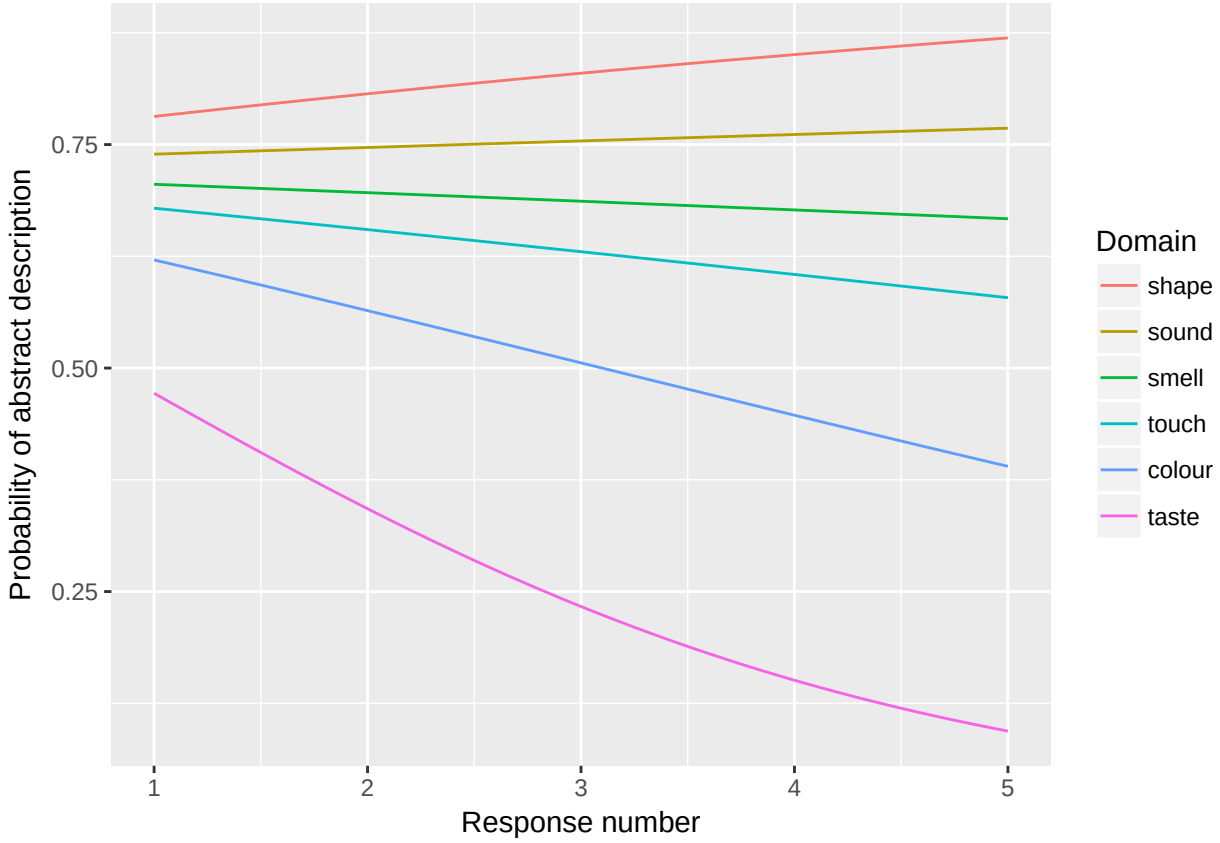
```
## (Intercept)
##         2.6
```

```
#percentage points after each response.
```

Random slopes for response number by domain significantly improve the fit of the model. Abstract descriptions are not less likely in later descriptions when controlling for this random slope. That is, the effect is stronger for some domains:

```
rint = fixef(mRD)[1] + ranef(mRD)$domain[,1]
rslope = fixef(mRD)[2] + ranef(mRD)$domain[,1]

xpoints = seq(1,5,length.out=100)

dx = data.frame(
```

```
  y=as.vector(sapply(xpoints,function(X){rint + (rslope*X)})),
  x=rep(xpoints,each=6),
  Domain=rep(levels(factor(d$domain)), 100))

dx$y = logit2prob(dx$y)

dx$Domain = factor(dx$Domain, levels=c("shape","sound",'smell',"touch",'colour','taste'))

ggplot(dx, aes(x=x,y=y,colour=Domain)) +
  geom_line() +
  xlab("Response number") +
  ylab("Probability of abstract description")
```



Summary

We found that they were less likely to use abstract descriptions for later responses (proportion of abstract terms in first description = 72%, in second description = 58%), but this was mainly driven by responses to taste and colour (random slope for response number by domain p<.001). The probability of producing an abstract description for taste drops from 47% to 9% over 5 responses.