Alternative analysis: Shapes determined by first 11PCs containing 90% of all morphological variance

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This analysis runs an alternative core script, where data are loaded and further processed, most models are defined and plots are drafted. The process prepares this document for a neat report. If you are interested in details, you can run the Core script manually outside of this report. This core script first decomposes the facial shape into 144PC, then evaluates, how many PCs are needed to explain 90% of facial variability then replaces all other PCs' eigenvectors with vectors of length 0, and multiplies the shape scores along with the reduced matrix of eigenvectors. The results of this analysis are virtually identical to the results that use complete facial shape variance.

```r
#Few additional functions that are used in the analysis
source("result_functions.R")

#Visualize the morphs. You can inspect the results directly here
source("visualization_morphs1.R")
```
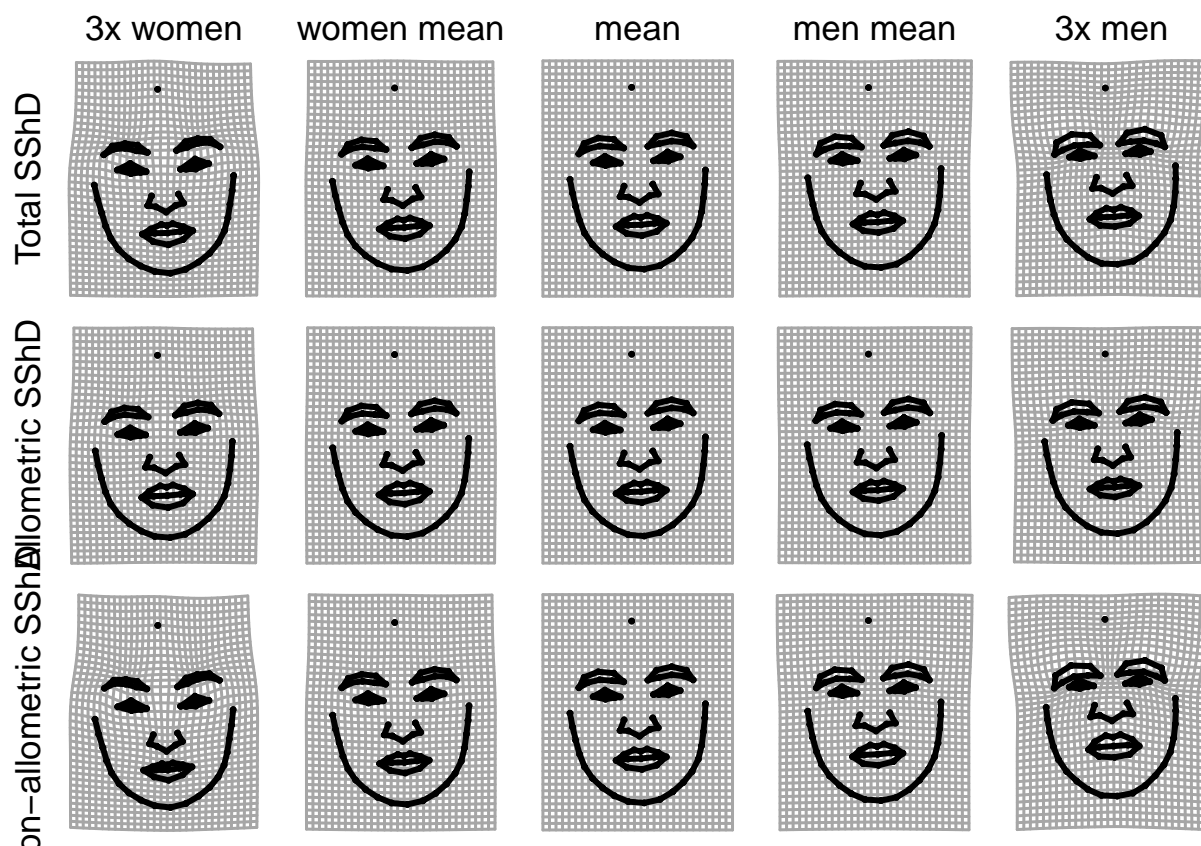

R Markdown report of sexual dimorphism in facial morphology

We report the national samples in following order

```
reord<-c(5,2,7,6,4,8,3,1)
(reord.labs<-c("Brazil","Cameroon","Colombia","Czech Republic","Namibia","Romania","Turkey","United King
```

```
## [1] "Namibia"        "Cameroon"       "Turkey"         "Romania"
## [5] "Czech Republic" "United Kingdom" "Colombia"       "Brazil"
```

In total we had

```
sum(summary(gtf$nat))
```

```
## [1] 1114
```

individuals from 8 different nations. Nation-wise sample sizes were

```
(Nall<-summary(gtf$nat)[reord])
```

```
##  NAM  CMR   TR   RO   CZ   UK  COL BRAZ
##   90  301  184   48  154   99  138  100
```

In this analysis we use the restricted sample, where the body height is known (N=1114). Which is essential for allometric/nonallometric decomposition. If you want to run parts of the analysis on the unrestricted sample (N=1317) load data file "Symmetrized_coordinates_all.RData". You can change this in the Core_script (see above)

```
(Nmales<-summary(gtf$nat[gtf$sex=="M"])[reord])
```
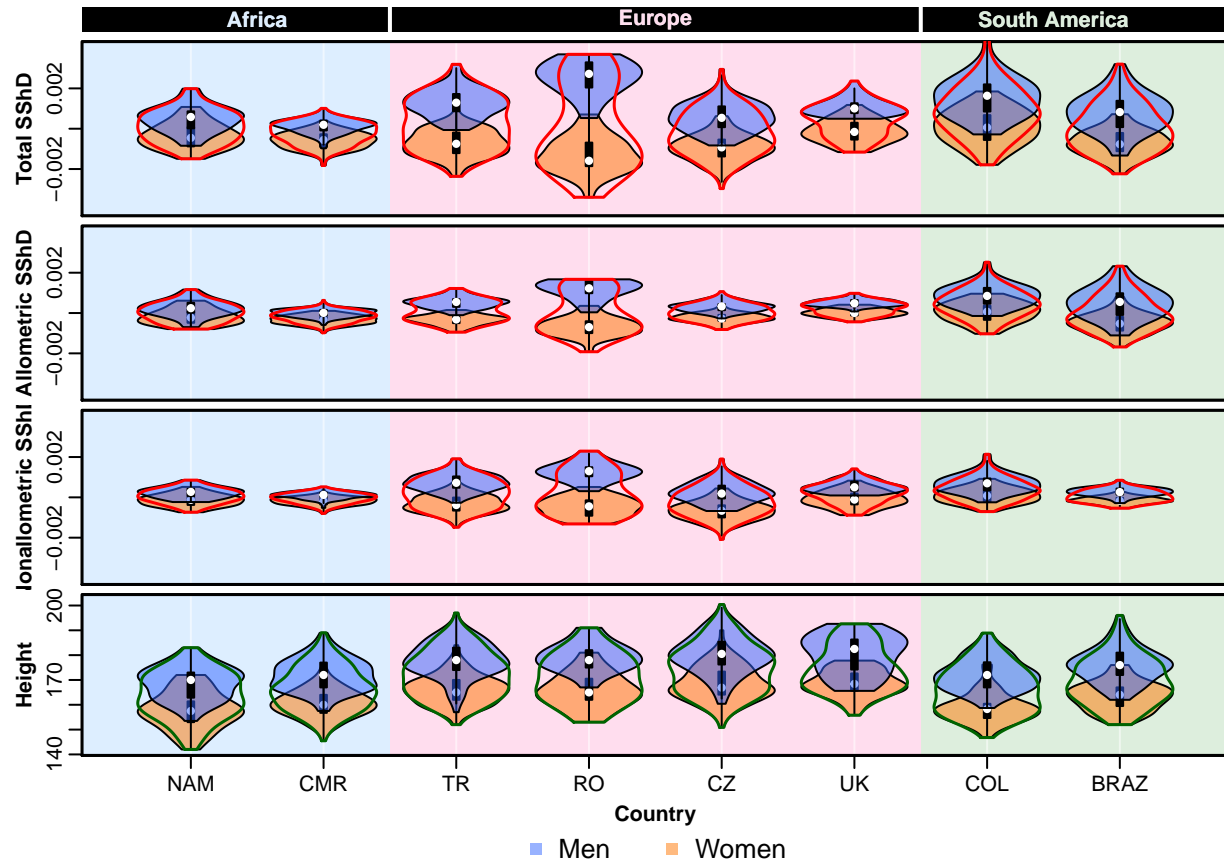
```
##  NAM  CMR   TR   RO   CZ   UK  COL BRAZ
##   48  150   91   17   76   49   72   49
```

```
(Nfemales<-summary(gtf$nat[gtf$sex=="F"])[reord])
```

```
##  NAM  CMR   TR   RO   CZ   UK  COL BRAZ
##   42  151   93   31   78   50   66   51
```

```
#Visualize vioplot
source("visualization_vio.R")
```

Calculate the angles between the allo/nonallo and sex vectors

```
labs<-c("all",names(tapply(sexscores1,gtf$nat,sd)))

#Name vectors accordingly
colnames(sex.vecs)<-labs
colnames(Asex.vecs)<-labs
colnames(Nsex.vecs)<-labs

#We are not intrested in the angles in the whole sample, so we can restrict the analysis in the nationa
sex.vecs<-sex.vecs[,-1]
Asex.vecs<-Asex.vecs[,-1]
Nsex.vecs<-Nsex.vecs[,-1]
```

Vectors between Allometric vector and overal maleness-femaleness vector (the same visualization as in Scheafer et al. 2004)

```
(Aang<-angles(sex.vecs,Asex.vecs))
```

```
##      BRAZ      CMR      COL       CZ      NAM       RO       TR       UK
## 16.67764 22.72219 15.21354 21.44228 27.72569 21.66161 19.92730 27.57360
```

Similar analysis for the non-allometric component of maleness-femaleness

```
(Nang<-angles(sex.vecs,Nsex.vecs))
```

```
##      BRAZ      CMR      COL       CZ      NAM       RO       TR       UK
## 29.73046 24.30062 17.85590 14.51385 28.99480 22.19945 17.21732 23.46776
```

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Angle between two components of Sexual shape dimorphism

```
(ANang<-angles(Asex.vecs,Nsex.vecs))
```

```
##      BRAZ      CMR      COL       CZ      NAM       RO       TR       UK
## 40.27016 35.58474 25.07914 32.69189 52.15651 34.22032 32.07091 42.81402
```

Sanity check: the sum of the two Allo(Nonallo)-total angles should be roughly the same as the angle between the Allo and nonallo component

```
ANang
```

```
##      BRAZ      CMR      COL       CZ      NAM       RO       TR       UK
## 40.27016 35.58474 25.07914 32.69189 52.15651 34.22032 32.07091 42.81402
```

```
Aang+Nang
```
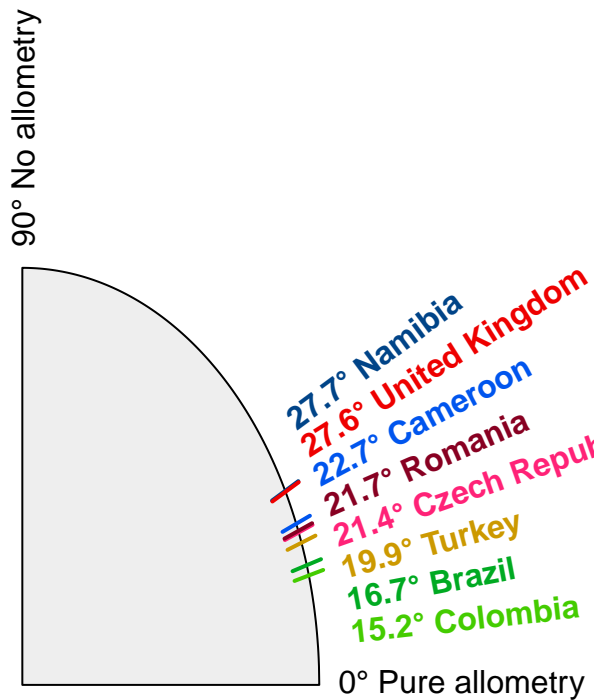
```
##      BRAZ      CMR      COL       CZ      NAM       RO       TR       UK
## 46.40810 47.02281 33.06944 35.95613 56.72049 43.86107 37.14463 51.04136
```
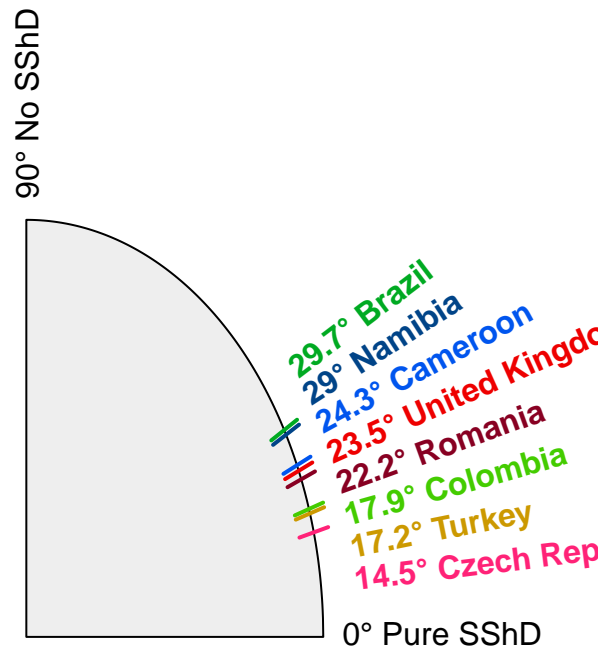
It fits :)

Visualize the results

```
cols<-c("#00AA22","#0055EE","#44CC00","#FF2277","#004488","#880022","#CC9900","#EE0000")
anglabs<-c("Brazil","Cameroon","Colombia","Czech Republic","Namibia","Romania","Turkey","United Kingdom

source("visualization_angles.R",encoding="UTF-8")
```


'

```r
mor.var<-data.frame(
  disp.pop = mdisp.1[[1]],
  disp.sex.cont = mdisp.1.sex[[1]],
  disp.m = mdisp.m[[1]],
  disp.f = mdisp.f[[1]]
)[reord,]

signif(mor.var,2)
```

```
##       disp.pop disp.sex.cont disp.m disp.f
## NAM    0.0033         0.0031 0.0037 0.0033
## CMR    0.0041         0.0040 0.0043 0.0046
## TR     0.0035         0.0031 0.0040 0.0030
## RO     0.0036         0.0032 0.0048 0.0029
## CZ     0.0036         0.0033 0.0037 0.0037
## UK     0.0030         0.0028 0.0033 0.0032
## COL    0.0036         0.0034 0.0049 0.0027
## BRAZ   0.0029         0.0025 0.0032 0.0028
```

All pairwise differences higher than

```r
disp.tab.sig(mdisp.1)
```

```
## [1] 0.0007410031
```

were statistically significant.

```r
disp.tab.sig(mdisp.1.sex)
```

```
## [1] 0.0006542499
```

for the morphological disparity controlled for sex

```r
disp.tab.sig(mdisp.m)
```

```
## [1] 0.001138923
```

for male faces only

```r
disp.tab.sig(mdisp.f)
```

```
## [1] 0.000897329
```

for female faces only

Male faces showed higher morphological disparity than female faces

```r
min(mdisp.sex[[3]])
```

```
## [1] 0.001
```

Procrustes variances for defined groups were

```r
mdisp.sex[[1]]
```

```
##           F          M
## 0.003343091 0.003815331
```

this was true even when morphological variation between nations was accounted for

```r
min(mdisp.sex.nat[[3]])
```

```
## [1] 0.045
```

```
mdisp.sex.nat[[1]]
```

```
##           F           M
## 0.002625049 0.002831242
```

We calculated differences between the group means for total SShD and for both subdimensions and other related measures

```
#Calculate difference between means from the sexscores
dif<-abs(tapply(fsexscores1,gtf$nat[gtf$sex=="F"],mean)-tapply(msexscores1,gtf$nat[gtf$sex=="M"],mean))

#Allometric
difA<-abs(tapply(fsexscoresA,gtf2$nat[gtf2$sex=="F"],mean)-tapply(msexscoresA,gtf2$nat[gtf2$sex=="M"],me

#Nonallometric
difN<-abs(tapply(fsexscoresN,gtf2$nat[gtf2$sex=="F"],mean)-tapply(msexscoresN,gtf2$nat[gtf2$sex=="M"],me

#Distinctivness and variability in height
meanH.f<-tapply(gtf2$height[gtf2$sex=="F"],gtf2$nat[gtf2$sex=="F"],mean)
meanH.m<-tapply(gtf2$height[gtf2$sex=="M"],gtf2$nat[gtf2$sex=="M"],mean)
meanH<-tapply(gtf2$height,gtf2$nat,mean)

difH<-abs(meanH.f-meanH.m)

dif.var<-data.frame(
  dif=dif,
  difA=difA,
  difN=difN,
  difH=difH
)[reord,]

signif(dif.var,2)
```

```
##         dif     difA     difN difH
## NAM  0.00087 0.00043 0.00040   11
## CMR  0.00073 0.00036 0.00031   12
## TR   0.00200 0.00087 0.00110   12
## RO   0.00380 0.00180 0.00180   14
## CZ   0.00160 0.00058 0.00095   12
## UK   0.00120 0.00050 0.00064   12
## COL  0.00150 0.00084 0.00063   13
## BRAZ 0.00150 0.00100 0.00043   13
```

The total SShd gets essentially pojected onto the Allometric and Nonallometric vectors.

```
cor.test(cos(deg2rad(Aang))*dif,difA)
```

```
##
##  Pearson's product-moment correlation
##
## data:  cos(deg2rad(Aang)) * dif and difA
## t = 8.4631, df = 6, p-value = 0.0001487
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.7919987 0.9930566
## sample estimates:
```

```
##       cor
## 0.9605748
```

```
cor.test(cos(deg2rad(Nang))*dif,difN)
```

```
##
##  Pearson's product-moment correlation
##
## data:  cos(deg2rad(Nang)) * dif and difN
## t = 8.544, df = 6, p-value = 0.000141
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.7953843 0.9931821
## sample estimates:
##       cor
## 0.9612758
```

It can be, therefore, stated that sexual shape dimrphism and its allometric and non-allometric components can be sufficiently described by the distributions on the original SShD components (top row in the vioplot) and angles of the total SShD vector with the alometric and non-allometric SShD vectors (figue with angles).

Mixed effect results - sextypicallity vs attractiveness

```
mixed.res1<-summary(mmodel1)[[10]]
nammixed<-colnames(mixed.res1)
mixed.res1<-cbind(round(mixed.res1[,1:2],3),round(mixed.res1[,3],1),round(mixed.res1[,4],2),round(mixed
colnames(mixed.res1)<-nammixed

mixed.resA1<-summary(mmodelA1)[[10]]
nammixed<-colnames(mixed.resA1)
mixed.resA1<-cbind(round(mixed.resA1[,1:2],3),round(mixed.resA1[,3],1),round(mixed.resA1[,4],2),round(m
colnames(mixed.resA1)<-nammixed

mixed.resN1<-summary(mmodelN1)[[10]]
nammixed<-colnames(mixed.resN1)
mixed.resN1<-cbind(round(mixed.resN1[,1:2],3),round(mixed.resN1[,3],1),round(mixed.resN1[,4],2),round(m
colnames(mixed.resN1)<-nammixed

mixed.res1
```

```
##                    Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)           0.001      0.042 901.0    0.03    0.977
## Sextypicality         0.187      0.046  14.9    4.10    0.001
## sexM                  0.000      0.059 958.7    0.01    0.995
## Sextypicality:sexM   -0.153      0.064   7.3   -2.40    0.046
```

```
mixed.resA1
```

```
##                     Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)            0.078      0.045 114.9    1.73    0.086
## Allometric_SShD        0.151      0.067   8.6    2.24    0.054
## sexM                  -0.024      0.091   3.7   -0.26    0.811
## Allometric_SShD:sexM  -0.003      0.115   5.6   -0.02    0.982
```

```
mixed.resN1
```

```
##                        Estimate Std. Error   df t value Pr(>|t|)
```

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```
## (Intercept)                      0.006     0.046  6.7    0.13    0.904
## Nonallometric_SShD               0.162     0.045 32.5    3.64    0.001
## sexM                            -0.004     0.062 23.1   -0.07    0.945
## Nonallometric_SShD:sexM         -0.199     0.062 40.6   -3.22    0.002
```

In total SShD and its Nonallometric component, sextypicality raises attractiveness in female faces, but not in male faces. The interaction term - the difference between regression coefficient for males and females is statistically significant. In allometric component, female faces get more attractive with allometric sextypicality, but the slope for males is not very different from the estimate for females.

We can visulaize the linear relationship of the interaction models above in all cultures separately and together

```
source("visualization_linear_models.R")

#Three main panels summarizing Sextypicality attractiveness
figuremain
```
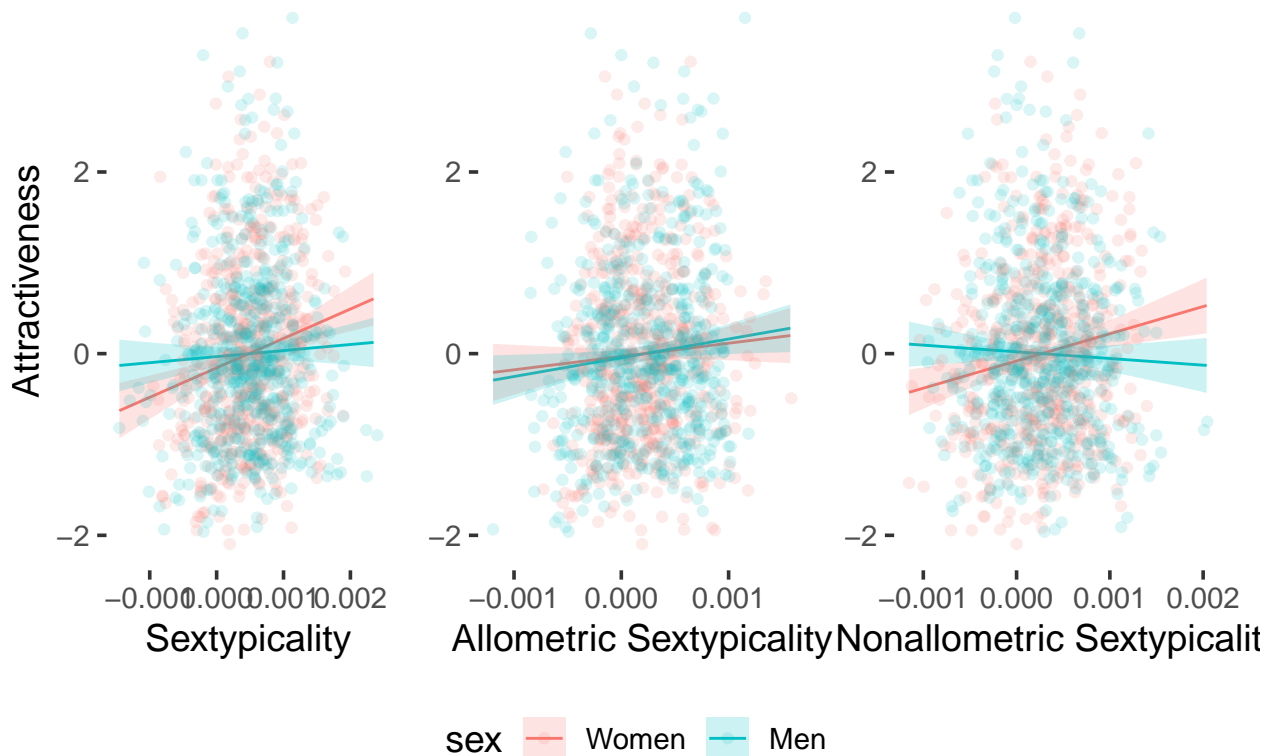

For comparison we add correltaions between body height and facial attractiveness. Faces of tall men are rated as attractive and there is no effect of body height on female facial attractiveness.

```
fall.cor.h
```

```
##
##  Pearson's product-moment correlation
##
## data:  fdat$height and fscores
## t = -0.10451, df = 560, p-value = 0.9168
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
```

```
##  -0.08709259  0.07832075
## sample estimates:
##          cor
## -0.004416127
```

mall.cor.h

```
##
##  Pearson's product-moment correlation
##
## data:  mdat$height and mscores
## t = 4.8651, df = 550, p-value = 1.496e-06
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##   0.1217328 0.2818016
## sample estimates:
##       cor
## 0.2031239
```

mean.dist<-`apply`(sex.vecs,`2`,`function`(x){`sqrt`(`sum`(x^2))})

this distance is almost perfectly correlated with the differences between the means of the pojections (dif - see above)

`cor.test`(mean.dist,dif)

```
##
##  Pearson's product-moment correlation
##
## data:  mean.dist and dif
## t = 17.971, df = 6, p-value = 1.909e-06
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##   0.9482488 0.9984068
## sample estimates:
##       cor
## 0.9908383
```

Which means it is also strongly correlated with the difference in body height

`cor.test`(difH,mean.dist)

```
##
##  Pearson's product-moment correlation
##
## data:  difH and mean.dist
## t = 2.8897, df = 6, p-value = 0.0277
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##   0.1257333 0.9544429
## sample estimates:
##       cor
## 0.7628197
```

The visualization of the linear model of the relationship between differences in bodz height and distance between sex-specific means in morphospace. The corridor is 89% bootstrapped compatibility interval.

Note that all auropean countries are above the line - they have higher difference between group means than expected and most non-european countries are below the line - they have lower difference between group

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means than expected. It contributes to our argument. Facial morphological dimorphism seems to be more important in european countries.

We will check the relationship between disparity and SShD distance between sexes in multidimensional morphospace

```
library(rethinking)
```

```
## Loading required package: rstan
```

```
## Loading required package: StanHeaders
```

```
## rstan (Version 2.19.2, GitRev: 2e1f913d3ca3)
```

```
## For execution on a local, multicore CPU with excess RAM we recommend calling
## options(mc.cores = parallel::detectCores()).
## To avoid recompilation of unchanged Stan programs, we recommend calling
## rstan_options(auto_write = TRUE)
```

```
## For improved execution time, we recommend calling
## Sys.setenv(LOCAL_CPPFLAGS = '-march=native')
## although this causes Stan to throw an error on a few processors.
```

```
##
## Attaching package: 'rstan'
```

```
## The following object is masked from 'package:tidyr':
##
##     extract
```

```
## The following object is masked from 'package:magrittr':
##
##     extract
```

```
## Loading required package: parallel
```

```
## Loading required package: dagitty
```

```
## rethinking (Version 1.93)
```

```
##
## Attaching package: 'rethinking'
```

```
## The following object is masked from 'package:mapplots':
##
##     make.grid
```

```
## The following object is masked from 'package:purrr':
##
##     map
```

```
## The following object is masked from 'package:standardize':
##
##     standardize
```

```
## The following object is masked from 'package:stats':
##
##     rstudent
```

```
source("visualization_differences.R")
```