

Alternative analysis: Shapes after controlling for body weight

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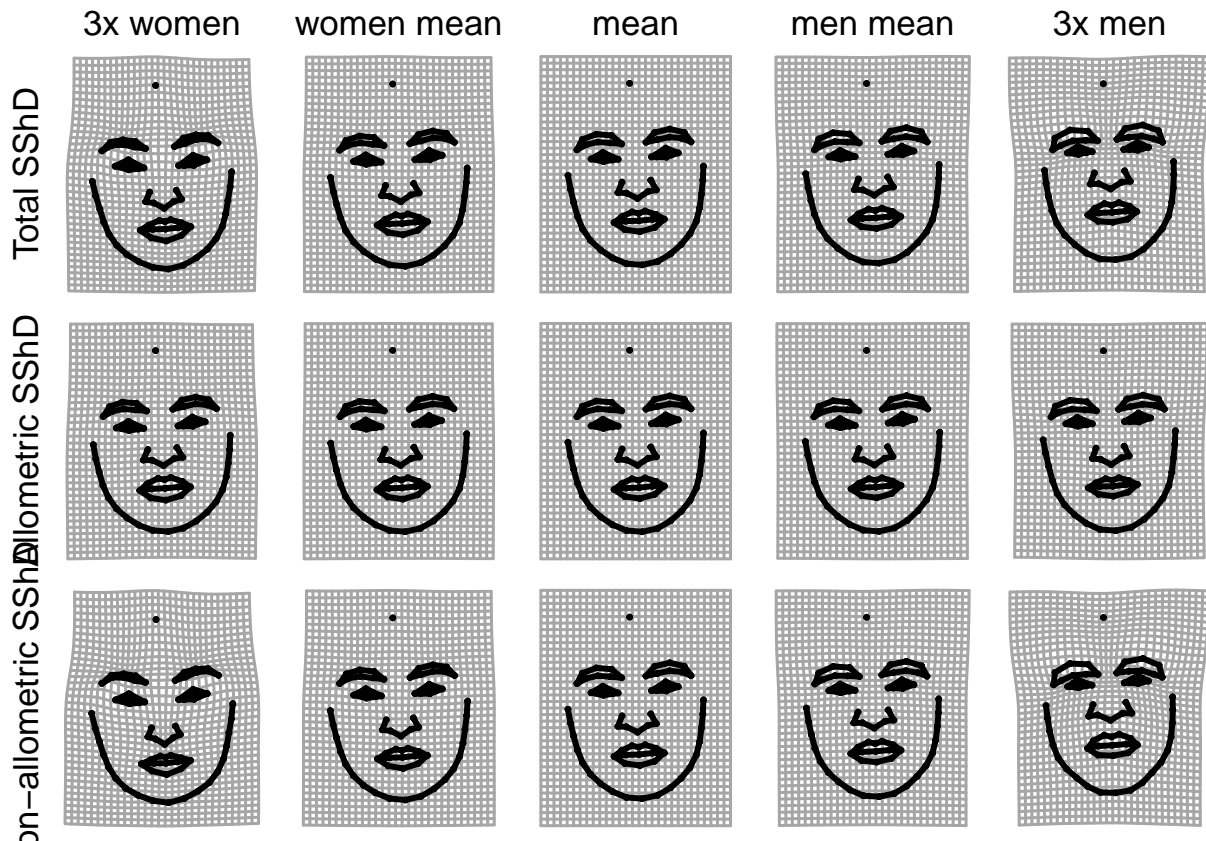
This analysis runs an alternative core script, where data are loaded and further processed, most models are defined and plots are drafted. Weight is significantly correlated with facial shape due to the effects of facial adiposity. This is also something that varies among populations and can, potentially, vary among sexes by population. We regress facial shape on weight in this study and consider only the residuals as a material for the other regression models and summarizations.

We have decided to report the analysis without accounting for weight in the manuscript, because that allowed us to include the data from United Kingdom, where the weight of female targets was not known.

The results of this analysis are very similar to the results of the analysis that does not account for body weight, which suggests that our findings are robust. It is true that the positive effect of non-allometric sextypicality (although present) gets slightly weaker in women, because the effect of body size is overcompensated by accounting for two intercorrelated measures (height and weight). The loss of statistical significance ($p=0.1$ for the effect of non-allometric sextypicality on attractiveness of female targets) might be also due to the lower sample size because of the necessity to exclude UK sample, where body weight was not known.

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

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

In total we had

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

```
## [1] 1015
```

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

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

```
##  NAM  CMR   TR   RO   CZ  COL  BRAZ
##   90  301  184   48  154  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])
```

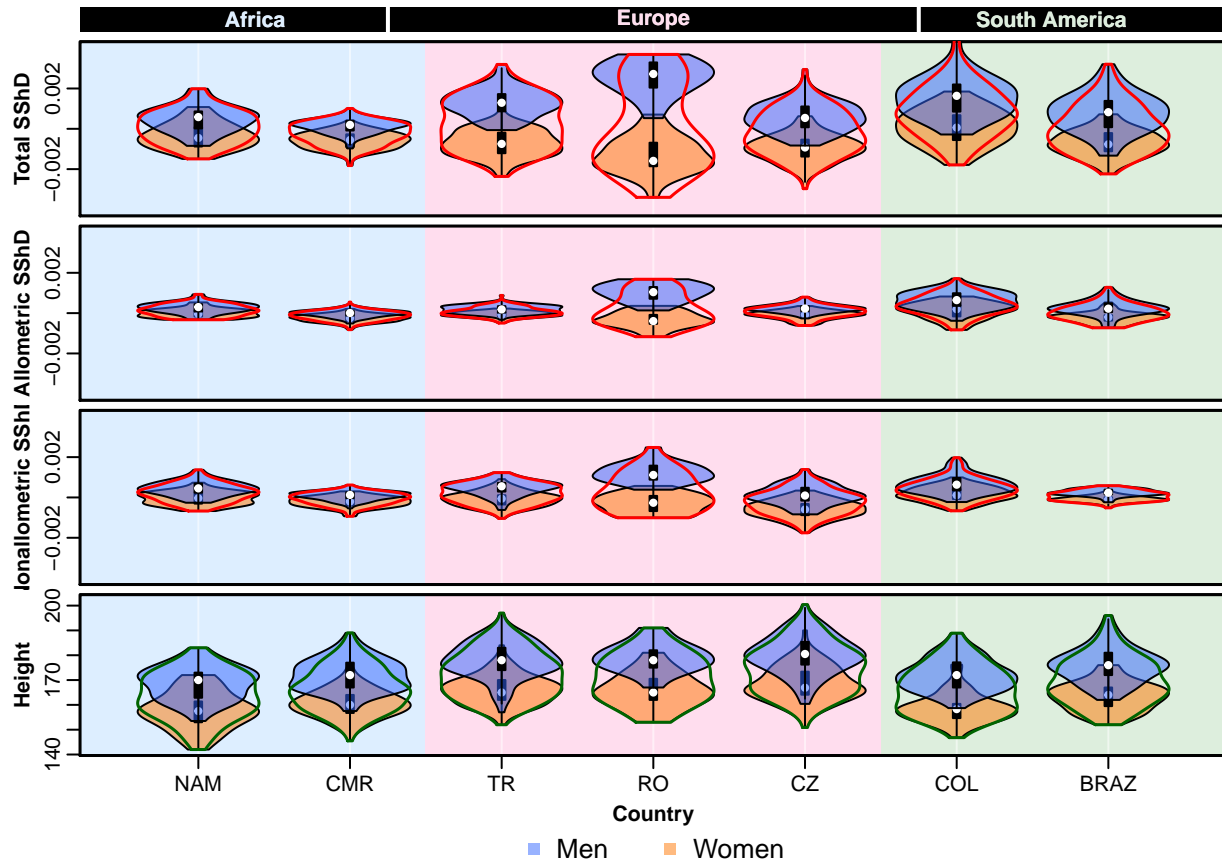
```
## NAM CMR TR RO CZ COL BRAZ
## 48 150 91 17 76 72 49
```

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

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

```
#Visualize vioplot
```

```
source("visualization_vio_withoutUK.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 national
```

```
sex.vecs<-sex.vecs[,-1]
```

```
Asex.vecs<-Asex.vecs[,-1]
```

```
Nsex.vecs<-Nsex.vecs[,-1]
```

Vectors between Allometric vector and overall 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
## 22.19617 34.45653 33.91081 45.89306 32.09015 29.32153 51.95369
```

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

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

```
##      BRAZ      CMR      COL      CZ      NAM      RO      TR
## 31.64457 17.94546 16.66451 13.39399 19.65199 24.98360 17.64217
```

Angle between two components of Sexual shape dimorphism

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

```
##      BRAZ      CMR      COL      CZ      NAM      RO      TR
## 44.63487 49.85073 45.22295 53.85792 51.49109 35.14593 63.25328
```

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
## 44.63487 49.85073 45.22295 53.85792 51.49109 35.14593 63.25328
```

```
Aang+Nang
```

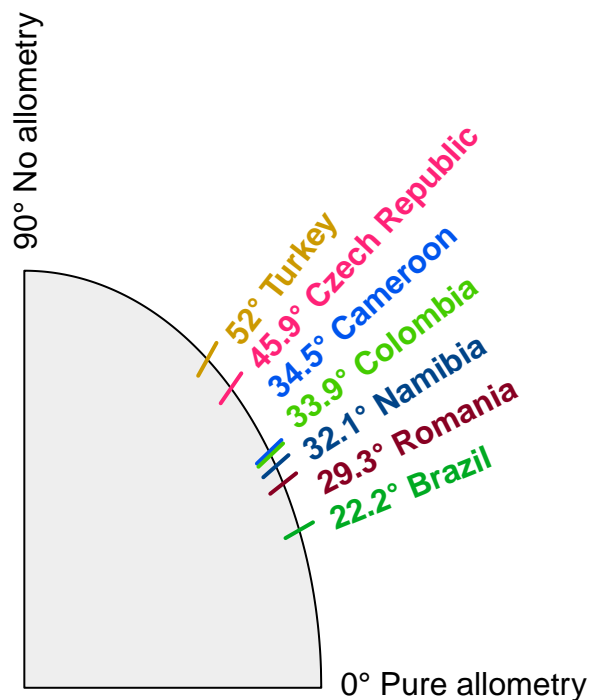
```
##      BRAZ      CMR      COL      CZ      NAM      RO      TR
## 53.84075 52.40199 50.57532 59.28706 51.74213 54.30513 69.59586
```

It fits :)

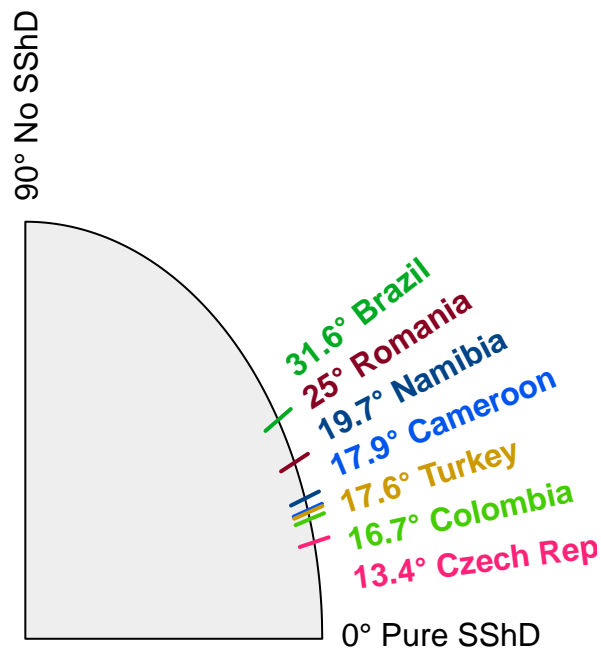
Visualize the results

```
cols<-c("#00AA22", "#0055EE", "#44CC00", "#FF2277", "#004488", "#880022", "#CC9900")
anglabs<-c("Brazil", "Cameroon", "Colombia", "Czech Republic", "Namibia", "Romania", "Turkey")
source("visualization_angles.R", encoding="UTF-8")
```

SShD and allometric SShD



SShD and nonallometric SShD



```
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      0.0035      0.0034 0.0037 0.0033
## CMR      0.0043      0.0042 0.0042 0.0045
## TR       0.0036      0.0035 0.0041 0.0031
## RO       0.0037      0.0036 0.0050 0.0029
## CZ       0.0039      0.0037 0.0038 0.0038
## COL      0.0038      0.0037 0.0048 0.0027
## BRAZ     0.0030      0.0028 0.0032 0.0028
```

All pairwise differences higher than

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

```
## [1] 0.0006508445
```

were statistically significant.

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

```
## [1] 0.0006509398
```

for the morphological disparity controlled for sex

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

```
## [1] 0.0008889934
```

for male faces only

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

```
## [1] 0.0007158646
```

for female faces only

Male faces showed higher morphological disparity than female faces

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

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

Procrustes variances for defined groups were

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

```
##           F           M
```

```
## 0.003584344 0.004097862
```

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

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

```
## [1] 0.014
```

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

```
##           F           M
```

```
## 0.002814809 0.003065143
```

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"],mean))
```

```
#Nonallometric
```

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

```
#Distinctiveness 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 0.00028 0.00051  11
## CMR  0.00073 0.00025 0.00034  12
## TR   0.00200 0.00027 0.00059  12
## RD   0.00380 0.00140 0.00150  14
## CZ   0.00160 0.00034 0.00075  12
## COL  0.00150 0.00054 0.00052  13
## BRAZ 0.00150 0.00049 0.00033  13

```

The total SShd gets essentially projected 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 = 9.5973, df = 5, p-value = 0.0002081
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.8284677 0.9962840
## sample estimates:
##          cor
## 0.9739153

```

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

```

##
## Pearson's product-moment correlation
##
## data: cos(deg2rad(Nang)) * dif and difN
## t = 5.504, df = 5, p-value = 0.002707
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.5735754 0.9893032
## sample estimates:
##          cor
## 0.9264617

```

It can be, therefore, stated that sexual shape dimorphism 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 allometric and non-allometric SShD vectors (figure with angles).

Mixed effect results - sextypicality 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.res1[,5],2))
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(mixed.resA1[,5],2))
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(mixed.resN1[,5],2))
colnames(mixed.resN1)<-nammixed
```

```
mixed.res1
```

##	Estimate	Std. Error	df	t value	Pr(> t)
## (Intercept)	0.002	0.044	1009.1	0.04	0.971
## Sextypicality	0.188	0.045	859.0	4.16	0.000
## sexM	-0.002	0.062	1007.5	-0.03	0.975
## Sextypicality:sexM	-0.145	0.062	766.1	-2.33	0.020

```
mixed.resA1
```

##	Estimate	Std. Error	df	t value	Pr(> t)
## (Intercept)	0.028	0.060	7.8	0.47	0.653
## Allometric_SShD	-0.078	0.083	1.7	-0.94	0.461
## sexM	0.010	0.080	5.6	0.13	0.903
## Allometric_SShD:sexM	0.181	0.112	2.8	1.61	0.211

```
mixed.resN1
```

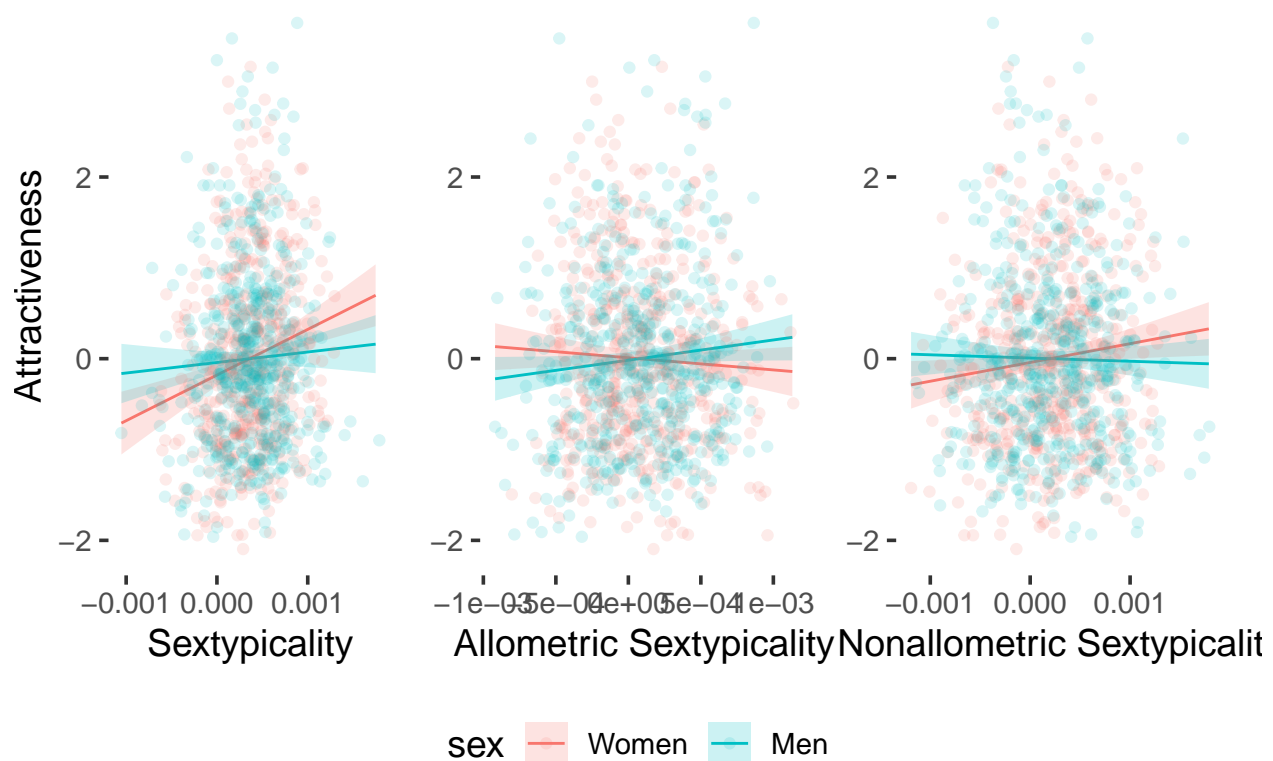
##	Estimate	Std. Error	df	t value	Pr(> t)
## (Intercept)	0.014	0.046	82.9	0.30	0.764
## Nonallometric_SShD	0.104	0.053	5.8	1.95	0.100
## sexM	-0.002	0.062	627.4	-0.03	0.974
## Nonallometric_SShD:sexM	-0.120	0.080	3.7	-1.49	0.214

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 visualize the linear relationship of the interaction models above in all cultures separately and together

```
source("visualization_linear_models_withoutUK.R")
```

```
#Three main panels summarizing Sextypicality attractiveness
figuremain
```

For comparison we add correlations 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 = -1.666, df = 510, p-value = 0.09632
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.15921369 0.01316716
## sample estimates:
## cor
## -0.07357278
```

```
mall.cor.h
```

```
##
## Pearson's product-moment correlation
##
## data: mdat$height and mscores
## t = 4.051, df = 501, p-value = 5.911e-05
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.09209543 0.26144765
## sample estimates:
```

```
##      cor
## 0.17809
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 = 16.199, df = 5, p-value = 1.634e-05
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.9351764 0.9986715
## sample estimates:
##      cor
## 0.9906072
```

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 = 2.5827, df = 5, p-value = 0.04927
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.006876153 0.961608368
## sample estimates:
##      cor
## 0.7560195
```

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 european 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 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")

```

