Report on Human sexual dimorphism

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03 02 2020

Running the core script, where data are loaded and further processed, most models are defined and plots are drafted, prepares this document for a neat report. If you are interested in details, you can run the Core script manually outside this report. We approach the visualizations in simmilar way. They are stored as separate scripts and sourced from this markdown file.

```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")
```
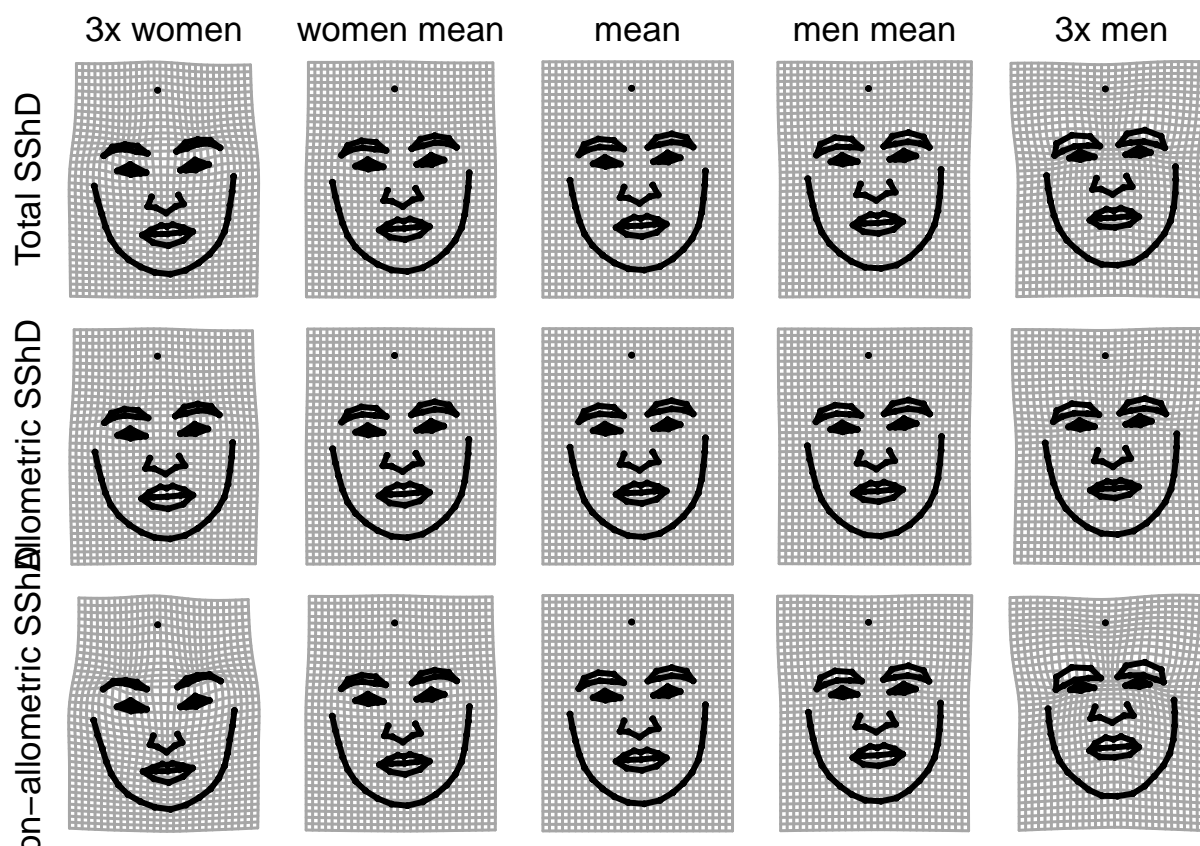

Similar analysis is conducted also nationwise - it sores the results into tiffs automatically for better resolution

R Markdown report of sexual dimorphism in facial morphology

We report the national samples in following order

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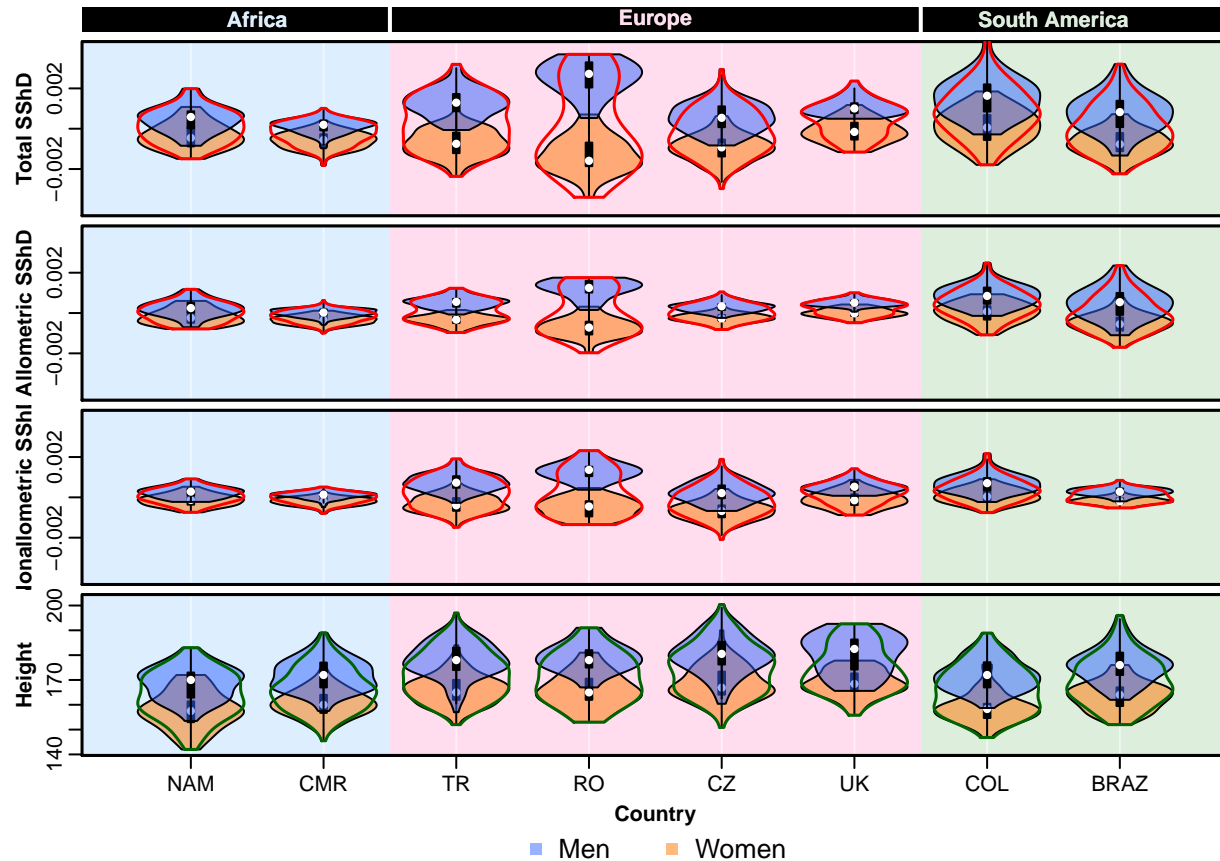
```
(Nfemales<-summary(gtf$nat[gtf$sex=="F"])[reord])
```

```
##  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
## 13.89478 17.51552 12.82013 20.51082 26.03176 18.29716 18.77206 24.14998
```

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

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

```
##      BRAZ      CMR      COL       CZ      NAM       RO       TR       UK
## 28.82597 19.27508 16.69510 12.95595 27.02477 19.16206 15.87865 19.25458
```

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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
## 42.18609 35.85257 28.73096 33.02488 52.89036 34.48556 32.54403 42.91370
```

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
## 42.18609 35.85257 28.73096 33.02488 52.89036 34.48556 32.54403 42.91370
```

```
Aang+Nang
```
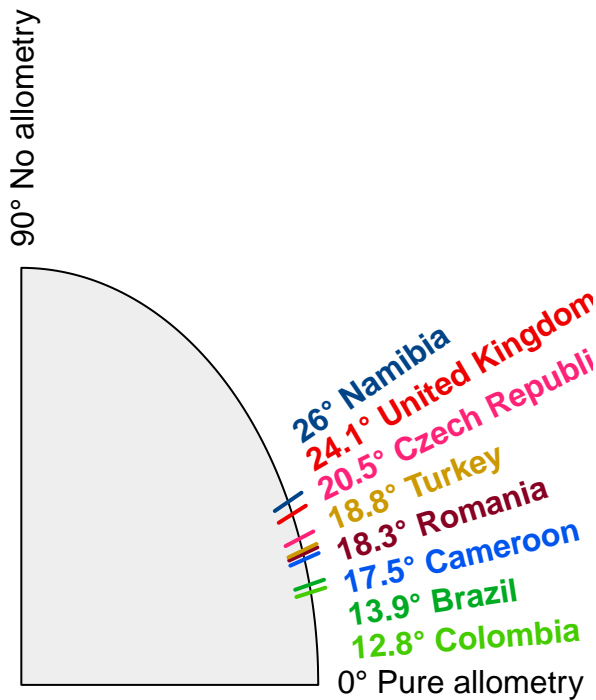
```
##      BRAZ      CMR      COL       CZ      NAM       RO       TR       UK
## 42.72075 36.79060 29.51522 33.46677 53.05653 37.45923 34.65071 43.40456
```
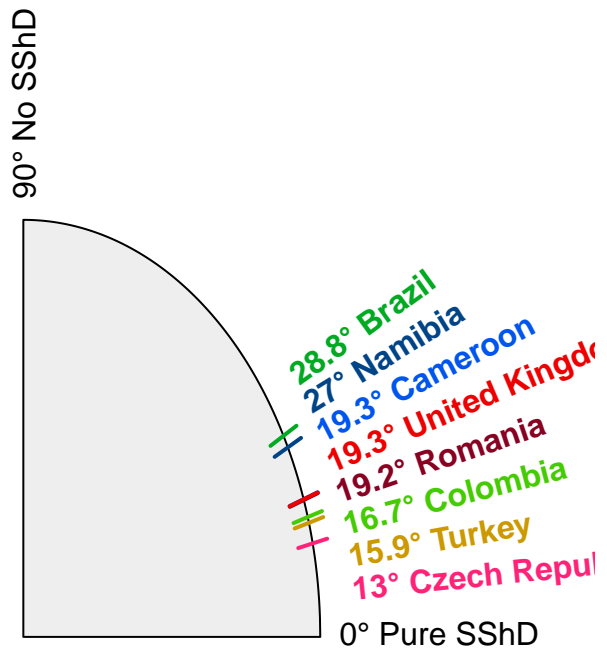
It fits :)

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    0.0037        0.0035 0.0037 0.0033
## CMR    0.0045        0.0044 0.0043 0.0046
## TR     0.0038        0.0034 0.0040 0.0030
## RO     0.0040        0.0035 0.0048 0.0029
## CZ     0.0040        0.0036 0.0037 0.0037
## UK     0.0034        0.0032 0.0033 0.0032
## COL    0.0039        0.0038 0.0049 0.0027
## BRAZ   0.0032        0.0029 0.0032 0.0028
```

All pairwise differences higher than

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

```
## [1] 0.0008213941
```

were statistically significant.

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

```
## [1] 0.0006361403
```

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
## 0.003705138 0.004197213
```

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

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

```
## [1] 0.026
```

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

```
##           F           M
## 0.002969885 0.003200536
```

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 0.00044 0.00042   11
## CMR  0.00073 0.00038 0.00034   12
## TR   0.00200 0.00089 0.00110   12
## RO   0.00380 0.00190 0.00180   14
## CZ   0.00160 0.00059 0.00097   12
## UK   0.00120 0.00053 0.00068   12
## COL  0.00150 0.00087 0.00065   13
## BRAZ 0.00150 0.00100 0.00046   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 = 8.7324, df = 6, p-value = 0.0001248
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.8029627 0.9934613
## sample estimates:
```

```
##       cor
## 0.9628372
```

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

```
##
##  Pearson's product-moment correlation
##
## data:  cos(deg2rad(Nang)) * dif and difN
## t = 9.0578, df = 6, p-value = 0.0001015
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.8151460 0.9939054
## sample estimates:
##       cor
## 0.9653252
```

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

```r
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      0.042 920.4    0.03    0.977
## Sextypicality         0.190      0.045  15.7    4.18    0.001
## sexM                  0.000      0.059 955.3    0.01    0.995
## Sextypicality:sexM   -0.155      0.063   7.5   -2.45    0.042
```

```r
mixed.resA1
```

```
##                      Estimate Std. Error     df t value Pr(>|t|)
## (Intercept)             0.079      0.045 115.1    1.75    0.082
## Allometric_SShD         0.153      0.068   8.6    2.26    0.051
## sexM                   -0.024      0.092   3.9   -0.26    0.805
## Allometric_SShD:sexM   -0.003      0.115   5.7   -0.03    0.977
```
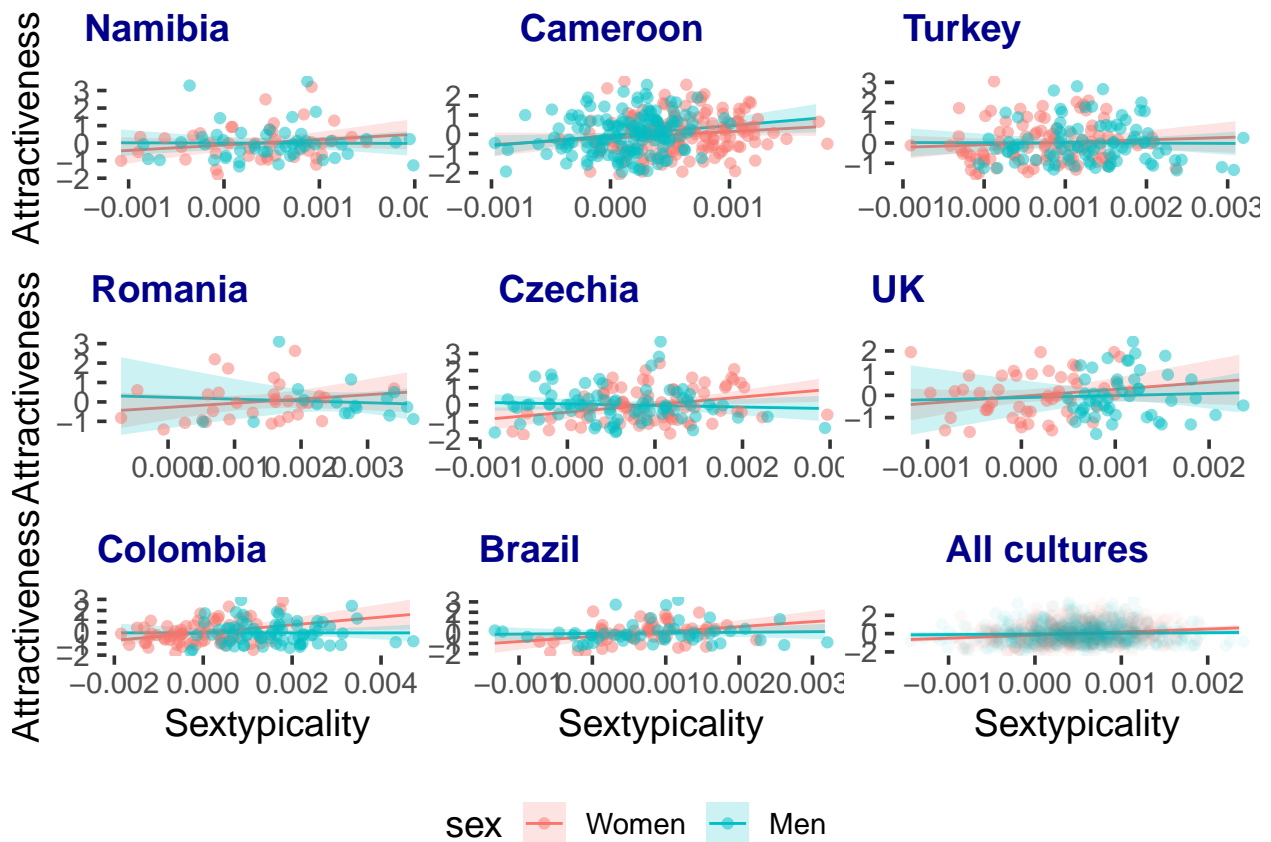
```r
mixed.resN1
```

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

```
## (Intercept)                    0.002    0.042 22.3    0.04   0.970
## Nonallometric_SShD              0.151    0.043  2.6    3.46   0.051
## sexM                           -0.001    0.060 96.1   -0.02   0.984
## Nonallometric_SShD:sexM        -0.188    0.060  5.9   -3.11   0.022
```
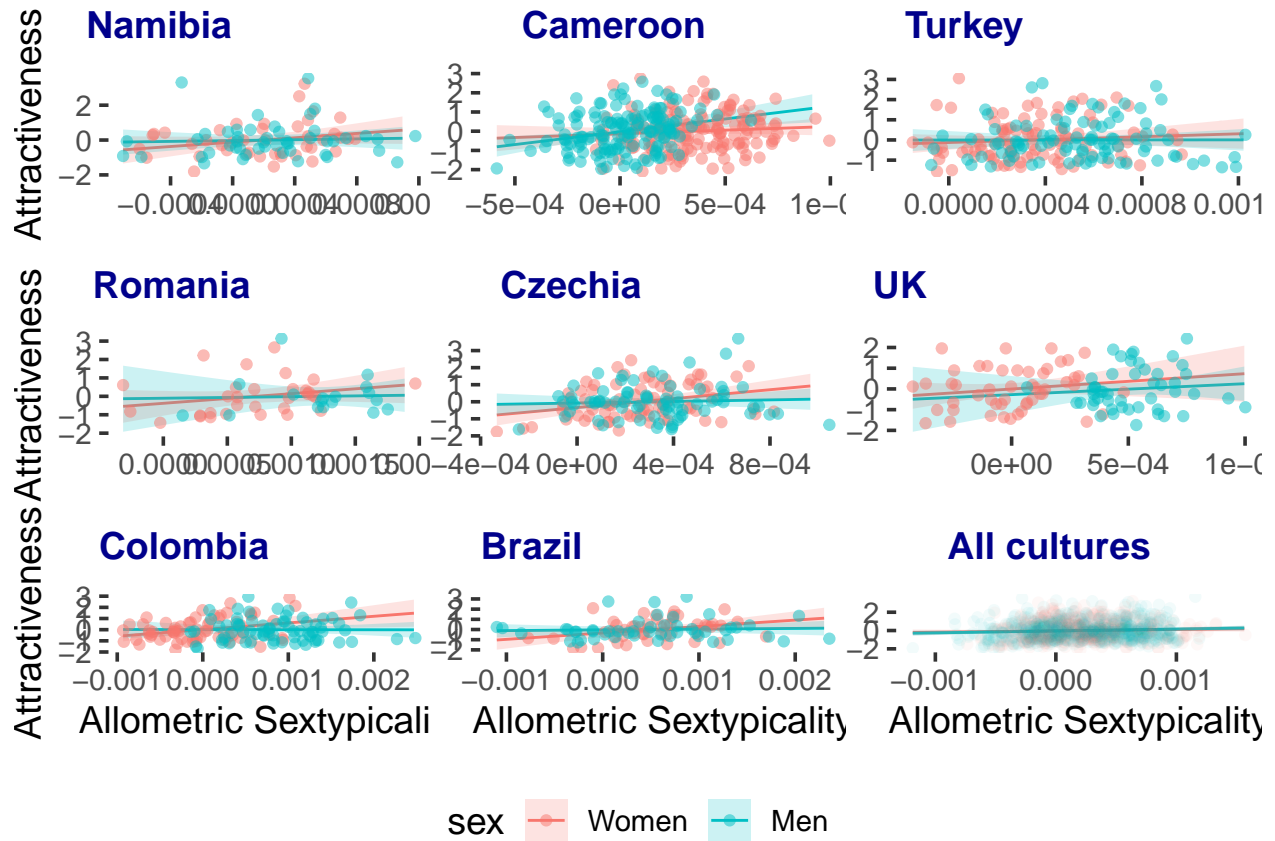
In total SShD and its Nonallometric component, sextypicality raises attractiveness in female faces, but not in male faces. The interaction term - the difference between regression coefficient for males and females is statistically significant. In allometric component, female faces get more attractive 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
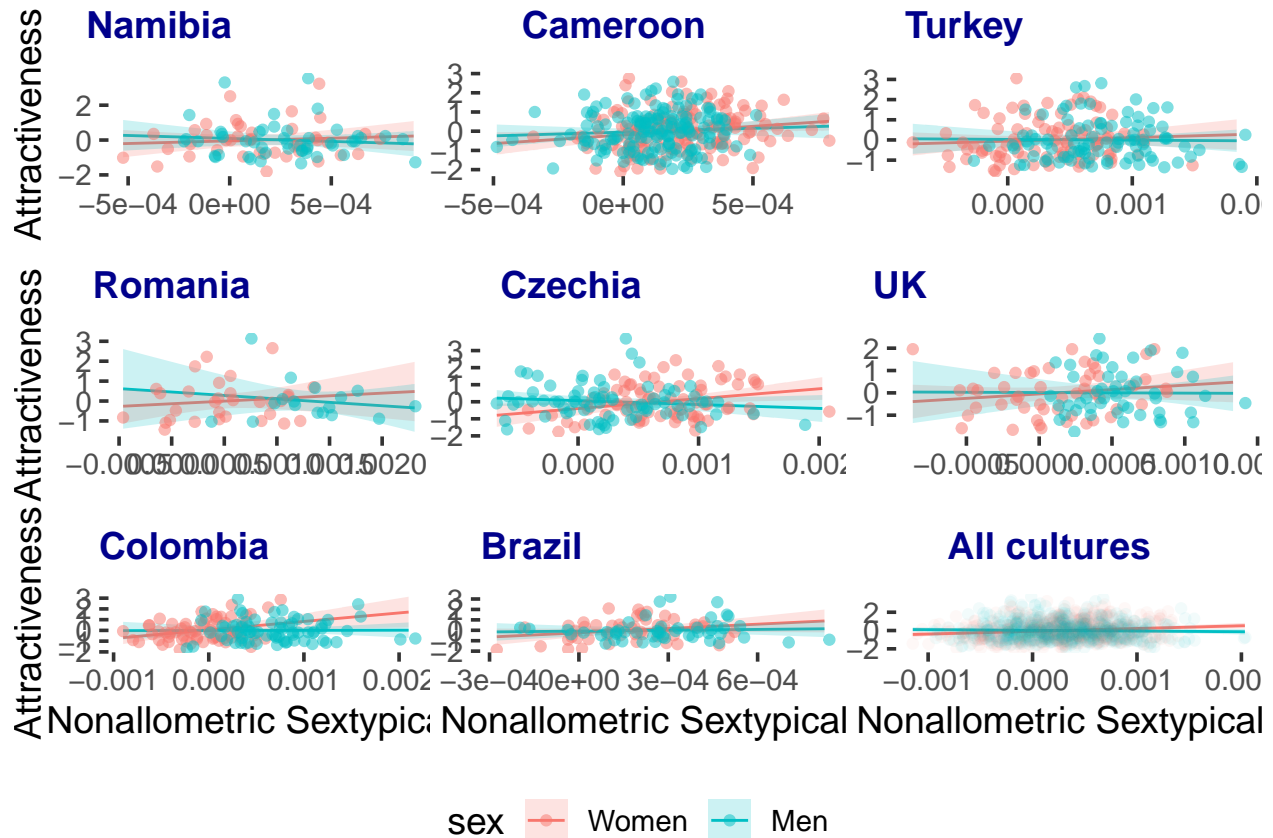
```
source("visualization_linear_models.R")
#Total SShD
figure1
```



```
#Allometric SShD
figureA
```

Namibia | Cameroon | Turkey
Romania | Czechia | UK
Colombia | Brazil | All cultures

Attractiveness

Allometric Sextypicality

sex — Women — Men

```
#Nonallometric SShD
figureN
```

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 = -0.093516, df = 560, p-value = 0.9255
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.08663169  0.07878229
## sample estimates:
##          cor
## -0.003951736
```

```
mall.cor.h
```

```
##
##  Pearson's product-moment correlation
##
## data:  mdat$height and mscores
## t = 4.8903, df = 550, p-value = 1.324e-06
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.1227678 0.2827685
## sample estimates:
```

```
##      cor
## 0.204131
```

```
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.

```
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
```
```r
source("visualization_differences.R")
```
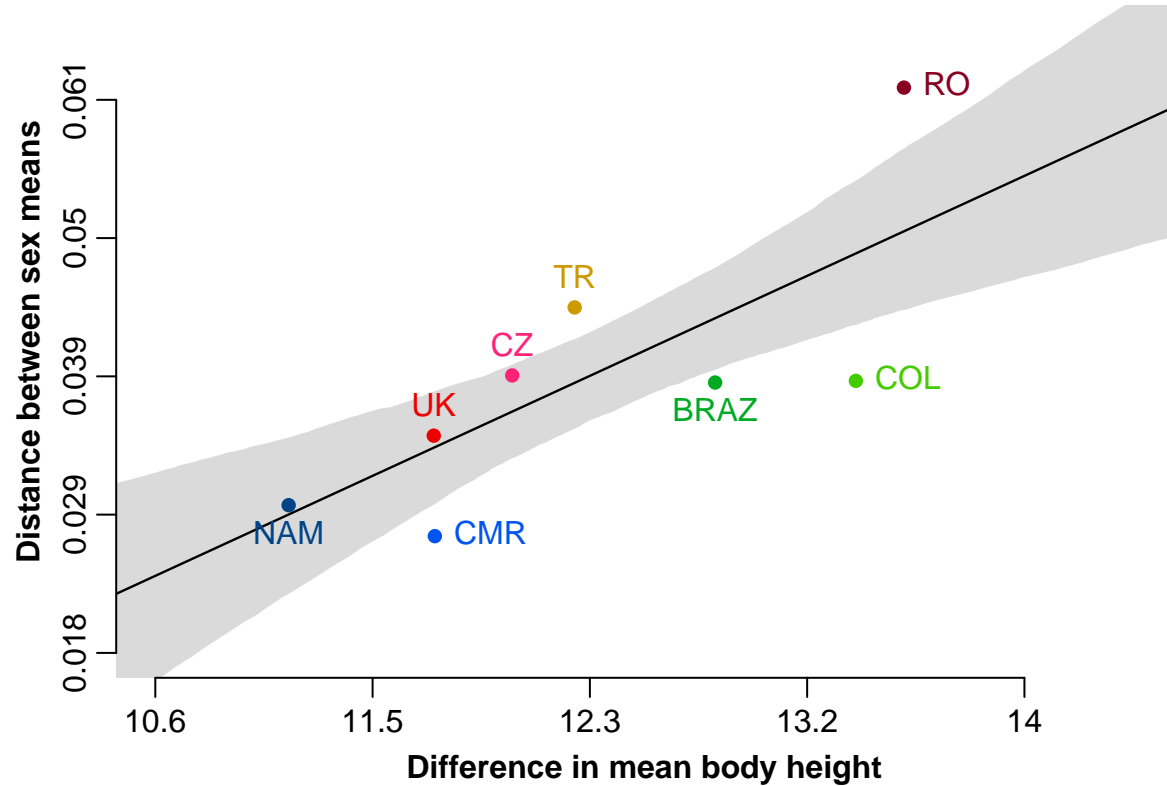
Note that all auropean countries are above the line - they have higher difference between group means than expected and most non-european countries are below the line - they have lower difference between group means than expected. It contributes to our argument. Facial morphological dimorphism seems to be more important in european countries.

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

```r
source("visualization_dimorphism.R")
```
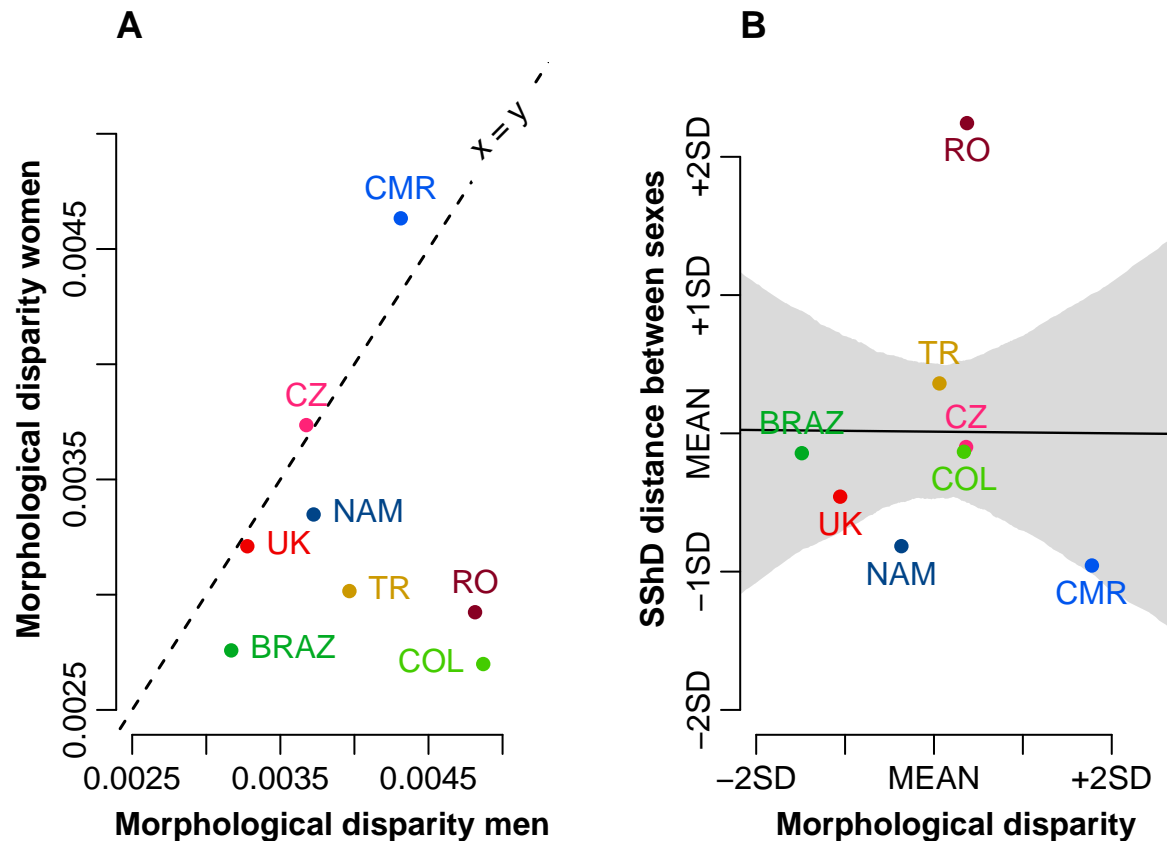
we explore the relationship between several demographic variables from World population prospects https://population.un.org/wpp/ and world urbanization prospects https://population.un.org/wup/, we use data from 2015 because this year provides entries in all investigated variables

```
dem<-read.table("demography.csv",sep="\t",header=T)
demnam<-dem[,1]

dem<-dem[,-1]
row.names(dem)<-demnam
round(dem,2)
```

```
##      urban density   popsize     GDP sexratio
## NAM  46.90    2.81   2314.90  5032.9    93.81
## CMR  54.58   49.29  23298.38  1327.0    99.86
## TR   73.61  102.04  78529.41 10948.7    96.92
## RO   53.89   86.57  19925.18  8977.5    94.86
## CZ   73.48  137.25  10601.39 17715.6    96.60
## UK   82.63  272.23  65860.15 44966.1    97.19
## COL  79.76   42.83  47520.67  6175.9    96.11
## BRAZ 85.77   24.46 204471.76  8814.0    96.96
```

```
reord<-c(5,2,7,6,4,8,3,1)

cols<-c("#00AA22","#0055EE","#44CC00","#FF2277","#004488","#880022","#CC9900","#EE0000")
coldem<-c("#555555","#FF6600","#0066DD","#008822")

pdem<-dem[,1:4]
```

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```
pdem<-pdem/rep(apply(pdem,2,max),each=8)*0.6

x<-rep(3:10)
y<-rep(0,8)

par(mar=c(0,0,0,0))
plot(1:10,1:10,bty="n",axes=F,xlab="",ylab="",xlim=c(0,10.2),ylim=c(-0.2,1.2),type="n")
text(x,y,rownames(dem),col=cols[reord],xpd=T)


offx<-0.1
offy<--0.2
demlwd<-2

for(i in 1:8){
  lines(rep(x[i]-offx/2-offx,2),c(y[i]-offy,y[i]-offy+pdem[i,1]),lwd=demlwd,col=coldem[1],xpd=T)
  lines(rep(x[i]-offx/2,2),c(y[i]-offy,y[i]-offy+pdem[i,2]),lwd=demlwd,col=coldem[2],xpd=T)
  lines(rep(x[i]+offx/2,2),c(y[i]-offy,y[i]-offy+pdem[i,3]),lwd=demlwd,col=coldem[3],xpd=T)
  lines(rep(x[i]+offx/2+offx,2),c(y[i]-offy,y[i]-offy+pdem[i,4]),lwd=demlwd,col=coldem[4],xpd=T)
    }

text(rep(-0.5,4),c(3,2,1,0)*0.25,c("Urbanization","Population density","Population size","GDP per capita
```
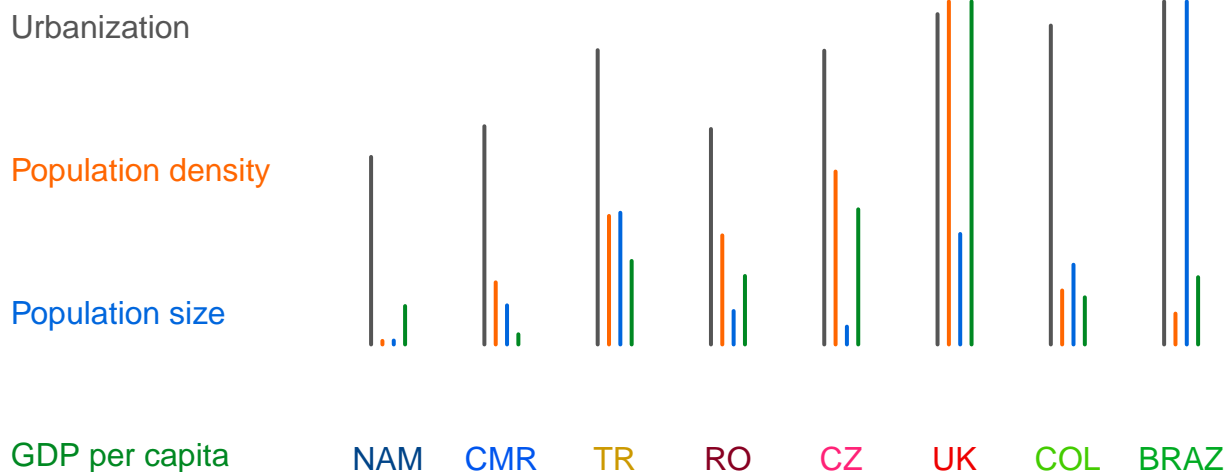

Less urbanized countries (african ones) have only relatively smaller SShD for a given total morphological disparity.