Alternative analysis: Standardized sexscores

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This analysis runs an alternative core script, with a different formula to capture score of sexual shape dimorphism. The formula we use to determine the sexscore is

$$sexscore(\vec{A}) = \vec{A} \bullet (MM \vec{-} FM),$$

whereas most studies so far used the formula in a standardized form

$$sexscore(\vec{A}) = \frac{\vec{A} \bullet (MM \vec{-} FM)}{\left\| MM \vec{-} FM \right\|^2}.$$

Here we demonstrate how our results change if we use the later instead of the former. Most findings including the effect of sextypicality on rated attractiveness holds, but we are no longer able to compare the magnitude of the vector connecting male and female mean shape between national samples, bacuse we calculate (and hence standardize) sexscores within each national sample separately.

```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")
```

	3x women	women mean	mean	men mean	3x men

Total SShD

Allometric SShD

Non-allometric SShD
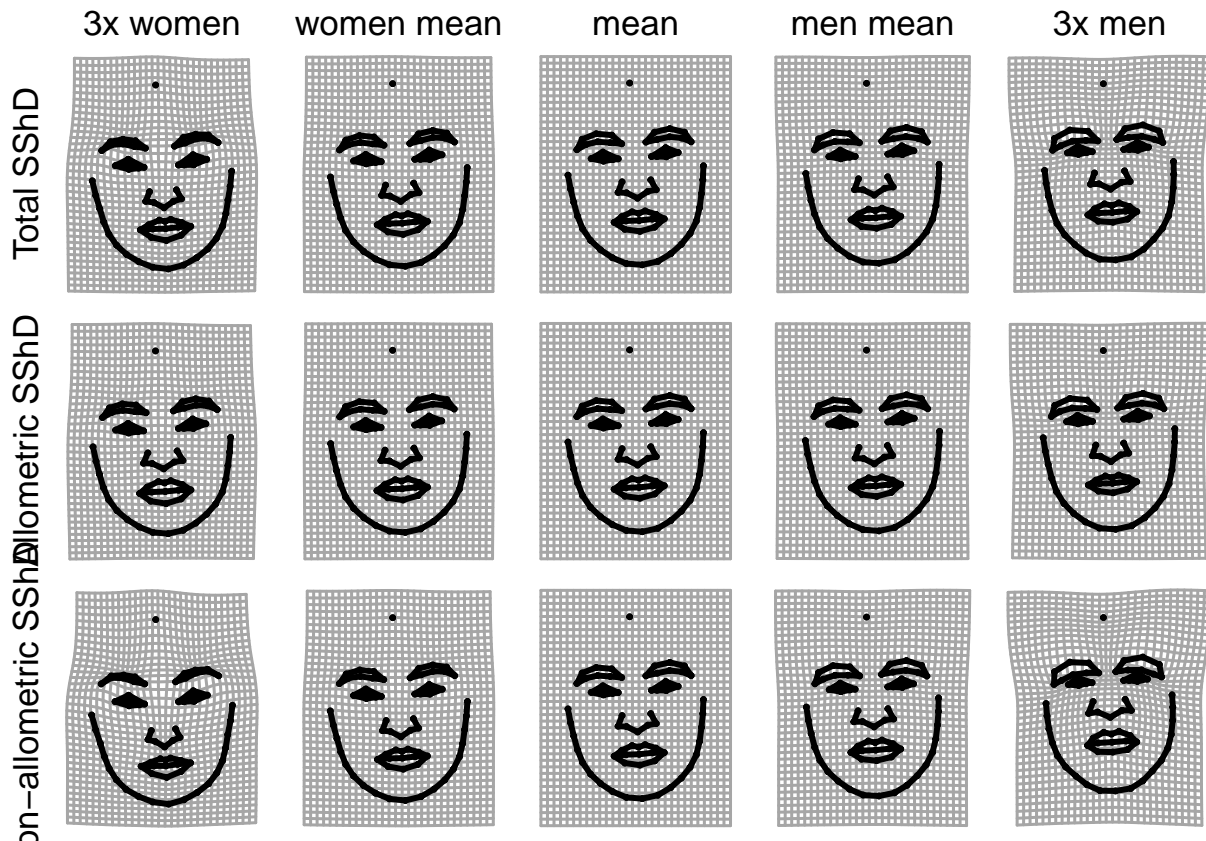
R Markdown report of sexual dimorphism in facial morphology

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

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

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

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

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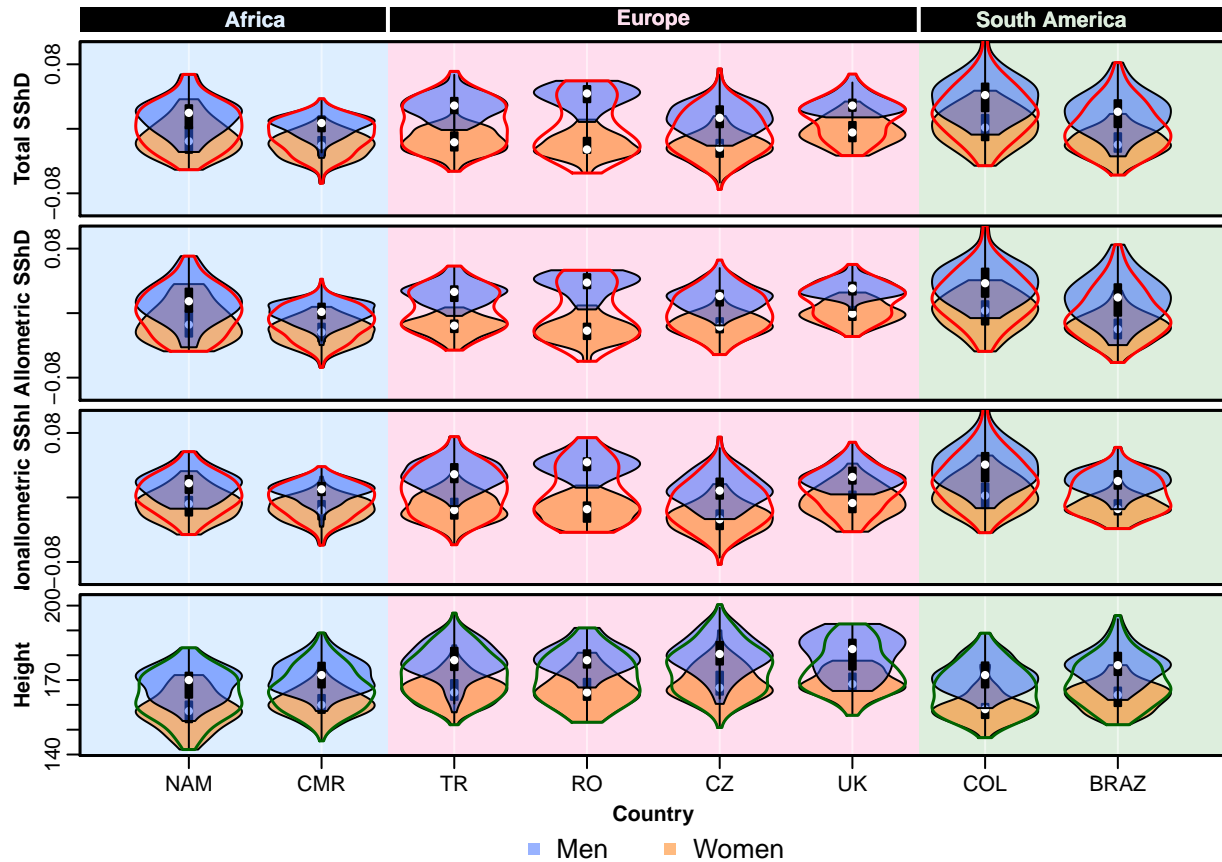
```r
(Nmales<-summary(gtf$nat[gtf$sex=="M"])[reord])
```

```
##  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_standardized.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)

3

```
(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
```

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
```
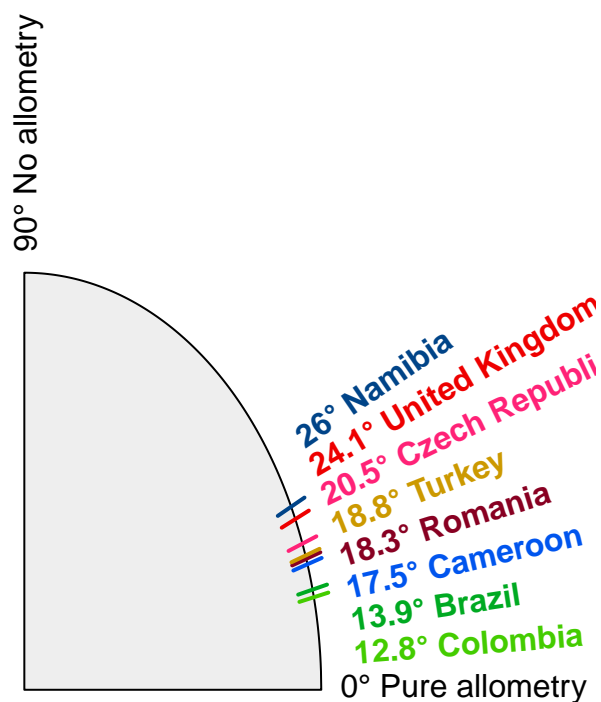
It fits :)

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")
```
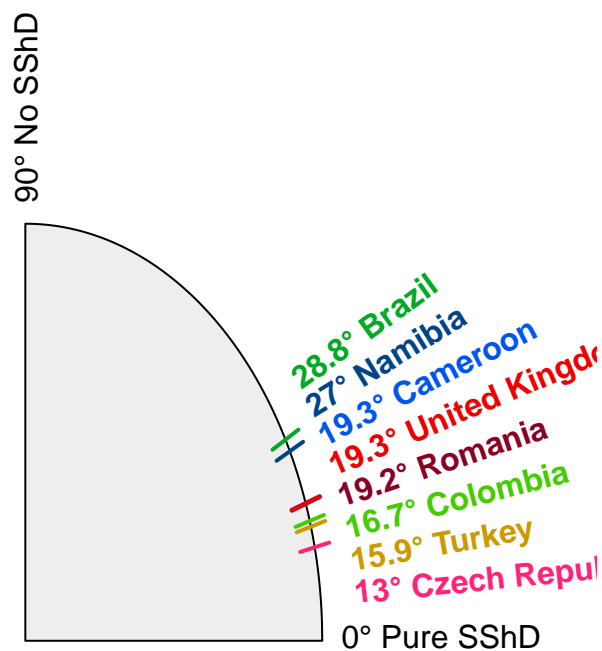
SShD and allometric SShD

90° No allometry

26° Namibia
24.1° United Kingdom
20.5° Czech Republic
18.8° Turkey
18.3° Romania
17.5° Cameroon
13.9° Brazil
12.8° Colombia

0° Pure allometry

SShD and nonallometric SShD

90° No SShD

28.8° Brazil
27° Namibia
19.3° Cameroon
19.3° United Kingdom
19.2° Romania
16.7° Colombia
15.9° Turkey
13° Czech Republic

0° Pure SShD

'

```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.

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

[1] 0.0006361403

for the morphological disparity controlled for sex

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

[1] 0.001138923

for male faces only

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

[1] 0.000897329

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
## 0.003705138 0.004197213
```

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

```
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

```r
#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  0.029 0.026 0.026   11
## CMR  0.027 0.026 0.025   12
## TR   0.045 0.042 0.043   12
## RO   0.062 0.059 0.058   14
## CZ   0.040 0.037 0.038   12
## UK   0.035 0.032 0.033   12
## COL  0.039 0.038 0.037   13
## BRAZ 0.039 0.038 0.034   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 = 1459.9, df = 6, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.9999919 0.9999998
## sample estimates:
##       cor
## 0.9999986
```

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

```
##
##   Pearson's product-moment correlation
##
## data:  cos(deg2rad(Nang)) * dif and difN
## t = 1279.2, df = 6, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.9999894 0.9999997
## sample estimates:
##       cor
## 0.9999982
```

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  920.1    0.03    0.977
## Sextypicality        0.190      0.045   15.8    4.18    0.001
## sexM                 0.000      0.059  955.4    0.01    0.995
## Sextypicality:sexM  -0.155      0.063    7.6   -2.45    0.042
```

```r
mixed.resA1
```

```
##                     Estimate Std. Error     df t value Pr(>|t|)
## (Intercept)            0.079      0.045  145.8    1.75    0.082
## Allometric_SShD        0.153      0.068    8.8    2.26    0.050
## sexM                  -0.024      0.092    6.3   -0.26    0.800
## Allometric_SShD:sexM  -0.004      0.115    6.9   -0.03    0.976
```

```r
mixed.resN1
```

```
##                        Estimate Std. Error     df t value Pr(>|t|)
## (Intercept)               0.002      0.042   23.3    0.04    0.970
## Nonallometric_SShD        0.151      0.043    2.7    3.46    0.047
## sexM                     -0.001      0.060  100.3   -0.02    0.984
## Nonallometric_SShD:sexM  -0.188      0.060    6.2   -3.11    0.020
```

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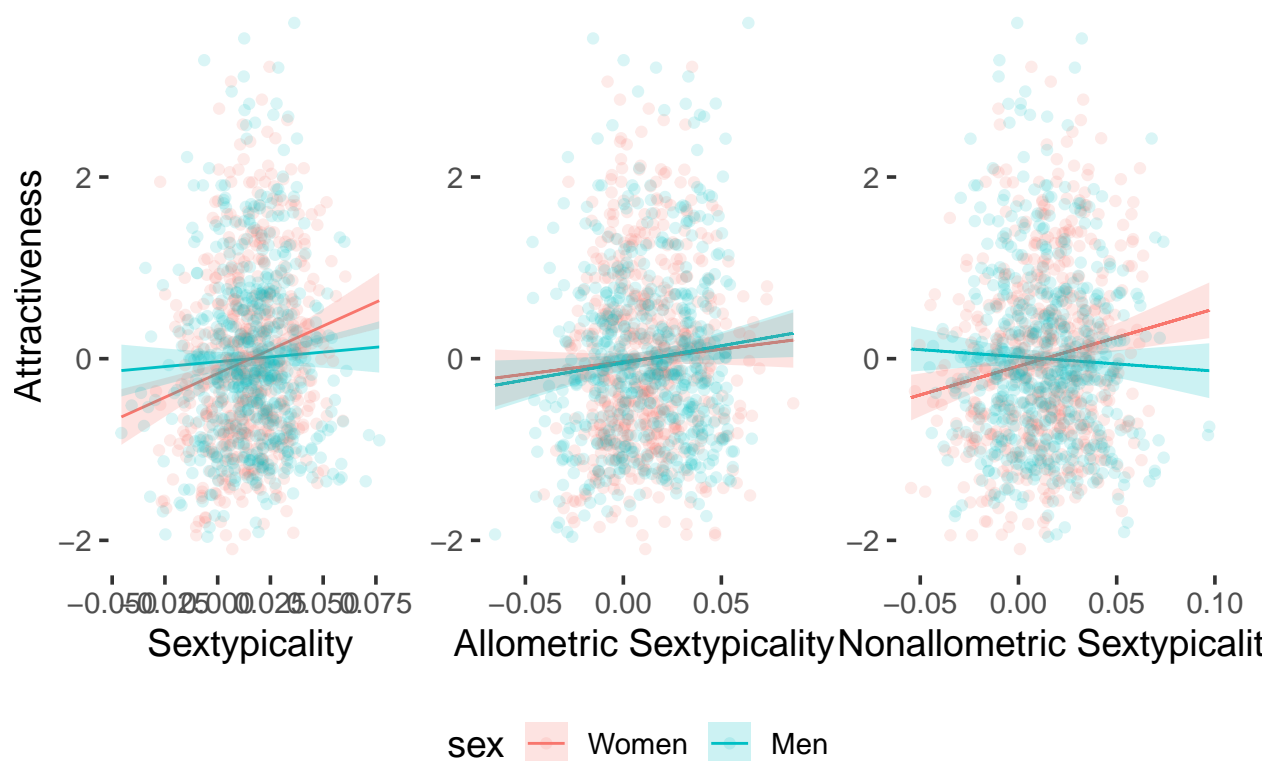
We can visulaize the linear relationship of the interaction models above in all cultures separately and together

```r
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 = -0.093516, 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 = 164382474, df = 6, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  1 1
## sample estimates:
## cor
##   1
```

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 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
```

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