

Alternative analysis: Accounting for focal length

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This analysis runs an alternative core script. We regress facial shape on logarithm of focal length (which varied slightly between the samples) and consider only the residuals of this regression as a material for the other regression models and summarizations.

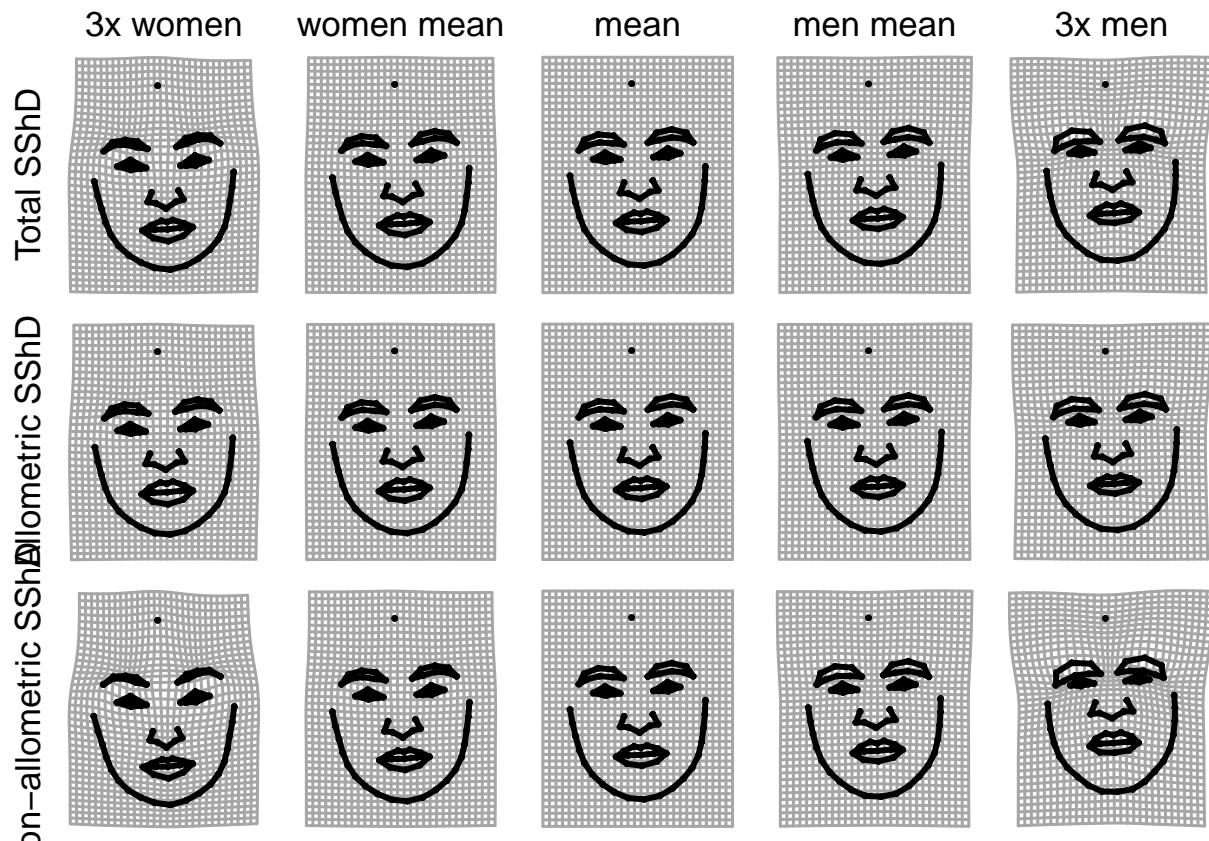
The results of this analysis are very similar to the results of the analysis that does not account for focal length which suggests that our findings are robust. Even visual inspection of the plot below can lead to the same conclusion, strikingly different samples in SShD such as African and south american samples had almost identical focal length, most variation in methodology was between european samples, which were, however, quite consistent in SShD patterns.

```
#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])
```

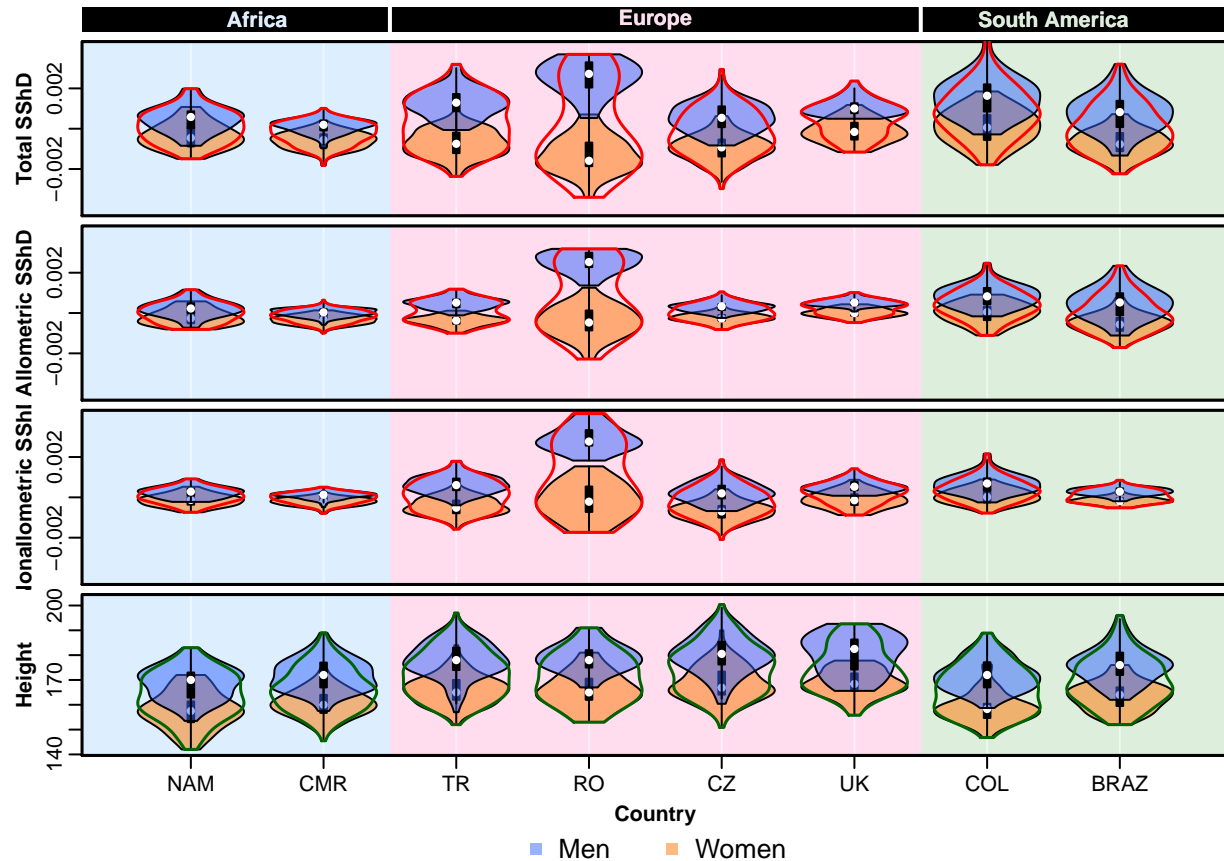
```
##  NAM  CMR   TR   RO   CZ   UK  COL  BRAZ
##   48  150   91   17   76   49   72   49
```

```
(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 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      UK
## 13.89478 17.56376 12.76535 20.42553 26.03176 21.03909 18.53715 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 19.35315 16.68541 12.94666 27.02477 24.97689 15.85960 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 35.98227 28.65915 32.92919 52.89036 28.10005 32.25908 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 35.98227 28.65915 32.92919 52.89036 28.10005 32.25908 42.91370
```

```
Aang+Nang
```

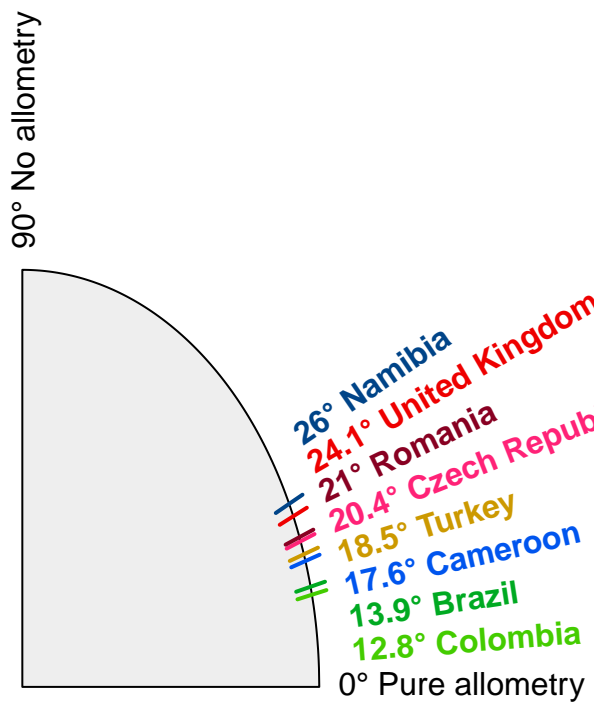
```
##      BRAZ      CMR      COL      CZ      NAM      RO      TR      UK
## 42.72075 36.91692 29.45076 33.37219 53.05653 46.01598 34.39675 43.40456
```

It fits :)

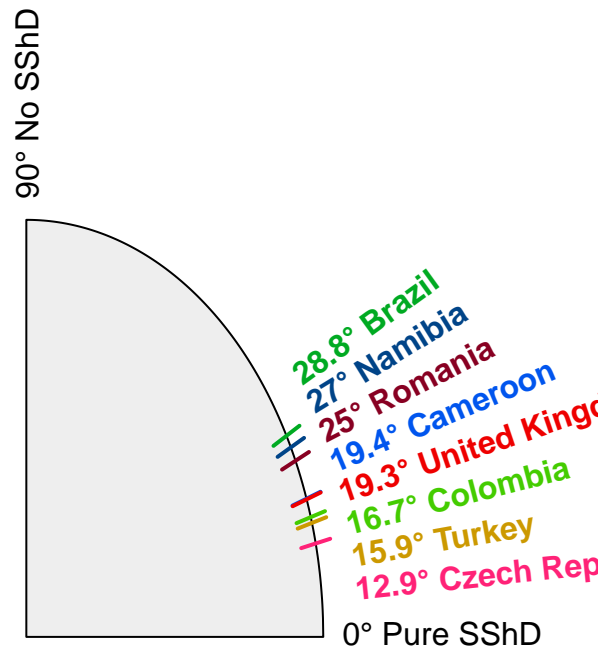
Visualize the results

```
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



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 0.0043 0.0046
## TR       0.0029      0.0025 0.0040 0.0030
## RO       0.0055      0.0051 0.0048 0.0029
## CZ       0.0040      0.0037 0.0037 0.0037
## UK       0.0035      0.0033 0.0033 0.0032
## COL      0.0039      0.0037 0.0049 0.0027
## BRAZ     0.0033      0.0030 0.0032 0.0028

```

All pairwise differences higher than

```

disp.tab.sig(mdisp.1)

```

```

## [1] 0.0005653633

```

were statistically significant.

```

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

```

```

## [1] 0.0004944467

```

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
## 0.003551074 0.004063041

```

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

```

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

```

```

## [1] 0.034

```

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

```
##           F           M
## 0.003012471 0.003237551
```

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 0.00044 0.00042   11
## CMR  0.00073 0.00038 0.00034   12
## TR   0.00200 0.00090 0.00110   12
## RO   0.00380 0.00300 0.00310   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 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 = 8.8171, df = 6, p-value = 0.0001182
```

```
## alternative hypothesis: true correlation is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## 0.8062424 0.9935814
```

```
## sample estimates:
```

```
##          cor
## 0.9635096

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

##
## Pearson's product-moment correlation
##
## data: cos(deg2rad(Nang)) * dif and difN
## t = 9.3875, df = 6, p-value = 8.296e-05
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.8264165 0.9943111
## sample estimates:
##          cor
## 0.9676027
```

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),round(mixed.res1[,6],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),round(mixed.resA1[,6],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),round(mixed.resN1[,6],2))
colnames(mixed.resN1)<-nammixed

mixed.res1
```

##	Estimate	Std. Error	df	t value	Pr(> t)
## (Intercept)	0.002	0.042	786.5	0.04	0.968
## Sextypicality	0.191	0.046	15.2	4.13	0.001
## sexM	0.001	0.059	822.3	0.02	0.987
## Sextypicality:sexM	-0.155	0.065	7.9	-2.39	0.044

```
mixed.resA1
```

##	Estimate	Std. Error	df	t value	Pr(> t)
## (Intercept)	0.079	0.045	107.7	1.75	0.083
## Allometric_SShD	0.196	0.073	8.1	2.70	0.027
## sexM	-0.041	0.090	6.2	-0.46	0.661
## Allometric_SShD:sexM	-0.053	0.116	7.3	-0.46	0.660

```
mixed.resN1
```

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

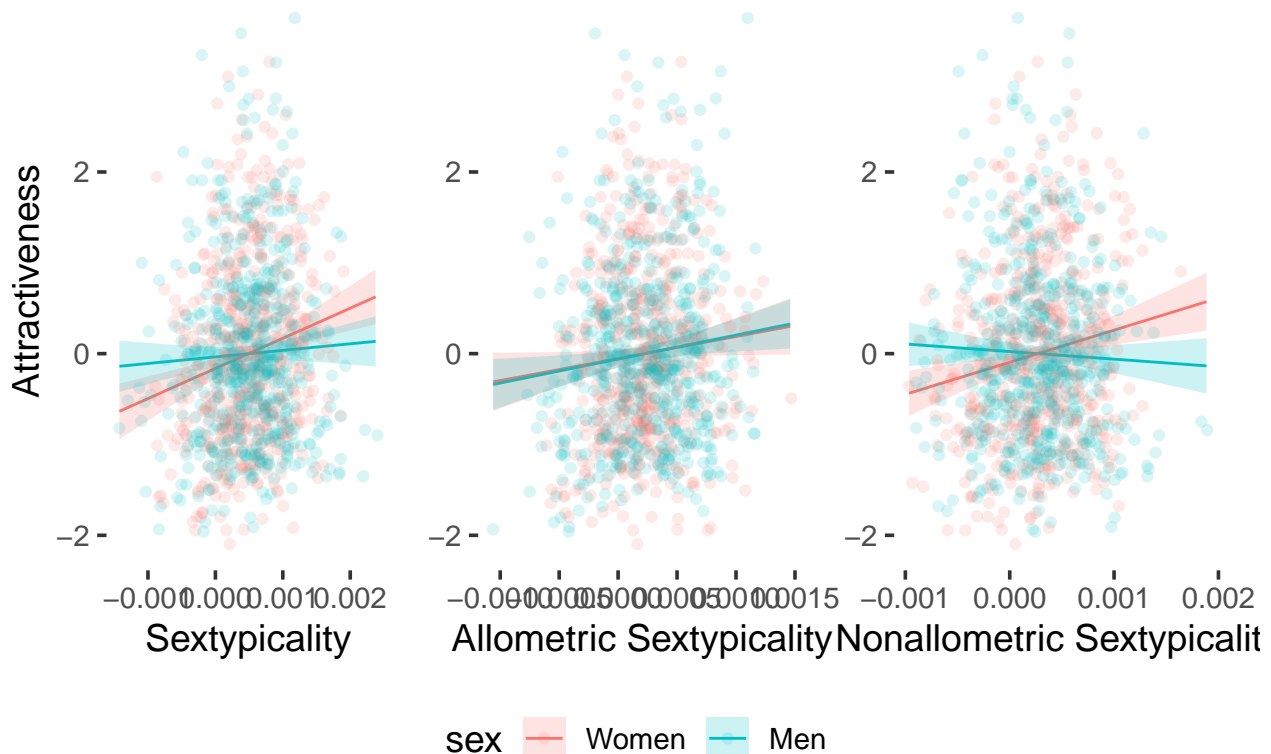
```
## (Intercept)          0.001      0.042 1110    0.02    0.983
## Nonallometric_SShD    0.156      0.043 1110    3.63    0.000
## sexM                 -0.001      0.059 1110   -0.01    0.991
## Nonallometric_SShD:sexM -0.193      0.059 1110   -3.25    0.001
```

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.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 = 0.22455, df = 560, p-value = 0.8224
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
```



```
## -0.07327719 0.09212456
## sample estimates:
##      cor
## 0.009488588
```

```
mall.cor.h
```

```
##
## Pearson's product-moment correlation
##
## data: mdat$height and mscores
## t = 5.1945, df = 550, p-value = 2.895e-07
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.1352411 0.2943966
## sample estimates:
##      cor
## 0.216255
```

```
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 auropcean 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")
```

