

Self-rated attractiveness predicts preferences for sexually dimorphic facial characteristics: Evidence from a culturally diverse sample

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Note: Code for data preparation is included below, though not necessary to replicate the data.

Load Packages and Custom Functions

```
library(tidyverse)
library(lme4)
library(lmerTest)

checkN <- function(data,label){
  print(paste(label,":",NROW(data),sep = ""))
  return(data)
}

z <- function(x,remove.outliers = FALSE,winsorise = FALSE){
  out <- (x - mean(x,na.rm = TRUE))/sd(x,na.rm = TRUE)
  if (remove.outliers == TRUE){
    out <- ifelse(out >3,NA,ifelse(out < -3,NA,out))
  }
}
```

```

    }
    if (winsorise == TRUE){
      out <- ifelse(out > 3,3,ifelse(out < -3,-3,out))
    }
    return(out)
  }
}

```

Load Data

Recode Country Values

```

country.codes <- read.csv("Country List.csv",stringsAsFactors = FALSE) %>%
  mutate( code = as.numeric(gsub("[^[:digit:]]","",country)),
          country = gsub("[[:digit:]]","",country),
          country = trimws(country))

```

Load Data

```

full.data <- read.csv("full.data.csv",stringsAsFactors = FALSE)

```

Participant Demographics

```

#Number of men and women in full sample
table(full.data$sex)

```

```

##
## Female    Male
##    8957    3473

```

```

#Total number of countries in full sample
NROW(unique(full.data$country))

```

```

## [1] 116

```

```

#Mean and SD for age in full sample
summarise(full.data, mean.age = mean(age,na.rm = TRUE),
          sd.age = sd(age,na.rm = TRUE))

```

```

##   mean.age   sd.age
## 1    27.624  9.172805

```

Prepare Data

Participant Data

```

participant.data <- full.data %>%
  select(ResponseId,country,sex,age,sexo,rs,sra,srh) %>% checkN("Full Sample") %>%
  filter(sexo == 1) %>% checkN("Exclusively Heterosexual") %>%
  filter(!is.na(country)) %>%
  group_by(country) %>%
  filter(n() >= 10) %>% checkN("More than 10 participants per country") %>%
  ungroup() %>%
  mutate( z.age = z(age,winsorise = TRUE),
          z.sra = z(sra,winsorise = TRUE),
          z.srh = z(srh,winsorise = TRUE))

```

```

## [1] "Full Sample: 13313"
## [1] "Exclusively Heterosexual: 9916"
## [1] "More than 10 participants per country: 9758"

```

```

#Number of men and women in full sample
table(participant.data$sex)

```

```

##
## Female    Male
##   6907    2851

```

```

#Total number of countries in full sample
NROW(unique(participant.data$country))

```

```

## [1] 41

```

```

sort(unique(participant.data$country))

```

```

## [1] "Argentina"
## [2] "Australia"
## [3] "Belgium"
## [4] "Brazil"
## [5] "Canada"
## [6] "China"
## [7] "Colombia"
## [8] "Croatia"
## [9] "Czech Republic"
## [10] "Denmark"
## [11] "Estonia"
## [12] "Finland"
## [13] "France"
## [14] "Germany"
## [15] "Iceland"
## [16] "Iran, Islamic Republic of..."
## [17] "Ireland"
## [18] "Italy"
## [19] "Japan"
## [20] "Latvia"
## [21] "Malaysia"
## [22] "Mexico"
## [23] "Nepal"
## [24] "Netherlands"
## [25] "New Zealand"
## [26] "Nigeria"
## [27] "Norway"

```

```
## [28] "Poland"
## [29] "Portugal"
## [30] "Romania"
## [31] "Russian Federation"
## [32] "Saudi Arabia"
## [33] "Singapore"
## [34] "Slovakia"
## [35] "Spain"
## [36] "Sweden"
## [37] "Switzerland"
## [38] "Turkey"
## [39] "Ukraine"
## [40] "United Kingdom of Great Britain and Northern Ireland"
## [41] "United States of America"
```

```
#Mean and SD for age in full sample
summarise(participant.data, mean.age = mean(age, na.rm = TRUE),
           sd.age = sd(age, na.rm = TRUE))
```

```
## # A tibble: 1 x 2
##   mean.age sd.age
##   <dbl>   <dbl>
## 1    27.9    9.37
```

Separate by participant sex and check for multicollinearity

Male Participants

```
male.data <- participant.data %>%
  filter(sex == "Male") %>%
  mutate( z.age = z(age, winsorise = TRUE),
          z.sra = z(sra, winsorise = TRUE),
          z.srh = z(srh, winsorise = TRUE))

cor.test(male.data$age, male.data$sra)

##
## Pearson's product-moment correlation
##
## data: male.data$age and male.data$sra
## t = -1.8744, df = 2647, p-value = 0.06098
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.074389204 0.001678067
## sample estimates:
## cor
## -0.03640831

cor.test(male.data$sra, male.data$srh)

##
## Pearson's product-moment correlation
##
## data: male.data$sra and male.data$srh
## t = 27.001, df = 2643, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
```

```
## 95 percent confidence interval:
## 0.4345669 0.4943310
## sample estimates:
##      cor
## 0.4649785

cor.test(male.data$age,male.data$srh)

##
## Pearson's product-moment correlation
##
## data: male.data$age and male.data$srh
## t = -1.2679, df = 2645, p-value = 0.2049
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.06268615 0.01346449
## sample estimates:
##      cor
## -0.02464658
```

Female Participants

```
female.data <- participant.data %>%
  filter(sex == "Female") %>%
  mutate( z.age = z(age,winsorise = TRUE),
          z.sra = z(sra,winsorise = TRUE),
          z.srh = z(srh,winsorise = TRUE))

cor.test(female.data$age,female.data$sra)

##
## Pearson's product-moment correlation
##
## data: female.data$age and female.data$sra
## t = 0.46536, df = 6578, p-value = 0.6417
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.01842782 0.02989646
## sample estimates:
##      cor
## 0.005737669

cor.test(female.data$sra,female.data$srh)

##
## Pearson's product-moment correlation
##
## data: female.data$sra and female.data$srh
## t = 39.616, df = 6565, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.4195181 0.4585631
## sample estimates:
##      cor
## 0.439248
```

```
cor.test(female.data$age,female.data$srh)

##
## Pearson's product-moment correlation
##
## data: female.data$age and female.data$srh
## t = 3.0976, df = 6587, p-value = 0.001959
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.01400466 0.06222730
## sample estimates:
## cor
## 0.03813818
```

Rating Data

```
rating.data <- select(full.data,ResponseId,m1:f20) %>%
  filter(ResponseId %in% participant.data$ResponseId) %>%
  gather(key = "faceId",value = "response",m1:f20)
```

Country Data

```
library(psych)
country.data <- read.csv("Updated Country.Data.csv",stringsAsFactors = FALSE) %>%
  mutate( mortality = ifelse(is.na(mortality) & na <= 2,mean(mortality,na.rm = TRUE),mortality),
    fertility = ifelse(is.na(fertility) & na <= 2,mean(fertility,na.rm = TRUE),fertility),
    yltd = ifelse(is.na(yltd) & na <= 2,mean(yltd,na.rm = TRUE),yltd),
    pathogen7 = ifelse(is.na(pathogen7) & na <= 2,mean(pathogen7,na.rm = TRUE),pathogen7),
    homicide = ifelse(is.na(homicide) & na <= 2,mean(homicide,na.rm = TRUE),homicide),
    urban = ifelse(is.na(urban) & na <= 2,mean(urban,na.rm = TRUE),urban),
    gdp = ifelse(is.na(gdp) & na <= 2,mean(gdp,na.rm = TRUE),gdp),
    hdi = ifelse(is.na(hdi) & na <= 2,mean(hdi,na.rm = TRUE),hdi),
    gini = ifelse(is.na(gini) & na <= 2,mean(gini,na.rm = TRUE),gini),
    gii = ifelse(is.na(gii) & na <= 2,mean(gii,na.rm = TRUE),gii),
    life.exp = ifelse(is.na(life.exp) & na <= 2,mean(life.exp,na.rm = TRUE),life.exp)
  ) %>%
  select(-health.fa,-inequality.fa)

d <- country.data %>%
  dplyr::select(fertility,yltd,pathogen7,homicide,urban,gdp,hdi,gini,gii,mortality,life.exp)

country.fa <- principal(d,nfactors = 2,rotate = "oblimin")

country.fa.loadings <- country.fa$loadings[1:11,1:2] %>%
  as.data.frame(row.names = row.names()) %>%
  rownames_to_column(var = "statistic") %>%
  arrange(desc(abs(TC1)))

country.fa.loadings
```

```
##      statistic      TC1      TC2
```

```
## 1      hdi -0.96577214 -0.008968194
## 2  life.exp -0.95937182  0.042021445
## 3     yltd  0.93450741  0.037799043
## 4 fertility  0.91425169 -0.053078297
## 5      gii  0.82615810  0.225659828
## 6     urban -0.78054822  0.249851878
## 7 pathogen7  0.63085232  0.247354059
## 8      gdp -0.27200740  0.075180591
## 9      gini  0.25925243  0.676239634
## 10 mortality  0.13127476 -0.590578993
## 11 homicide -0.05234705  0.714529156

country.fa.scores <- cbind(country.data$Country, country.data$region, country.fa$scores) %>%
  as.data.frame(stringsAsFactors = FALSE) %>%
  rename(Country = V1, region = V2, health.fa = TC1, inequality.fa = TC2) %>%
  mutate(health.fa = c(scale(as.numeric(health.fa) * -1)),
         inequality.fa = c(scale(as.numeric(inequality.fa)))) %>%
  filter(Country %in% participant.data$country) %>%
  mutate(health.fa = z(health.fa, winsorise = TRUE),
         inequality.fa = z(inequality.fa, winsorise = TRUE)) %>%
  select(Country, region, health.fa, inequality.fa)

analysis.male <- left_join(male.data, rating.data, by = "ResponseId") %>%
  left_join(country.fa.scores, by = c("country" = "Country")) %>%
  mutate(response = recode(response, "0" = 1, "1" = 0))

analysis.female <- left_join(female.data, rating.data, by = "ResponseId") %>%
  left_join(country.fa.scores, by = c("country" = "Country"))
```

Analyses - Is Self-Rated Attractiveness and Self-Rated Health Associated with Masculinity Preferences

Female Participants rating Male Faces

Linear Mixed Effects Model

```
model.f <- glmer(response ~ z.age + z.sra + z.srh +
  (1 | ResponseId) +
  (1 + z.age + z.sra + z.srh || faceId) +
  (1 + z.age + z.sra + z.srh || country) +
  (1 + z.age + z.sra + z.srh || region), data = analysis.female, family = "binomial")

save(model.f, file = "model.f.Rdata")

load("model.f.Rdata")
summary(model.f)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial (logit)
## Formula:
## response ~ z.age + z.sra + z.srh + (1 | ResponseId) + (1 + z.age +
```

```
##      z.sra + z.srh || faceId) + (1 + z.age + z.sra + z.srh ||
##      country) + (1 + z.age + z.sra + z.srh || region)
## Data: analysis.female
##
##      AIC      BIC    logLik deviance df.resid
## 131399.1 131564.0 -65682.6 131365.1   120479
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -8.1261 -0.6458  0.2237  0.6280  8.4500
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## ResponseId (Intercept) 1.584e+00 1.259e+00
## country     z.srh      1.295e-12 1.138e-06
## country.1   z.sra      6.185e-04 2.487e-02
## country.2   z.age      1.877e-02 1.370e-01
## country.3   (Intercept) 6.946e-02 2.636e-01
## faceId      z.srh      0.000e+00 0.000e+00
## faceId.1    z.sra      0.000e+00 0.000e+00
## faceId.2    z.age      7.878e-03 8.876e-02
## faceId.3    (Intercept) 1.164e+00 1.079e+00
## region      z.srh      0.000e+00 0.000e+00
## region.1    z.sra      0.000e+00 0.000e+00
## region.2    z.age      0.000e+00 0.000e+00
## region.3    (Intercept) 1.562e-01 3.952e-01
## Number of obs: 120496, groups:
## ResponseId, 6325; country, 41; faceId, 21; region, 7
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.042573   0.295008   0.144 0.885255
## z.age        0.166733   0.048133   3.464 0.000532 ***
## z.sra        0.072037   0.023548   3.059 0.002220 **
## z.srh       -0.001544   0.020101  -0.077 0.938771
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) z.age  z.sra
## z.age  0.022
## z.sra -0.009  0.001
## z.srh -0.003 -0.035 -0.377
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Plot Data

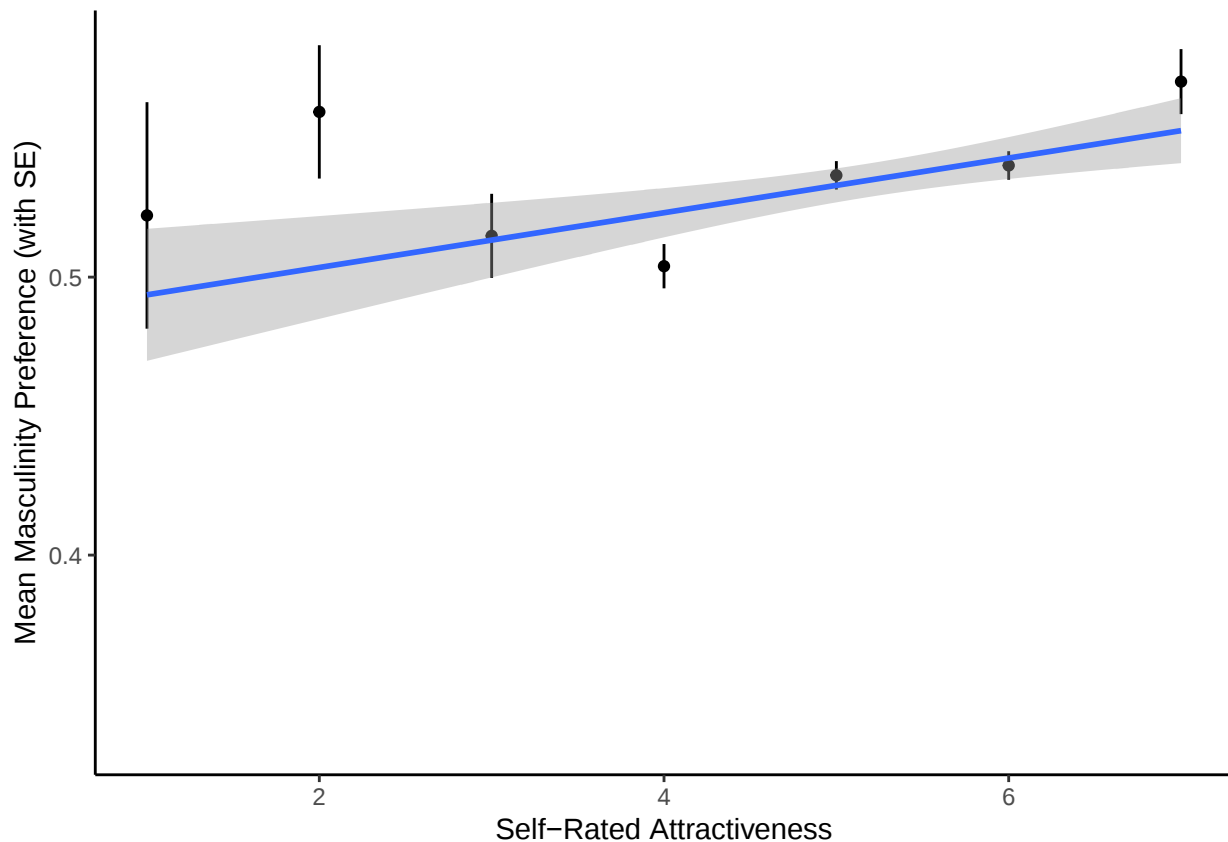
```
plot.data <- analysis.female %>%
  group_by(ResponseId,sra) %>%
  summarise(
    mean.response = mean(response,na.rm = TRUE)
  ) %>%
```

```

filter(!is.na(mean.response))
plot.data2 <- group_by(plot.data,sra) %>%
  summarise(se = sd(mean.response,na.rm = TRUE)/sqrt(n()),
            mean.response = mean(mean.response,na.rm = TRUE))

ggplot(plot.data2,aes(x = sra,y = mean.response)) +
  stat_summary(fun.y=mean,geom="point") +
  geom_linerange(aes(ymin = mean.response - se,ymax = mean.response + se)) +
  geom_smooth(data = plot.data,method = "lm") +
  theme_classic() +
  xlab("Self-Rated Attractiveness") +
  ylab("Mean Masculinity Preference (with SE)")

```



```

ggsave(filename = "fig1.png")

```

Male Participants rating Female Faces

Linear Mixed Effects Model

```

model.m <- glmer(response ~ z.age + z.sra + z.srh +
  (1 | ResponseId) +
  (1 + z.age + z.sra + z.srh || faceId) +
  (1 + z.age + z.sra + z.srh || country) +
  (1 + z.age + z.sra + z.srh || region),data = analysis.male,family = "binomial")

```

```
save(model.m,file = "model.m.Rdata")
```

```
load("model.m.Rdata")
```

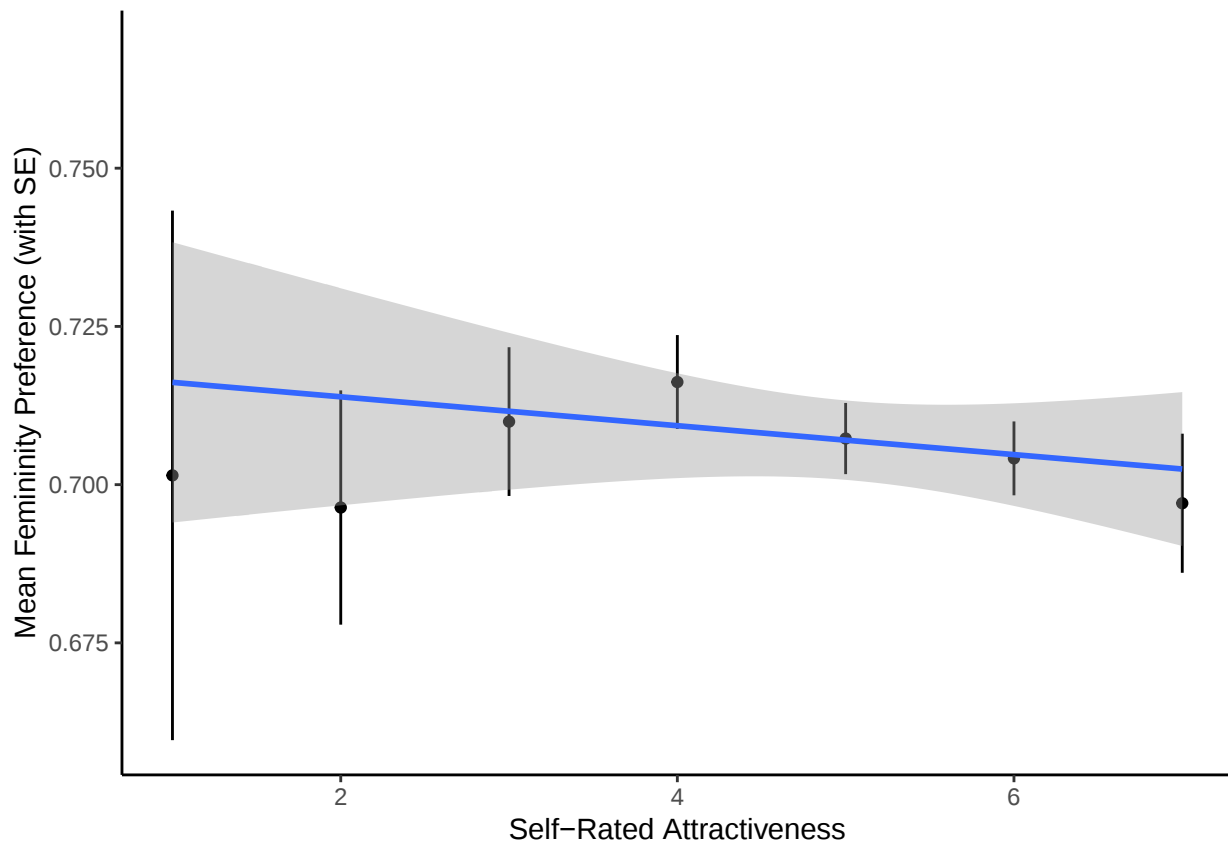
```
summary(model.m)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula:
## response ~ z.age + z.sra + z.srh + (1 | ResponseId) + (1 + z.age +
## z.sra + z.srh || faceId) + (1 + z.age + z.sra + z.srh ||
## country) + (1 + z.age + z.sra + z.srh || region)
## Data: analysis.male
##
##      AIC      BIC    logLik deviance df.resid
## 50507.6 50657.4 -25236.8 50473.6   49697
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -6.1200 -0.5407  0.3858  0.5547  4.6970
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## ResponseId (Intercept) 4.395e-01 6.630e-01
## country     z.srh      3.321e-09 5.763e-05
## country.1   z.sra      1.907e-09 4.366e-05
## country.2   z.age      1.016e-09 3.187e-05
## country.3   (Intercept) 2.818e-02 1.679e-01
## faceId      z.srh      0.000e+00 0.000e+00
## faceId.1    z.sra      2.791e-03 5.283e-02
## faceId.2    z.age      1.057e-02 1.028e-01
## faceId.3    (Intercept) 1.035e+00 1.017e+00
## region      z.srh      8.736e-05 9.347e-03
## region.1    z.sra      1.217e-10 1.103e-05
## region.2    z.age      5.919e-09 7.694e-05
## region.3    (Intercept) 1.170e-01 3.421e-01
## Number of obs: 49714, groups:
## ResponseId, 2606; country, 41; faceId, 20; region, 7
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.95522    0.26942   3.545 0.000392 ***
## z.age        -0.11785    0.03057  -3.855 0.000116 ***
## z.sra         0.04965    0.02366   2.098 0.035898 *
## z.srh        -0.01281    0.05018  -0.255 0.798569
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) z.age  z.sra
## z.age  0.005
## z.sra -0.009 -0.006
## z.srh -0.021 -0.057 -0.188
## convergence code: 0
```

```
## boundary (singular) fit: see ?isSingular
```

Plot Data

```
plot.data <- analysis.male %>%  
  group_by(ResponseId,sra) %>%  
  summarise(  
    mean.response = mean(response,na.rm = TRUE)  
  ) %>%  
  filter(!is.na(mean.response))  
plot.data2 <- group_by(plot.data,sra) %>%  
  summarise(se = sd(mean.response,na.rm = TRUE)/sqrt(n()),  
    mean.response = mean(mean.response,na.rm = TRUE))  
  
ggplot(plot.data2,aes(x = sra,y = mean.response)) +  
  stat_summary(fun.y=mean,geom="point") +  
  geom_linerange(aes(ymin = mean.response - se,ymax = mean.response + se)) +  
  geom_smooth(data = plot.data,method = "lm") +  
  theme_classic() +  
  xlab("Self-Rated Attractiveness") +  
  ylab("Mean Femininity Preference (with SE)")
```



```
ggsave("fig4.png")
```

Analysis with Ecological Factors

Female Participants rating Male Faces

Linear Mixed Effects Model

```
model.f2 <- glmer(response ~ z.age*health.fa + z.sra*health.fa + z.srh*health.fa +
  z.age*inequality.fa + z.sra*inequality.fa + z.srh*inequality.fa +
  (1 + health.fa + inequality.fa || ResponseId) +
  (1 + z.age:inequality.fa + z.sra:inequality.fa +
    z.srh:inequality.fa + z.age:health.fa + z.sra:health.fa +
    z.srh:health.fa || faceId) +
  (1 + z.age + z.sra + z.srh || country) +
  (1 + z.age:inequality.fa + z.sra:inequality.fa +
    z.srh:inequality.fa + z.age:health.fa + z.sra:health.fa +
    z.srh:health.fa || region),
  data = analysis.female,family = "binomial")

save(model.f2,file = "model.f2.Rdata")

load("model.f2.Rdata")
summary(model.f2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula:
## response ~ z.age * health.fa + z.sra * health.fa + z.srh * health.fa +
## z.age * inequality.fa + z.sra * inequality.fa + z.srh * inequality.fa +
## (1 + health.fa + inequality.fa || ResponseId) + (1 + z.age:inequality.fa +
## z.sra:inequality.fa + z.srh:inequality.fa + z.age:health.fa +
## z.sra:health.fa + z.srh:health.fa || faceId) + (1 + z.age +
## z.sra + z.srh || country) + (1 + z.age:inequality.fa + z.sra:inequality.fa +
## z.srh:inequality.fa + z.age:health.fa + z.sra:health.fa +
## z.srh:health.fa || region)
## Data: analysis.female
##
##      AIC      BIC   logLik deviance df.resid
## 131290.6 131610.7 -65612.3 131224.6   120463
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -8.1272 -0.6437  0.2236  0.6267  7.4748
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## ResponseId  inequality.fa        2.255e-08 1.502e-04
## ResponseId.1 health.fa          0.000e+00 0.000e+00
## ResponseId.2 (Intercept)        1.594e+00 1.263e+00
```

```

## country      z.srh      4.970e-10 2.229e-05
## country.1    z.sra      7.853e-09 8.862e-05
## country.2    z.age      1.200e-02 1.095e-01
## country.3    (Intercept) 4.537e-02 2.130e-01
## faceId       z.srh:health.fa 1.512e-04 1.230e-02
## faceId.1     z.sra:health.fa 5.253e-03 7.247e-02
## faceId.2     z.age:health.fa 3.641e-02 1.908e-01
## faceId.3     inequality.fa:z.srh 3.575e-04 1.891e-02
## faceId.4     inequality.fa:z.sra 2.392e-04 1.547e-02
## faceId.5     z.age:inequality.fa 4.453e-03 6.673e-02
## faceId.6     (Intercept) 1.224e+00 1.106e+00
## region       z.srh:health.fa 1.403e-10 1.185e-05
## region.1     z.sra:health.fa 0.000e+00 0.000e+00
## region.2     z.age:health.fa 0.000e+00 0.000e+00
## region.3     inequality.fa:z.srh 0.000e+00 0.000e+00
## region.4     inequality.fa:z.sra 0.000e+00 0.000e+00
## region.5     z.age:inequality.fa 1.522e-10 1.234e-05
## region.6     (Intercept) 1.612e-01 4.016e-01
## Number of obs: 120496, groups:
## ResponseId, 6325; country, 41; faceId, 21; region, 7
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.0761328  0.3140568   0.242 0.808457
## z.age          0.1576698  0.0391176   4.031 5.56e-05 ***
## health.fa      0.2266693  0.0969417   2.338 0.019377 *
## z.sra          0.0758840  0.0208601   3.638 0.000275 ***
## z.srh          0.0003913  0.0204558   0.019 0.984736
## inequality.fa  0.1941969  0.0947811   2.049 0.040472 *
## z.age:health.fa -0.0657335  0.0740501  -0.888 0.374708
## health.fa:z.sra 0.0253283  0.0319028   0.794 0.427240
## health.fa:z.srh -0.0114122  0.0288689  -0.395 0.692613
## z.age:inequality.fa -0.0013402  0.0398198  -0.034 0.973150
## z.sra:inequality.fa 0.0087815  0.0218948   0.401 0.688364
## z.srh:inequality.fa -0.0120628  0.0213756  -0.564 0.572532
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) z.age hlth.f z.sra  z.srh  inqlt. z.g:h. helth.f:z.sr
## z.age          0.009
## health.fa      0.215 -0.101
## z.sra          0.000 0.002 0.033
## z.srh          -0.010 -0.039 0.004 -0.432
## inequality.f   -0.175 -0.058 0.052 -0.018 0.020
## z.ag:hlth.f    -0.017 -0.076 0.083 0.006 0.004 0.038
## helth.f:z.sr   0.025 0.002 -0.005 -0.045 0.047 -0.021 0.003
## hlth.f:z.srh   0.027 0.009 0.003 0.054 -0.112 -0.013 -0.041 -0.382
## z.g:nqlty.f    -0.009 -0.054 0.068 0.011 0.001 0.067 0.394 0.002
## z.sr:nqlty.     0.008 0.004 -0.009 0.113 -0.042 -0.035 0.003 0.404
## z.srh:nqlt.     0.011 0.008 -0.006 -0.039 0.061 -0.002 -0.017 -0.187
##              hlth.f:z.srh z.g:n. z.sr:n.
## z.age
## health.fa

```

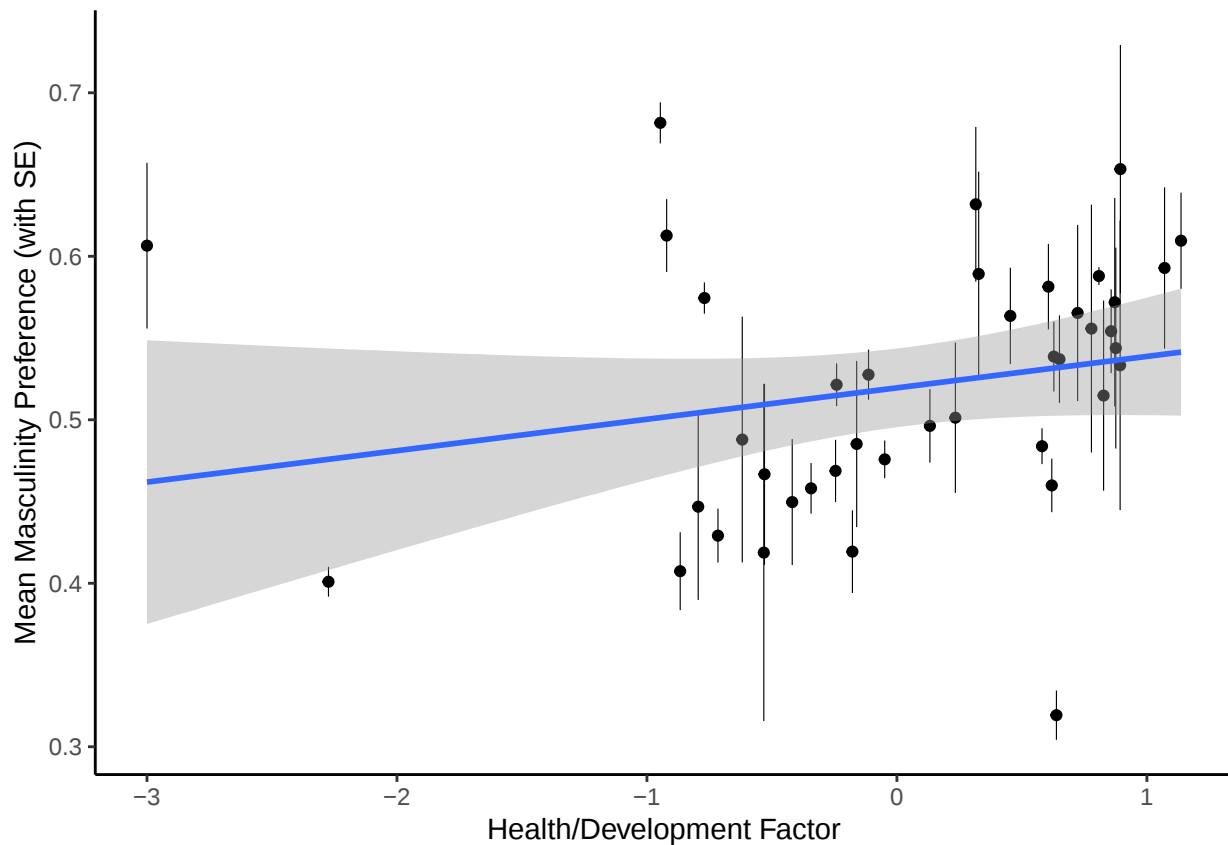
```
## z.sra
## z.srh
## inequality.f
## z.ag:hlth.f
## helth.f:z.sr
## hlth.f:z.srh
## z.g:nqlty.f -0.023
## z.sr:nqlty. -0.200      0.011
## z.srh:nqlt.  0.475      -0.030 -0.433
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Plot Data

Health/Development Factor

```
plot.data3 <- analysis.female %>%
  group_by(country,health.fa,inequality.fa,ResponseId) %>%
  summarise(meanMasc = mean(response,na.rm = TRUE)) %>%
  ungroup() %>%
  group_by(country,health.fa,inequality.fa) %>%
  summarise(mean = mean(meanMasc,na.rm = TRUE),
            se = sd(meanMasc,na.rm = TRUE)/sqrt(n()))

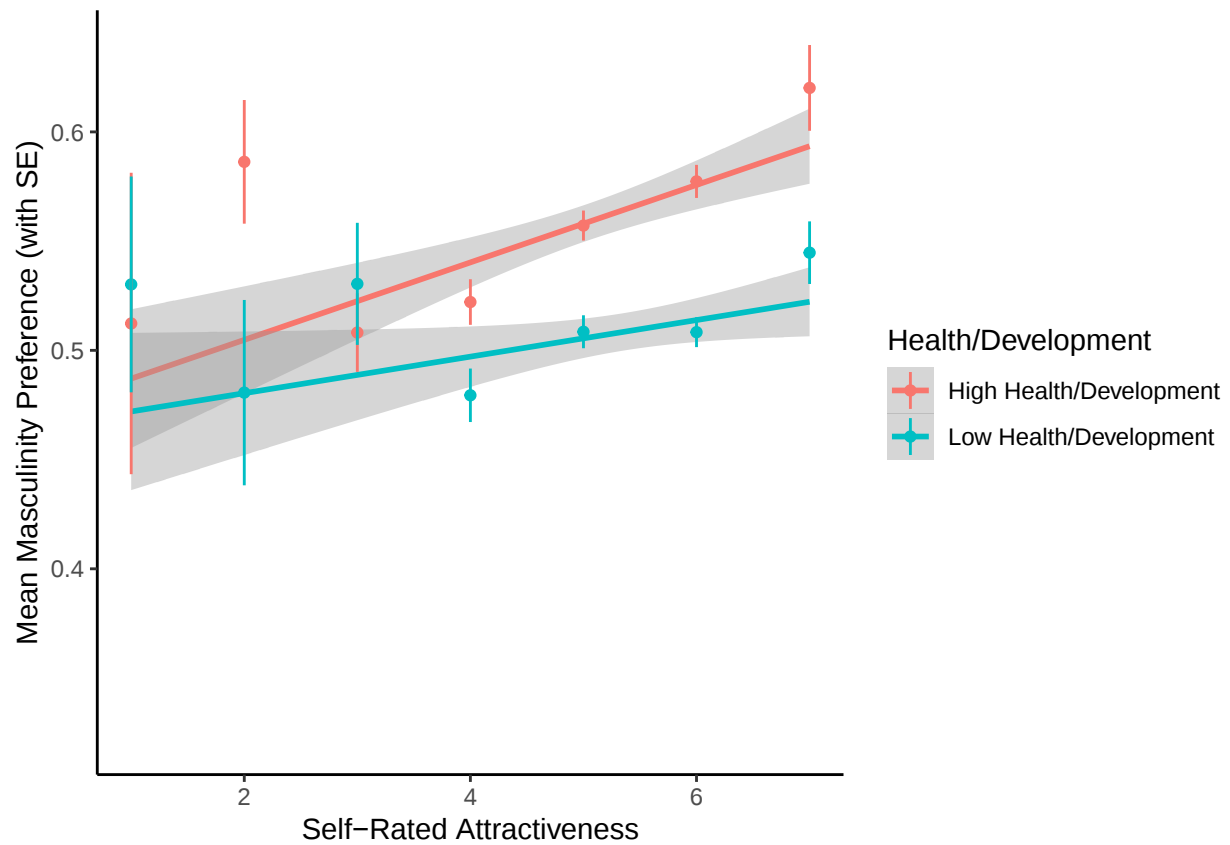
ggplot(plot.data3,aes(x = health.fa,y = mean)) +
  geom_pointrange(aes(ymin = mean - se,ymax = mean + se),size = .2) +
  geom_smooth(method = "lm") +
  xlab("Health/Development Factor") +
  ylab("Mean Masculinity Preference (with SE)") +
  theme_classic()
```



```
ggsave("fig2.png")

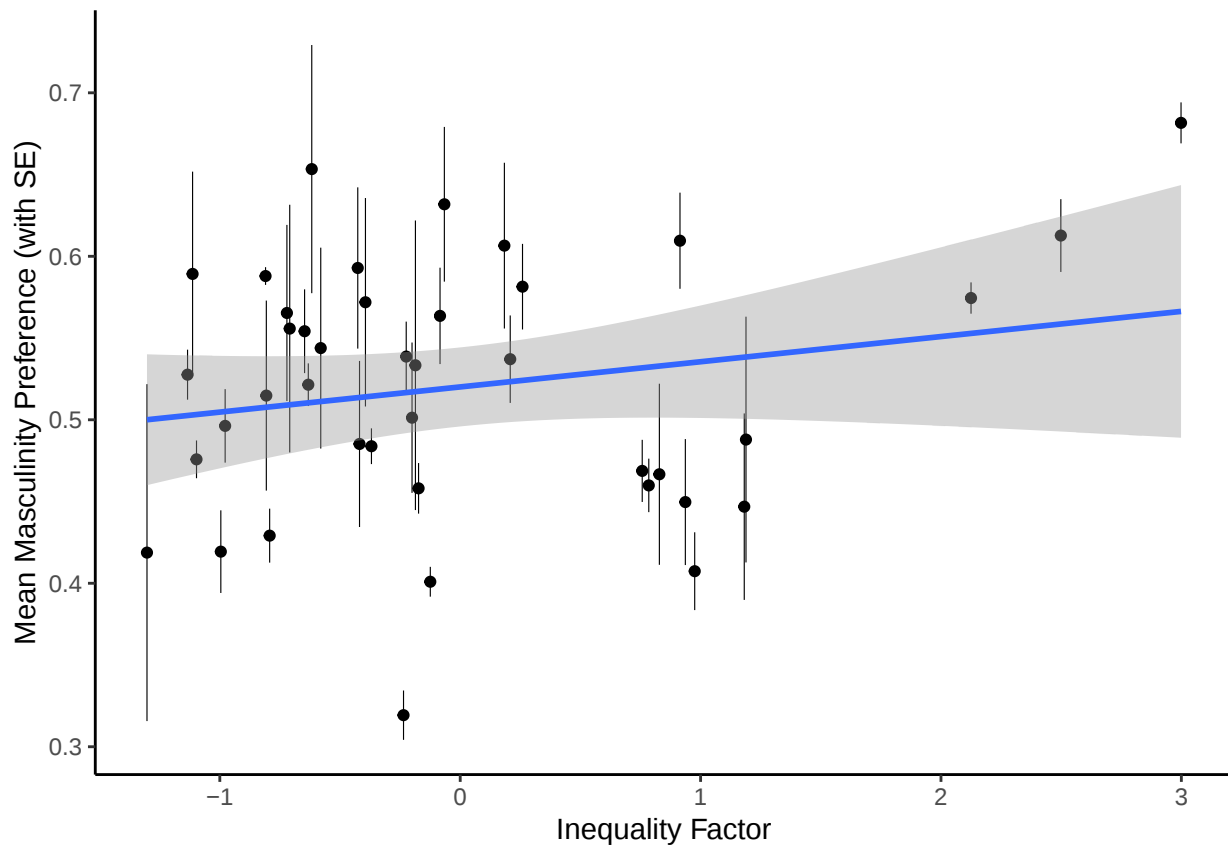
plot.data <- analysis.female %>%
  mutate(health.cat = ifelse(health.fa > 0, "High Health/Development", "Low Health/Development"),
         inequality.cat = ifelse(inequality.fa > 0, "High Inequality", "Low Inequality")) %>%
  group_by(ResponseId, sra, health.cat) %>%
  summarise(
    mean.response = mean(response, na.rm = TRUE)
  ) %>%
  filter(!is.na(mean.response))
plot.data2 <- group_by(plot.data, sra, health.cat) %>%
  summarise(se = sd(mean.response, na.rm = TRUE) / sqrt(n()),
            mean.response = mean(mean.response, na.rm = TRUE))

ggplot(plot.data2, aes(x = sra, y = mean.response, group = health.cat, colour = health.cat)) +
  geom_smooth(data = plot.data, method = "lm") +
  stat_summary(fun.y = mean, geom = "point") +
  geom_linerange(aes(ymin = mean.response - se, ymax = mean.response + se)) +
  theme_classic() +
  xlab("Self-Rated Attractiveness") +
  ylab("Mean Masculinity Preference (with SE)") +
  labs(colour = "Health/Development")
```



Inequality

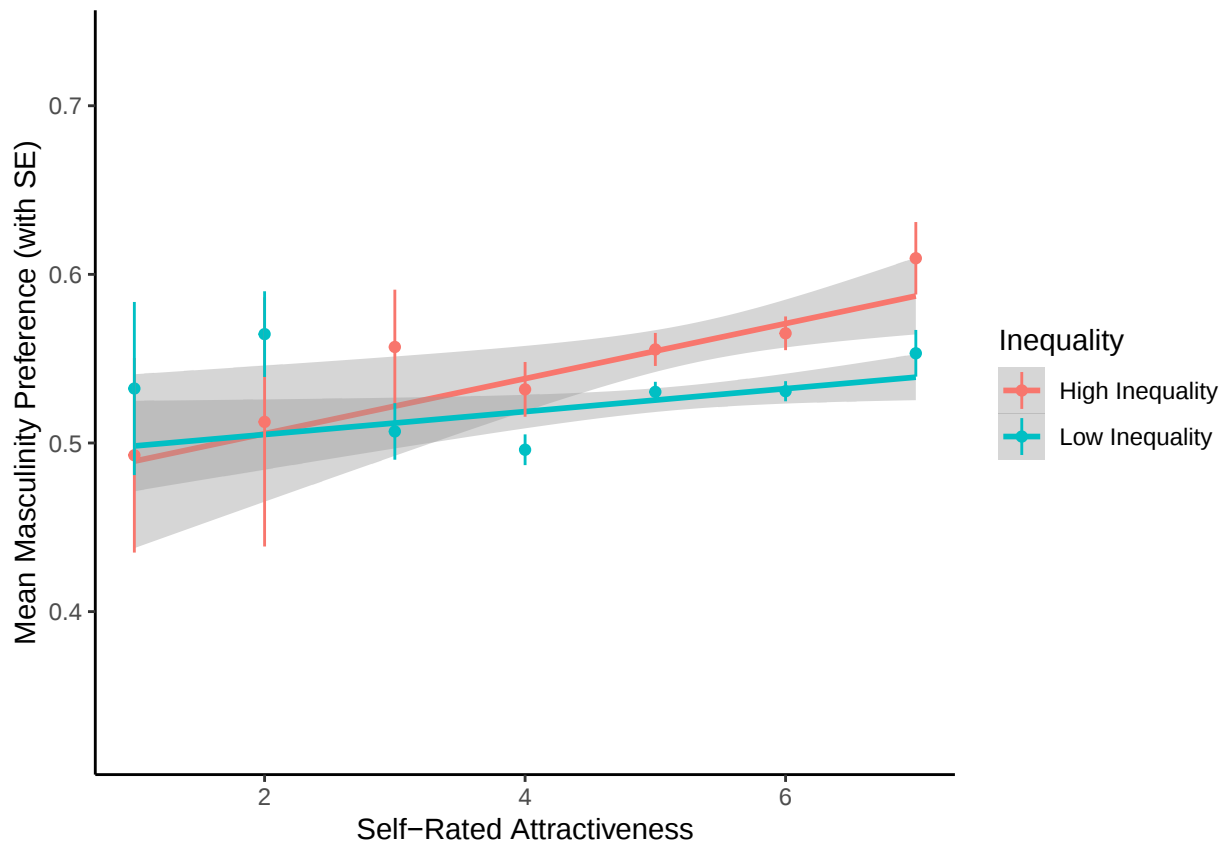
```
ggplot(plot.data3,aes(x = inequality.fa,y = mean)) +
  geom_pointrange(aes(ymin = mean - se,ymax = mean + se),size = .2) +
  geom_smooth(method = "lm") +
  xlab("Inequality Factor") +
  ylab("Mean Masculinity Preference (with SE)") +
  theme_classic()
```



```
ggsave("fig3.png")

plot.data <- analysis.female %>%
  mutate(health.cat = ifelse(health.fa > 0, "High Health", "Low Health"),
         inequality.cat = ifelse(inequality.fa > 0, "High Inequality", "Low Inequality")) %>%
  group_by(ResponseId, sra, inequality.cat) %>%
  summarise(
    mean.response = mean(response, na.rm = TRUE)
  ) %>%
  filter(!is.na(mean.response))
plot.data2 <- group_by(plot.data, sra, inequality.cat) %>%
  summarise(se = sd(mean.response, na.rm = TRUE) / sqrt(n()),
            mean.response = mean(mean.response, na.rm = TRUE))

ggplot(plot.data2, aes(x = sra, y = mean.response, group = inequality.cat, colour = inequality.cat)) +
  geom_smooth(data = plot.data, method = "lm") +
  stat_summary(fun.y = mean, geom = "point") +
  geom_linerange(aes(ymin = mean.response - se, ymax = mean.response + se)) +
  theme_classic() +
  xlab("Self-Rated Attractiveness") +
  ylab("Mean Masculinity Preference (with SE)") +
  labs(colour = "Inequality")
```



Male Analysis

Linear Mixed Effects Model

```
model.m2 <- glmer(response ~ z.age*health.fa + z.sra*health.fa + z.srh*health.fa +
  z.age*inequality.fa + z.sra*inequality.fa + z.srh*inequality.fa +
  (1 + health.fa + inequality.fa || ResponseId) +
  (1 + z.age:inequality.fa + z.sra:inequality.fa +
    z.srh:inequality.fa + z.age:health.fa + z.sra:health.fa +
    z.srh:health.fa || faceId) +
  (1 + z.age + z.sra + z.srh || country) +
  (1 + z.age:inequality.fa + z.sra:inequality.fa +
    z.srh:inequality.fa + z.age:health.fa + z.sra:health.fa +
    z.srh:health.fa || region),
  data = analysis.male,family = "binomial")
```

```
save(model.m2,file = "model.m2.2.Rdata")
```

```
load("model.m2.Rdata")
```

```
summary(model.m2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula:
## response ~ z.age * health.fa + z.sra * health.fa + z.srh * health.fa +
```

```

##      z.age * inequality.fa + z.sra * inequality.fa + z.srh * inequality.fa +
##      (1 + health.fa + inequality.fa || ResponseId) + (1 + z.age:inequality.fa +
##      z.sra:inequality.fa + z.srh:inequality.fa + z.age:health.fa +
##      z.sra:health.fa + z.srh:health.fa || faceId) + (1 + z.age +
##      z.sra + z.srh || country) + (1 + z.age:inequality.fa + z.sra:inequality.fa +
##      z.srh:inequality.fa + z.age:health.fa + z.sra:health.fa +
##      z.srh:health.fa || region)
##      Data: analysis.male
##
##      AIC      BIC    logLik deviance df.resid
## 50430.8 50721.5 -25182.4 50364.8    49521
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -5.1718 -0.5558 -0.3868  0.5442  6.4301
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
## ResponseId  inequality.fa    2.312e-02 1.521e-01
## ResponseId.1 health.fa      3.728e-08 1.931e-04
## ResponseId.2 (Intercept)    4.144e-01 6.438e-01
## country      z.srh          2.167e-09 4.655e-05
## country.1     z.sra          1.010e-09 3.179e-05
## country.2     z.age          2.042e-03 4.519e-02
## country.3     (Intercept)    1.541e-02 1.241e-01
## faceId        z.srh:health.fa 2.537e-03 5.037e-02
## faceId.1      z.sra:health.fa 3.893e-04 1.973e-02
## faceId.2      z.age:health.fa 3.289e-03 5.735e-02
## faceId.3      inequality.fa:z.srh 1.834e-08 1.354e-04
## faceId.4      inequality.fa:z.sra 4.036e-09 6.353e-05
## faceId.5      z.age:inequality.fa 2.411e-05 4.910e-03
## faceId.6      (Intercept)    1.023e+00 1.011e+00
## region        z.srh:health.fa 0.000e+00 0.000e+00
## region.1      z.sra:health.fa 1.054e-08 1.027e-04
## region.2      z.age:health.fa 1.243e-08 1.115e-04
## region.3      inequality.fa:z.srh 7.168e-08 2.677e-04
## region.4      inequality.fa:z.sra 2.558e-09 5.058e-05
## region.5      z.age:inequality.fa 4.263e-10 2.065e-05
## region.6      (Intercept)    3.768e-02 1.941e-01
## Number of obs: 49554, groups:
## ResponseId, 2598; country, 39; faceId, 20; region, 7
##
## Fixed effects:
##
##      Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.079467    0.248222  -4.349 1.37e-05 ***
## z.age        0.107760    0.022893   4.707 2.51e-06 ***
## health.fa    -0.145185    0.052961  -2.741 0.00612 **
## z.sra        -0.059842    0.020174  -2.966 0.00301 **
## z.srh         0.001629    0.020249   0.080 0.93588
## inequality.fa -0.026891    0.068589  -0.392 0.69502
## z.age:health.fa 0.012851    0.027499   0.467 0.64027
## health.fa:z.sra -0.053060    0.021822  -2.431 0.01504 *
## health.fa:z.srh 0.027139    0.024184   1.122 0.26178
## z.age:inequality.fa 0.021079    0.023282   0.905 0.36527

```

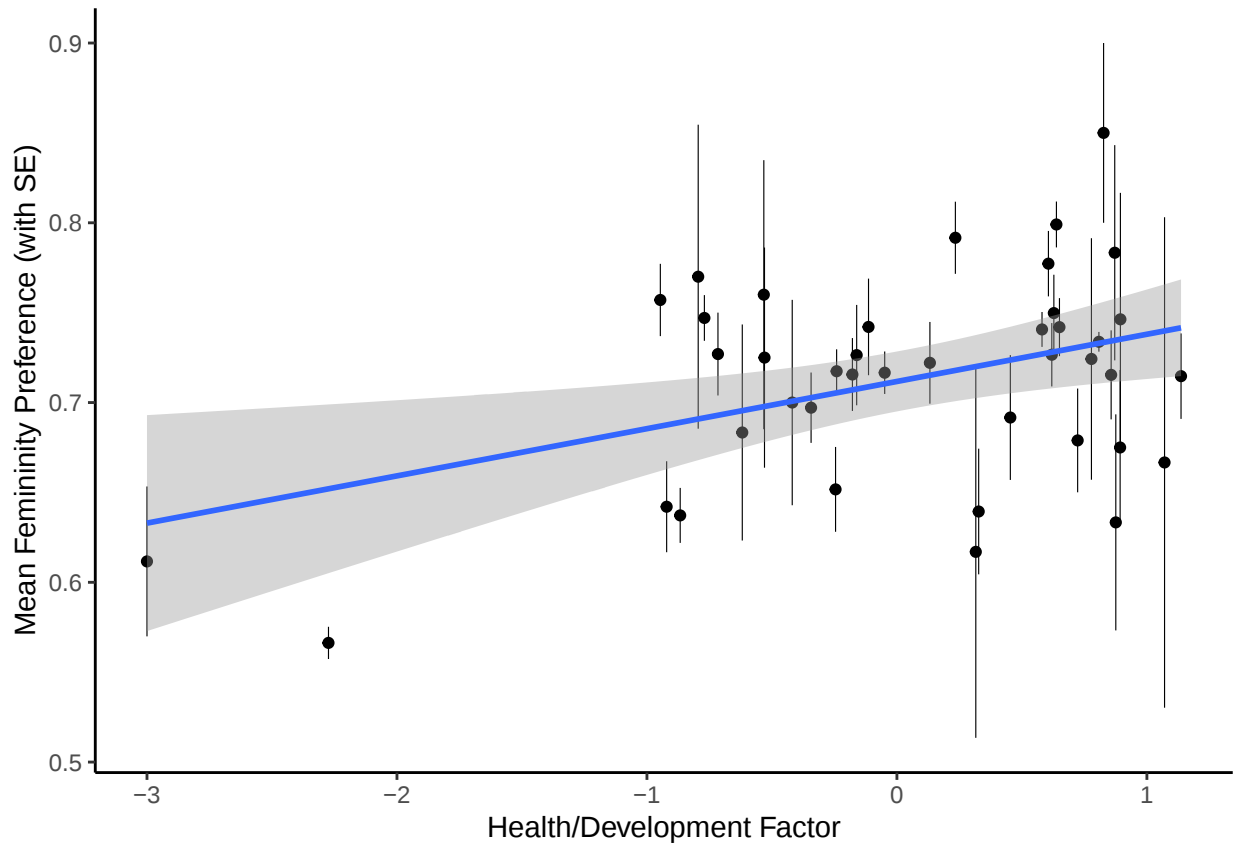
```
## z.sra:inequality.fa -0.029571 0.023346 -1.267 0.20530
## z.srh:inequality.fa -0.023073 0.023293 -0.991 0.32189
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) z.age  hlth.f z.sra  z.srh  inqlt. z.g:h. hlth.f:z.sr
## z.age          -0.002
## health.fa       0.149 -0.001
## z.sra           0.001 -0.022 -0.001
## z.srh          -0.001 -0.037 -0.005 -0.449
## inequality.f    -0.104 0.004 0.138 -0.002 0.000
## z.ag:hlth.f     -0.003 0.219 -0.009 -0.007 -0.015 0.001
## hlth.f:z.sr     0.002 0.003 0.005 0.088 -0.027 0.001 0.027
## hlth.f:z.srh   -0.001 -0.005 -0.008 -0.024 0.089 -0.003 0.037 -0.447
## z.g:nqlty.f     0.001 0.043 -0.001 0.000 -0.041 -0.009 0.183 -0.001
## z.sr:nqlty.     0.000 -0.006 -0.001 0.251 -0.118 -0.006 0.003 0.360
## z.srh:nqlt.    -0.001 -0.034 -0.003 -0.118 0.249 0.006 0.009 -0.179
##              hlth.f:z.srh z.g:n. z.sr:n.
## z.age
## health.fa
## z.sra
## z.srh
## inequality.f
## z.ag:hlth.f
## hlth.f:z.sr
## hlth.f:z.srh
## z.g:nqlty.f -0.001
## z.sr:nqlty. -0.162      0.012
## z.srh:nqlt. 0.327      -0.077 -0.474
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Plot Data

Health/Development Factor

```
plot.data3 <- analysis.male %>%
  group_by(country,health.fa,inequality.fa,ResponseId) %>%
  summarise(meanMasc = mean(response,na.rm = TRUE)) %>%
  ungroup() %>%
  group_by(country,health.fa,inequality.fa) %>%
  summarise(mean = mean(meanMasc,na.rm = TRUE),
            se = sd(meanMasc,na.rm = TRUE)/sqrt(n()))

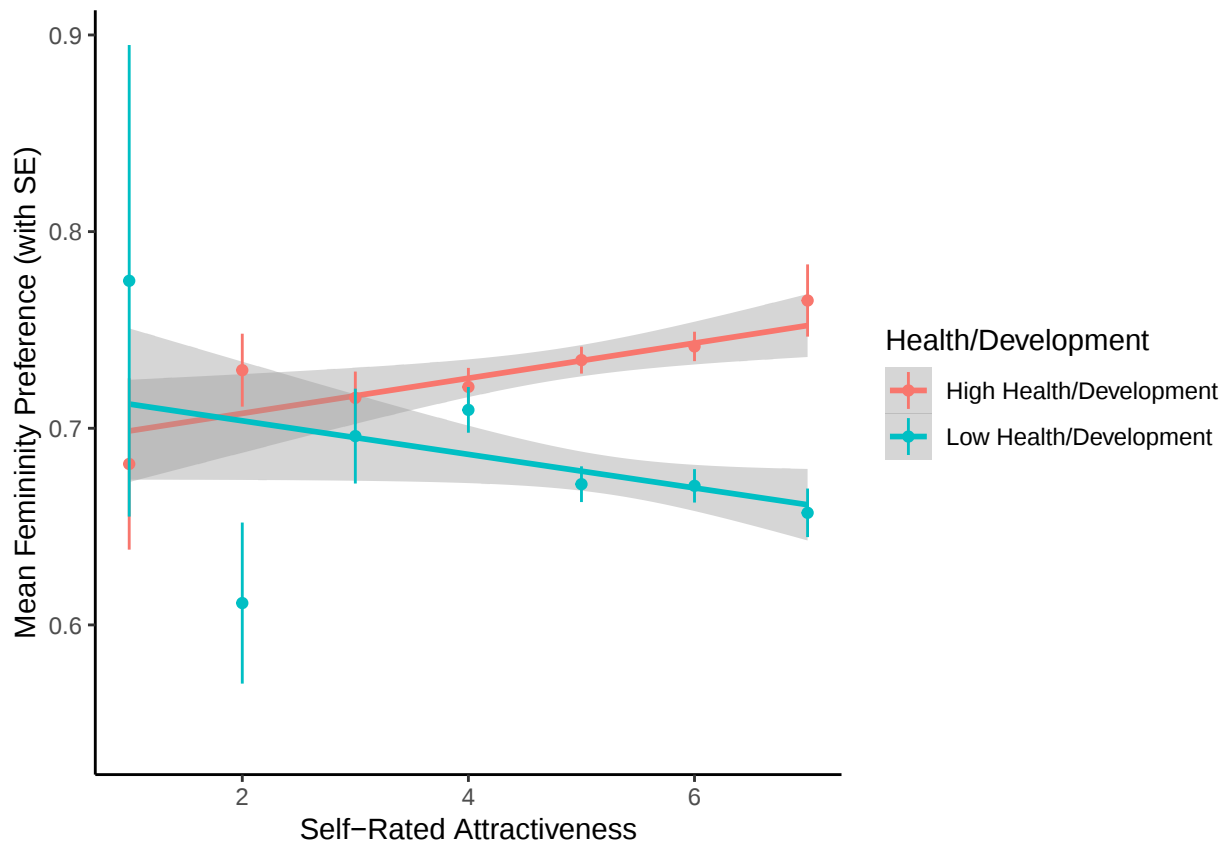
ggplot(plot.data3,aes(x = health.fa,y = mean)) +
  geom_pointrange(aes(ymin = mean - se,ymax = mean + se),size = .2) +
  geom_smooth(method = "lm") +
  xlab("Health/Development Factor") +
  ylab("Mean Femininity Preference (with SE)") +
  theme_classic()
```



```
ggsave("Fig5.png")
```

```
plot.data <- analysis.male %>%
  mutate(health.cat = ifelse(health.fa > 0, "High Health/Development", "Low Health/Development"),
         inequality.cat = ifelse(inequality.fa > 0, "High Inequality", "Low Inequality")) %>%
  group_by(ResponseId, sra, health.cat) %>%
  summarise(
    mean.response = mean(response, na.rm = TRUE)
  ) %>%
  filter(!is.na(mean.response))
plot.data2 <- group_by(plot.data, sra, health.cat) %>%
  summarise(se = sd(mean.response, na.rm = TRUE) / sqrt(n()),
            mean.response = mean(mean.response, na.rm = TRUE))

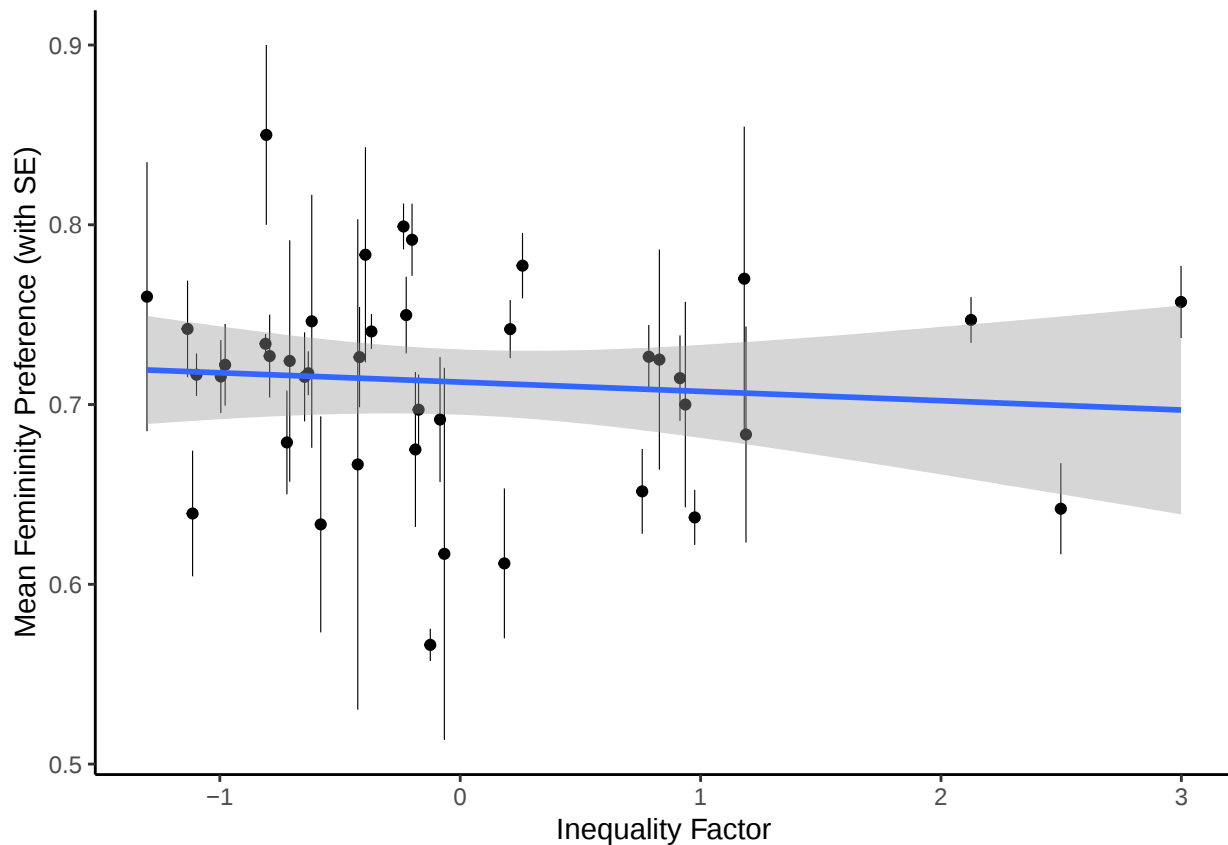
ggplot(plot.data2, aes(x = sra, y = mean.response, group = health.cat, colour = health.cat)) +
  geom_smooth(data = plot.data, method = "lm") +
  stat_summary(fun.y = mean, geom = "point") +
  geom_linerange(aes(ymin = mean.response - se, ymax = mean.response + se)) +
  theme_classic() +
  xlab("Self-Rated Attractiveness") +
  ylab("Mean Femininity Preference (with SE)") +
  labs(colour = "Health/Development")
```



```
ggsave("fig6.png")
```

Inequality

```
ggplot(plot.data3,aes(x = inequality.fa,y = mean)) +
  geom_pointrange(aes(ymin = mean - se,ymax = mean + se),size = .2) +
  geom_smooth(method = "lm") +
  xlab("Inequality Factor") +
  ylab("Mean Femininity Preference (with SE)") +
  theme_classic()
```



```
ggsave("fig3.png")

plot.data <- analysis.male %>%
  mutate(health.cat = ifelse(health.fa > 0, "High Health", "Low Health"),
         inequality.cat = ifelse(inequality.fa > 0, "High Inequality", "Low Inequality")) %>%
  group_by(ResponseId, sra, inequality.cat) %>%
  summarise(
    mean.response = mean(response, na.rm = TRUE)
  ) %>%
  filter(!is.na(mean.response))
plot.data2 <- group_by(plot.data, sra, inequality.cat) %>%
  summarise(se = sd(mean.response, na.rm = TRUE) / sqrt(n()),
            mean.response = mean(mean.response, na.rm = TRUE))

ggplot(plot.data2, aes(x = sra, y = mean.response, group = inequality.cat, colour = inequality.cat)) +
  geom_smooth(data = plot.data, method = "lm") +
  stat_summary(fun.y = mean, geom = "point") +
  geom_linerange(aes(ymin = mean.response - se, ymax = mean.response + se)) +
  theme_classic() +
  xlab("Self-Rated Attractiveness") +
  ylab("Mean Femininity Preference (with SE)") +
  labs(colour = "Inequality")
```

