

Supplementary Online Material (SOM):

Variability in energy expenditure is much greater in males than females

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R script (R v. 3.5.3; R Core Team, 2013)

```
library(MCMCglmm)
library(dplyr)
rm( list = ls())
#
#this annotated code accompanies the article:
#Title:
#"Variability in energy expenditure is much greater in males than females"
#
#Authors:
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#Lewis Halsey L.Halsey@roehampton.ac.uk
#
#The code below can be used to reproduce results in the article,
#using the IAEA DLW database v. 3.1.2
#
DATA<-read.table(file="DLW database v3.1.1 abbreviated.csv", header=T, sep=",")
summary(DATA)
#
#
##### PREPARING DATA
##### PREPARING DATA
#TO ENSURE SAMPLE SIZE DOESN'T CHANGE DEPENDING ON WHICH
COVARIATES IS INCLUDED
#WE NEED TO REMOVE ANY NAs IN THE COVARIATES
# get rid of rows without height as want this as a control variable
nrow(DATA) # 6787
DATA<-DATA[!is.na(DATA$ht),]
nrow(DATA) # 6434
```

```

# get rid of rows without lean body mass as want this as a control variable
DATA<-DATA[!is.na(DATA$LBM),]
nrow(DATA) # 6397
# get rid of rows without age as want this as a control variable
DATA<-DATA[!is.na(DATA$Age),]
nrow(DATA) # 6397
#
# get rid of non-adults
DATA<-DATA[which(DATA$Age>17.999),]
nrow(DATA) # 5016
#
# Get rid of individuals that have repeated measures (thus multiple [two ] rows of
data for each of them)
length(unique(DATA$IND_ID)) # 4647
nrow(DATA) # 5016
DATA.tmp<-DATA
DATA.tmp$NBR<-NA
for(i in unique(DATA.tmp$IND_ID)) DATA.tmp$NBR[which(DATA.tmp$IND_ID==i)]<-
nrow(subset(DATA.tmp,IND_ID==i))
hist(DATA.tmp$NBR)
REPEAT<-subset(DATA.tmp, NBR>1)
SINGLE<-subset(DATA.tmp, NBR==1)
length(unique(REPEAT$IND_ID)) # 364
nrow(SINGLE) # 4283
length(unique(SINGLE$IND_ID)) # 4283
SINGLE2<-REPEAT[!duplicated(REPEAT$IND_ID),]
DATA<-rbind(SINGLE,SINGLE2)
nrow(DATA) # 4647
length(unique(DATA$IND_ID)) # 4647
#
# get rid of people engaged in extreme forms of physical activity

```

```

#(no need to do this with version 10.2 but seems to be required in version 3.1)
DATA$sath<-factor(DATA$sath)
summary(DATA$sath)
nrow(DATA)
DATA<-DATA[-which(DATA$sath=="NotAUA"),]
DATA<-DATA[-which(DATA$sath=="PA"),]
DATA<-DATA[-which(DATA$sath=="AANCT"),]
nrow(DATA) # 4612 # Number of TEE data points
length(which(DATA$BEE>0)) # Number of BEE data points = 1760
#
DATA<-DATA[!is.na(DATA$TEE),]
nrow(DATA) #4602
#
# Derive additional variables for analysis
DATA$AEE<-0.9*DATA$TEE-DATA$BEE #activity energy expenditure (AEE)
DATA$FAT<-DATA$wt_av-DATA$LBM #fat mass
#
#description: percent AEE over TEE
DATA_AEE<-DATA[!is.na(DATA$AEE),]
nrow(DATA_AEE) #1756
mean(DATA_AEE$AEE)/mean(DATA_AEE$TEE)*100
MEANS<-aggregate(TEE~Sex,DATA_AEE,FUN=mean)
MEANS$AEE<-aggregate(AEE~Sex,DATA_AEE,FUN=mean)$AEE
MEANS$BEE<-aggregate(BEE~Sex,DATA_AEE,FUN=mean)$BEE
MEANS$PCT.AEE<-MEANS$AEE/MEANS$TEE*100
plot(BEE~AEE,DATA_AEE)
#
#
##### Descriptives about the sample (as requested by JHE referees) #####
dim(DATA) # 4602 independent data points

```



```

unique(DATA$ISO) # representing 30 different countries
dim(filter(DATA, ISO=="USA")) # But, the majority of those data points (3008) are
from the USA
summarise(
  group_by(DATA, Sex), Tally=n())
#
# Age distributions?
summarise(
  group_by(DATA, Sex), Mean.age=mean(na.exclude(Age))) # females 5 years older
summarise(
  group_by(filter(DATA, Age>60), Sex), Tally=n())
#
### Centre each predictor variable
# note: the non-centred version will be used when they are an outcome variable
DATA$FATc <- DATA$FAT-mean(DATA$FAT, na.rm=TRUE)
DATA$Agec <- DATA$Age-mean(DATA$Age, na.rm=TRUE)
DATA$htc <- DATA$ht-mean(DATA$ht, na.rm=TRUE)
DATA$wt_avc <- DATA$wt_av-mean(DATA$wt_av, na.rm=TRUE)
DATA$LBMc <- DATA$LBM-mean(DATA$LBM, na.rm=TRUE)
#
#get "complete cases" sample sizes
test<-lm(TEE~0+Sex+
          Sex*poly(LBMc,2,raw=TRUE)+
          Sex*poly(FATc,2,raw=TRUE)+
          Sex*poly(Agec,2,raw=TRUE)+
          LBMc*poly(Agec,2,raw=TRUE)+
          FATc*poly(Agec,2,raw=TRUE),data=DATA)
length(resid(test)) #4602 observations in total
DATA$RES_TEE<-resid(test)
nrow(DATA)

```

```
length(DATA$BEE[which(DATA$Sex=="F")]) #3108 observations in females AEE
and BEE
```

```
length(DATA$BEE[which(DATA$Sex=="M")]) #1494 observations in males AEE
and BEE
```

```
#
```

```
#
```

```
DATA_BEE_focus<-DATA[!is.na(DATA$BEE),]
```

```
test<-lm(BEE~0+Sex+
```

```
Sex*poly(LBMc,2,row=TRUE)+
```

```
Sex*poly(FATc,2,row=TRUE)+
```

```
Sex*poly(Agec,2,row=TRUE)+
```

```
LBMc*poly(Agec,2,row=TRUE)+
```

```
FATc*poly(Agec,2,row=TRUE),data=DATA_BEE_focus)
```

```
length(resid(test)) #1756 BEE observations in total
```

```
DATA_BEE_focus$RES_TEE<-resid(test)
```

```
nrow(DATA_BEE_focus)
```

```
### BEE
```

```
length(DATA_BEE_focus$BEE[which(DATA_BEE_focus$Sex=="F")]) #1063
observations in females AEE and BEE
```

```
length(DATA_BEE_focus$BEE[which(DATA_BEE_focus$Sex=="M")]) #693
observations in males AEE and BEE
```

```
##### RUN MODELS FOR EACH VARIABLE
#####
```

```
##### RUN MODELS FOR EACH VARIABLE
#####
```

```
##### RUN MODELS FOR EACH VARIABLE
#####
```

```
##### RUN MODELS FOR EACH VARIABLE
#####
```

```
##### RUN MODELS FOR EACH VARIABLE
#####
```

```
##### RUN MODELS FOR EACH VARIABLE
#####
```

```
#run one model for the variables subsequently included as covariates:
```

```
#Height (cm)
```

```
#LBM (kg)
```

```
#Fat mass (kg)
```

```
#Age (y)
```

```
#
```

```
#then run models for the metabolic variables with different covariates
```

```
#TEE1 = TEE without covariates (MJ d-1)
```

```
#BEE1 = BEE without covariates (MJ d-1)
```

```
#AEE1 = AEE without covariates (MJ d-1)
```

```
#
```

```
#TEE2 = TEE with Height and LBM as covariates
```

```
#BEE2 = BEE with Height and LBM as covariates
```

```
#AEE2 = AEE with Height and LBM as covariates
```

```
#
```

```
#TEE3 = TEE with Height, LBM, fat mass, age as covariates
```

```
#BEE3 = BEE with Height, LBM, fat mass, age as covariates
```

```
#AEE3 = AEE with Height, LBM, fat mass, age as covariates
```

```
#
```

```
#TEE4 = TEE with Height, LBM, fat mass, age, age-squared as covariates plus  
all 2-way interactions
```

```
#BEE4 = BEE with Height, LBM, fat mass, age, age-squared as covariates plus  
all 2-way interactions
```

```
#AEE4 = AEE with Height, LBM, fat mass, age, age-squared as covariates plus  
all 2-way interactions
```

```
#set sampling to have good MCMC convergence
```

n=20; NITT=13000*n; BURN=3000*n; THIN=10*n # n=5

#note: instead of running the models each time, simply load the models (see below)

#covariates

```
MC.height<-MCMCglmm(ht~0+Sex,  
  family="gaussian",  
  random=~ISO,  
  rcov=~idh(Sex):units,  
  #prior =prior.2,  
  nitt=NITT,thin=THIN,burnin=BURN,  
  data=DATA)
```

```
MC.lean<-MCMCglmm(LBM~0+Sex,  
  family="gaussian",  
  random=~ISO,  
  rcov=~idh(Sex):units,  
  #prior =prior.2,  
  nitt=NITT,thin=THIN,burnin=BURN,  
  data=DATA)
```

```
MC.fat<-MCMCglmm(FAT~0+Sex,  
  family="gaussian",  
  random=~ISO,  
  rcov=~idh(Sex):units,  
  #prior =prior.2,  
  nitt=NITT,thin=THIN,burnin=BURN,  
  data=DATA)
```

```
MC.age<-MCMCglmm(Age~0+Sex,  
  family="gaussian",  
  random=~ISO,  
  rcov=~idh(Sex):units,  
  #prior =prior.2,
```

```
nitt=NITT,thin=THIN,burnin=BURN,  
data=DATA)
```

```
#TEE
```

```
MC.TEE1<-MCMCglmm(TEE~0+Sex,  
family="gaussian",  
random=~ISO,  
rcov=~idh(Sex):units,  
#prior =prior.2,  
nitt=NITT,thin=THIN,burnin=BURN,  
data=DATA)
```

```
MC.TEE2<-MCMCglmm(TEE~0+Sex+htc+LBMc,  
family="gaussian",  
random=~ISO,  
rcov=~idh(Sex):units,  
#prior =prior.2,  
nitt=NITT,thin=THIN,burnin=BURN,  
data=DATA)
```

```
MC.TEE3<-MCMCglmm(TEE~0+Sex+htc+LBMc+FATc+Agec,  
family="gaussian",  
random=~ISO,  
rcov=~idh(Sex):units,  
#prior =prior.2,  
nitt=NITT,thin=THIN,burnin=BURN,  
data=DATA)
```

```
MC.TEE4<-MCMCglmm(TEE~0+Sex+htc+  
Sex*poly(LBMc,2,raw=TRUE)+  
Sex*poly(FATc,2,raw=TRUE)+  
Sex*poly(Agec,2,raw=TRUE)+  
LBMc*poly(Agec,2,raw=TRUE)+  
FATc*poly(Agec,2,raw=TRUE),
```

```
family="gaussian",
random=~ISO,
rcov=~idh(Sex):units,
#prior =prior.2,
nitt=NITT,thin=THIN,burnin=BURN,
data=DATA)
```

```
#BEE
```

```
MC.BEE1<-MCMCglmm(BEE~0+Sex,
family="gaussian",
random=~ISO,
rcov=~idh(Sex):units,
#prior =prior.2,
nitt=NITT,thin=THIN,burnin=BURN,
data=DATA)
```

```
MC.BEE2<-MCMCglmm(BEE~0+Sex+htc+LBMc,
family="gaussian",
random=~ISO,
rcov=~idh(Sex):units,
#prior =prior.2,
nitt=NITT,thin=THIN,burnin=BURN,
data=DATA)
```

```
MC.BEE3<-MCMCglmm(BEE~0+Sex+htc+LBMc+FATc+Agec,
family="gaussian",
random=~ISO,
rcov=~idh(Sex):units,
#prior =prior.2,
nitt=NITT,thin=THIN,burnin=BURN,
data=DATA)
```

```
MC.BEE4<-MCMCglmm(BEE~0+Sex+htc+
Sex*poly(LBMc,2,raw=TRUE)+
```

```

Sex*poly(FATc,2,raw=TRUE)+
Sex*poly(Agec,2,raw=TRUE)+
LBMc*poly(Agec,2,raw=TRUE)+
FATc*poly(Agec,2,raw=TRUE),
family="gaussian",
random=~ISO,
rcov=~idh(Sex):units,
#prior =prior.2,
nitt=NITT,thin=THIN,burnin=BURN,
data=DATA)

```

#AEE

```

MC.AEE1<-MCMCglmm(AEE~0+Sex,
family="gaussian",
random=~ISO,
rcov=~idh(Sex):units,
#prior =prior.2,
nitt=NITT,thin=THIN,burnin=BURN,
data=DATA)

MC.AEE2<-MCMCglmm(AEE~0+Sex+htc+LBMc,
family="gaussian",
random=~ISO,
rcov=~idh(Sex):units,
#prior =prior.2,
nitt=NITT,thin=THIN,burnin=BURN,
data=DATA)

```

```

MC.AEE3<-MCMCglmm(AEE~0+Sex+htc+LBMc+FATc+Agec,
family="gaussian",
random=~ISO,
rcov=~idh(Sex):units,

```

```
#prior =prior.2,  
nitt=NITT,thin=THIN,burnin=BURN,  
data=DATA)
```

```
MC.AEE4<-MCMCglmm(AEE~0+Sex+htc+  
  Sex*poly(LBMc,2,raw=TRUE)+  
  Sex*poly(FATc,2,raw=TRUE)+  
  Sex*poly(Agec,2,raw=TRUE)+  
  LBMc*poly(Agec,2,raw=TRUE)+  
  FATc*poly(Agec,2,raw=TRUE),  
family="gaussian",  
random=~ISO,  
rcov=~idh(Sex):units,  
#prior =prior.2,  
nitt=NITT,thin=THIN,burnin=BURN,  
data=DATA)
```

```
#save the models as R objects
```

```
save(MC.height,  
  MC.lean,  
  MC.fat,  
  MC.age,  
  MC.TEE1,  
  MC.TEE2,  
  MC.TEE3,  
  MC.TEE4,  
  MC.BEE1,  
  MC.BEE2,  
  MC.BEE3,  
  MC.BEE4,  
  MC.AEE1,
```



```
MC.AEE2,  
MC.AEE3,  
MC.AEE4, file="MCMC_models.RData")
```

```
load("MCMC_models.RData")
```

```
##### check model convergence #####
```

```
#check effective sample sizes for sex-specific averages
```

```
EFF.sample.fixed<-
```

```
c(summary(MC.height)$solutions[1:2,4],  
summary(MC.lean)$solutions[1:2,4],  
summary(MC.fat)$solutions[1:2,4],  
summary(MC.age)$solutions[1:2,4],  
summary(MC.TEE1)$solutions[1:2,4],  
summary(MC.TEE2)$solutions[1:2,4],  
summary(MC.TEE3)$solutions[1:2,4],  
summary(MC.TEE4)$solutions[1:2,4],  
summary(MC.BEE1)$solutions[1:2,4],  
summary(MC.BEE2)$solutions[1:2,4],  
summary(MC.BEE3)$solutions[1:2,4],  
summary(MC.BEE4)$solutions[1:2,4],  
summary(MC.AEE1)$solutions[1:2,4],  
summary(MC.AEE2)$solutions[1:2,4],  
summary(MC.AEE3)$solutions[1:2,4],  
summary(MC.AEE4)$solutions[1:2,4])
```

```
range(EFF.sample.fixed)
```

```
#check effective sample sizes for sex-specific variances
```

```
EFF.sample.resid<-
```

```
c(summary(MC.height)$Rcovariances[,4],
summary(MC.lean)$Rcovariances[,4],
summary(MC.fat)$Rcovariances[,4],
summary(MC.age)$Rcovariances[,4],
summary(MC.TEE1)$Rcovariances[,4],
summary(MC.TEE2)$Rcovariances[,4],
summary(MC.TEE3)$Rcovariances[,4],
summary(MC.TEE4)$Rcovariances[,4],
summary(MC.BEE1)$Rcovariances[,4],
summary(MC.BEE2)$Rcovariances[,4],
summary(MC.BEE3)$Rcovariances[,4],
summary(MC.BEE4)$Rcovariances[,4],
summary(MC.AEE1)$Rcovariances[,4],
summary(MC.AEE2)$Rcovariances[,4],
summary(MC.AEE3)$Rcovariances[,4],
summary(MC.AEE4)$Rcovariances[,4])
```

```
range(EFF.sample.resid)
```

```
#[1] 860.3274 1529.8571
```

```
#check mode summaries
```

```
summary(MC.height)
```

```
summary(MC.lean)
```

```
summary(MC.fat)
```

```
summary(MC.age)
```

```
summary(MC.TEE1)
```

```
summary(MC.TEE2)
```

```
summary(MC.TEE3)
```

```
summary(MC.TEE4)
```

```
summary(MC.BEE1)
```

```
summary(MC.BEE2)
summary(MC.BEE3)
summary(MC.BEE4)
summary(MC.AEE1)
summary(MC.AEE2)
summary(MC.AEE3)
summary(MC.AEE4)
```

```
#explanation of model outputs
```

```
summary(MC.height)
```

```
#SexF.units is the variance in females
```

```
#SexF is the female mean
```

```
#these can be retrieved from
```

```
mean(MC.height$VCV[,"SexF.units"])
```

```
mean(MC.height$Sol[,"SexF"])
```

```
#you can look at the posterior distribution for these by doing:
```

```
plot(MC.height$VCV[,"SexF.units"])
```

```
plot(MC.height$Sol[,"SexF"])
```

```
#To get the Coefficient of Variation, we can divide the mean variance by the mean average:
```

```
mean(MC.height$VCV[,"SexF.units"])/mean(MC.height$Sol[,"SexF"])
```

```
#But even better, divide the variance by the mean for each posterior,
```

```
POST.F<-MC.height$VCV[,"SexF.units"]/MC.height$Sol[,"SexF"]
```

```
plot(POST.F) #this is the posterior distribution for the Coefficient of Variation
```

```
#therefore, we can calculate the mean and 95% CI for Coefficient of Variation like this:
```

```
posterior.mode(POST.F)
```

```
HPDinterval(POST.F)
```

```
#in one go we can do:
```

```
posterior.mode(MC.height$VCV[,"SexF.units"]/MC.height$Sol[,"SexF"])
```

```
HPDinterval(MC.height$VCV[,"SexF.units"]/MC.height$Sol[, "SexF"])
```

#below we will extract sex-specific means, variances, and coefficient of variances from each model

#first, set up a data.frame to receive the estimates

```
ESTIMATES<-data.frame(Trait=c("Height","LBM","Fat mass","Age",  
    "TEE1","TEE2","TEE3","TEE4",  
    "BEE1","BEE2","BEE3","BEE4",  
    "AEE1","AEE2","AEE3","AEE4"),  
    Mean.M=NA,  
    Mean.M.LC=NA,  
    Mean.M.UC=NA,  
    Mean.F=NA,  
    Mean.F.LC=NA,  
    Mean.F.UC=NA,  
    V.M=NA,  
    V.M.LC=NA,  
    V.M.UC=NA,  
    V.F=NA,  
    V.F.LC=NA,  
    V.F.UC=NA,  
    CV.M=NA,  
    CV.M.LC=NA,  
    CV.M.UC=NA,  
    CV.F=NA,  
    CV.F.LC=NA,  
    CV.F.UC=NA,  
    Ratio=NA,  
    Ratio.LC=NA,  
    Ratio.UC=NA)
```

```

#compile estimates from each model
#Average in males
Mean.M<-c(
posterior.mode(MC.height$Sol)["SexM"],
posterior.mode(MC.lean$Sol)["SexM"],
posterior.mode(MC.fat$Sol)["SexM"],
posterior.mode(MC.age$Sol)["SexM"],
posterior.mode(MC.TEE1$Sol)["SexM"],
posterior.mode(MC.TEE2$Sol)["SexM"],
posterior.mode(MC.TEE3$Sol)["SexM"],
posterior.mode(MC.TEE4$Sol)["SexM"],
posterior.mode(MC.BEE1$Sol)["SexM"],
posterior.mode(MC.BEE2$Sol)["SexM"],
posterior.mode(MC.BEE3$Sol)["SexM"],
posterior.mode(MC.BEE4$Sol)["SexM"],
posterior.mode(MC.AEE1$Sol)["SexM"],
posterior.mode(MC.AEE2$Sol)["SexM"],
posterior.mode(MC.AEE3$Sol)["SexM"],
posterior.mode(MC.AEE4$Sol)["SexM"])
ESTIMATES$Mean.M<-round(Mean.M,2)
#95% credible intervals
Mean.M.CI<-rbind(
HPDinterval(MC.height$Sol[,2]),
HPDinterval(MC.lean$Sol[,2]),
HPDinterval(MC.fat$Sol[,2]),
HPDinterval(MC.age$Sol[,2]),
HPDinterval(MC.TEE1$Sol[,2]),
HPDinterval(MC.TEE2$Sol[,2]),
HPDinterval(MC.TEE3$Sol[,2]),

```

```

HPDinterval(MC.TEE4$Sol[,2]),
HPDinterval(MC.BEE1$Sol[,2]),
HPDinterval(MC.BEE2$Sol[,2]),
HPDinterval(MC.BEE3$Sol[,2]),
HPDinterval(MC.BEE4$Sol[,2]),
HPDinterval(MC.AEE1$Sol[,2]),
HPDinterval(MC.AEE2$Sol[,2]),
HPDinterval(MC.AEE3$Sol[,2]),
HPDinterval(MC.AEE4$Sol[,2])
ESTIMATES$Mean.M.LC<-round(Mean.M.CI[,1],2)
ESTIMATES$Mean.M.UC<-round(Mean.M.CI[,2],2)
#Average in females
Mean.F<-c(
posterior.mode(MC.height$Sol)["SexF"],
posterior.mode(MC.lean$Sol)["SexF"],
posterior.mode(MC.fat$Sol)["SexF"],
posterior.mode(MC.age$Sol)["SexF"],
posterior.mode(MC.TEE1$Sol)["SexF"],
posterior.mode(MC.TEE2$Sol)["SexF"],
posterior.mode(MC.TEE3$Sol)["SexF"],
posterior.mode(MC.TEE4$Sol)["SexF"],
posterior.mode(MC.BEE1$Sol)["SexF"],
posterior.mode(MC.BEE2$Sol)["SexF"],
posterior.mode(MC.BEE3$Sol)["SexF"],
posterior.mode(MC.BEE4$Sol)["SexF"],
posterior.mode(MC.AEE1$Sol)["SexF"],
posterior.mode(MC.AEE2$Sol)["SexF"],
posterior.mode(MC.AEE3$Sol)["SexF"],
posterior.mode(MC.AEE4$Sol)["SexF"])
ESTIMATES$Mean.F<-round(Mean.F,2)

```

```

#95% credible intervals
Mean.F.CI<-rbind(
HPDinterval(MC.height$Sol[,1]),
HPDinterval(MC.lean$Sol[,1]),
HPDinterval(MC.fat$Sol[,1]),
HPDinterval(MC.age$Sol[,1]),
HPDinterval(MC.TEE1$Sol[,1]),
HPDinterval(MC.TEE2$Sol[,1]),
HPDinterval(MC.TEE3$Sol[,1]),
HPDinterval(MC.TEE4$Sol[,1]),
HPDinterval(MC.BEE1$Sol[,1]),
HPDinterval(MC.BEE2$Sol[,1]),
HPDinterval(MC.BEE3$Sol[,1]),
HPDinterval(MC.BEE4$Sol[,1]),
HPDinterval(MC.AEE1$Sol[,1]),
HPDinterval(MC.AEE2$Sol[,1]),
HPDinterval(MC.AEE3$Sol[,1]),
HPDinterval(MC.AEE4$Sol[,1]))
ESTIMATES$Mean.F.LC<-round(Mean.F.CI[,1],2)
ESTIMATES$Mean.F.UC<-round(Mean.F.CI[,2],2)
#variance in males
V.M<-c(
posterior.mode(MC.height$VCV["SexM.units"]),
posterior.mode(MC.lean$VCV["SexM.units"]),
posterior.mode(MC.fat$VCV["SexM.units"]),
posterior.mode(MC.age$VCV["SexM.units"]),
posterior.mode(MC.TEE1$VCV["SexM.units"]),
posterior.mode(MC.TEE2$VCV["SexM.units"]),
posterior.mode(MC.TEE3$VCV["SexM.units"]),
posterior.mode(MC.TEE4$VCV["SexM.units"]),

```

```

posterior.mode(MC.BEE1$VCV[, "SexM.units"]),
posterior.mode(MC.BEE2$VCV[, "SexM.units"]),
posterior.mode(MC.BEE3$VCV[, "SexM.units"]),
posterior.mode(MC.BEE4$VCV[, "SexM.units"]),
posterior.mode(MC.AEE1$VCV[, "SexM.units"]),
posterior.mode(MC.AEE2$VCV[, "SexM.units"]),
posterior.mode(MC.AEE3$VCV[, "SexM.units"]),
posterior.mode(MC.AEE4$VCV[, "SexM.units"]))
ESTIMATES$V.M<-round(V.M,2)
#95% credible intervals in residual variance in males
V.M.CI<-rbind(
HPDinterval(MC.height$VCV[, "SexM.units"]),
HPDinterval(MC.lean$VCV[, "SexM.units"]),
HPDinterval(MC.fat$VCV[, "SexM.units"]),
HPDinterval(MC.age$VCV[, "SexM.units"]),
HPDinterval(MC.TEE1$VCV[, "SexM.units"]),
HPDinterval(MC.TEE2$VCV[, "SexM.units"]),
HPDinterval(MC.TEE3$VCV[, "SexM.units"]),
HPDinterval(MC.TEE4$VCV[, "SexM.units"]),
HPDinterval(MC.BEE1$VCV[, "SexM.units"]),
HPDinterval(MC.BEE2$VCV[, "SexM.units"]),
HPDinterval(MC.BEE3$VCV[, "SexM.units"]),
HPDinterval(MC.BEE3$VCV[, "SexM.units"]),
HPDinterval(MC.AEE1$VCV[, "SexM.units"]),
HPDinterval(MC.AEE2$VCV[, "SexM.units"]),
HPDinterval(MC.AEE3$VCV[, "SexM.units"]),
HPDinterval(MC.AEE4$VCV[, "SexM.units"]))
ESTIMATES$V.M.LC<-round(V.M.CI[,1],2)
ESTIMATES$V.M.UC<-round(V.M.CI[,2],2)
# variance in females

```



```

V.F<-c(
posterior.mode(MC.height$VCV["SexF.units"]),
posterior.mode(MC.lean$VCV["SexF.units"]),
posterior.mode(MC.fat$VCV["SexF.units"]),
posterior.mode(MC.age$VCV["SexF.units"]),
posterior.mode(MC.TEE1$VCV["SexF.units"]),
posterior.mode(MC.TEE2$VCV["SexF.units"]),
posterior.mode(MC.TEE3$VCV["SexF.units"]),
posterior.mode(MC.TEE4$VCV["SexF.units"]),
posterior.mode(MC.BEE1$VCV["SexF.units"]),
posterior.mode(MC.BEE2$VCV["SexF.units"]),
posterior.mode(MC.BEE3$VCV["SexF.units"]),
posterior.mode(MC.BEE4$VCV["SexF.units"]),
posterior.mode(MC.AEE1$VCV["SexF.units"]),
posterior.mode(MC.AEE2$VCV["SexF.units"]),
posterior.mode(MC.AEE3$VCV["SexF.units"]),
posterior.mode(MC.AEE4$VCV["SexF.units"]))
ESTIMATES$V.F<-round(V.F,2)
#95% credible intervals in residual variance in females
V.F.CI<-rbind(
HPDinterval(MC.height$VCV["SexF.units"]),
HPDinterval(MC.lean$VCV["SexF.units"]),
HPDinterval(MC.fat$VCV["SexF.units"]),
HPDinterval(MC.age$VCV["SexF.units"]),
HPDinterval(MC.TEE1$VCV["SexF.units"]),
HPDinterval(MC.TEE2$VCV["SexF.units"]),
HPDinterval(MC.TEE3$VCV["SexF.units"]),
HPDinterval(MC.TEE4$VCV["SexF.units"]),
HPDinterval(MC.BEE1$VCV["SexF.units"]),
HPDinterval(MC.BEE2$VCV["SexF.units"]),

```

```

HPDinterval(MC.BEE3$VCV["SexF.units"]),
HPDinterval(MC.BEE4$VCV["SexF.units"]),
HPDinterval(MC.AEE1$VCV["SexF.units"]),
HPDinterval(MC.AEE2$VCV["SexF.units"]),
HPDinterval(MC.AEE3$VCV["SexF.units"]),
HPDinterval(MC.AEE4$VCV["SexF.units"]))
ESTIMATES$V.F.LC<-round(V.F.CI[,1],2)
ESTIMATES$V.F.UC<-round(V.F.CI[,2],2)
#CoV in males
CV.M<-c(
posterior.mode(MC.height$VCV["SexM.units"])/MC.height$Sol["SexM"]),
posterior.mode(MC.lean$VCV["SexM.units"] /MC.lean$Sol["SexM"]),
posterior.mode(MC.fat$VCV["SexM.units"] /MC.fat$Sol["SexM"]),
posterior.mode(MC.age$VCV["SexM.units"] /MC.age$Sol["SexM"]),
posterior.mode(MC.TEE1$VCV["SexM.units"] /MC.TEE1$Sol["SexM"]),
posterior.mode(MC.TEE2$VCV["SexM.units"] /MC.TEE2$Sol["SexM"]),
posterior.mode(MC.TEE3$VCV["SexM.units"] /MC.TEE3$Sol["SexM"]),
posterior.mode(MC.TEE4$VCV["SexM.units"] /MC.TEE4$Sol["SexM"]),
posterior.mode(MC.BEE1$VCV["SexM.units"] /MC.BEE1$Sol["SexM"]),
posterior.mode(MC.BEE2$VCV["SexM.units"] /MC.BEE2$Sol["SexM"]),
posterior.mode(MC.BEE3$VCV["SexM.units"] /MC.BEE3$Sol["SexM"]),
posterior.mode(MC.BEE4$VCV["SexM.units"] /MC.BEE4$Sol["SexM"]),
posterior.mode(MC.AEE1$VCV["SexM.units"] /MC.AEE1$Sol["SexM"]),
posterior.mode(MC.AEE2$VCV["SexM.units"] /MC.AEE2$Sol["SexM"]),
posterior.mode(MC.AEE3$VCV["SexM.units"] /MC.AEE3$Sol["SexM"]),
posterior.mode(MC.AEE4$VCV["SexM.units"] /MC.AEE4$Sol["SexM"]))
ESTIMATES$CV.M<-round(CV.M,2)
#95% credible intervals in CoV males
CV.M.CI<-rbind(
HPDinterval(MC.height$VCV["SexM.units"])/MC.height$Sol["SexM"]),

```

```

HPDinterval(MC.lean$VCV["SexM.units"] /MC.lean$Sol["SexM"]),
HPDinterval(MC.fat$VCV["SexM.units"] /MC.fat$Sol["SexM"]),
HPDinterval(MC.age$VCV["SexM.units"] /MC.age$Sol["SexM"]),
HPDinterval(MC.TEE1$VCV["SexM.units"] /MC.TEE1$Sol["SexM"]),
HPDinterval(MC.TEE2$VCV["SexM.units"] /MC.TEE2$Sol["SexM"]),
HPDinterval(MC.TEE3$VCV["SexM.units"] /MC.TEE3$Sol["SexM"]),
HPDinterval(MC.TEE4$VCV["SexM.units"] /MC.TEE4$Sol["SexM"]),
HPDinterval(MC.BEE1$VCV["SexM.units"] /MC.BEE1$Sol["SexM"]),
HPDinterval(MC.BEE2$VCV["SexM.units"] /MC.BEE2$Sol["SexM"]),
HPDinterval(MC.BEE3$VCV["SexM.units"] /MC.BEE3$Sol["SexM"]),
HPDinterval(MC.BEE4$VCV["SexM.units"] /MC.BEE4$Sol["SexM"]),
HPDinterval(MC.AEE1$VCV["SexM.units"] /MC.AEE1$Sol["SexM"]),
HPDinterval(MC.AEE2$VCV["SexM.units"] /MC.AEE2$Sol["SexM"]),
HPDinterval(MC.AEE3$VCV["SexM.units"] /MC.AEE3$Sol["SexM"]),
HPDinterval(MC.AEE4$VCV["SexM.units"] /MC.AEE4$Sol["SexM"]))
ESTIMATES$CV.M.LC<-round(CV.M.CI[,1],2)
ESTIMATES$CV.M.UC<-round(CV.M.CI[,2],2)
#CoV in females
CV.F<-c(
posterior.mode(MC.height$VCV["SexF.units"])/MC.height$Sol["SexF"]),
posterior.mode(MC.lean$VCV["SexF.units"] /MC.lean$Sol["SexF"]),
posterior.mode(MC.fat$VCV["SexF.units"] /MC.fat$Sol["SexF"]),
posterior.mode(MC.age$VCV["SexF.units"] /MC.age$Sol["SexF"]),
posterior.mode(MC.TEE1$VCV["SexF.units"] /MC.TEE1$Sol["SexF"]),
posterior.mode(MC.TEE2$VCV["SexF.units"] /MC.TEE2$Sol["SexF"]),
posterior.mode(MC.TEE3$VCV["SexF.units"] /MC.TEE3$Sol["SexF"]),
posterior.mode(MC.TEE4$VCV["SexF.units"] /MC.TEE4$Sol["SexF"]),
posterior.mode(MC.BEE1$VCV["SexF.units"] /MC.BEE1$Sol["SexF"]),
posterior.mode(MC.BEE2$VCV["SexF.units"] /MC.BEE2$Sol["SexF"]),
posterior.mode(MC.BEE3$VCV["SexF.units"] /MC.BEE3$Sol["SexF"]),

```

```

posterior.mode(MC.BEE4$VCV[, "SexF.units"] /MC.BEE4$Sol[, "SexF"]),
posterior.mode(MC.AEE1$VCV[, "SexF.units"] /MC.AEE1$Sol[, "SexF"]),
posterior.mode(MC.AEE2$VCV[, "SexF.units"] /MC.AEE2$Sol[, "SexF"]),
posterior.mode(MC.AEE3$VCV[, "SexF.units"] /MC.AEE3$Sol[, "SexF"]),
posterior.mode(MC.AEE4$VCV[, "SexF.units"] /MC.AEE4$Sol[, "SexF"]))
ESTIMATES$CV.F<-round(CV.F,2)
#95% credible intervals in CoV males
CV.F.CI<-rbind(
HPDinterval(MC.height$VCV[, "SexF.units"]/MC.height$Sol[, "SexF"]),
HPDinterval(MC.lean$VCV[, "SexF.units"] /MC.lean$Sol[, "SexF"]),
HPDinterval(MC.fat$VCV[, "SexF.units"] /MC.fat$Sol[, "SexF"]),
HPDinterval(MC.age$VCV[, "SexF.units"] /MC.age$Sol[, "SexF"]),
HPDinterval(MC.TEE1$VCV[, "SexF.units"] /MC.TEE1$Sol[, "SexF"]),
HPDinterval(MC.TEE2$VCV[, "SexF.units"] /MC.TEE2$Sol[, "SexF"]),
HPDinterval(MC.TEE3$VCV[, "SexF.units"] /MC.TEE3$Sol[, "SexF"]),
HPDinterval(MC.TEE4$VCV[, "SexF.units"] /MC.TEE4$Sol[, "SexF"]),
HPDinterval(MC.BEE1$VCV[, "SexF.units"] /MC.BEE1$Sol[, "SexF"]),
HPDinterval(MC.BEE2$VCV[, "SexF.units"] /MC.BEE2$Sol[, "SexF"]),
HPDinterval(MC.BEE3$VCV[, "SexF.units"] /MC.BEE3$Sol[, "SexF"]),
HPDinterval(MC.BEE4$VCV[, "SexF.units"] /MC.BEE4$Sol[, "SexF"]),
HPDinterval(MC.AEE1$VCV[, "SexF.units"] /MC.AEE1$Sol[, "SexF"]),
HPDinterval(MC.AEE2$VCV[, "SexF.units"] /MC.AEE2$Sol[, "SexF"]),
HPDinterval(MC.AEE3$VCV[, "SexF.units"] /MC.AEE3$Sol[, "SexF"]),
HPDinterval(MC.AEE4$VCV[, "SexF.units"] /MC.AEE4$Sol[, "SexF"]))
ESTIMATES$CV.F.LC<-round(CV.F.CI[,1],2)
ESTIMATES$CV.F.UC<-round(CV.F.CI[,2],2)
#Ratio Male/female
Ratio<-c(
posterior.mode(MC.height$VCV[, "SexM.units"]/MC.height$VCV[, "SexF.units"]),
posterior.mode(MC.lean$VCV[, "SexM.units"]/MC.lean$VCV[, "SexF.units"]),

```

```

posterior.mode(MC.fat$VCV[, "SexM.units"]/MC.fat$VCV[, "SexF.units"]),
posterior.mode(MC.age$VCV[, "SexM.units"]/MC.age$VCV[, "SexF.units"]),
posterior.mode(MC.TEE1$VCV[, "SexM.units"]/MC.TEE1$VCV[, "SexF.units"]),
posterior.mode(MC.TEE2$VCV[, "SexM.units"]/MC.TEE2$VCV[, "SexF.units"]),
posterior.mode(MC.TEE3$VCV[, "SexM.units"]/MC.TEE3$VCV[, "SexF.units"]),
posterior.mode(MC.TEE4$VCV[, "SexM.units"]/MC.TEE4$VCV[, "SexF.units"]),
posterior.mode(MC.BEE1$VCV[, "SexM.units"]/MC.BEE1$VCV[, "SexF.units"]),
posterior.mode(MC.BEE2$VCV[, "SexM.units"]/MC.BEE2$VCV[, "SexF.units"]),
posterior.mode(MC.BEE3$VCV[, "SexM.units"]/MC.BEE3$VCV[, "SexF.units"]),
posterior.mode(MC.BEE4$VCV[, "SexM.units"]/MC.BEE4$VCV[, "SexF.units"]),
posterior.mode(MC.AEE1$VCV[, "SexM.units"]/MC.AEE1$VCV[, "SexF.units"]),
posterior.mode(MC.AEE2$VCV[, "SexM.units"]/MC.AEE2$VCV[, "SexF.units"]),
posterior.mode(MC.AEE3$VCV[, "SexM.units"]/MC.AEE3$VCV[, "SexF.units"]),
posterior.mode(MC.AEE4$VCV[, "SexM.units"]/MC.AEE4$VCV[, "SexF.units"])

```

```
ESTIMATES$Ratio<-round(Ratio,2)
```

```
#95% credible intervals of Ratio
```

```
Ratio.CI<-rbind(
```

```

HPDinterval(MC.height$VCV[, "SexM.units"]/MC.height$VCV[, "SexF.units"]),
HPDinterval(MC.lean$VCV[, "SexM.units"]/MC.lean$VCV[, "SexF.units"]),
HPDinterval(MC.fat$VCV[, "SexM.units"]/MC.fat$VCV[, "SexF.units"]),
HPDinterval(MC.age$VCV[, "SexM.units"]/MC.age$VCV[, "SexF.units"]),
HPDinterval(MC.TEE1$VCV[, "SexM.units"]/MC.TEE1$VCV[, "SexF.units"]),
HPDinterval(MC.TEE2$VCV[, "SexM.units"]/MC.TEE2$VCV[, "SexF.units"]),
HPDinterval(MC.TEE3$VCV[, "SexM.units"]/MC.TEE3$VCV[, "SexF.units"]),
HPDinterval(MC.TEE4$VCV[, "SexM.units"]/MC.TEE4$VCV[, "SexF.units"]),
HPDinterval(MC.BEE1$VCV[, "SexM.units"]/MC.BEE1$VCV[, "SexF.units"]),
HPDinterval(MC.BEE2$VCV[, "SexM.units"]/MC.BEE2$VCV[, "SexF.units"]),
HPDinterval(MC.BEE3$VCV[, "SexM.units"]/MC.BEE3$VCV[, "SexF.units"]),
HPDinterval(MC.BEE4$VCV[, "SexM.units"]/MC.BEE4$VCV[, "SexF.units"]),
HPDinterval(MC.AEE1$VCV[, "SexM.units"]/MC.AEE1$VCV[, "SexF.units"]),

```

```

HPDinterval(MC.AEE2$VCV[,"SexM.units"]/MC.AEE2$VCV[,"SexF.units"]),
HPDinterval(MC.AEE3$VCV[,"SexM.units"]/MC.AEE3$VCV[,"SexF.units"]),
HPDinterval(MC.AEE4$VCV[,"SexM.units"]/MC.AEE4$VCV[,"SexF.units"])
ESTIMATES$Ratio.LC<-round(Ratio.CI[,1],2)
ESTIMATES$Ratio.UC<-round(Ratio.CI[,2],2)
##### Save for Table for manuscript #####
ESTIMATES.round<-round(ESTIMATES[,2:22],1)

#write.table(ESTIMATES, file="ESTIMATES_with_country_as_random_effect.csv",
sep=",")
#write.table(ESTIMATES.round, file="ESTIMATES.round.csv", sep=",")
#####

##### make figure 1
#####

##### make figure 1
#####

##### make figure 1
#####

##### make figure 1
#####

##### make figure 1
#####

##### make figure 1
#####

ESTIMATES$Xmale <-
c(0.9,1.9,2.9,3.9,5.9,6.9,7.9,8.9,10.9,11.9,12.9,13.9,15.9,16.9,17.9,18.9)
ESTIMATES$Xfemale<-
c(1.1,2.1,3.1,4.1,6.1,7.1,8.1,9.1,11.1,12.1,13.1,14.1,16.1,17.1,18.1,19.1)
#
par(las=1,mar=c(5,5,0.5,0.5))
plot(V.M~Xmale, ESTIMATES,
pch=16,col=1,cex=1.25,ylim=c(0.26,6.85),xlim=c(6,19),xaxt="n",xlab="",ylab="Varian
ce (±95%CI)")

```

```

points(V.F~Xfemale,ESTIMATES, pch=17,col=1,cex=1.25)
arrows(ESTIMATES$Xmale, ESTIMATES$V.M.LC, ESTIMATES$Xmale,
ESTIMATES$V.M.UC,col=1,code=3,length=0.05,angle=90)

arrows(ESTIMATES$Xfemale,ESTIMATES$V.F.LC,ESTIMATES$Xfemale,ESTIMA
TES$V.F.UC,col=1,code=3,length=0.05,angle=90)

abline(v=10)
abline(v=15)

mtext("TEE",side=3,adj=0.125,line=-1.2)
mtext("BEE",side=3,adj=0.5,line=-1.2)
mtext("AEE",side=3,adj=0.875,line=-1.2)
axis(1,c(6,7,8,9,11,12,13,14,16,17,18,19), las=3,
labels=c("none","set 1","set 2","set 3",
"none","set 1","set 2","set 3",
"none","set 1","set 2","set 3"))
mtext("Covariates", side=1,line=3.5)

```

```
##### testing for a sex x age interaction in variance
#####
```

```
##### testing for a sex x age interaction in variance
#####
```

```
##### testing for a sex x age interaction in variance
#####
```

```
##### testing for a sex x age interaction in variance
#####
```

```
##### testing for a sex x age interaction in variance
#####
```

```
##### testing for a sex x age interaction in variance
#####
```

```
#reviewer comment:
```

#The effect of age on EE is controlled for in some of the analyses, but is the variance ratio affected by age?

#Sexual selection based explanations would predict that variance would be relatively higher among young men.

```
hist(DATA$Age)
```

#split the data into 4 equal age periods

```
quantile(DATA$Age)
```

```
DATA$AGE_cat<-1
```

```
DATA$AGE_cat[which(DATA$Age>32)]<-2
```

```
DATA$AGE_cat[which(DATA$Age>48)]<-3
```

```
DATA$AGE_cat[which(DATA$Age>69)]<-4
```

```
DATA$AGE_cat<-factor(DATA$AGE_cat)
```

```
plot(Age~AGE_cat,DATA)
```

```
DATA$n<-1
```

```
aggregate(n~AGE_cat,DATA,FUN=sum)
```

#look at sex-specific sample sizes

```
DATA$SEX_AGE<-factor(paste(DATA$Sex,DATA$AGE_cat,sep="_"))
```

```
aggregate(n~SEX_AGE,DATA,FUN=sum)
```

#set priors for 8 separate residual variances

```
prior.3<-list(R=list(R1=list(V=diag(8), nu=1.002)))
```

#run the model with 8 separate residual variances (4 for females and 4 for males)

```
MC.hete.5<-MCMCglmm(TEE~0+SEX_AGE+  
    Sex*poly(LBMc,2,raw=TRUE)+  
    Sex*poly(FATc,2,raw=TRUE)+  
    Sex*poly(Agec,2,raw=TRUE)+  
    LBMc*poly(Agec,2,raw=TRUE)+  
    FATc*poly(Agec,2,raw=TRUE),  
    family="gaussian",
```



```
random=~ISO,  
rcov=~idh(SEX_AGE):units,  
# prior =prior.3,  
nitt=NITT,thin=THIN,burnin=BURN,  
data=DATA)
```

```
save(MC.hete.5,file="MC.hete.5.RData")
```

```
load(file="MC.hete.5.RData")
```

```
summary(MC.hete.5)
```

```
V<-c(
```

```
posterior.mode(MC.hete.5$VCV["SEX_AGEF_1.units"]),  
posterior.mode(MC.hete.5$VCV["SEX_AGEF_2.units"]),  
posterior.mode(MC.hete.5$VCV["SEX_AGEF_3.units"]),  
posterior.mode(MC.hete.5$VCV["SEX_AGEF_4.units"]),  
posterior.mode(MC.hete.5$VCV["SEX_AGEM_1.units"]),  
posterior.mode(MC.hete.5$VCV["SEX_AGEM_2.units"]),  
posterior.mode(MC.hete.5$VCV["SEX_AGEM_3.units"]),  
posterior.mode(MC.hete.5$VCV["SEX_AGEM_4.units"]))
```

```
#
```

```
CI<-rbind(
```

```
HPDinterval(MC.hete.5$VCV["SEX_AGEF_1.units"]),  
HPDinterval(MC.hete.5$VCV["SEX_AGEF_2.units"]),  
HPDinterval(MC.hete.5$VCV["SEX_AGEF_3.units"]),  
HPDinterval(MC.hete.5$VCV["SEX_AGEF_4.units"]),  
HPDinterval(MC.hete.5$VCV["SEX_AGEM_1.units"]),  
HPDinterval(MC.hete.5$VCV["SEX_AGEM_2.units"]),  
HPDinterval(MC.hete.5$VCV["SEX_AGEM_3.units"]),  
HPDinterval(MC.hete.5$VCV["SEX_AGEM_4.units"]))
```

```
#
```

```

CV<-c(
posterior.mode(MC.hete.5$VCV["SEX_AGEF_1.units"]/MC.hete.5$Sol["SEX_AGE
F_1"]),
posterior.mode(MC.hete.5$VCV["SEX_AGEF_2.units"]/MC.hete.5$Sol["SEX_AGE
F_2"]),
posterior.mode(MC.hete.5$VCV["SEX_AGEF_3.units"]/MC.hete.5$Sol["SEX_AGE
F_3"]),
posterior.mode(MC.hete.5$VCV["SEX_AGEF_4.units"]/MC.hete.5$Sol["SEX_AGE
F_4"]),
posterior.mode(MC.hete.5$VCV["SEX_AGEM_1.units"]/MC.hete.5$Sol["SEX_AGE
M_1"]),
posterior.mode(MC.hete.5$VCV["SEX_AGEM_2.units"]/MC.hete.5$Sol["SEX_AGE
M_2"]),
posterior.mode(MC.hete.5$VCV["SEX_AGEM_3.units"]/MC.hete.5$Sol["SEX_AGE
M_3"]),
posterior.mode(MC.hete.5$VCV["SEX_AGEM_4.units"]/MC.hete.5$Sol["SEX_AGE
M_4"]))
#
CV.CI<-rbind(
HPDinterval(MC.hete.5$VCV["SEX_AGEF_1.units"]/MC.hete.5$Sol["SEX_AGEF_1
"]),
HPDinterval(MC.hete.5$VCV["SEX_AGEF_2.units"]/MC.hete.5$Sol["SEX_AGEF_2
"]),
HPDinterval(MC.hete.5$VCV["SEX_AGEF_3.units"]/MC.hete.5$Sol["SEX_AGEF_3
"]),
HPDinterval(MC.hete.5$VCV["SEX_AGEF_4.units"]/MC.hete.5$Sol["SEX_AGEF_4
"]),
HPDinterval(MC.hete.5$VCV["SEX_AGEM_1.units"]/MC.hete.5$Sol["SEX_AGEM_
1"]),
HPDinterval(MC.hete.5$VCV["SEX_AGEM_2.units"]/MC.hete.5$Sol["SEX_AGEM_
2"]),
HPDinterval(MC.hete.5$VCV["SEX_AGEM_3.units"]/MC.hete.5$Sol["SEX_AGEM_
3"]),
HPDinterval(MC.hete.5$VCV["SEX_AGEM_4.units"]/MC.hete.5$Sol["SEX_AGEM_
4"]))
#

```

```

V.AGE<-data.frame(cbind(V,CI,CV,CV.CI))
V.AGE$x<-c(0.95,1.95,2.95,3.95,1.05,2.05,3.05,4.05)
V.AGE$COL<-
c("pink2","pink2","pink2","pink2","paleturquoise3","paleturquoise3","paleturquoise3","
paleturquoise3")
V.AGE$PCH<-c(17,17,17,17,16,16,16,16)
#Ratio Male/female #Ratio Male/female #Ratio Male/female #Ratio Male/female
#Ratio Male/female #Ratio Male/female #Ratio Male/female #Ratio Male/female
#Ratio Male/female #Ratio Male/female #Ratio Male/female #Ratio Male/female
RATIO<-c(
posterior.mode(MC.hete.5$VCV[,"SEX_AGEM_1.units"]/MC.hete.5$VCV[,"SEX_AG
EF_1.units"]),
posterior.mode(MC.hete.5$VCV[,"SEX_AGEM_2.units"]/MC.hete.5$VCV[,"SEX_AG
EF_2.units"]),
posterior.mode(MC.hete.5$VCV[,"SEX_AGEM_3.units"]/MC.hete.5$VCV[,"SEX_AG
EF_3.units"]),
posterior.mode(MC.hete.5$VCV[,"SEX_AGEM_4.units"]/MC.hete.5$VCV[,"SEX_AG
EF_4.units"]))
RATIO.CI<-rbind(
HPDinterval(MC.hete.5$VCV[,"SEX_AGEM_1.units"]/MC.hete.5$VCV[,"SEX_AGEF
_1.units"]),
HPDinterval(MC.hete.5$VCV[,"SEX_AGEM_2.units"]/MC.hete.5$VCV[,"SEX_AGEF
_2.units"]),
HPDinterval(MC.hete.5$VCV[,"SEX_AGEM_3.units"]/MC.hete.5$VCV[,"SEX_AGEF
_3.units"]),
HPDinterval(MC.hete.5$VCV[,"SEX_AGEM_4.units"]/MC.hete.5$VCV[,"SEX_AGEF
_4.units"]))

# Figure 3
x11(7,3)
par(mfrow=c(1,3),las=1,mar=c(6,5,0.5,0.5))
plot(V~x, V.AGE,
pch=PCH,col=1,ylim=c(0,4.5),xlim=c(0.5,4.54),xaxt="n",xlab="",ylab="Variance
(±95%CI)")

```

```

arrows(V.AGE$x, V.AGE$lower, V.AGE$x, V.AGE$upper,
col=1,code=3,length=0.05,angle=90)
axis(1,c(1,2,3,4), las=3,labels=c("18 to 32","33 to 48","49 to 69","70 to 96"))
mtext("Age category", side=1,line=4.5)
mtext("A", side=3,line=-1.2,adj=0.02)
#add sample sizes
text(1,1.40,"734",cex=0.8)
text(2,1.25,"677",cex=0.8)
text(3,0.95,"797",cex=0.8)
text(4,0.70,"900",cex=0.8)
#
text(1,3.1,"413",cex=0.8)
text(2,3.3,"441",cex=0.8)
text(3,2.1,"364",cex=0.8)
text(4,1.6,"276",cex=0.8)
#plot CVs
plot(CV~x, V.AGE,
pch=PCH,col=1,ylim=c(0,0.8),xlim=c(0.5,4.5),xaxt="n",xlab="",ylab="Coefficient of
variance ( $\pm 95\%$ CI)")
arrows(V.AGE$x, V.AGE$lower.1, V.AGE$x, V.AGE$upper.1,
col=1,code=3,length=0.05,angle=90)
axis(1,c(1,2,3,4), las=3,labels=c("18 to 32","33 to 48","49 to 69","70 to 96"))
mtext("Age category", side=1,line=4.5)
mtext("B", side=3,line=-1.2,adj=0.02)
#
plot(1:4,RATIO,
pch=16,col=1,ylim=c(1.5,3.1),xlim=c(0.5,4.54),xaxt="n",xlab="",ylab="M:F variance
ratio ( $\pm 95\%$ CI)")
arrows(1:4, RATIO.CI[,1], 1:4, RATIO.CI[,2], col=1,code=3,length=0.05,angle=90)
axis(1,c(1,2,3,4), las=3,labels=c("18 to 32","33 to 48","49 to 69","70 to 96"))
mtext("C", side=3,line=-1.2,adj=0.02)
mtext("Age category", side=1,line=4.5)

```

```
#check country if USA (or USA as 'West') have different variance than elsewhere in the world
```

```
#check country if USA (or USA as 'West') have different variance than elsewhere in the world
```

```
#check country if USA (or USA as 'West') have different variance than elsewhere in the world
```

```
#check country if USA (or USA as 'West') have different variance than elsewhere in the world
```

```
#check country if USA (or USA as 'West') have different variance than elsewhere in the world
```

```
#check country if USA (or USA as 'West') have different variance than elsewhere in the world
```

```
summary(DATA)
```

```
DATA$ISO<-factor(DATA$ISO)
```

```
plot(TEE~ISO,DATA)
```

```
DATA$n<-1
```

```
aggregate(n~ISO,DATA,FUN=sum)
```

```
DATA$USA<-"USA"
```

```
DATA$USA[which(DATA$ISO=="BOL")]<-"other" #Bolivia
```

```
#DATA$USA[which(DATA$ISO=="CHE")]<-"other" #Switzerland ### Removed by Lewis 21.12.10th
```

```
DATA$USA[which(DATA$ISO=="Chile")]<-"other" #Chile
```

```
DATA$USA[which(DATA$ISO=="CHN")]<-"other" #China
```

```
DATA$USA[which(DATA$ISO=="ECU")]<-"other" #Ecuador
```

```
DATA$USA[which(DATA$ISO=="GHA")]<-"other" #Ghana
```

```
DATA$USA[which(DATA$ISO=="JAM")]<-"other" #Jamaica
```

```
DATA$USA[which(DATA$ISO=="JPN")]<-"other" #Japan
```

```
DATA$USA[which(DATA$ISO=="KEN")]<-"other" #Kenya
```

```
DATA$USA[which(DATA$ISO=="MUS")]<-"other" #Mauritius ### Added by Lewis 21.12.10th
```

```

DATA$USA[which(DATA$ISO=="NGA")]<-"other" #Nigeria
DATA$USA[which(DATA$ISO=="NPL")]<-"other" #Nepal
DATA$USA[which(DATA$ISO=="SYC")]<-"other" #Seychelles
DATA$USA[which(DATA$ISO=="TZA")]<-"other" #Tanzania
DATA$USA[which(DATA$ISO=="ZAF")]<-"other" #South Africa
## Thee above leaves the following countries under USA (aka West): USA, DEU,
NLD, AUS, FIN, BEL, SWE, FRA,
## GBR, NOR, GRC, CHE[Switz]

```

```
# Ethnicity within Western v. other
```

```

summarise(
  group_by(DATA, eth1, USA), Tally=n())

```

```
# Occupation within Western v. Other. DATA TOO PIECEMEAL? ALSO
SHOULDN'T R (RETIRED) BY IN THE JAPAN
```

```
# PART OF THE NON-WEST GROUP?
```

```

summarise(
  group_by(DATA, occ_ISCO, USA), Tally=n())

```

```
DATA$USA<-factor(DATA$USA)
```

```
plot(TEE~USA,DATA)
```

```
aggregate(n~USA,DATA,FUN=sum)
```

```
DATA$SEX_USA<-factor(paste(DATA$Sex,DATA$USA,sep="_"))
```

```
aggregate(n~SEX_USA,DATA,FUN=sum)
```

```
#run the model with 8 separate residual variances (4 for females and 4 for males)
```

```

MC.hete.USA<-MCMCglmm(TEE~0+Sex+
  Sex*poly(LBMc,2,raw=TRUE)+
  Sex*poly(FATc,2,raw=TRUE)+

```

```

Sex*poly(Agec,2,raw=TRUE)+
LBMc*poly(Agec,2,raw=TRUE)+
FATc*poly(Agec,2,raw=TRUE),
family="gaussian",
random=~ISO,
rcov=~idh(SEX_USA):units,
#prior =prior.3,
#nitt=NITT,thin=THIN,burnin=BURN,
data=DATA)

```

```
summary(MC.hete.USA)
```

```

V.USA<-c(
posterior.mode(MC.hete.USA$VCV["SEX_USAM_USA.units"]),
posterior.mode(MC.hete.USA$VCV["SEX_USAF_USA.units"]),
posterior.mode(MC.hete.USA$VCV["SEX_USAM_other.units"]),
posterior.mode(MC.hete.USA$VCV["SEX_USAF_other.units"]))

```

```

V.USA.CI<-rbind(
HPDinterval(MC.hete.USA$VCV["SEX_USAM_USA.units"]),
HPDinterval(MC.hete.USA$VCV["SEX_USAF_USA.units"]),
HPDinterval(MC.hete.USA$VCV["SEX_USAM_other.units"]),
HPDinterval(MC.hete.USA$VCV["SEX_USAF_other.units"]))

```

```
USA<-data.frame(cbind(V.USA,V.USA.CI))
```

```
USA$x<-c(0.95,1.05,1.95,2.05)
```

```
USA$COL<-1
```

```
USA$PCH<-c(16,17,16,17)
```

```
#Ratio Male/female #Ratio Male/female #Ratio Male/female #Ratio Male/female
```

```
#Ratio Male/female #Ratio Male/female #Ratio Male/female #Ratio Male/female
```

```
#Ratio Male/female #Ratio Male/female #Ratio Male/female #Ratio Male/female
```

```

#make figure S1
x11(4,4)
par(las=1,mar=c(5,5,1,1))
  plot(V.USA~x, USA,
pch=PCH,col=COL,ylim=c(0.5,4),xlim=c(0.5,2.5),xaxt="n",xlab="",ylab="Variance
(±95%CI)")
arrows(USA$x, USA$lower, USA$x, USA$upper,
col=USA$COL,code=3,length=0.05,angle=90)
axis(1,c(1,2), las=1,labels=c("West","Other"))
#add sample sizes
text(0.95,2.90,"1226",cex=0.8)
text(1.05,1.0,"2689",cex=0.8)
text(1.95,3.10,"268",cex=0.8)
text(2.05,0.9,"419",cex=0.8)

```

```

##### TWO-STEP ANALYSIS using residuals
#####

```

```

##### TWO-STEP ANALYSIS using residuals
#####

```

```

##### TWO-STEP ANALYSIS using residuals
#####

```

```

##### TWO-STEP ANALYSIS using residuals
#####

```

```

##### TWO-STEP ANALYSIS using residuals
#####

```

```

##### TWO-STEP ANALYSIS using residuals
#####

```

```

#covariates
LM.height<-lm(htc~Sex,data=DATA)

```



```

LM.lean<-lm(LBM~Sex,data=DATA)
LM.fat<-lm(FAT~Sex,data=DATA)
LM.age<-lm(Age~Sex,data=DATA)
#Tee
LM.TEE1<-lm(TEE~Sex,data=DATA)
LM.TEE2<-lm(TEE~Sex+htc+LBM,data=DATA)
LM.TEE3<-lm(TEE~Sex+htc+LBM+FAT+Age,data=DATA)

#BEE
LM.BEE1<-lm(BEE~Sex,data=DATA_BEE_focus)
LM.BEE2<-lm(BEE~Sex+htc+LBM,data=DATA_BEE_focus)
LM.BEE3<-lm(BEE~Sex+htc+LBM+FAT+Age,data=DATA_BEE_focus)

DATA_AEE_focus<-DATA[!is.na(DATA$AEE),]
#AEE
LM.AEE1<-lm(AEE~Sex,data=DATA_BEE_focus)
LM.AEE2<-lm(AEE~Sex+htc+LBM,data=DATA_BEE_focus)
LM.AEE3<-lm(AEE~Sex+htc+LBM+FAT+Age,data=DATA_BEE_focus)

DATA$res.height <- resid(LM.height)
DATA$res.lean <-resid(LM.lean)
DATA$res.fat <-resid(LM.fat)
DATA$res.age <-resid(LM.age)
#
DATA$res.TEE1<-resid(LM.TEE1)
DATA$res.TEE2<-resid(LM.TEE2)
DATA$res.TEE3<-resid(LM.TEE3)
#
DATA_BEE_focus$res.BEE1<-resid(LM.BEE1)

```

```

DATA_BEE_focus$res.BEE2<-resid(LM.BEE2)
DATA_BEE_focus$res.BEE3<-resid(LM.BEE3)
#
DATA_AEE_focus$res.AEE1<-resid(LM.AEE1)
DATA_AEE_focus$res.AEE2<-resid(LM.AEE2)
DATA_AEE_focus$res.AEE3<-resid(LM.AEE3)

LM.ESTIMATES<-data.frame(Trait=c("Height","LBM","Fat mass","Age",
      "TEE1","TEE2","TEE3",
      "BEE1","BEE2","BEE3",
      "AEE1","AEE2","AEE3"),
      Vmale=NA,
      Vfemale=NA)

LM.Vmale<-c(
var(DATA$res.height[which(DATA$Sex=="M")]),
var(DATA$res.lean[which(DATA$Sex=="M")]) ,
var(DATA$res.fat[which(DATA$Sex=="M")]) ,
var(DATA$res.age[which(DATA$Sex=="M")]) ,
var(DATA$res.TEE1[which(DATA$Sex=="M")]) ,
var(DATA$res.TEE2[which(DATA$Sex=="M")]) ,
var(DATA$res.TEE3[which(DATA$Sex=="M")]) ,
var(DATA_BEE_focus$res.BEE1[which(DATA_BEE_focus$Sex=="M")]) ,
var(DATA_BEE_focus$res.BEE2[which(DATA_BEE_focus$Sex=="M")]) ,
var(DATA_BEE_focus$res.BEE3[which(DATA_BEE_focus$Sex=="M")]) ,
var(DATA_AEE_focus$res.AEE1[which(DATA_AEE_focus$Sex=="M")]) ,
var(DATA_AEE_focus$res.AEE2[which(DATA_AEE_focus$Sex=="M")]) ,
var(DATA_AEE_focus$res.AEE3[which(DATA_AEE_focus$Sex=="M")]) )
LM.ESTIMATES$Vmale<-LM.Vmale

```

```

LM.Vfemale<-c(
var(DATA$res.height[which(DATA$Sex=="F")]),
var(DATA$res.lean[which(DATA$Sex=="F")]) ,
var(DATA$res.fat[which(DATA$Sex=="F")]) ,
var(DATA$res.age[which(DATA$Sex=="F")]) ,
var(DATA$res.TEE1[which(DATA$Sex=="F")]) ,
var(DATA$res.TEE2[which(DATA$Sex=="F")]) ,
var(DATA$res.TEE3[which(DATA$Sex=="F")]) ,
var(DATA_BEE_focus$res.BEE1[which(DATA_BEE_focus$Sex=="F")]) ,
var(DATA_BEE_focus$res.BEE2[which(DATA_BEE_focus$Sex=="F")]) ,
var(DATA_BEE_focus$res.BEE3[which(DATA_BEE_focus$Sex=="F")]) ,
var(DATA_AEE_focus$res.AEE1[which(DATA_AEE_focus$Sex=="F")]) ,
var(DATA_AEE_focus$res.AEE2[which(DATA_AEE_focus$Sex=="F")]) ,
var(DATA_AEE_focus$res.AEE3[which(DATA_AEE_focus$Sex=="F")]) )
LM.ESTIMATES$Vfemale<-LM.Vfemale

```

```

LM.meanmale<-c(
mean(DATA$res.height[which(DATA$Sex=="M")]),
mean(DATA$res.lean[which(DATA$Sex=="M")]) ,
mean(DATA$res.fat[which(DATA$Sex=="M")]) ,
mean(DATA$res.age[which(DATA$Sex=="M")]) ,
mean(DATA$res.TEE1[which(DATA$Sex=="M")]) ,
mean(DATA$res.TEE2[which(DATA$Sex=="M")]) ,
mean(DATA$res.TEE3[which(DATA$Sex=="M")]) ,
mean(DATA_BEE_focus$res.BEE1[which(DATA_BEE_focus$Sex=="M")]) ,
mean(DATA_BEE_focus$res.BEE2[which(DATA_BEE_focus$Sex=="M")]) ,
mean(DATA_BEE_focus$res.BEE3[which(DATA_BEE_focus$Sex=="M")]) ,
mean(DATA_AEE_focus$res.AEE1[which(DATA_AEE_focus$Sex=="M")]) ,
mean(DATA_AEE_focus$res.AEE2[which(DATA_AEE_focus$Sex=="M")]) ,
mean(DATA_AEE_focus$res.AEE3[which(DATA_AEE_focus$Sex=="M")]) )

```

```
LM.ESTIMATES$meanmale<-LM.meanmale
```

```
LM.meanfemale<-c(
  mean(DATA$res.height[which(DATA$Sex=="F")]),
  mean(DATA$res.lean[which(DATA$Sex=="F")]) ,
  mean(DATA$res.fat[which(DATA$Sex=="F")]) ,
  mean(DATA$res.age[which(DATA$Sex=="F")]) ,
  mean(DATA$res.TEE1[which(DATA$Sex=="F")]) ,
  mean(DATA$res.TEE2[which(DATA$Sex=="F")]) ,
  mean(DATA$res.TEE3[which(DATA$Sex=="F")]) ,
  mean(DATA_BEE_focus$res.BEE1[which(DATA_BEE_focus$Sex=="F")]) ,
  mean(DATA_BEE_focus$res.BEE2[which(DATA_BEE_focus$Sex=="F")]) ,
  mean(DATA_BEE_focus$res.BEE3[which(DATA_BEE_focus$Sex=="F")]) ,
  mean(DATA_AEE_focus$res.AEE1[which(DATA_AEE_focus$Sex=="F")]) ,
  mean(DATA_AEE_focus$res.AEE2[which(DATA_AEE_focus$Sex=="F")]) ,
  mean(DATA_AEE_focus$res.AEE3[which(DATA_AEE_focus$Sex=="F")]) )
LM.ESTIMATES$meanfemale<-LM.meanfemale
```

```
##### Calculating means for male and female
#####
```

```
# See Schielzeth et al. (2010)
```

```
# Create dummy variable for sex M=0, F=1
```

```
DATA$Dummy <- DATA$Sex
```

```
DATA$Dummy <- gsub("M", "0", DATA$Dummy)
```

```
DATA$Dummy <- gsub("F", "1", DATA$Dummy)
```

```
DATA_BEE_focus$Dummy <- DATA_BEE_focus$Sex
```

```
DATA_BEE_focus$Dummy <- gsub("M", "0", DATA_BEE_focus$Dummy)
```

```
DATA_BEE_focus$Dummy <- gsub("F", "1", DATA_BEE_focus$Dummy)
```

```

DATA_AEE_focus$Dummy <- DATA_AEE_focus$Sex
DATA_AEE_focus$Dummy <- gsub("M", "0", DATA_AEE_focus$Dummy)
DATA_AEE_focus$Dummy <- gsub("F", "1", DATA_AEE_focus$Dummy)

# Run lm's, without predictor variable centring, to calculate means and SEs
LM.ht.mean<-summary(LM.height<-lm(ht~0+Dummy, data=DATA))
LM.LBM.mean<-summary(LM.LBM<-lm(LBM~0+Dummy, data=DATA))
LM.FAT.mean<-summary(LM.FAT<-lm(FAT~0+Dummy, data=DATA))
LM.Age.mean<-summary(LM.Age<-lm(Age~0+Dummy, data=DATA))
LM.TEE1.mean<-summary(LM.TEE1<-lm(TEE~0+Dummy, data=DATA))
LM.TEE2.mean<-summary(LM.TEE2<-lm(TEE~0+Dummy+ht+LBM, data=DATA))
LM.TEE3.mean<-summary(LM.TEE3<-lm(TEE~0+Dummy+ht+LBM+FAT+Age,
data=DATA))
LM.BEE1.mean<-summary(LM.BEE1<-lm(BEE~0+Dummy,
data=DATA_BEE_focus))
LM.BEE2.mean<-summary(LM.BEE2<-lm(BEE~0+Dummy+ht+LBM,
data=DATA_BEE_focus))
LM.BEE3.mean<-summary(LM.BEE3<-lm(BEE~0+Dummy+ht+LBM+FAT+Age,
data=DATA_BEE_focus))
LM.AEE1.mean<-summary(LM.AEE1<-lm(AEE~0+Dummy,
data=DATA_AEE_focus))
LM.AEE2.mean<-summary(LM.AEE2<-lm(AEE~0+Dummy+ht+LBM,
data=DATA_AEE_focus))
LM.AEE3.mean<-summary(LM.AEE3<-lm(AEE~0+Dummy+ht+LBM+FAT+Age,
data=DATA_AEE_focus))

MEANS <- data.frame(variables=c("height", "LBM", "FAT", "Age", "TEE1", "TEE2",
"TEE3",
                                "BEE1", "BEE2", "BEE3", "AEE1", "AEE2", "AEE3"),
"MeanM"=NA)

MEANS$MeanM <- round(c(LM.ht.mean$coefficients[1],
LM.LBM.mean$coefficients[1],LM.FAT.mean$coefficients[1],

```

```

LM.Age.mean$coefficients[1], LM.TEE1.mean$coefficients[1],
LM.TEE2.mean$coefficients[1],

LM.TEE3.mean$coefficients[1], LM.BEE1.mean$coefficients[1],
LM.BEE2.mean$coefficients[1],

LM.BEE3.mean$coefficients[1], LM.AEE1.mean$coefficients[1],
LM.AEE2.mean$coefficients[1],

LM.AEE3.mean$coefficients[1]),2)
MEANS$MeanF <- round(c(LM.ht.mean$coefficients[2],
LM.LBM.mean$coefficients[2],LM.FAT.mean$coefficients[2],

LM.Age.mean$coefficients[2], LM.TEE1.mean$coefficients[2],
LM.TEE2.mean$coefficients[2],

LM.TEE3.mean$coefficients[2], LM.BEE1.mean$coefficients[2],
LM.BEE2.mean$coefficients[2],

LM.BEE3.mean$coefficients[2], LM.AEE1.mean$coefficients[2],
LM.AEE2.mean$coefficients[2],

LM.AEE3.mean$coefficients[2]),2)
MEANS$SE.M <- round(c(LM.ht.mean$coefficients[3],
LM.LBM.mean$coefficients[3],LM.FAT.mean$coefficients[3],

LM.Age.mean$coefficients[3], LM.TEE1.mean$coefficients[3],
LM.TEE2.mean$coefficients[5],

LM.TEE3.mean$coefficients[7], LM.BEE1.mean$coefficients[3],
LM.BEE2.mean$coefficients[5],

LM.BEE3.mean$coefficients[7], LM.AEE1.mean$coefficients[3],
LM.AEE2.mean$coefficients[5],

LM.AEE3.mean$coefficients[7]),2)
MEANS$SE.F <- round(c(LM.ht.mean$coefficients[4],
LM.LBM.mean$coefficients[4],LM.FAT.mean$coefficients[4],

LM.Age.mean$coefficients[4], LM.TEE1.mean$coefficients[4],
LM.TEE2.mean$coefficients[6],

LM.TEE3.mean$coefficients[8], LM.BEE1.mean$coefficients[4],
LM.BEE2.mean$coefficients[6],

LM.BEE3.mean$coefficients[8], LM.AEE1.mean$coefficients[4],
LM.AEE2.mean$coefficients[6],

LM.AEE3.mean$coefficients[8]),2)

write.table(file="MEANS.txt", MEANS, sep=",")

```

```

ALL <- cbind(ESTIMATES,MEANS)
write.table(file="ALL.txt", ALL, sep=",")

LM.ESTIMATES$Xmale <-c(0.9,1.9,2.9,3.9,5.9,6.9,7.9,9.9,10.9,11.9,13.9,14.9,15.9)
LM.ESTIMATES$Xfemale<-
c(1.1,2.1,3.1,4.1,6.1,7.1,8.1,10.1,11.1,12.1,14.1,15.1,16.1)

#check LM.ESTIMATES versus MCMC. ESTIMATES
library(png)
library("ggplot2")

#####
##### Plot figures of variance #####
#####

library(gridExtra)

# dev.new()

get_png <- function(filename) {
  grid::rasterGrob(png::readPNG(filename), interpolate = TRUE) #
https://www.markhw.com/blog/logos
}
#standing.pic <- get_png("Person standing.png")
#basal.pic <- get_png("Person basal.png")
#active1.pic <- get_png("Person activity 1.png")
#active2.pic <- get_png("Person activity 2.png")

# jpeg(file="Figure 2.jpg", units = "in", width = 12, height = 12, res=300)

```

```
pdf(file="Figure 2.pdf", width = 12, height = 12)
```

```
f1 <- ggplot(DATA, aes(res.TEE1, fill = Sex)) + geom_density(alpha = 0.2) +  
  #geom_vline(xintercept = mean(DATA$res.TEE1[which(DATA$Sex=="F")],  
na.rm=TRUE),  
  #    linetype="dotted", color = "pink", size=1.25) +  
  #geom_vline(xintercept = mean(DATA$res.TEE1[which(DATA$Sex=="M")],  
na.rm=TRUE),  
  #    linetype="dotted", color = "cyan", size=1.2) +  
  annotate(geom="text", x=-8, y=0.4, label="A", size=8) +  
  annotate(geom="text", x=-8, y=0.5, label=" Adjusted for sex", size=6) +  
  coord_cartesian(xlim = c(-8, 22), ylim = c(0, 0.4)) +  
  theme_bw() +  
  theme(legend.position = "none", panel.grid.major = element_blank(),  
panel.grid.minor = element_blank()) +  
  xlab("") +  
  ylab("") +  
  ggtitle("")  
  #annotation_custom(standing.pic, xmin = 15, xmax = 20, ymin = 0.1, ymax = 0.25)
```

```
f2 <- ggplot(DATA, aes(res.TEE2, fill = Sex)) + geom_density(alpha = 0.2) +  
  #geom_vline(xintercept = mean(DATA$res.TEE2[which(DATA$Sex=="F")],  
na.rm=TRUE),  
  #    linetype="dotted", color = "pink", size=1.25) +  
  #geom_vline(xintercept = mean(DATA$res.TEE2[which(DATA$Sex=="M")],  
na.rm=TRUE),  
  #    linetype="dotted", color = "cyan", size=1.2) +  
  annotate(geom="text", x=-8, y=0.4, label="B", size=8) +  
  annotate(geom="text", x=-8, y=0.5, label="Adjusted for sex, height and lean  
mass", size=6) +  
  coord_cartesian(xlim = c(-8, 22), ylim = c(0, 0.4)) +
```



```

theme_bw() +
theme(legend.position = "none", panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(), plot.title = element_text(size = 13.5),
      axis.title.x = element_text(size = 17)) +
xlab("Total energy expenditure (MJ/d)") +
ylab("") +
ggtitle("Adj. for height and fat free mass")
#annotation_custom(standing.pic, xmin = 15, xmax = 20, ymin = 0.1, ymax = 0.25)

f3 <- ggplot(DATA, aes(res.TEE3, fill = Sex)) + geom_density(alpha = 0.2) +
  #geom_vline(xintercept = mean(DATA$res.TEE3[which(DATA$Sex=="F")],
na.rm=TRUE),
  #
  linetype="dotted", color = "pink", size=1.25) +
  #geom_vline(xintercept = mean(DATA$res.TEE3[which(DATA$Sex=="M")],
na.rm=TRUE),
  #
  linetype="dotted", color = "cyan", size=1.2) +
  annotate(geom="text", x=-8, y=0.4, label="C", size=8) +
  #annotate(geom="text", x=-8, y=0.4, label="Adjusted for sex, height, lean mass,
fat mass and age", size=5) +
  coord_cartesian(xlim = c(-8, 22), ylim = c(0, 0.4)) +
  theme_bw() +
  theme(legend.position = "none", panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(), plot.title = element_text(size = 13.5)) +
  xlab("") +
  ylab("") +
  ggtitle("Adj. height, fat free mass, fat mass, age")
#annotation_custom(standing.pic, xmin = 15, xmax = 20, ymin = 0.1, ymax = 0.25)

g1 <- ggplot(DATA_BEE_focus, aes(res.BEE1, fill = Sex)) + geom_density(alpha =
0.2) +

```

```

#geom_vline(xintercept =
mean(DATA_BEE_focus$res.BEE1[which(DATA_BEE_focus$Sex=="F")],
na.rm=TRUE),

#      linetype="dotted", color = "pink", size=1.25) +

#geom_vline(xintercept =
mean(DATA_BEE_focus$res.BEE1[which(DATA_BEE_focus$Sex=="M")],
na.rm=TRUE),

#      linetype="dotted", color = "cyan", size=1.2) +
annotate(geom="text", x=-4, y=0.7, label="D", size=8) +
coord_cartesian(xlim = c(-4, 7), ylim = c(0, 0.7)) +
theme_bw() +

theme(legend.position = "none", panel.grid.major = element_blank(),
panel.grid.minor = element_blank(),

axis.title.y = element_text(size = 17)) +
xlab("") +
ylab("Density")

#annotation_custom(basal.pic, xmin = 3.0, xmax = 6.5, ymin = 0.2, ymax = 0.6)

g2 <- ggplot(DATA_BEE_focus, aes(res.BEE2, fill = Sex)) + geom_density(alpha =
0.2) +

#geom_vline(xintercept =
mean(DATA_BEE_focus$res.BEE2[which(DATA_BEE_focus$Sex=="F")],
na.rm=TRUE),

#      linetype="dotted", color = "pink", size=1.25) +

#geom_vline(xintercept =
mean(DATA_BEE_focus$res.BEE2[which(DATA_BEE_focus$Sex=="M")],
na.rm=TRUE),

#      linetype="dotted", color = "cyan", size=1.2) +
annotate(geom="text", x=-4, y=0.7, label="E", size=8) +
coord_cartesian(xlim = c(-4, 7), ylim = c(0, 0.7)) +
theme_bw() +

theme(legend.position = "none", panel.grid.major = element_blank(),
panel.grid.minor = element_blank(),

axis.title.x = element_text(size = 17)) +

```

```

xlab("Basal energy expenditure (MJ/d)") +
ylab("")

#annotation_custom(basal.pic, xmin = 3.0, xmax = 6.5, ymin = 0.2, ymax = 0.6)

g3 <- ggplot(DATA_BEE_focus, aes(res.BEE3, fill = Sex)) + geom_density(alpha =
0.2) +
  #geom_vline(xintercept =
mean(DATA_BEE_focus$res.BEE3[which(DATA_BEE_focus$Sex=="F")],
na.rm=TRUE),
  #      linetype="dotted", color = "pink", size=1.25) +
  #geom_vline(xintercept =
mean(DATA_BEE_focus$res.BEE3[which(DATA_BEE_focus$Sex=="M")],
na.rm=TRUE),
  #      linetype="dotted", color = "cyan", size=1.2) +
  annotate(geom="text", x=-4, y=0.7, label="F", size=8) +
  coord_cartesian(xlim = c(-4, 7), ylim = c(0, 0.7)) +
  theme_bw() +
  theme(legend.position = "none", panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(), axis.title.x = element_text(size = 9)) +
  xlab("") +
  ylab("")

#annotation_custom(basal.pic, xmin = 3.0, xmax = 6.5, ymin = 0.2, ymax = 0.6)

h1 <- ggplot(DATA_AEE_focus, aes(res.AEE1, fill = Sex)) + geom_density(alpha =
0.2) +
  #geom_vline(xintercept =
mean(DATA_AEE_focus$res.AEE1[which(DATA_AEE_focus$Sex=="F")],
na.rm=TRUE),
  #      linetype="dotted", color = "pink", size=1.25) +
  #geom_vline(xintercept =
mean(DATA_AEE_focus$res.AEE1[which(DATA_AEE_focus$Sex=="M")],
na.rm=TRUE),
  #      linetype="dotted", color = "cyan", size=1.2) +
  annotate(geom="text", x=-6, y=0.4, label="G", size=8) +

```

```

coord_cartesian(xlim = c(-6, 9), ylim = c(0, 0.4)) +
theme_bw() +
theme(legend.position = "none", panel.grid.major = element_blank(),
panel.grid.minor = element_blank()) +
xlab("") +
ylab("")
#annotation_custom(active1.pic, xmin = 3.5, xmax = 8, ymin = 0.1, ymax = 0.3)

h2 <- ggplot(DATA_AEE_focus, aes(res.AEE2, fill = Sex)) + geom_density(alpha =
0.2) +
#geom_vline(xintercept =
mean(DATA_AEE_focus$res.AEE2[which(DATA_AEE_focus$Sex=="F")],
na.rm=TRUE),
# linetype="dotted", color = "pink", size=1.25) +
#geom_vline(xintercept =
mean(DATA_AEE_focus$res.AEE2[which(DATA_AEE_focus$Sex=="M")],
na.rm=TRUE),
# linetype="dotted", color = "cyan", size=1.2) +
annotate(geom="text", x=-6, y=0.4, label="H", size=8) +
coord_cartesian(xlim = c(-6, 9), ylim = c(0, 0.4)) +
theme_bw() +
theme(legend.position = "none", panel.grid.major = element_blank(),
panel.grid.minor = element_blank(),
axis.title.x = element_text(size = 17)) +
xlab("Activity energy expenditure (MJ/d)") +
ylab("")
#annotation_custom(active1.pic, xmin = 3.5, xmax = 8, ymin = 0.1, ymax = 0.3)

h3 <- ggplot(DATA_AEE_focus, aes(res.AEE3, fill = Sex)) + geom_density(alpha =
0.2) +
#geom_vline(xintercept =
mean(DATA_AEE_focus$res.AEE3[which(DATA_AEE_focus$Sex=="F")],
na.rm=TRUE),
# linetype="dotted", color = "pink", size=1.25) +

```

```

#geom_vline(xintercept =
mean(DATA_AEE_focus$res.AEE3[which(DATA_AEE_focus$Sex=="M")],
na.rm=TRUE),

#   linetype="dotted", color = "cyan", size=1.2) +
annotate(geom="text", x=-6, y=0.4, label="I", size=8) +
coord_cartesian(xlim = c(-6, 9), ylim = c(0, 0.4)) +
theme_bw() +
theme(legend.position = "none", panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(), axis.title.x = element_text(size = 9)) +
xlab("") +
ylab("")

#annotation_custom(active1.pic, xmin = 3.5, xmax = 8, ymin = 0.1, ymax = 0.3)

grid.arrange(f1, f2, f3, g1, g2, g3, h1, h2, h3, nrow=3)

dev.off()

```

SOM Table S1

Unique participant identifiers for the IAEA DLW database v. 3.1.2.

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SOM Table S2

Disaggregation of the data into 'Western' and 'non-Western' countries. Western countries: United States, Germany, The Netherlands, Australia, Finland, Belgium, Sweden, France, UK, Norway, Greece. Non-western countries: Bolivia, Chile, China, Ecuador, Ghana, Jamaica, Japan, Kenya, Mauritius, Nigeria, Nepal, Seychelles, Tanzania, South Africa.

SOM Table S3

The ethnic makeup of Western and non-Western countries based on available data.

Ethnicity	Western/non-Western countries	%
African	non-West	61.0
African American	West	18.0
Asian	non-West	26.0
Asian	West	1.7
Caucasian	non-West	1.3
Caucasian	West	77.0
Hunter-gatherer	non-West	0.9
Hunter-gatherer	West	2.7
Other	non-West	10.7
Other	West	0.7

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