Analysis of Body measurements and proportions between male and female

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In this article we compare the *empirical characteristic function* (Tukey 1977; Becker et al. 1988) to a *moment-generating-functional form* to compute the proportion of hypotheses m that are rejected under the null hypothesis.

Here is a second paragraph of the abstract (if necessary), and with the pipe notation it doesn't break. Notice it still needs to be indented.

Generally, we write this abstract last. Often it is called the executive summary. It should succinctly summarize the entire document. You can include references such as this one to the Appendices section 6 if necessary.

Keywords: boxplots; multivariate chi-square distribution; nonlinear growth curves; Richard's curve; simulated critical points

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1 Introduction

The global mean height of women is about four and a half inches, or 12 centimeters shorter than that of men. Globally, the ratio is 1.07, meaning that on average, men are about 7% taller than women. Across the world, this relative difference between the sexes can vary from only 2-3% to over 12% (Max Roser and Ritchie 2013). It is well-established knowledge that men are taller than women on average throughout the globe. This study will further examine the anatomical differences between men and women. More specifically, in the context of standing height, leg length, wingspan, hand length, foot length, and head height.

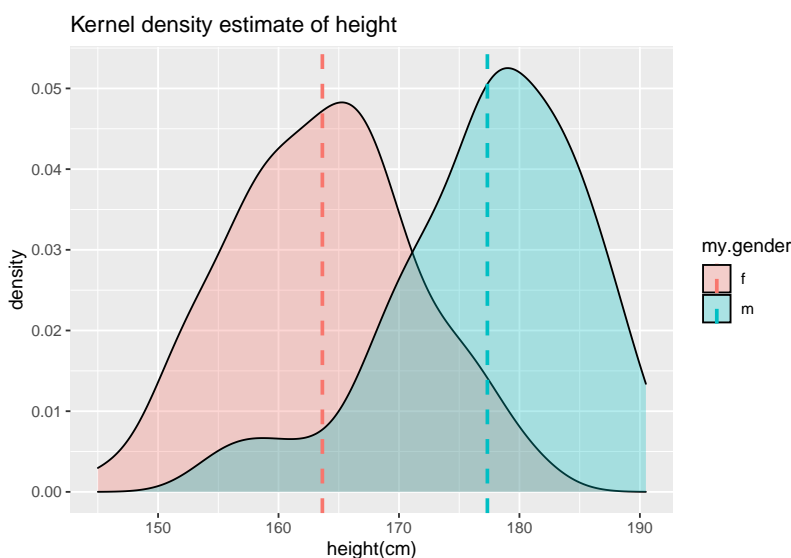### Figure 1: Height distribution between male and female

Figure 1 visualizes the height distributions of males and females in the sample data. The red line indicates the mean value of the female height sample, and the blue line indicates the mean value of the male height sample. The difference between the average height is about 13.7cm, which is 1.3cm greater than the global mean difference of 12cm, according to (Max Roser and Ritchie 2013). In our sample data, men are about 8.4% taller than the female on average. The result verifies our sample data is within the norm of global height difference.

2   Research Question: Male and female comparison of body measurements and proportions

2.1   *How are male and female differ in terms of body measurements*

Figure 2: boxplots of male and female measurements
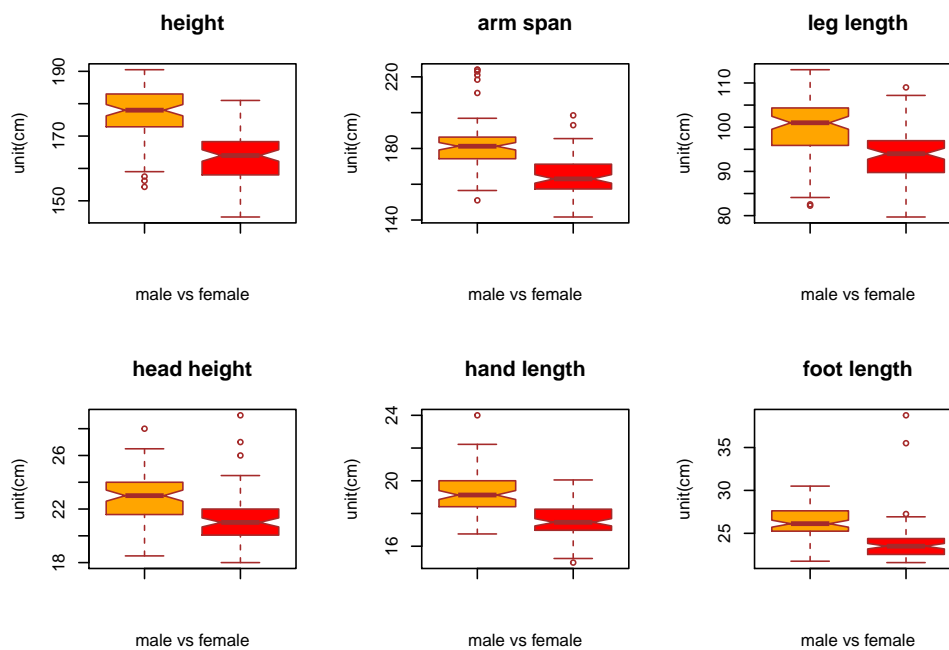
The sample data measurement differs between males and females. Figure 2 reveal the distribution of each variable between men and women. All variables median value lie outside of the box of opposite sex box plots. That is, there is likely to be a difference between the two genders. Observation of Interquartile ranges(the box) shows a similar dispersion between males and females. The overall spread of the boxplots reveals men vary more in head height and foot length in comparison to women. Some of the outliers in head height, hand length, and foot length are likely due to a measurement error. It is very unlikely that the normal human head height and foot length exceed 30cm. Extreme outliers will be removed for the hypothesis testing.

Further investigating the measurement between male and female with another factor variable ethnicity. In our sample, we are only comparing Asians and whites. Figure 3 displays boxplots of Asian male and female measurements on the top row and white male and female measurements on the bottom row. The boxplots are closer together and overlap more in Asians than whites. This indicates there is less difference between genders in Asians than whites. It is interesting to observe leg length between Asian males and females, they seem to have the same median value although Asian male's median height value is about 10cm taller. Do Asian women have longer leg lengths relative to height than Asian men? Note the distribution of Asian males varies greater than of Asian females across every measurement variables. The distribution of white males

Figure 3: boxplots of white/asian male and female body measurements
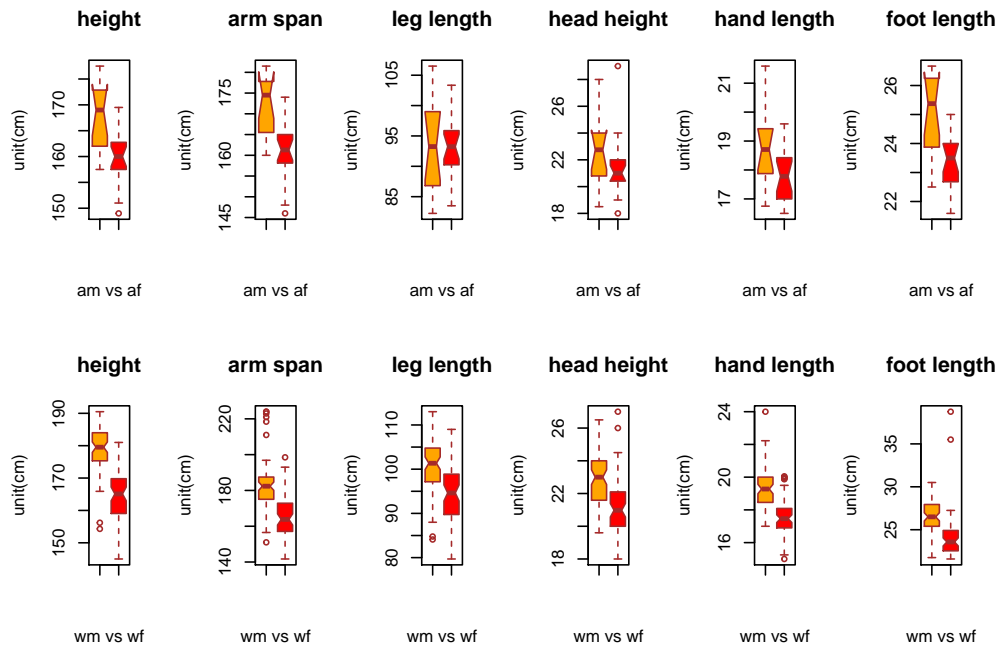
and females is very similar to the average distribution between males and females. However, the average measurement values in whites are slightly higher than the average sample data.

2.2   *How are male and female differ in terms of body proportions*

In Figure 4 The proportion of boxplots between male and female sample data reveal the distribution of body proportions relative to height. It is clear to see the distributions are very similar to each other. Body proportion between males and females doesn't seem to differ much. On average, the arm span is about the same as the height of a person. The median head height proportion is about 0.13, which is about 7.7 heads will fit into a person's standing height.

Figure **??** breaks down the male-female proportion boxplots between Asian and white. Again, the boxplots overlap with each other. However, the Asian male/female boxplots median values differ slightly. Asian male boxplots show longer arm span and hand length, and shorter leg length compared to Asian female proportions. In the next section, the study reviews the significance of the difference in body measurements and the proportion between genders.

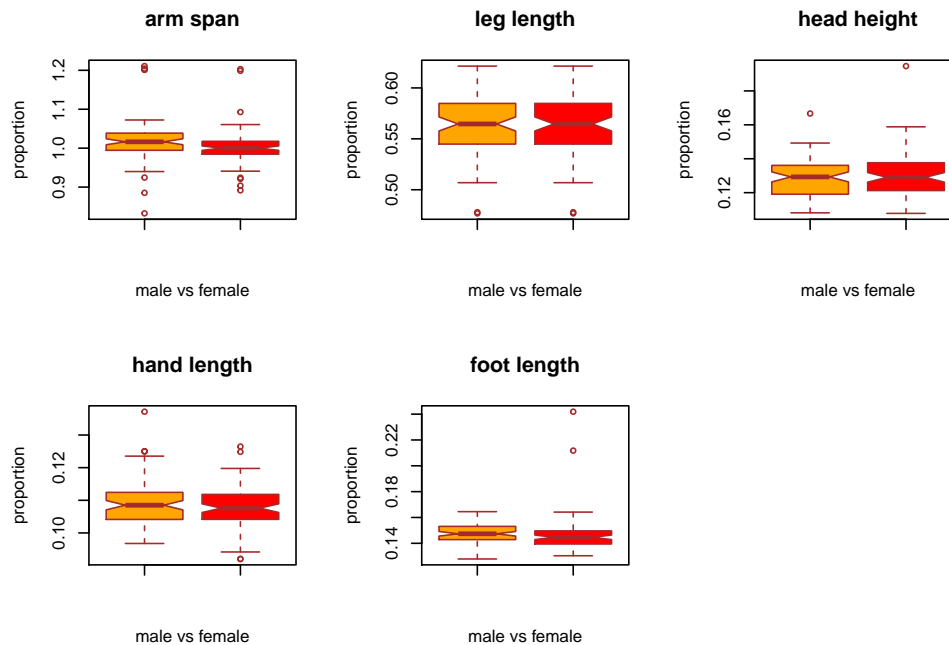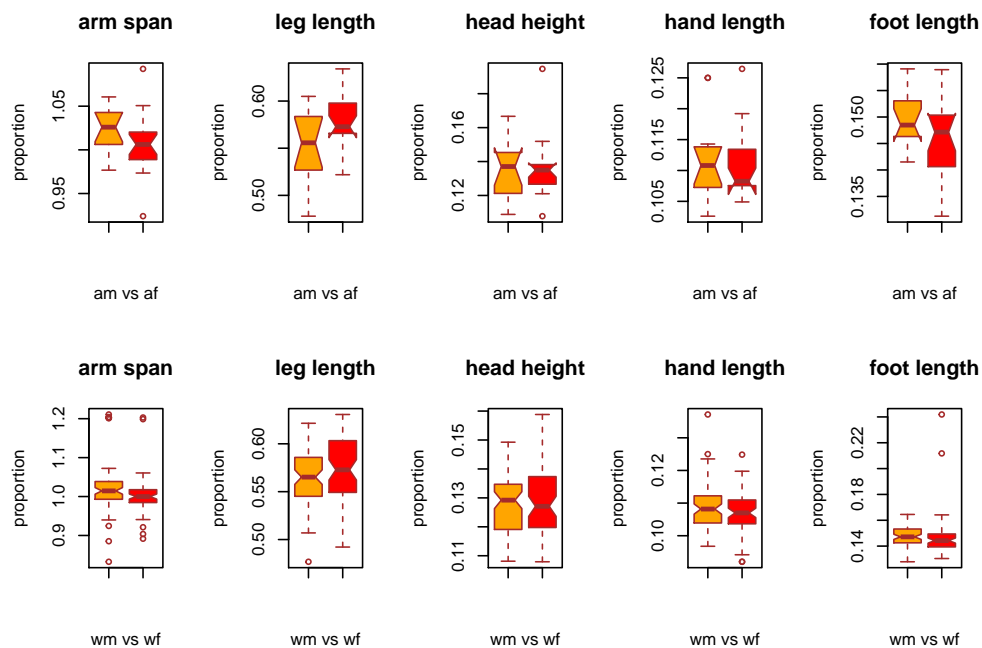**Figure 4: boxplots of male and female body proportions**

Figure 5: boxplots of white/asian male and female body proportions

3   Data Description

Data was collected by each classmate. Each classmate created handouts for data collection and collected 10 individuals measurements. The original data initially contained 428 observations. After the data cleaning process, the observation reduced to 190 individuals. Some of the measurements measured right and left side of the body have been merged into one averaged value. All the measurement units were converted to centimeters.

Sample data constraints individuals at age 18 or above. The measurements contain individuals' height, leg length, arm span, head height, hand length, and foot length. The sample data also contains proportions of each measurement relative to height. Other variables used in the sample data include gender, sex, and age.

Reference the section in the Appendix with greater detail about the data provenance 6.

3.1   Summary of Sample

Figure6 shows the sample data counts grouped by gender and ethnicity. A total of 167 observations are in sample data which contains 83 females and 84 males. About 70% of the sample data is white and about 30% Asian.

Figure 6: sample data grouping by gender and ethnicity

	my.gender	my.ethnicity	count
1	f	a	19
2	f	w	64
3	m	a	12
4	m	w	72

Figure7 histogram shows the density of the sample data in the different age groups. About 45% of the participants are aged between 20 and 30.

3.2   Summary Statistics of Data

See table 1 and 2.
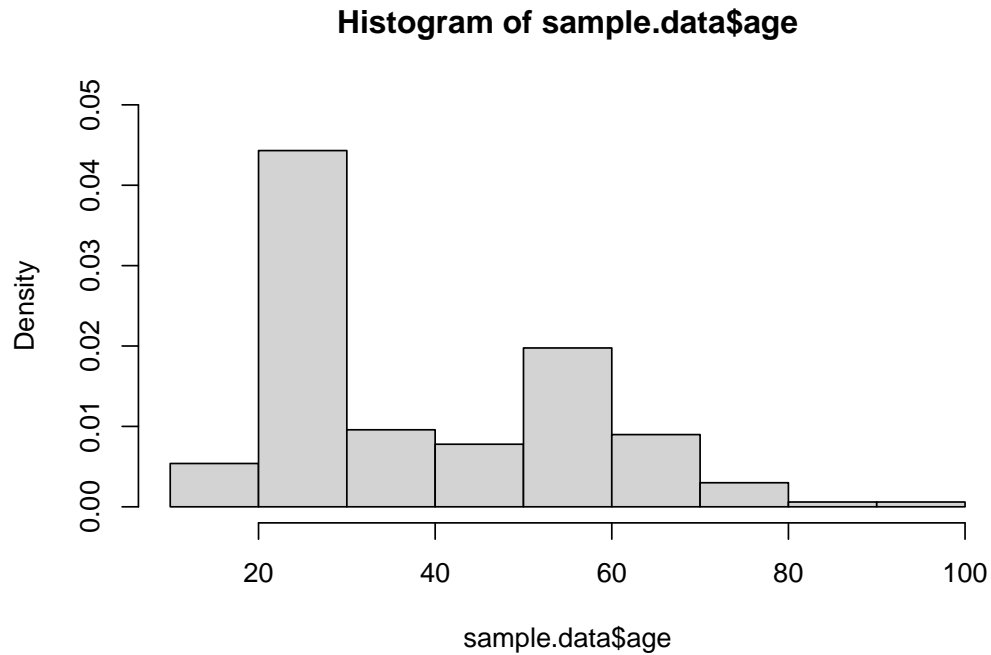
Figure 7: sample data age distribution

Histogram of sample.data$age

Table 1: Descriptive Statistics and Correlation Analysis in male

		M	SD	1	2	3	4	5
1	**height**	177.3	7.89	1				
2	**head.height**	22.8	1.70	-.05	1			
3	**arm.span**	181.5	14.21	.60***	-.29**	1		
4	**hand.length**	19.3	1.30	.34**	.29**	-.02	1	
5	**foot.length**	26.3	1.76	.68***	.08	.29**	.56***	1
6	**floor.hip**	99.9	6.82	.64***	.13	.28**	.23*	.43***

Notes: Pearson pairwise correlations are reported;
a two-side test was performed to report correlation significance.

$^\dagger p < .10$ $^* p < .05$ $^{**} p < .01$ $^{***} p < .001$

Table 2: Descriptive Statistics and Correlation Analysis in female

		M	SD	1	2	3	4	5
1	**height**	163.6	7.65	1				
2	**head.height**	21.3	1.88	-.05	1			
3	**arm.span**	164.2	10.49	.71***	-.15	1		
4	**hand.length**	17.6	1.12	.47***	.01	.33**	1	
5	**foot.length**	23.9	2.51	.33**	.04	.32**	.38***	1
6	**floor.hip**	94.0	5.47	.49***	.05	.38***	.41***	.31**

Notes: Pearson pairwise correlations are reported;
a two-side test was performed to report correlation significance.

$^{†}p < .10$ $^{*}p < .05$ $^{**}p < .01$ $^{***}p < .001$

4   Key Findings

5   Conclusion

This was a new page
This is a newline.
Here is some more text.
Below are some example code that may benefit you in preparing your document.

Please state your name: _____

I was born on _____ in _____

$$Y_{jt} = \alpha + \boldsymbol{\beta} X_{jt} + v_j + \varepsilon_{jt}, \tag{1}$$

where α is the grand mean, v_j is the fixed-time country mean, X_{jt} (country j at time t) is the matrix of country-level observations for the vector of aforementioned parameters $\boldsymbol{\beta}$, and ε_{jt} represents the residual idiosyncratic disturbance. Our panel data set consists of repeated observations of countries over time. Therefore, we employ cross-section time-series models. This approach redefines Equation~1 by subtracting time-demeaned values. This *within* transformation subtracts constant country effects for the dependent variable $\bar{Y}_j$, the predictor variables $\bar{X}_j$, and the intercept $\bar{v}_j$:

$$(Y_{jt} - \theta\bar{Y}_j) = (1 - \theta)\alpha + \boldsymbol{\beta}(X_{jt} - \bar{X}_j) + (v_{jt} - \theta\bar{v}_j), \tag{2}$$

If $\theta = 0$, the model reduces to a basic pooled ordinary-least-squares (OLS) model; if $\theta = 1$, the model reduces to a fixed-effects model; otherwise the model represents a random-effects model. The pooled OLS estimation is biased if country effects exist (Hsiao 2003). The random-effects model may be susceptible to omitted-variable bias (Wooldridge 2006): bias because a predictor was excluded from the model specification. Conversely, the fixed-effects model is not susceptible to this bias as it captures unobserved intracountry variation around its average country-level "fixed effect." Panel-data analysis commonly has issues with heteroskedasticity, serial autocorrelation, and cross-sectional autocorrelation.
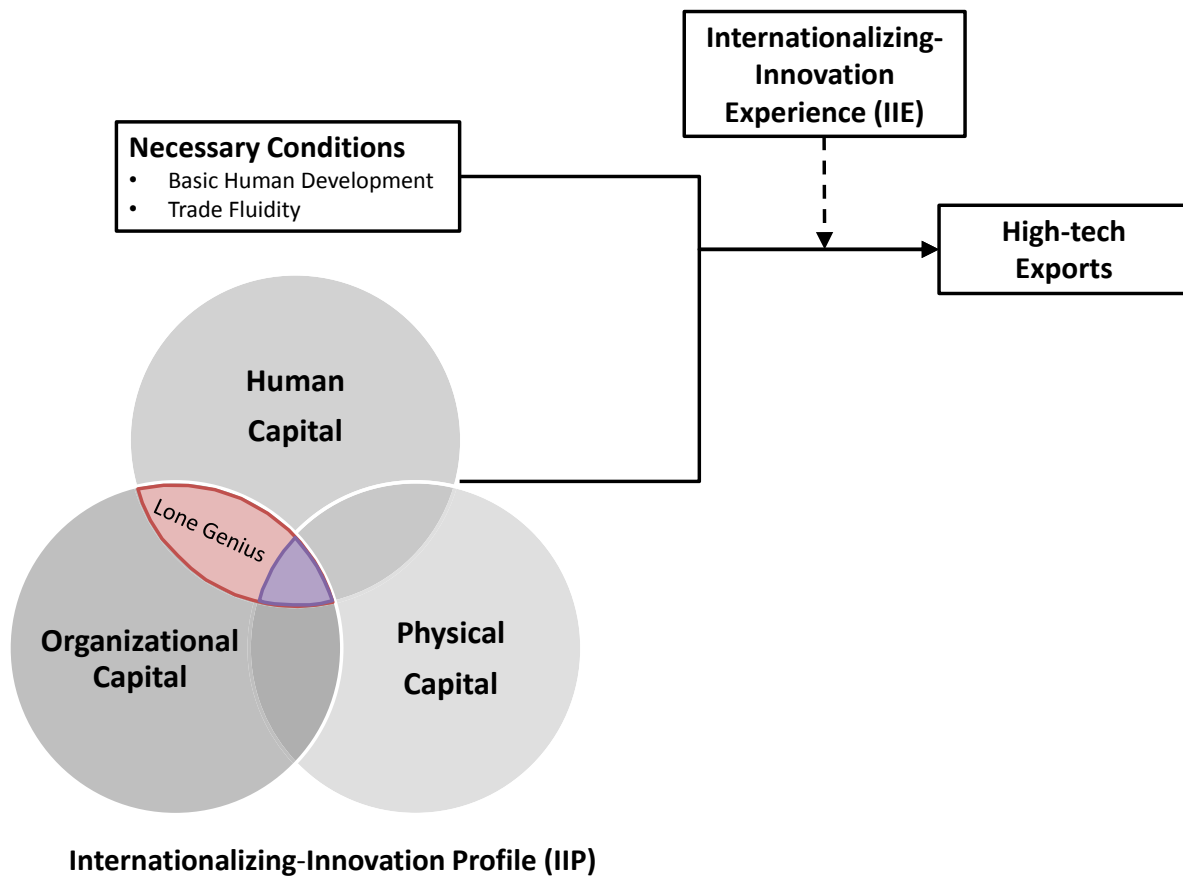
$i = 1$ and

$$i = 1$$

1	2	3	4	5
6	7	8	9	10

See Figure 8.

Figure 8: Conceptual Model

This is a footnote[1] that can be placed within a document.

Refer to the Appendices in section~6 where I am going to cite John (Tukey 1962, pp. 2-3).
Here is a quote by Tukey (1962, pp. 2-3):

> For a long time I have thought I was a statistician, interested in inferences from the particular to the general. But as I have watched mathematical statistics evolve, I have had to cause to wonder and to doubt. [...] All in all, I have come to feel that my central interest is in *data analysis*, which I take to include among other things: procedures for analyzing data, techniques for interpreting the results of such procedures, ways of planning the gathering of data to make its analysis easier, more precise or more accurate, and all the machinery and results of (mathematical) statistics which apply to analyzing the data.

Large parts of data analysis are inferential in the sample-to-population sense, but these are only parts, not the whole. Large parts of data analysis are incisive, laying bare indications which we could not perceive by simple and direct examination of the raw data, but these too are only parts, not the whole. Some parts of data analysis, as the term is her stretch beyond its philology, are allocation, in the sense that they guide us in the distribution of effort and other valuable considerations in observation, experimentation, or analysis. Data analysis is a larger and more varied field than inference, or incisive procedures, or allocation.

Statistics has contributed much to data analysis. In the future it can, and in my view should, contribute more. For such contributions to exist, and be valuable, it is not necessary that they be direct. They need not provide new techniques, or better tables for old techniques, in order to influence the practice of data analysis.

6   APPENDICES

6.1   Data Provenance

6.1.1   Data Collection Handout

Figure 9: Handout Page 1

WSU STATS419 Measure Project Data Collection Handout

Part 1. Please fill out the questions below

Name:

Gender: Age:

Ethnicity:

Dominant Eye (right, left, or equal):   Eye color:

Dominant arm for swing a bat (right, left, or both):   Dominant writing hand (right, left, or both):

Notes/Comments:

Part 2. Measurements

- You will need a soft measuring tape
- Please record how long it took you to finish part2.
- Measure the following locations in cm. Measure right and left if applicable.
  Please refer to the next page for visual representation for measurement locations.

|	Description	Right (cm)	Left (cm)
1.Height	Standing height (head to floor with no shoes on)		
2.Floor to knee pit	Distance from the floor to the knee pit		
3.Floor to hip	Distance from the floor to the hip bone		
4.Floor to navel	Distance from the floor to the belly button		
5.Floor to armpit	Distance from the floor to the armpit		
6.Standing reach	Standing flatfooted, length from floor to the extended arm maximum point.		
7.Wingspan	middle finger of each hand fully stretched out		
8.Middle finger to elbow	Distance from middle finger to elbow (measure from the inside)		
9.Elbow to armpit	Distance from the elbow to armpit		
10.Length of foot	Distance from back of the heal to the longest toe		
11.Head height	Distance from the top of the head to below the chin		
12.Head circumference	Distance around head, measured right above ears/eyes		
13.Hand length	Distance from middle finger to wrist (horizontal line just below the palm)		
14.Hand span	Distance from pinkie to thumb fully stretched		

Time spent on part2:

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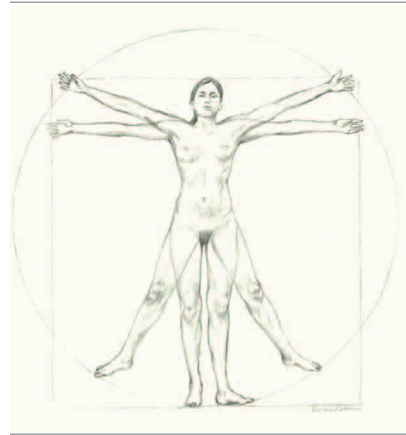Minju.lee@wsu.edu
SID:11638071

Figure 10: Handout Page 2
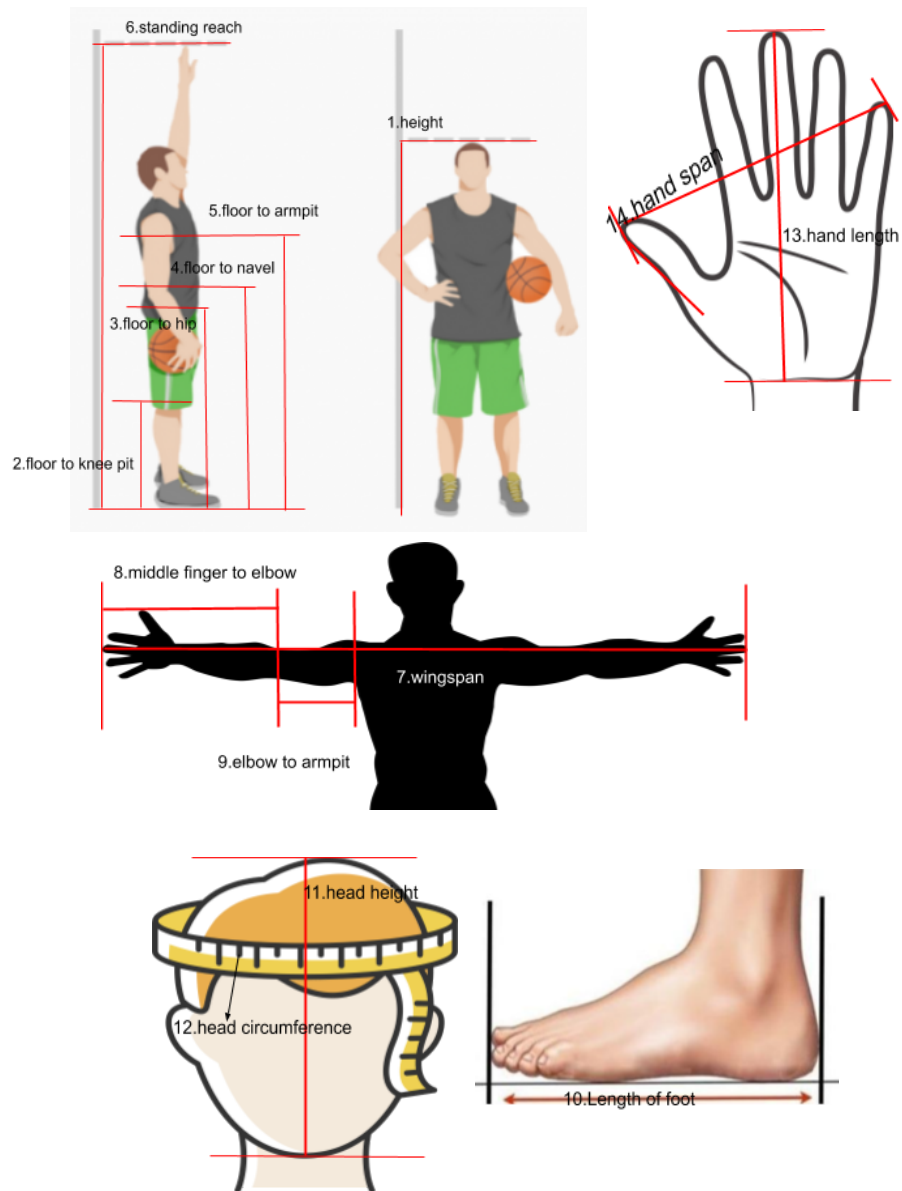
Minju Lee
Minju.lee@wsu.edu
SID:11638071
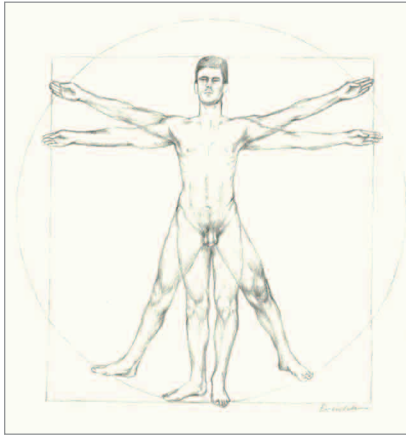
(a) Thomas et al. (2020) discuss this.

(b) Schnitt realer Sensor (Thomas et al. 2020)

Figure 11:   Der Sensor in Theorie und Verwirklichung... caption at bottom instead?   I can write a really long caption if I want.

This is using "crop" to include one image and trim it to appear as two. Likely you will have two separate images if you use this option, so you would set the trim parameters all equal to 0.

This figure has subfigures which each also have a possible caption.

6.2 Preparing the Report Workspace as a subsection

6.2.1 prepare sample data

Below is the necessary functions and libraries required to run the code referenced in this document.

```
library(devtools);          # required for source_url
```

```
## Loading required package: usethis
```

```
path.humanVerseWSU = "https://raw.githubusercontent.com/MonteShaffer/humanVerseWSU/"
source_url( paste0(path.humanVerseWSU,"master/misc/functions-project-measure.R") );
```

```
## SHA-1 hash of file is 091aa1c443f262dce181395047d037a756331a65
```

```
## Loading required package: lattice
```

```
## Loading required package: survival
```

```
## Loading required package: Formula
```

```
## Loading required package: ggplot2
```

```
##
## Attaching package: 'Hmisc'
```

```
## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
source_url( paste0(path.humanVerseWSU,"master/humanVerseWSU/R/functions-dataframe.R") );
```

```
## SHA-1 hash of file is e1fdfd5e02a4d25ef4a57cfd79df4bba1222788b
```

```
source_url( paste0(path.humanVerseWSU,"master/humanVerseWSU/R/functions-EDA.R") );
```

```
## SHA-1 hash of file is 9a397c6d1f50caa6caad70bf01c17242731350b9
```

```
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

```
##
## Attaching package: 'psych'
```

```
## The following object is masked from 'package:Hmisc':
##
##     describe
```

```
## The following objects are masked from 'package:ggplot2':
##
##     %+%, alpha
```

Below is the code to load the data and prepare it for analysis.

```
path.project = "C:/_git_/WSU_STATS419_FALL2020/project-measure/";
path.to.secret = "C:/Users/13608/Dropbox/WSU-419/Fall 2020/__student_access__/_SECRET_/"

measure = utils::read.csv( paste0(path.to.secret, "measure-students.txt"), header=TRUE, quote="", sep="
getOne = c("hand.length", "hand.width", "hand.elbow", "elbow.armpit", "arm.reach", "foot.length", "floor

#############################################################################################
path.github = "https://raw.githubusercontent.com/minju-lee92/WSU_STATS419_FALL2020/";
source_url( paste0(path.github,"master/functions/functions-project-measure.R") );
```

```
## SHA-1 hash of file is 5aa82ee87a0a62bfc9b04ccc942d44c0cc3ed092
```

```
# this is your function
# covert unit into cm
measureAscm <-convert.inchestocm(measure)
# build merged left/right value cols
merged.df <-merge.left.right(measureAscm, getOne)
# remove nas, duplicates, create categorical variables... etc
cleaned.df = prepareMeasureData(merged.df)

# create scaled variables using height
colnum = c(3:7,20:28)
new.colname = c("p.height", "p.head.h", "p.head.c", "p.arm.span", "p.floor.navel","p.hand.length","p.ha

v1.df =build.scale.variables(cleaned.df, colnum, new.colname, cleaned.df$height)

# final sample data for the analysis
sample.df <-v1.df[,c(1:4,6,20,25,27,13,29:31,36,37,39,41,46,48)]
sample.data <- sample.df[sample.df$my.gender !='o'& sample.df$my.ethnicity=='a'|sample.df$my.ethnicity==

# age over 18
sample.data <- sample.data[sample.data$age >=18,]
summary(sample.data)
# getting rid of outliers.
sample.data <- sample.data[sample.data$height >= 145 & sample.data$arm.span>100 & sample.data$hand.leng

saveRDS(sample.data,"sample.data.rds");
    utils::write.table(sample.data, file="sample.data.txt", quote=FALSE, col.names=TRUE, row.names=FALSE
```

6.2.2 generate summary of sample

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:Hmisc':
##
##      src, summarize

## The following objects are masked from 'package:stats':
##
##      filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
sample.data <- na.omit(sample.data)
dist.sample <- sample.data %>% group_by(my.gender, my.ethnicity) %>% dplyr::summarise(count = n())
```

```
## 'summarise()' regrouping output by 'my.gender' (override with '.groups' argument)
```

```
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
pdf("pdfs/sample.pdf", height=2, width=3)
grid.table(dist.sample)
dev.off()
```

```
hist(sample.data$age, breaks=seq(10,100,10), ylim=c(0,0.05), freq=FALSE)
```

```
dim(sample.data)
str(sample.data)
summary.sample <-summary(sample.data[,c(13:18)])
library(gridExtra)
pdf("pdfs/summary-sample.pdf", height=3, width=10)
grid.table(summary.sample)
dev.off()
```

6.2.3   generate summary statistic tables

Below is the code to generate the summary statistics and save them as a table that you see in Section **??**.

```
path.project = "C:/_git_/WSU_STATS419_FALL2020/project-measure/";
path.tables = paste0(path.project,"tables/");
  createDirRecursive(path.tables);
```

```
file.correlation = paste0(path.tables,"correlation-table.tex")
myData = as.matrix(sample.data[,c(3:8)])  # numeric values only, only what will appear in table
# https://www.overleaf.com/read/srzhrcryjpwn
# keepaspectratio of include graphics
# could scale \input if still too big ...
# https://tex.stackexchange.com/questions/13460/scalebox-knowing-how-much-it-scales#13487
buildLatexCorrelationTable(myData,
  rotateTable = FALSE,
  width.table = 0.80, # best for given data ... 0.95 when rotateTable = FALSE
                  # 0.60 when rotateTable = TRUE
  myCaption = "Overall Descriptive Statistics and Correlation Analysis",
```

```r
  myFile = file.correlation,
  myNames = colnames(myData),
  showOnes = "left")
Sys.sleep(2) # in case Knit-PDF doesn't like that I just created the file...
```

```r
file.correlation = paste0(path.tables,"male-correlation-table.tex")

male_sample.data <- sample.data[sample.data$my.gender=='m',]
myData = as.matrix(male_sample.data[,c(3:8)])   # numeric values only, only what will appear in table
# https://www.overleaf.com/read/srzhrcryjpwn
# keepaspectratio of include graphics
# could scale \input if still too big ...
# https://tex.stackexchange.com/questions/13460/scalebox-knowing-how-much-it-scales#13487
buildLatexCorrelationTable(myData,
  myLabel = "table:male-correlation",
  rotateTable = FALSE,
  width.table = 0.80, # best for given data ... 0.95 when rotateTable = FALSE
                      # 0.60 when rotateTable = TRUE
  myCaption = "Descriptive Statistics and Correlation Analysis in male",
  myFile = file.correlation,
  myNames = colnames(myData),
  width.names = "15mm",
  space.M.SD = "0.1mm",
  space.SD.corr = "0.5mm",
  space.between = "0.1mm",
  showOnes = "center")
Sys.sleep(2) # in case Knit-PDF doesn't like that I just created the file...
```

```r
file.correlation = paste0(path.tables,"female-correlation-table.tex")

female_sample.data <- sample.data[sample.data$my.gender=='f',]
myData = as.matrix(female_sample.data[,c(3:8)])   # numeric values only, only what will appear in table
# https://www.overleaf.com/read/srzhrcryjpwn
# keepaspectratio of include graphics
# could scale \input if still too big ...
# https://tex.stackexchange.com/questions/13460/scalebox-knowing-how-much-it-scales#13487
buildLatexCorrelationTable(myData,
  myLabel = "table:female-correlation",
  rotateTable = FALSE,
  width.table = 0.80, # best for given data ... 0.95 when rotateTable = FALSE
                      # 0.60 when rotateTable = TRUE
  myCaption = "Descriptive Statistics and Correlation Analysis in female",
  myFile = file.correlation,
  myNames = colnames(myData),
  width.names = "15mm",
  space.M.SD = "0.1mm",
  space.SD.corr = "0.5mm",
  space.between = "0.1mm",
  showOnes = "center")
Sys.sleep(2) # in case Knit-PDF doesn't like that I just created the file...
```

6.2.4   generate summary statistic figures

```r
height.m <- sample.data$height[sample.data$my.gender == 'm']
height.f <- sample.data$height[sample.data$my.gender == 'f']
arm.span.m <- sample.data$arm.span[sample.data$my.gender == 'm']
arm.span.f <- sample.data$arm.span[sample.data$my.gender == 'f']
floor.hip.m <- sample.data$floor.hip[sample.data$my.gender == 'm']
floor.hip.f <- sample.data$floor.hip[sample.data$my.gender == 'f']
head.height.m <- sample.data$head.height[sample.data$my.gender == 'm']
head.height.f <- sample.data$head.height[sample.data$my.gender == 'f']
hand.length.m <- sample.data$hand.length[sample.data$my.gender == 'm']
hand.length.f <- sample.data$hand.length[sample.data$my.gender == 'f']
foot.length.m <- sample.data$foot.length[sample.data$my.gender == 'm']
foot.length.f <- sample.data$foot.length[sample.data$my.gender == 'f']


par(mfrow = c(2,3))

boxplot(height.m, height.f,
        main = "height",
        xlab = "male vs female",
        ylab = "unit(cm)",
        ylim = c(140,220),
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(arm.span.m, arm.span.f,
        main = "arm span",
        xlab = "male vs female",
        ylab = "unit(cm)",
        ylim = c(140,220),
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(floor.hip.m, floor.hip.f,
        main = "leg length",
        xlab = "male vs female",
        ylab = "unit(cm)",
        ylim = c(80,160),
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(head.height.m, head.height.f,
        main = "head height",
        xlab = "male vs female",
        ylab = "unit(cm)",
        ylim = c(16,35),
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(hand.length.m, hand.length.f,
        main = "hand length",
        xlab = "male vs female",
        ylab = "unit(cm)",
```

```r
        ylim = c(16,35),
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(foot.length.m, foot.length.f,
        main = "foot length",
        xlab = "male vs female",
        ylab = "unit(cm)",
        ylim = c(16,35),
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```r
# Would certain ethnicity change the measurements between male and female?
a.height.m <- sample.data$height[sample.data$my.gender == 'm' &sample.data$my.ethnicity =='a']
a.height.f <- sample.data$height[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='a']

a.arm.span.m <- sample.data$arm.span[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='a']
a.arm.span.f <- sample.data$arm.span[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='a']

a.floor.hip.m <- sample.data$floor.hip[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='a']
a.floor.hip.f <- sample.data$floor.hip[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='a']
a.head.height.m <- sample.data$head.height[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='a']
a.head.height.f <- sample.data$head.height[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='a']
a.hand.length.m <- sample.data$hand.length[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='a']
a.hand.length.f <- sample.data$hand.length[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='a']
a.foot.length.m <- sample.data$foot.length[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='a']
a.foot.length.f <- sample.data$foot.length[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='a']

w.height.m <- sample.data$height[sample.data$my.gender == 'm' &sample.data$my.ethnicity =='w']
w.height.f <- sample.data$height[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='w']

w.arm.span.m <- sample.data$arm.span[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='w']
w.arm.span.f <- sample.data$arm.span[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='w']

w.floor.hip.m <- sample.data$floor.hip[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='w']
w.floor.hip.f <- sample.data$floor.hip[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='w']
w.head.height.m <- sample.data$head.height[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='w']
w.head.height.f <- sample.data$head.height[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='w']
w.hand.length.m <- sample.data$hand.length[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='w']
w.hand.length.f <- sample.data$hand.length[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='w']
w.foot.length.m <- sample.data$foot.length[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='w']
w.foot.length.f <- sample.data$foot.length[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='w']

par(mfrow = c(2,6))
boxplot(a.height.m, a.height.f,
        main = "height",
        xlab = "am vs af",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```r
## Warning in bxp(list(stats = structure(c(157.5, 162, 169, 172.86, 177.5, : some
```

```
## notches went outside hinges ('box'): maybe set notch=FALSE
```

```r
boxplot(a.arm.span.m, a.arm.span.f,
        main = "arm span",
        xlab = "am vs af",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```
## Warning in bxp(list(stats = structure(c(160, 165.5, 174.5, 177.8, 181.5, : some
## notches went outside hinges ('box'): maybe set notch=FALSE
```

```r
boxplot(a.floor.hip.m, a.floor.hip.f,
        main = "leg length",
        xlab = "am vs af",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(a.head.height.m, a.head.height.f,
        main = "head height",
        xlab = "am vs af",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```
## Warning in bxp(list(stats = structure(c(18.5, 20.795, 22.75, 24, 28, 19, : some
## notches went outside hinges ('box'): maybe set notch=FALSE
```

```r
boxplot(a.hand.length.m, a.hand.length.f,
        main = "hand length",
        xlab = "am vs af",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(a.foot.length.m, a.foot.length.f,
        main = "foot length",
        xlab = "am vs af",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```
## Warning in bxp(list(stats = structure(c(22.5, 23.875, 25.375, 26.25, 26.67, :
## some notches went outside hinges ('box'): maybe set notch=FALSE
```

```r
boxplot(w.height.m, w.height.f,
        main = "height",
        xlab = "wm vs wf",
        ylab = "unit(cm)",
```

```r
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(w.arm.span.m, w.arm.span.f,
        main = "arm span",
        xlab = "wm vs wf",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(w.floor.hip.m, w.floor.hip.f,
        main = "leg length",
        xlab = "wm vs wf",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(w.head.height.m, w.head.height.f,
        main = "head height",
        xlab = "wm vs wf",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(w.hand.length.m, w.hand.length.f,
        main = "hand length",
        xlab = "wm vs wf",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(w.foot.length.m, w.foot.length.f,
        main = "foot length",
        xlab = "wm vs wf",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```r
par(mfrow = c(2,3))
boxplot(w.height.m, a.height.f,
        main = "height",
        xlab = "white male vs asian female",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(w.arm.span.m, a.arm.span.f,
        main = "arm span",
        xlab = "white male vs asian female",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
```

```r
              notch = TRUE)
boxplot(w.floor.hip.m, a.floor.hip.f,
        main = "leg length",
        xlab = "white male vs asian female",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(w.head.height.m, a.head.height.f,
        main = "head height",
        xlab = "white male vs asian female",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(w.hand.length.m, a.hand.length.f,
        main = "hand length",
        xlab = "white male vs asian female",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(w.foot.length.m, a.foot.length.f,
        main = "foot length",
        xlab = "white male vs asian female",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```r
par(mfrow = c(2,3))
boxplot(a.height.m, w.height.f,
        main = "height",
        xlab = "asian male vs white female",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```
## Warning in bxp(list(stats = structure(c(157.5, 162, 169, 172.86, 177.5, : some
## notches went outside hinges ('box'): maybe set notch=FALSE
```

```r
boxplot(a.arm.span.m, w.arm.span.f,
        main = "arm span",
        xlab = "asian male vs white female",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```
## Warning in bxp(list(stats = structure(c(160, 165.5, 174.5, 177.8, 181.5, : some
## notches went outside hinges ('box'): maybe set notch=FALSE
```

```r
boxplot(a.floor.hip.m, w.floor.hip.f,
        main = "leg length",
        xlab = "asian male vs white female",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(a.head.height.m, w.head.height.f,
        main = "head height",
        xlab = "asian male vs white female",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```
## Warning in bxp(list(stats = structure(c(18.5, 20.795, 22.75, 24, 28, 18, : some
## notches went outside hinges ('box'): maybe set notch=FALSE
```

```r
boxplot(a.hand.length.m, w.hand.length.f,
        main = "hand length",
        xlab = "asian male vs white female",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(a.foot.length.m, w.foot.length.f,
        main = "foot length",
        xlab = "asian male vs white female",
        ylab = "unit(cm)",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```
## Warning in bxp(list(stats = structure(c(22.5, 23.875, 25.375, 26.25, 26.67, :
## some notches went outside hinges ('box'): maybe set notch=FALSE
```

What is the best to way to represent proportions of measurments? .

```r
p.arm.span.m <- sample.data$p.arm.span[sample.data$my.gender == 'm']
p.arm.span.f <- sample.data$p.arm.span[sample.data$my.gender == 'f']
p.floor.hip.m <- sample.data$p.floor.hip[sample.data$my.gender == 'm']
p.floor.hip.f <- sample.data$p.floor.hip[sample.data$my.gender == 'f']

p.head.h.m <- sample.data$p.head.h[sample.data$my.gender == 'm']
p.head.h.f <- sample.data$p.head.h[sample.data$my.gender == 'f']
p.hand.length.m <- sample.data$p.hand.length[sample.data$my.gender == 'm']
p.hand.length.f <- sample.data$p.hand.length[sample.data$my.gender == 'f']
p.foot.length.m <- sample.data$p.foot.length[sample.data$my.gender == 'm']
p.foot.length.f <- sample.data$p.foot.length[sample.data$my.gender == 'f']

par(mfrow = c(2,3))
boxplot(p.arm.span.m, p.arm.span.f,
        main = "arm span",
        xlab = "male vs female",
```

```r
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(p.floor.hip.m, p.floor.hip.m,
        main = "leg length",
        xlab = "male vs female",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(p.head.h.m, p.head.h.f,
        main = "head height",
        xlab = "male vs female",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(p.hand.length.m, p.hand.length.f,
        main = "hand length",
        xlab = "male vs female",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(p.foot.length.m, p.foot.length.f,
        main = "foot length",
        xlab = "male vs female",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```r
ap.arm.span.m <- sample.data$p.arm.span[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='a']
ap.arm.span.f <- sample.data$p.arm.span[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='a']
ap.floor.hip.m <- sample.data$p.floor.hip[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='a']
ap.floor.hip.f <- sample.data$p.floor.hip[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='a']

ap.head.h.m <- sample.data$p.head.h[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='a']
ap.head.h.f <- sample.data$p.head.h[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='a']
ap.hand.length.m <- sample.data$p.hand.length[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='a
ap.hand.length.f <- sample.data$p.hand.length[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='a
ap.foot.length.m <- sample.data$p.foot.length[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='a
ap.foot.length.f <- sample.data$p.foot.length[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='a

wp.arm.span.m <- sample.data$p.arm.span[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='w']
wp.arm.span.f <- sample.data$p.arm.span[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='w']
wp.floor.hip.m <- sample.data$p.floor.hip[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='w']
wp.floor.hip.f <- sample.data$p.floor.hip[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='w']

wp.head.h.m <- sample.data$p.head.h[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='w']
wp.head.h.f <- sample.data$p.head.h[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='w']
wp.hand.length.m <- sample.data$p.hand.length[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='
```

```
wp.hand.length.f <- sample.data$p.hand.length[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='
wp.foot.length.m <- sample.data$p.foot.length[sample.data$my.gender == 'm'&sample.data$my.ethnicity =='
wp.foot.length.f <- sample.data$p.foot.length[sample.data$my.gender == 'f'&sample.data$my.ethnicity =='

par(mfrow = c(2,5))
boxplot(ap.arm.span.m, ap.arm.span.f,
        main = "arm span",
        xlab = "am vs af",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(ap.floor.hip.m, ap.floor.hip.f,
        main = "leg length",
        xlab = "am vs af",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```
## Warning in bxp(list(stats = structure(c(0.477941176470588, 0.526795735129068, :
## some notches went outside hinges ('box'): maybe set notch=FALSE
```

```
boxplot(ap.head.h.m, ap.head.h.f,
        main = "head height",
        xlab = "am vs af",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```
## Warning in bxp(list(stats = structure(c(0.108823529411765, 0.121212121212121, :
## some notches went outside hinges ('box'): maybe set notch=FALSE
```

```
boxplot(ap.hand.length.m, ap.hand.length.f,
        main = "hand length",
        xlab = "am vs af",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```
## Warning in bxp(list(stats = structure(c(0.102601156069364, 0.107252706993406, :
## some notches went outside hinges ('box'): maybe set notch=FALSE
```

```
boxplot(ap.foot.length.m, ap.foot.length.f,
        main = "foot length",
        xlab = "am vs af",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```
## Warning in bxp(list(stats = structure(c(0.141509433962264, 0.146318342151675, :
## some notches went outside hinges ('box'): maybe set notch=FALSE
```

```
boxplot(wp.arm.span.m, wp.arm.span.f,
        main = "arm span",
        xlab = "wm vs wf",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(wp.floor.hip.m, wp.floor.hip.f,
        main = "leg length",
        xlab = "wm vs wf",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(wp.head.h.m, wp.head.h.f,
        main = "head height",
        xlab = "wm vs wf",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(wp.hand.length.m, wp.hand.length.f,
        main = "hand length",
        xlab = "wm vs wf",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
boxplot(wp.foot.length.m, wp.foot.length.f,
        main = "foot length",
        xlab = "wm vs wf",
        ylab = "proportion",
        col = c("orange", 'red'),
        border = "brown",
        notch = TRUE)
```

```
comb<-c('af','am','wf','wm')
comb <-as.factor(comb)
mean<-c(1,1,1,1)
height <- data.frame(comb, mean)
mean<-c(mean(ap.head.h.f), mean(ap.head.h.m), mean(wp.head.h.f), mean(wp.head.h.m))
head_height <- data.frame(comb, mean)
mean<-c(mean(ap.arm.span.f), mean(ap.arm.span.m), mean(wp.arm.span.f), mean(wp.arm.span.m))
arm_span <- data.frame(comb, mean)
mean<-c(mean(ap.floor.hip.f), mean(ap.floor.hip.m), mean(wp.floor.hip.f), mean(wp.floor.hip.m))
leg_length <- data.frame(comb, mean)
mean<-c(mean(ap.hand.length.f), mean(ap.hand.length.m), mean(wp.hand.length.f), mean(wp.hand.length.m))
hand_length <- data.frame(comb, mean)
mean<-c(mean(ap.foot.length.f), mean(ap.foot.length.m), mean(wp.foot.length.f), mean(wp.foot.length.m))
foot_length <- data.frame(comb, mean)
```

```r
head_height$name <-'head_height'
arm_span$name <-'arm_span'
leg_length$name <-'leg_length'
hand_length$name <-'hand_length'
foot_length$name <- 'foot_length'

d <- rbind(head_height, arm_span, leg_length, hand_length, foot_length)
p <- ggplot(d, aes(comb, mean, fill=name))+
     geom_bar(position = 'dodge', stat='identity')+
     xlab("Aisn/white male and female")+
     ylab("proportion as a function of height")
p
```

```r
# Two-way ANOVA with interaction effect
res.aov2 <- aov(height ~ my.gender * my.ethnicity, data = sample.data)
summary(res.aov2)
```

```r
two.way <- aov(height ~ my.gender * my.ethnicity, data = sample.data)

summary(two.way)
```

```r
t.test(height.m, height.f,
       alternative = "greater",
       mu = 0, paired = FALSE, var.equal = FALSE)
```

```r
t.test(a.height.m, w.height.f,
       alternative = "greater",
       mu = 0, paired = FALSE, var.equal = FALSE)
```

```r
t.test(a.floor.hip.m, a.floor.hip.f,
       alternative = "greater",
       mu = 0, paired = FALSE, var.equal = FALSE)
```

```r
library(ggplot2)
library(plyr)
library(dplyr)

csample.data <- ddply(sample.data, "my.gender", summarise, height.mean=mean(height))
csample.data <- na.omit(csample.data)
csample.data
# Density plots with semi-transparent fill
ggplot(sample.data, aes(x=height, fill=my.gender)) + geom_density(alpha=.3) +
     geom_vline(data=csample.data, aes(xintercept=height.mean,  colour=my.gender), linetype="dashed"
     labs(x = "height(cm)",
          title = "Kernel density estimate of height")
```

```r
asample.data <- ddply(sample.data, "my.gender", summarise, arm.span.mean=mean(arm.span))
asample.data <- na.omit(asample.data)

ggplot(sample.data, aes(x=arm.span, fill=my.gender)) + geom_density(alpha=.3) +
     geom_vline(data=asample.data, aes(xintercept=arm.span.mean,  colour=my.gender), linetype="dashe
```

```r
ggplot(sample.data, aes(x=floor.hip, fill=my.gender)) + geom_density(alpha=.3)
```

```r
ggplot(sample.data, aes(x=head.height, fill=my.gender)) + geom_density(alpha=.3)
```

```r
ggplot(sample.data, aes(x=hand.length, fill=my.gender)) + geom_density(alpha=.3)
```

```r
ggplot(sample.data, aes(x=foot.length, fill=my.gender)) + geom_density(alpha=.3)
```

```r
# cols = colnames(sample.data[,-c(1:2)]);
# rows = sample.data$my.gender;
#
# df = removeColumnsFromDataFrame(sample.data, "my.gender");
# df.t = transposeMatrix(df);
# colnames(df.t) = rows;
#
# sample.t = as.data.frame(df.t);
# sample.t;
#
# X = removeColumnsFromDataFrame(sample.data,"my.gender");
# X
# X.kmeans = kmeans(X, 3);  # default algorithm
# stars(X.kmeans$centers, len = 0.5, key.loc = c(4, 3),
#        main = "Algorithm: DEFAULT [Hartigan-Wong] \n Stars of KMEANS=3", draw.segments = TRUE);
# print(X.kmeans)
```

ENDNOTES

[1] This is a footnote that can be really long.

You can have multiple paragraphs in the footnote. You can have <u>underline</u> or **bold** or *italics.* You can even have a math equation inline.

In this section, we review the regression results to summarize our findings. First, we examine each model for significance, and conclude the hypothesized models fit well with the data. Second, we conclude that the fixed country effects represent consistent and unbiased parameter estimates. Third, with the use of the Driscoll and Kraay (1998) robust standard errors, we adjust any variance bias to ascertain the significance of these consistent estimates. Therefore, we are able to make inferences about the hypotheses using our model estimates. For ease of interpretation across these 12 models, we introduce $_{\text{Total}}^{\text{M1}}\hat{\beta}_1$ as notation to refer to parameter estimate $\hat{\beta}_1$ (HDI) for the Total Sample and (M1) Model 1: Main Effects. We proceed by reporting findings for the total sample.

The footnotes are automatically converted to "endnotes" and will be included at the end of the document. It will finish when you have that outer brace like this.

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