



**University of  
Zurich<sup>UZH</sup>**

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**From a "Spiel Popeye und miss deine Greifkraft" activity  
to Swiss norms for handgrip strength**

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Master Thesis in Biostatistics (STA 495)

by

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Vithersan Somasundaram  
January 2023





# Abstract

The handgrip strength (HGS) is an important, non-invasive, and cost effective measure of health in medical therapy and sports. To assess HGS in practice, norms of HGS have been developed worldwide. Though, there are still numerous open questions. First of all, the question arises whether the Swiss HGS norms developed in 2009 are still valid for Swiss adults in the year 2022. Moreover, whether HGS norms could be developed for Swiss children. One should thereby clarify which position would be preferred and whether the rigid American Society of Hand Therapist regime could be relaxed for children. Furthermore, one can ask whether a children-friendly experimental design could be developed. It also remains to be inspected whether sample sizes for the development of Swiss norms in each age category guarantee reliable norms. Moreover, clear recommendations for the optimal sample sizes for the development of refined HGS norms are needed. Finally, this master thesis should provide replicable open-source R code.

To address the issues discussed above, this master thesis evolves through several steps. First, we developed a "Spiel Popeye und miss deine Greifkraft!" activity for the Day of Open Doors on July 9, 2022, at Epidemiology, Biostatistics and Prevention Institute at the University of Zurich. This activity was based on a playful experimental study design that is applicable to children, adults and elderly people with the easy-to-use Jamar dynamometer. HGS measurements and demographic specifications were collected with Google forms. Afterwards, collected data were automatically extracted from Google forms into the R environment and analysed in a reproducible way. Finally, a literature review was conducted to gain insights into previously discovered findings on HGS. We used the following statistical methods: descriptive statistics, boxplots, violin-plots, Bland-Altman plot, scattergrams, QQ-plots, confidence intervals, one-sample t-test, two-sample Welch t-test, repeated measure ANOVA and linear mixed-effects model. Results of tests with p-values smaller than 0.05 are interpreted as statistically significant.

Our results provide insights into the preferred posture-elbow position and validate existing Swiss norms for adults. Furthermore, we make recommendations for the development of future norms based on optimal sample sizes for Swiss adults and children. Moreover, the report and the R code of the analysis are available online and accessible to the public and to all interested researchers in the field of HGS norms and beyond. These resources can facilitate the development of future HGS norms for Swiss children and adults based on a playful but scientifically correct experiment to obtain HGS measurements. Such future HGS norms can help physicians and physiotherapists to reliably and non-invasively assess the muscle strength and health of Swiss population in each age category for both children and adults, preventing development of muscular diseases and thus actively contribute to the reduction of costs and overload of the health care system.

**Keywords:** Hand grip strength (HGS), Jamar dynamometer, HGS norms, Reproducibility



# Chapter 1

## Introduction

The handgrip strength (HGS) is an important measure of health in medical therapy and sports which serves several purposes such as clinical diagnosis, evaluation and comparison of surgical techniques, documentation of the progress during rehabilitation, response to treatment and the level of disability after injury ([Shiratori et al., 2014](#)). Aside from that, HGS is an important measurement assessing a person's health status as well as the physical performance of the population with increasing age. The advantage of HGS measure is that it is non-invasive, cost effective and easily accessible ([Roberts et al., 2011](#); [Shiratori et al., 2014](#); [Bohannon, 2008](#); [Soysal et al., 2021](#); [Leong et al., 2015](#)).

To assess HGS, norms of HGS have been developed ([Mathiowetz et al., 1985, 1986](#)). Swiss norms were developed by [Werle et al. \(2009\)](#) for males and females aged 18 to 96. In general, HGS norms are higher in men than in women, differ between dominant and non-dominant hand and show a curvilinear relationship with age ([Bohannon et al., 2006](#); [Werle et al., 2009](#); [Sousa-Santos and Amaral, 2017](#); [Peters et al., 2011](#)). An age-dependent decline of HGS norm values can be observed in both genders after 60 years ([Werle et al., 2009](#); [Peters et al., 2011](#)).

Swiss norms developed by [Werle et al. \(2009\)](#) are based on HGS measured in the seated position with the elbow flexed in right angle. [Werle et al. \(2009\)](#) used the recommended measuring position by the American Society of Hand Therapist (ASHT) ([Kuzala and Vargo, 1992](#)). They considered sample sizes of at most 47 participants in each age category. They recorded the mean of three successive HGS measurements per participant. Finally, they calculated the mean and SD of HGS for adults in each age category. These Swiss norms were developed in 2009 reflecting the health status of Swiss adults more than a decade ago. One may speculate, whether the Swiss HGS norms are still valid for Swiss adults in year 2022. Furthermore, one may ask whether similar norms could be developed for Swiss children.

The most widely used device to measure the HGS is the Jamar dynamometer. This device is also recommended by the ASHT for measuring HGS. The Jamar dynamometer is an easy-to-use and highly reliable device ([Innes, 1999](#); [Härkönen et al., 1993](#)). According to ASHT's recommendation, HGS should be measured with its handle in the second position in a seated, elbow flexed, 90 degree position ([Kuzala and Vargo, 1992](#); [Bohannon et al., 2006](#)), because the position can affect HGS measurements ([Sousa-Santos and Amaral, 2017](#); [Innes, 1999](#)). For example, HGS was higher in a standing than in a sitting position ([Sousa-Santos and Amaral, 2017](#); [Peters et al., 2011](#)) and the effect of the elbow position yielded conflicting results ([Mathiowetz et al., 1985](#); [Innes, 1999](#); [Werle et al., 2009](#)). Nonetheless, the length of the resting period did not affect the fatigue of HGS values ([Trossman and Li, 1989](#)). None of these studies investigated which position would be preferred by patients. Moreover, none of them investigated whether the rigid ASHT regime could be relaxed for children to develop a children-friendly experimental design.

Typically, HGS norms for both genders are represented by reference quantile curves for HGS which are based on mean and SD of HGS in each age category ([Hanten et al., 1999](#); [Werle et al., 2009](#); [Massy-Westropp et al., 2011](#); [Mathiowetz et al., 1985](#)). A closer look at the sample sizes used for the development of these norms indicates that although the total size of the study is large, for each age category and gender only very few people were measured ([Innes, 1999](#); [Werle et al., 2009](#); [Mathiowetz et al., 1985](#)). To the best of our knowledge, little attention has been paid to the development of representative normative values for the HGS. It remains to be inspected whether sample sizes used by [Werle et al. \(2009\)](#) in each age category are sufficient for the development of reliable and representative HGS norms. Moreover, clear recommendations for the optimal sample sizes for the development of HGS norms are needed.

Modern science is done with the help of computers, shared software and data in ways that were once unthinkable. Reproducibility ensures high efficiency and quality of research, playing a central role in the modern science. Reproducibility supports a more efficient distribution of knowledge in modern science and enhances the transparency and credibility of research. Therefore, it is necessary that other researchers can reproduce and replicate findings ([Begley and Ioannidis, 2015](#); [National Academies of Sciences, Engineering, and Medicine and others, 2019](#)). None of the studies which developed HGS norms ([Mathiowetz et al., 1985](#); [Innes, 1999](#); [Hanten et al., 1999](#); [Werle et al., 2009](#); [Massy-Westropp et al., 2011](#); [Wong, 2016](#)) provided the source code for the analysis. Hence, it is necessary that this master thesis provides replicable open-source R code.

To address the issues discussed above, this master thesis evolves around several steps. First, we developed a "Spiel Popeye und miss deine Greifkraft!" activity for the Day of Open Doors (DOOD) at Epidemiology, Biostatistics and Prevention Institute (EBPI). This activity was based on a playful experimental study design that was applicable to children, adults and elderly people with the easy-to-use Jamar dynamometer. HGS measurements and demographic specifications were collected with Google forms. Afterwards, collected data were automatically extracted from Google forms into the R environment and analysed in a reproducible way. Finally, a literature review was conducted to gain insights into previously discovered findings on HGS.

Results provided in the following Sections 3.1–3.8 provide insights into the preferred posture-elbow position and validate existing Swiss norms for adults. Furthermore, they provide recommendations for the development of future HGS norms based on optimal sample sizes for Swiss adults and children. Finally, the report and the R code of the analysis in the Appendix B.2 are available online and accessible to the public and to all interested researchers in the field of HGS norms and beyond.

## Chapter 2

# Materials and Methods

### 2.1 Review of the Literature

A review of eleven publications is conducted to gain some insights from previous studies. These eleven publications are [Mathiowetz et al. \(1985\)](#), [Hanten et al. \(1999\)](#), [Innes \(1999\)](#), [Watanabe et al. \(2005\)](#), [España-Romero et al. \(2008\)](#), [Werle et al. \(2009\)](#), [Massy-Westropp et al. \(2011\)](#), [Wong \(2016\)](#), [Sousa-Santos and Amaral \(2017\)](#), [McGrath et al. \(2018\)](#) and [Wearing et al. \(2018\)](#). The aim is to collect relevant information on the hand grip strength (HGS) and to identify study designs of previous studies including

1. In which position was the HGS measured?
2. How many participated in the experiment?
3. How is age divided into categories?
4. How is strength development in people with increasing age?
5. How are norms established?

Whereas a detailed review is provided in Appendix [A](#), our main findings are summarized below. We also found two publications [Bobos et al. \(2020\)](#) and [Bohannon \(2019\)](#) that address the minimally important difference (MID), which is a clinically relevant difference that is reflected in a person's better health or quality of life. According to [Bobos et al. \(2020\)](#), MIDs for healthy individuals range from 2.4 kg to 2.7 kg.

The publications [Mathiowetz et al. \(1985\)](#), [Innes \(1999\)](#), [Hanten et al. \(1999\)](#), [Werle et al. \(2009\)](#), [Massy-Westropp et al. \(2011\)](#) and [Wong \(2016\)](#) discuss how the norms are developed. The others do not focus on the development of norms. In general, mean and standard deviation are used to develop norms, which are grouped according to gender and age categories.

Usually, the recommended position by American Society of Hand Therapist (ASHT) is used for the measurement of HGS. The most common testing position is standing, with the elbow extended 0° rather than flexed at 90°. It has been shown by [Sousa-Santos and Amaral \(2017\)](#) and [Innes \(1999\)](#) that variations in testing position when using the same instrument can significantly affect the results and should therefore be avoided. For example, it has been shown that the HGS is higher when using the same instrument in a standing rather than in a sitting position ([Sousa-Santos and Amaral, 2017](#)). Studies on the effect of elbow position on grip strength have yielded conflicting results ([Mathiowetz et al., 1985](#); [Innes, 1999](#); [Werle et al., 2009](#)).

In some studies, HGS was measured once, in others several times. In general, HGS was measured three times and then average was taken. It is expected that participant fatigue may be a problem when multiple maximal efforts are demanded in a short period of time. Therefore, in some studies, a short recovery period was included between the trials. [Trossman and Li \(1989\)](#) examined the effects of resting periods between five trials. They concluded that there is no significant difference in resting periods of 60 seconds, 30 seconds, and 15 seconds between trials. However, there is a pattern of decreasing HGS across the five trials. When asked how long the dynamometer should be pressed on each trial, [Smith and Lukens \(1983\)](#) concluded that grasping for 3 seconds is usually sufficient, to record the maximum HGS.

From the reviewed publications, the following studies have used the Jamar dynamometer: [Hanten et al. \(1999\)](#); [Massy-Westropp et al. \(2011\)](#); [Mathiowetz et al. \(1985\)](#); [Werle et al. \(2009\)](#); [Wearing et al. \(2018\)](#); [Bohannon \(2008\)](#). All data collected with the Jamar dynamometer have a high test-retest reliability of  $ICC > 0.93$  according to [Innes \(1999\)](#). He also showed that there is a positive correlation between grip strength, body weight and height in healthy participants.

When it comes to the question if handedness plays a role in determining HGS, there is disagreement about whether there is a consistent difference in HGS between the dominant and nondominant hand. [España-Romero et al. \(2008\)](#) demonstrated that hand span and optimal grip span have a significant linear relationship in children. They established an equation for grip span as a function of hand span in boys  $y = x/4 + 0.44$  and in girls  $y = 0.3x - 0.52$ . Where  $x$  is the hand span (width between the first and fifth fingers) and  $y$  is the optimal grip span.

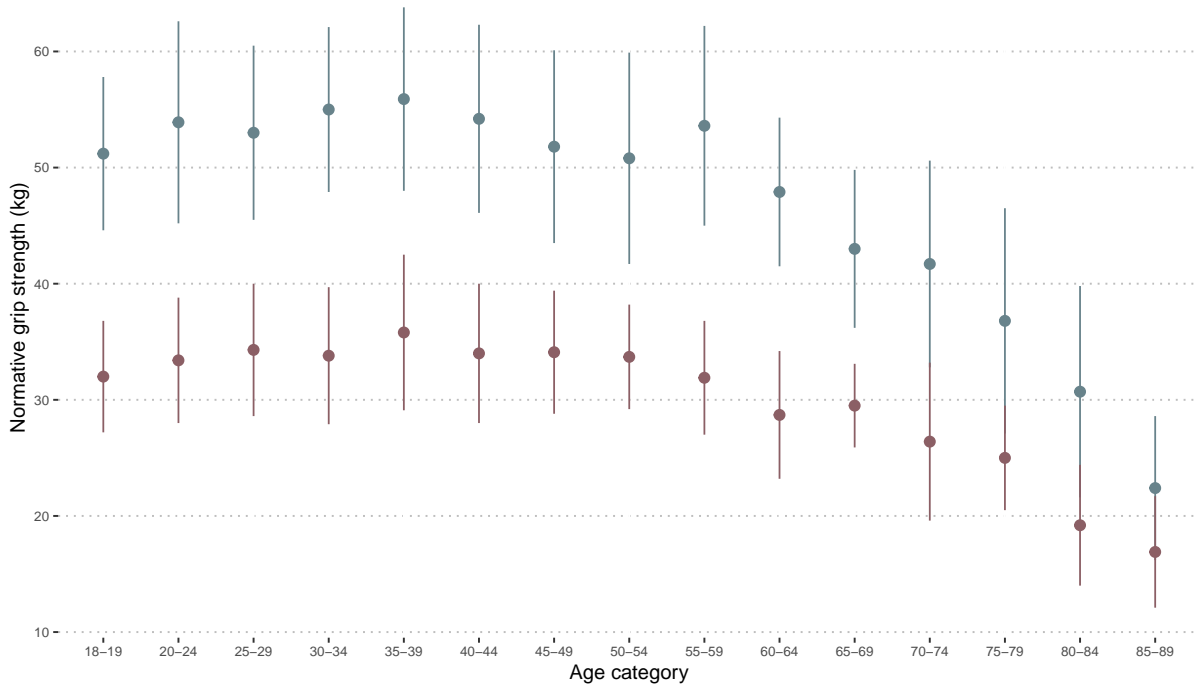
A literature review of the HGS was also conducted by [Innes \(1999\)](#). He concludes that the total samples of the studies are usually large. However, when grouped by gender and age, there are very few participants in each strata. Age groups are usually broken down into 5 year or 10 year intervals. Samples subdivided in this way usually comprise about 20-40 participants, which is quite small to determine representative normative values based on quantiles. Nevertheless, there is no clear indication in the literature of what sample size would be appropriate for developing normative values in general.

Nonetheless, HGS norms are very important for making clear judgements about a person's health status in comparison to the general population. HGS can be used both to describe the condition of the hand and to characterize the overall strength of the upper extremity. [Bohannon et al. \(2006\)](#) conducted a meta-analysis in a multinational setting. Their goal was to consolidate normative data that were consistent with ASHT recommendations and to obtain a better understanding of the HGS. The norms for HGS obtained in this way show that the maximum HGS is highest between 40 and 44 years in men and highest between 45 and 49 years in women.

## 2.2 Quantile Norms for Adults and Children

We plotted quantile norms for Swiss adults between 18 and 89 years using the data from the paper [Werle et al. \(2009\)](#). In their study he sampled 978 subjects (496 men and 482 women) from the German-speaking population in Switzerland. For a better coverage of the total population, he collected data from 11 different cantons, including urban, suburban and rural areas. When stratified for age and gender subgroups, a minimum of 29 subjects were tested in each age category. [Werle et al. \(2009\)](#) considered this to be an adequate sample size. Mean values of three measurements of HGS with the Jamar dynamometer (in kg) were computed. Mean and SD HGS for each age category are provided in Table 2 of [Werle et al. \(2009\)](#). They are split by dominant and non-dominant hand and by gender. Figure 2.1 shows the median normative grip strength of

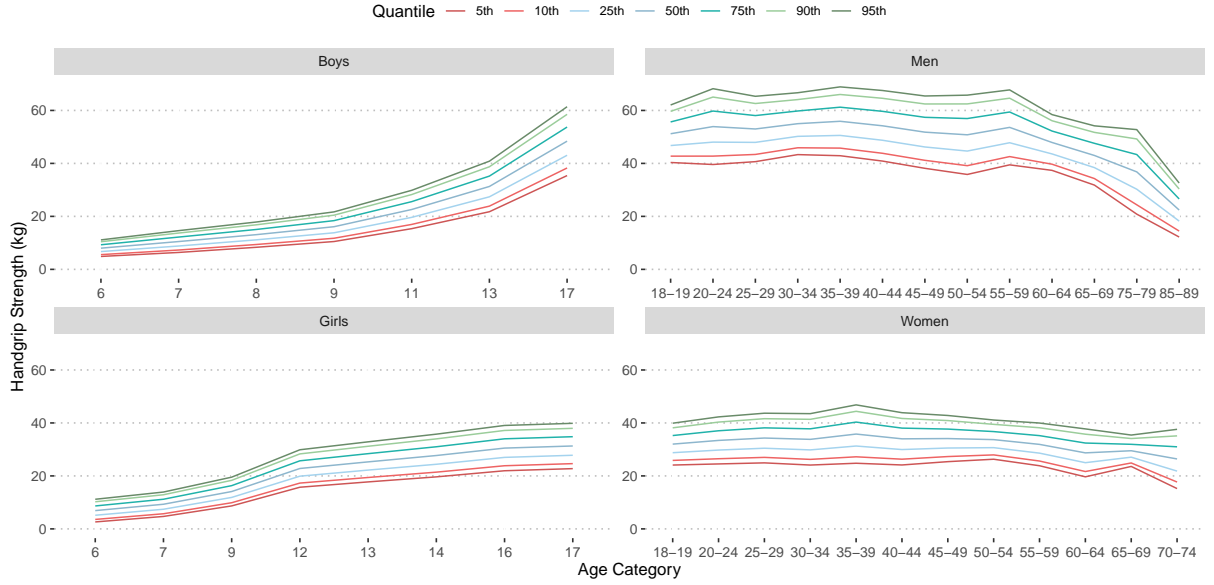
the dominant hand, indicated as a dot with its standard deviation.



**Figure 2.1:** HGS mean values with its SD from [Werle et al. \(2009\)](#). Only the dominant hand is considered.

For the creation of the quantile norms for Swiss adults, it was assumed that the HGS is normally distributed. Based on the assumption of normality and by using the mean and standard deviation from Table 2 of [Werle et al. \(2009\)](#), the quantiles were calculated for each age category (see Section 2.4.2 and Figure 2.2). For the development of the norms only the values of the dominant hand were used.

Dr. Fabio Baressi, from the Department of Occupational and Environmental Medicine at EBPI, approximated the quantile norms for children for DOOD. As no norms are available for Swiss children, quantiles were calculated from a Canadian study based on Table 3 of [Wong \(2016\)](#). The values were given as the maximum HGS. For this purpose, the data for the age categories 20 to 79 years and the age categories 18 and 19 years from [Werle et al. \(2009\)](#) and [Wong \(2016\)](#) were compared. Using these comparisons and the data from Canada for the age categories 6 to 17 years, the mean and standard deviation of HGS were approximated for Swiss children. Finally, using these means and standard deviations, the quantile norms of the HGS were estimated for each age category. Figure 2.2 shows the quantile norms for 5th, 10th, 25th, 50th, 75th, 90th and 95th quantiles for children and adults categorized by age and gender (female, male). See Section 2.4.2 for more information how these quantile norms were calculated.



**Figure 2.2:** Quantile norms of HGS for adults and children by gender used on Day of Open Doors.

## 2.3 Study Population and Study Design

The analysis and recommendations in this report are based on the data collected from the first run of the activity "Spiel Popeye und miss Deine Greifkraft" and on the Day of Open Doors (DOOD) at the Institute for Epidemiology, Biostatistics and Prevention (EBPI) at the University of Zurich on the 9th of July 2022. For data collection, all volunteers interested in participating in this activity were allowed to participate. For the statistical analysis, participants who did not fulfil the inclusion criteria were removed from the data.

### 2.3.1 Exclusion Criteria

Several medical conditions and chronic diseases make recruited participants unsuitable for statistical analysis. Therefore, a list of potential conditions and diseases that could affect the analysis on HGS was compiled. These are listed here:

- age  $\leq 6$  years
- any physical disability
- major surgery during the last 6 month
- injuries to the hand, wrist, elbow or shoulder
- diabetes
- neurological diseases
- carpal tunnel syndrome
- muscular diseases
- cancer disease
- arthrosis of shoulder, elbow, wrist
- bed rest for the last 3 month
- pain in hand, wrist, elbow or shoulder



### 2.3.2 Jamar Dynamometer Device

The Jamar handgrip dynamometer is used to measure the maximal isometric HGS of all participants at DOOD. The Jamar dynamometer is a valid and highly reliable device used in many previous studies and medical institutes, as described in Section 2.1. Further, it is also recommended by the ASHT to measure HGS.

The Jamar dynamometer is a hydraulic instrument for recording grip strength with an analogue display on two scales (see Figure 2.3). The device displays HGS in pounds and kilograms up to 200 pounds or 90 kilograms. The highest reading is automatically maintained until manually reset. In addition, the handle is adjustable in five positions, so that the measuring instrument can be suitably adjusted to the hand size of the respective participant.

Six of the calibrated Jamar dynamometers were available for the DOOD. The grip width on the second level was selected as default for all participants. This position was tested by the team internally to ensure that the thumb touches the index finger when gripping the Jamar dynamometer. This approach agrees with the findings of Sousa-Santos and Amaral (2017). If the thumb was not touching the index finger for a participant, the grip width was adjusted accordingly.

### 2.3.3 Day of Open Doors



Universität  
Zürich<sup>UZH</sup>

Institut für Epidemiologie, Biostatistik und Prävention (EBPI)

## Spiel Popeye und miss Deine Greifkraft! Entwicklung von Normwerten für Kinder und Erwachsene

#### Ziel der Studie

Die Greifkraft ist ein wichtiger Parameter, um die Kraft der oberen Extremität zu messen. Sie entspricht der maximalen Kraft, die Du mit Hilfe Deiner Hand- und Unterarmmuskeln zustande bringst.

Diese Greifkraft ist ein wichtiger Parameter der allgemeinen Muskelkraft und Muskelmasse, sowie des Ernährungszustands.

Eine gute Greifkraft geht mit einer besseren Gesundheit einher, mit einem geringeren Risiko für Unfälle und mit einer besseren Mobilität.

Um die Greifkraft jedes Einzelnen einzuschätzen, braucht es Normwerte. Dein eigener Wert kann so mit Werten von vielen Personen mit dem gleichen Alter und Geschlecht verglichen werden.

Diese Normwerte sind vielleicht unterschiedlich, je nach dem, wie die Greifkraft gemessen wird: stehend – sitzend – mit gestrecktem oder gebeugtem Arm – links oder rechts.

Wir möchten deshalb untersuchen, wie übereinstimmend die Werte sind, je nach dem wie die Greifkraft gemessen wird.



Figur 2: Messgerät, mit dem wir die Greifkraft messen

#### Wer kann mitmachen?

Alle, die gesund sind und Spass daran haben. Kinder unter 14 Jahren brauchen die Einwilligung Ihrer Eltern.

#### Was musst Du tun?

Du gibst uns Auskunft über Grösse – Gewicht – Geschlecht

Du misst die Greifkraft in verschiedenen Positionen wie im Bild gezeigt.



Figur 1: Hier siehst Du alle Positionen, in denen wir Deine Greifkraft messen: stehend – sitzend, mit gestrecktem oder gebeugtem Ellbogen, rechts – links

**Figure 2.3:** Poster for the "Spiel Popeye und miss Deine Greifkraft" activity, which was used on the Day of Open Doors. It provides additional information for the participants of the study, displays the goal of the study and the eight different measuring positions.

Figure 2.3 served as a welcome poster for the DOOD. It gave the first hints and information about the conducted experiment to the participants. In addition, a short description of the study was given. Furthermore, it demonstrated all positions for measuring the HGS.

All visitors who were interested in the study could get information at the Welcome Desk (right side on Figure 2.4). If they agreed to participate, they received the registration form (see Figure 2.5). Throughout the duration of the study, participants were accompanied by the same supervisor. This supervisor explained the setup and conducted measurements. For the DOOD on the 9th July 2022, thirteen supervisors from the EBPI were available to run the experiment. Supervisors were divided into two groups so that groups could alternate every hour.



**Figure 2.4:** Experimental setting on the Day of Open Doors at the Institute for Epidemiology, Biostatistics and Prevention at the University of Zurich. The Welcome Desk is on the right hand side.

### 2.3.4 Registration Form



## Spiel Popeye und miss deine Greifkraft!

- Teilnehmer-ID: NA
- Alter:
- Geschlecht: weiblich | männlich
- Grösse:
- Gewicht:
- Chronische Krankheit: nein | ja
- Start (randomisiert): 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8

Start	Hand	Bedingung	Flex	Messung
1	Links	stehend	0	
2	Rechts	stehend	0	
3	Links	stehend	90	
4	Rechts	stehend	90	
5	Links	sitzend	0	
6	Rechts	sitzend	0	
7	Links	sitzend	90	
8	Rechts	sitzend	90	

- Welche Position war für dich am angenehmsten?:

Um deine Resultate einzugeben, scanne folgenden QR Code



**Figure 2.5:** Registration form with QR Code to collect personal data of the participants.

The registration form in Figure 2.5 served to collect the data during the experimental run. On this sheet demographic data and the HGS measurements were recorded. It was also possible to enter the data online into a web based documentation system via the QR-Code on the registration form.

### 2.3.5 Testing Position

According to the registration form in Figure 2.5, HGS was measured in four different positions with one attempt on each, left and right, side:

1. upright sitting position on a chair without armrests, with the feet on the floor, neutral shoulder position, approximately  $90^\circ$  arm flexion and neutral forearm position
2. upright sitting position on a chair without armrests, with the feet on the floor, neutral shoulder position, approximately  $0^\circ$  arm flexion and neutral forearm position
3. upright standing position without armrests, with the feet on the floor, neutral shoulder position, approximately  $90^\circ$  arm flexion and neutral forearm position
4. upright standing position without armrests, with the feet on the floor, neutral shoulder position, approximately  $0^\circ$  arm flexion and neutral forearm position

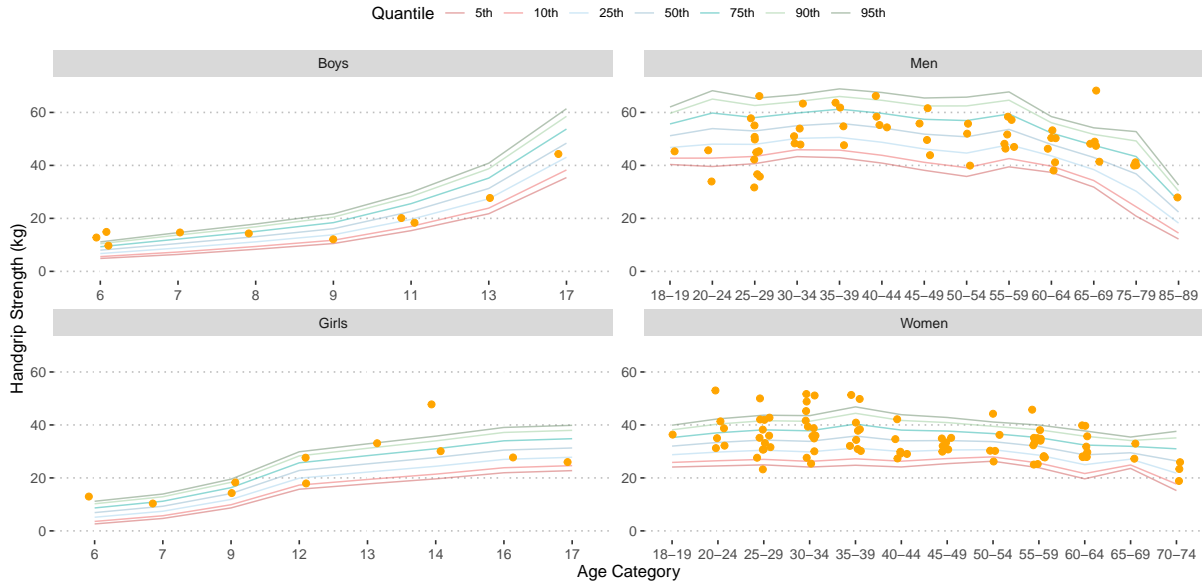
The experimental procedure was explained before the experiment started. In particular, it was stressed that the aim of the measurement was to record the maximal possible HGS in different positions. We did not ask about the dominant hand, as we assumed that the participants would be most comfortable with their dominant hand and intuitively favour the hand that they would use the most.

### 2.3.6 Experimental Setting

The experimental setting shown in Figure 2.4 allows for up to six simultaneous measurements. Two height-adjustable round tables were used to measure the positions standing,  $90^\circ$ , right/left and non-height-adjustable tables for sitting,  $90^\circ$ , right/left. Attention was paid to ensure that the wrist was free and not supported by the table. The exact measuring positions are shown in Figure 2.3.

### 2.3.7 Data Collection

For the test run of the activity all volunteers started with position 1 (Left, standing,  $0^\circ$  flex). To randomize the starting position on the DOOD, participants rolled an eight-sided dice. Then, the handgrip strength measurement and the demographic data needed for the study (age, sex, height, weight, chronic disease and preference) was recorded on the registration form (Figure 2.5) or online into a web-based documentation system ([Google Forms](#)) via QR Code. This allowed for an immediate visual evaluation of the personal maximal HGS on the quantile norms (Figure 2.2). For this purpose, the highest, measured value of HGS was used, regardless of the position and the hand to plot on the HGS quantiles and/or to mark it with an orange dot on the pre-printed Paper (Figure 2.6).



**Figure 2.6:** Quantile norms of HGS for Swiss adults and children by gender. Dots marked with orange are representing the maximal HGS of each participant.

Each position was measured once, starting with the randomly assigned position followed by the position on the registration form (Figure 2.5). After the last measurement, before marking their maximum HGS on the printed quantile norms, participants were asked which position they were most comfortable with for measuring HGS.

## 2.4 Methods

### 2.4.1 Descriptive Statistics and Visualization

For the descriptive statistics, the data set were presented in Tables 3.1–3.3 with the mean, standard deviation, minimum, quantiles, median, maximum, absolute and relative frequencies. For the description of statistical methods the books by [Stahel \(2013\)](#), [Leps and Smilauer \(2020\)](#) and [Dalgaard \(2020\)](#) were considered.

#### Boxplot

Boxplot and scatter plot were used to describe the data. The boxplot is used as a graphical representation of the observed distribution introduced by [Tukey \(1977\)](#). It contains information about skewness, location, potential outliers and spread. It is a quick way to summarize the distribution of the observed data. The box which indicates the interquartile range (IQR) shows the area where the 50% of all values are located. The bottom of the box is the point where the 25% of the data is accumulated (25% quantile). The median is typically marked by a solid line. This is where 50% of the data is accumulated (50% quantile) and the top of the box marks the point where 75% of all values are accumulated (75% quantile). The dispersion indicates how widely the data are distributed around the median. Aside from that, it allows to see immediately if there are any possible outliers. Whiskers mark the extrema of the distribution in the dataset. An extension of the boxplot is the violin plot which combines the boxplot with a density. In addition, a scatterplot can be added to display the frequency of the data values.

The advantages of this is that the reader can see how the data are distributed (Potter et al., 2006).

### Bland-Altman plot

The Bland-Altman plot is used to describe the agreement between two quantitative measures by constructing limits of agreement (LoA). The statistical limits are calculated by using the mean and the standard deviation of the difference between two measures. The resulting graph is a scatter plot. The y-axis shows the difference between the two measured values and the x-axis represents the average of these measures. The average of the differences between the two measures gives us the bias. LoA indicate in which range the difference between the two measures can be expected to lie for approximately 95% of the points. Usually, this type of plot is used to test if two measurements assess exactly the same characteristic on the same scale (Bland and Altman, 1986).

### 2.4.2 Quantile Norms Based on Mean and Standard Deviation

The empirical  $p$ -quantile is the value at which  $p \times 100\%$  of the data points are smaller and  $(1 - p) \times 100\%$  of the data points are greater. For the formal definition, we introduce the ordered values:

$$x_{(1)} \leq x_{(2)} \leq \dots \leq x_{(n)}. \quad (2.1)$$

The  $p$ -quantile is then equal to:

$$\tilde{x}_p = \begin{cases} \frac{1}{2} (x_{(pn)} + x_{(pn+1)}) , & \text{if } p \cdot n \text{ is an integer,} \\ x_{[k]} \text{ where } k = pn + \frac{1}{2} & \text{if } p \cdot n \text{ is not an integer.} \end{cases} \quad (2.2)$$

The median is the empirical 50% quantile: i.e., it shows the middle observation when the data have been sorted. In other words, the quantile represents a measure of the location of the data. The interquartile range (IQR):

$$75\text{-quantile} - 25\text{-quantile} \quad (2.3)$$

is a measure of statistical dispersion for the data. Median and IQR have the advantage that they are robust. They are much less influenced by extreme observations than the arithmetic mean and standard deviation.

As an example, let us determine the 5% quantile of a frequency distribution: For this we have to sort the data first. Next we calculate the 5% quantile with  $p = 0.05$  and assume that  $n = 116$ . This results in  $n \cdot p = 116 \cdot 0.05 = 5.8$ . Because this number is not an integer, we need to use the lower line of the quantile formula (2.2). This means, we have to round 6.3 to the next integer so:  $\tilde{x}_{.05} = x_{[6.3]} = x_6$ . Now we only need to read the 6th value from the sorted data.

Alternatively, quantiles can be defined by using distribution functions. The  $p$ -quantile is defined as the value  $\tilde{x}_p$  such that the probability of the random variable  $X$  is:

$$\tilde{x}_p = \inf \{x \in \mathbb{R}, F(x) \geq p\}, \quad (2.4)$$

where  $p$  is a given probability. Thus, the 5% quantile  $\tilde{x}_{.05}$  denotes at which value the probability of  $X \leq \tilde{x}_{.05}$  is 5%. To determine the quantile we have to solve the inequality:

$$\mathbb{P}(X \leq \tilde{x}_p) \geq p \Leftrightarrow F(\tilde{x}_p) \geq p \Leftrightarrow \tilde{x}_p \geq F^{-1}(p). \quad (2.5)$$

The quantile can be determined with the inverse function of the CDF, also known as the quantile function. Example: To determine the 5% quantile of a 30-34 year old woman we assume the normal distribution where  $X \sim \mathcal{N}(\mu = 33.8, \sigma = 5.9)$ . These numbers were taken from Table 2 of [Werle et al. \(2009\)](#). Since the calculation of the CDF of the normal distribution is difficult to handle, the calculation usually has to be done with software or tables. An important property of the normal distribution family is that its mean is equal its median. Moreover, the normal distribution can be traced back to the case of the standard normal distribution (Gaussian distribution):

$$F_x(x) = F_{\mathcal{N}(33.8, 5.9)}(x) = \Phi\left(\frac{x - 33.8}{5.9}\right), \quad (2.6)$$

so we get

$$\Phi\left(\frac{x - 33.8}{5.9}\right) \stackrel{!}{=} 0.05 \quad (2.7)$$

$$\frac{x - 33.8}{5.9} = \Phi^{-1}(0.05) = -1.645 \quad (2.8)$$

$$x = -1.645 \cdot 5.9 + 33.8 \quad (2.9)$$

$$x = 24.095 \quad (2.10)$$

even easier with statistical software R:

```
round(qnorm(p = 0.05, mean = 33.8, sd = 5.9), 3)
## [1] 24.095
```

### 2.4.3 Standard Deviation Scores

Standardization of an observation is a transformation of an observation by shifting and scaling the value. So that the expected value is zero and the variance  $\sigma^2$  is one. The standard deviation  $\sigma = \sqrt{\sigma^2}$  is therefore also equal to one. If the population mean  $\mu$  and standard deviation  $\sigma$  are known, an observation can be converted into a standard deviation score (SDS) (frequently also called  $z$ -score) by:

$$z = \frac{x - \mu}{\sigma} \quad (2.11)$$

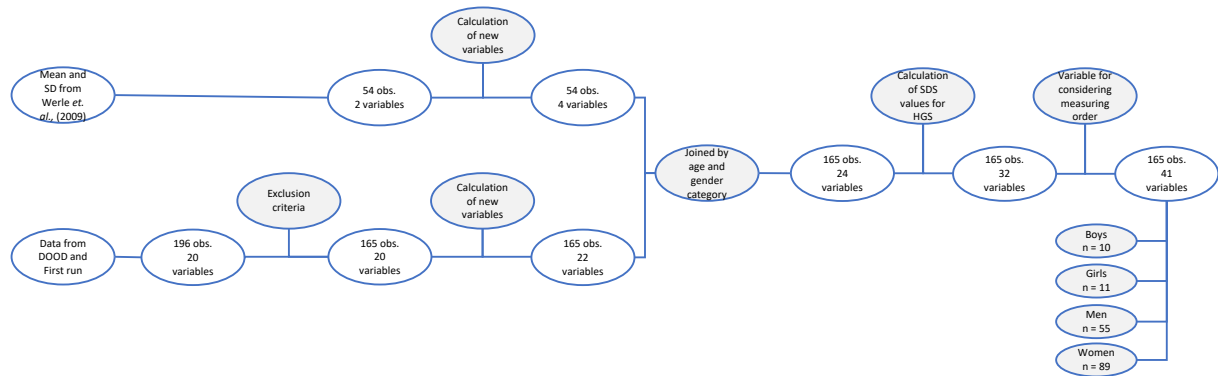
where  $\mu$  is the true mean of the population and  $\sigma$  the standard deviation of the population. The resulting SDS allows to make a universal interpretable statement of how far the distribution is distributed from the mean. Example: A female participant in the age category 30-34 for the position right, sitting, 90 flex has a HGS of 31 kg. Then the SDS would be:

$$z = \frac{31 - 33.8}{5.9} = -0.47 \quad (2.12)$$

A negative SDS indicates that the raw HGS is 0.47 standard deviation below the true mean (median).



### 2.4.4 Data Input, Curation, Preparation, Implementation and Computational Details



**Figure 2.7:** Flow-Chart of Data Input, Curation and Preparation

#### Data Input

For the analysis, the data from the DOOD entered via the (Google Forms) has to be accessed and correctly merged with the norm dataset. The extraction of the data from the (Google Forms) is described in more detail in the R code/01 Data Preparation.R in B.2.2. In General, a function was written which pulls the data automatically from Google Forms and stores it correctly in a data frame as a csv file.

#### Reference Quantile Curves and Merging with Experimental Data

The norm values and the calculation of the quantile norms of 0.05, 0.10, 0.25, 0.50, 0.75, 0.90 and 0.95 is well described in the R code/03 OOD norms.R in B.2.2. For the merging of the two dataset the function `merge` from R Core Team (2021) has been used. By doing so two data sets are generated. One dataset contains the quantile norms which is used to create the Figure 2.2 and Figure 2.6. The second dataset is merged only with the norm mean  $\mu$  and standard deviation  $\sigma$ . This dataset is used for the statistical analysis. The two datasets are merged using the variable `agecat`, which contains the age categories, and the variable `category`, which divides gender into men, boys, women, and girls. The corresponding code in R is:

```
# Data Frame With Quantile Norms in Wide Format:
dd_wide_pct <- merge(dd, subset(dd_nms, select = -c(lwr, upr)),
                    by = c("agecat", "category"))

# Data Frame With Out Quantile Norms in Wide Format:
dd_wide <- merge(dd, subset(dd_nms, select = c(mean, sd, agecat, category)),
                by = c("agecat", "category"))
```



For more details see R code/04 Data Analysis.R: in [B.2.2](#). The cleaned dataset is saved as .csv document. Both in long format and wide format.

### Consideration of the Order of the Measurement Sequence

To consider the effect of fatigue, a new variable is generated that takes into account the order of the measurement sequence. This is done as follows:

```
# Ordering the measurement according to the order on the entry sheet:
```

```
# 1 : Left, standing, 0 flex
# 2 : Right, standing, 0 flex
# 3 : Left, sitting, 90 flex
# 4 : Right, sitting, 90 flex
# 5 : Left, sitting, 0 flex
# 6 : Right, sitting, 0 flex
# 7 : Left, sitting, 90 flex
# 8 : Right, sitting, 90 flex
```

```
dd_wide$Start <- as.numeric(dd_wide$Start)
```

```
dd_wide <- dd_wide %>%
  mutate(Pos1 = Start)%>%
  mutate(Pos2 = ifelse(Pos1 !=8, Pos1 + 1,1)) %>%
  mutate(Pos3 = ifelse(Pos2 !=8, Pos2 + 1,1)) %>%
  mutate(Pos4 = ifelse(Pos3 !=8, Pos3 + 1,1)) %>%
  mutate(Pos5 = ifelse(Pos4 !=8, Pos4 + 1,1)) %>%
  mutate(Pos6 = ifelse(Pos5 !=8, Pos5 + 1,1)) %>%
  mutate(Pos7 = ifelse(Pos6 !=8, Pos6 + 1,1)) %>%
  mutate(Pos8 = ifelse(Pos7 !=8, Pos7 + 1,1))
```

```
print(head(dd_wide)[c("ID", "Pos1", "Pos2", "Pos3",
                      "Pos4", "Pos5", "Pos6", "Pos7", "Pos8")],
      row.names = FALSE)
```

```
##   ID Pos1 Pos2 Pos3 Pos4 Pos5 Pos6 Pos7 Pos8
## 103    4    5    6    7    8    1    2    3
##   66    3    4    5    6    7    8    1    2
##   96    2    3    4    5    6    7    8    1
##  180    1    2    3    4    5    6    7    8
##  174    2    3    4    5    6    7    8    1
##  159    4    5    6    7    8    1    2    3
```

```
# Pos1 : First measuring Position
# Pos2 : Second measuring Position
# . : ...
```

```
# From wide to long Format:
```

```
dd_long <- dd_long %>%
  gather(., key = "Sequence of measurement", value = "Position",
         "Pos1", "Pos2", "Pos3", "Pos4",
         "Pos5", "Pos6", "Pos7", "Pos8")
```

The wide data format is then transformed into long data format with the corresponding variable name `Sequence of measurement` which considers the order of the measurement sequence.

### Computational Details

Further, all analysis are performed in the R programming language (R Core Team, 2021) using base packages and the following analysis-specific packages: `ggplot2` for the creation of graphics (Wickham, 2016), `vtable` to generate summary statistics (Huntington-Klein, 2022). In addition, `rstatix` is used for performing basic statistical test including t-Test and repeated measures ANOVA (Kassambara, 2021). `BlandAltmanLeh` for Bland-Atman statistics (Lehnert, 2015). Further, `lme4` and `lmerTest` is used for the linear mixed-effects model (Bates et al., 2015; Kuznetsova et al., 2017). Test results with p-values smaller than 0.05 are interpreted as statistically significant.

#### 2.4.5 One-Sample t-Test

There are a few assumptions made with the  $t$ -statistic. It assumes that all observations are independent and data comes from a population for which the data would be normally distributed. The one-sample t-test is used to compare the mean of one sample to a known theoretical mean  $\mu_0$  specified in  $H_0: \mu = \mu_0$ . The null hypothesis assumes that the mean of the population is equal to the specified value. The alternative hypothesis is given by  $H_A: \mu \neq \mu_0$ . Thus t-test assumes that the data is normally distributed. Then t-statistic can be calculated as follows:

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}} \quad (2.13)$$

where,  $\bar{x}$  is the sample mean,  $\mu_0$  the theoretical mean,  $s$  is the standard deviation of the sample and  $n$  is the number of sample observations. The quantities which are the standard errors by which a value deviates from  $\mu_0$ . For large  $n$ , the shape of the t-distribution is similar to the standard normal distribution. If the sample size is small, the distribution is flatter. Therefore, the t-distribution needs an additional parameter that changes its variance. These are called the degree of freedom ( $df$ ) and can be calculated as  $df = n - 1$ , where  $n$  is the sample size.

#### 2.4.6 Confidence Interval

To make a statement about the true mean  $\mu$  the 95% confidence interval of the mean  $\mu$  (95%CI( $\mu$ )) can be considered:

$$\bar{x} - t_{.975} \times \frac{s}{\sqrt{n}} \leq \mu \leq \bar{x} + t_{.975} \times \frac{s}{\sqrt{n}} \quad (2.14)$$

There is an analogy between the one-sample t-test and the 95%CI( $\mu$ ). If  $\mu_0$  is included between the lower and upper limits, we can state that there is no significant difference from  $\mu_0$ . If this is not the case, there is a significant difference between the mean value of the population and the specified value,  $\mu_0$ . The 95% CI for probability was obtained according to Wilson (Wilson, 1927), using the R package `DescTools` (Andri et al., 2022).

#### 2.4.7 Two-Sample Welch t-Test

The two-sample t-test is used to compare whether the means of two independent groups are different. Like the one-sample t-test, the two-sample t-test assumes normality and that the vari-

ances of the two groups are equal (homoscedasticity). But this is rarely true in real life.

If the variances of the groups are different (heteroscedasticity), it is possible to use the Welch t-test, which is an adapted version:

$$t = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}} \quad (2.15)$$

where  $\bar{x}$  represents the sample mean,  $n$  the number of the sample observations and  $s^2$  the variance for the group 1 respectively group 2. The main difference to the Student's t-test (uses the pooled variance) is that Welch t-test involves the variance of each of the groups. This means that the standard error calculation is different. Further, the distribution of the test statistic is a t-distribution with the degree of freedom which is given by:

$$df = \frac{\left(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}\right)^2}{\left(\frac{s_1^4}{n_1^2(n_1-1)} + \frac{s_2^4}{n_2^2(n_2-1)}\right)} \quad (2.16)$$

This equation indicates, that the  $df$  of the Welch t-test doesn't have to be a whole number.

#### 2.4.8 Repeated Measures ANOVA

Repeated measures ANOVA (rmANOVA) is similar to one-way ANOVA. The one-way ANOVA is used when we want test two independent groups if there is a difference between them. The main difference to rmANOVA is, that rmANOVA tests rather use dependent groups and not independent groups. For example, we measure HGS of the same participant in different positions. The independent variable is the position, which is usually called the within-subject factor and the dependent variable is the HGS. The null hypothesis  $H_0$  for the rmANOVA is that the HGS is identical across all positions.

#### Decomposition of the F-statistic

To judge the differences among the groups in a one-way ANOVA we need the variability of the data within and between the groups. Both sum up to total sums of squares ( $SS_{total}$ ):

$$SS_{total} = SS_{between} + SS_{within} \quad (2.17)$$

In rmANOVA we are interested in the variability within a participant ( $SS_{within}$ ). This is explained by the model  $SS_{model}$  and by  $SS_{error}$ . The  $SS_{error}$  is the amount of variance that the model does not account for:

$$SS_{within} = \sum_{i=1}^n \sum_{j=1}^k (X_{ij} - \bar{X}_i)^2 \quad (2.18)$$

$$SS_{model} = n \sum_{j=1}^k (\bar{X}_j - \bar{X})^2 \quad (2.19)$$

$$SS_{error} = SS_{within} - SS_{model} \quad (2.20)$$

Our observations are split in  $k$  groups, which are the measuring positions. The number of observations are  $n$ . The average values of the  $i$ -th participant is labelled as  $\bar{X}_i$ , the overall average is  $\bar{X}$ . The degrees of freedom ( $df$ ) corresponding to this are:

$$df_{model} = k - 1 \quad (2.21)$$

$$df_{error} = (k - 1) \cdot (n - 1) \quad (2.22)$$

The error mean square is then the sum of squares divided by the degrees of freedom:

$$MS_{model} = \frac{SS_{model}}{df_{model}} \quad (2.23)$$

$$MS_{error} = \frac{SS_{error}}{df_{error}} \quad (2.24)$$

We can use an F test to compare these two variance estimates. The F statistic is calculated as the ratio of the larger sample variance to the smaller one:

$$F = \frac{MS_{model}}{MS_{error}} \quad (2.25)$$

If the null hypothesis is correct then the test statistic comes from a F distribution with  $df_{model}$ ,  $df_{error}$ . Then the F statistic can be compared with a given distribution in order to determine the probability that we obtain such a large F value if  $H_0$  is correct. So strictly speaking, if  $SS_{model}$  is large and  $SS_{error}$  is small, then the variation is explained by the model, which results in large F-value. In this case, we can conclude that the means across the groups are not equal.

### Test Assumption

The rmANOVA has its own assumptions. The primary assumption of the test is that the dependent variable is interval scaled and approximately normally distributed. This can be checked with the Shapiro-Wilk normality test introduced by [Shapiro and Wilk \(1965\)](#), which is a supplementary test to the graphical assessment of normality by the QQ-plot. The Shapiro-Wilk test is based on the statistic:

$$W = \frac{(\sum_{i=1}^n a_i X_{(i)})^2}{\sum_{i=1}^n (X_i - \bar{X})^2}, \quad (2.26)$$

where  $X_i$  are ordered values of the sample and  $a_i$  are tabulated constants. When the test statistic of the Shapiro-Wilk is not significant,  $p < .05$ , then  $H_0$  is accepted and data is called normally distributed. In statistics, a QQ-plot is a scatter plot where observed value are plotted against the expected values. Data that is normally distributed, the data points on a QQ-plot should lie on a straight line ([Hanusz and Tarasińska, 2015](#); [Das and Imon, 2016](#)).

Further, the assumption of sphericity must be checked. Sphericity can be linked to the homogeneity of variances in a one-way ANOVA. It is the condition where the variance of the difference between all possible pairs of within-subject are equal. The present of sphericity is represented by a statistic called epsilon ( $\varepsilon$ ):

$$\varepsilon = \frac{(\sum_a \zeta_{a,a})^2}{(A-1) \sum_{a,a'} \zeta_{a,a'}^2}, \quad (2.27)$$

where  $\zeta_{a,a'}$  is the entries of an  $A \times A$  table, which is the population covariance matrix. Epsilon of one indicates that the assumption is given. The further epsilon decreases ( $0 < \varepsilon < 1$ ) the greater the violation of the assumption. If sphericity assumption is violated, the probability of Typ I error increases (Abdi, 2010).

Mauchly's sphericity test can be used to validate this assumption. Mauchly's sphericity test tests the null hypothesis  $H_0$  which assumes that the variance of the difference are equal. If violated  $p < .05$ , correction must be made to achieve a valid F-value. This can be achieved by applying a correction factor to the  $df$ . The Greenhouse-Geisser adjustment is used to correct for sphericity violation, which estimates the correction factor ( $\hat{\varepsilon}$ ). In general, the population covariance matrix is not known. Therefore, we need to transform the sample covariance matrix. This procedure is called "double-centering". For further details see: Abdi (2010). From this matrix we can compute the correction factor ( $\hat{\varepsilon}$ ) :

$$\hat{\varepsilon} = \frac{(\sum_a s_{a,a})^2}{(A-1) \sum_{a,a'} s_{a,a'}^2}. \quad (2.28)$$

We use  $\hat{\varepsilon}$  to correct the  $df$ :

$$df_{model} = \hat{\varepsilon}(k-1) \quad (2.29)$$

$$df_{error} = \hat{\varepsilon}(k-1)(n-1) \quad (2.30)$$

where  $k$  indicates the number of repeated measures and  $n$  the number of participants. This correction does not lead to a different F-statistics, since the correction factor are cancelled out:

$$F = \frac{MS_{model}}{MS_{error}} = \frac{SS_{model}/df_{model}}{SS_{error}/df_{error}} = \frac{SS_{model} \cdot \hat{\varepsilon}(k-1)(n-1)}{SS_{error} \cdot \hat{\varepsilon}(k-1)}, \quad (2.31)$$

but this will change the  $p$ -value to compensate the violation of sphericity. A statistically significant rmANOVA only informs that at least one of the compared means is different from the others. To identify where the means differ, we use the procedure of multiple comparisons, so called post-hoc tests.

When we perform multiple comparisons, we have to deal with multiplicity problems. We control the Type I error by applying the Bonferroni correction to adjust the significance level  $\alpha$ . The Bonferroni method compares the  $p$ -values  $p_1, \dots, p_k$ , not with  $\alpha$ , but with the threshold  $\alpha/k$ ,  $k$  indicating the number of outcomes (Park et al., 2009; Leps and Smilauer, 2020).

### 2.4.9 Linear Mixed-Effects Models

Linear mixed-effects models are used to describe a relationship between a response variable and some of the covariates that have been measured along with the response. In linear mixed-effects models with random intercepts, several observations for the same person are possible.

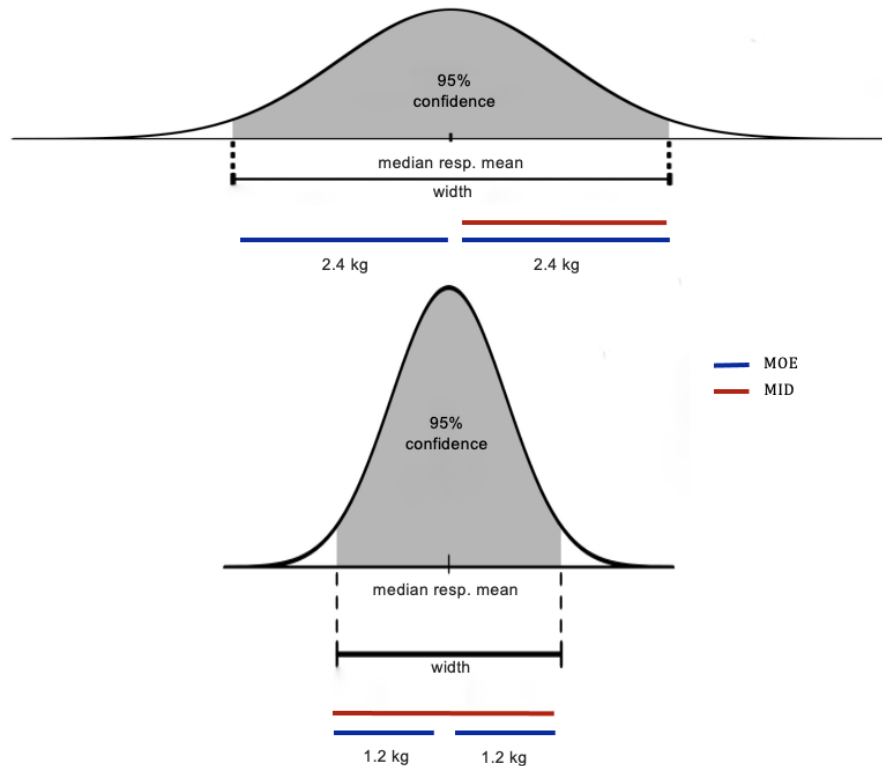
Longitudinal data consist of repeated measurements on the same subject taken over time. In general, to characterize the time trends within subjects and between subjects. Therefore, linear mixed-effects model is an alternative statistical analysis method to the rmANOVA. Such models can be fitted using the R package `lme4` (Bates et al., 2015). Covariates are distinguished between fixed-effects and random effects:

$$\text{observation} = \text{fixed effects} + \text{random effects} + \text{error}$$

Fixed effect parameters are a set of possible levels of covariates which are observable. In contrast, random effects are variables where levels represent realisation of a latent random variable rendering a random sample from the set of all possible levels. The advantage of the linear mixed-effects model is that it incorporates both, fixed effects parameters and a random effect variable (Brown and Prescott, 2015).

#### 2.4.10 Sample Size Calculation Based on Confidence Interval

Confidence interval represents how appropriate the amount of a sample size for a study is. In a small sample the population uncertainty will be large. So the CI gives a range of values that is likely to include the population value with a certain degree of confidence. As an example we take the 95% CI. This states that we can be 95% confident that the true mean respectively the median of the population lies in the interval. As the sample size increases, the range of the interval will get narrower.



**Figure 2.8:** Graphical illustration of sample size calculation based on the width of the CI. MOE: margin of error and MID: minimal important difference

In our case we want to determine the needed sample size to ensure, that the margin of error (MOE) is sufficiently small to be informative based on the information of the minimal important difference (MID) from the paper [Bobos et al. \(2020\)](#) and the information from DOOD.

CI take any parameter in the following form:

$$\text{Point Estimate} \pm \text{MOE} \quad (2.32)$$

We derive the formula for the mean as:

$$\bar{X} \pm Z_{1-\alpha/2} \frac{\sigma}{\sqrt{n}} \quad (2.33)$$

We want the MOE to be not more than 2.4 to 2.7 kg according to [Bobos et al. \(2020\)](#). Meaning that the 95% CI would have a width of 4.8 kg or more conservatively 2.4 kg to one side. The MOE in the one sample CI for the mean can be written as:

$$\text{MOE} = Z_{1-\alpha/2} \frac{\sigma}{\sqrt{n}} \quad (2.34)$$

Since our goal is to determine the sample size which ensures MOE, we solve the equation above for the variable  $n$ :

$$n = \left( \frac{Z_{1-\alpha/2} \cdot \sigma}{\text{MOE}} \right)^2 \quad (2.35)$$

This formula will give the minimum needed sample size for the median. This ensures that the half length of the 95% CI will not exceed the MOE.



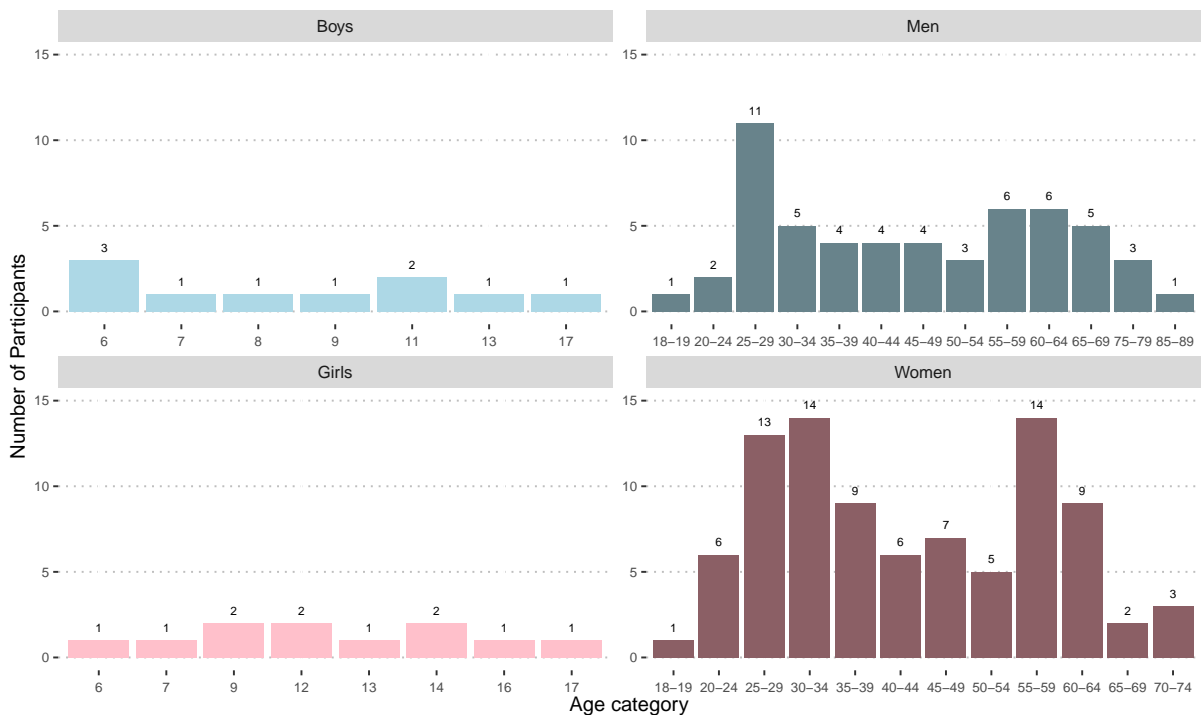


# Chapter 3

## Results

### 3.1 Descriptive Statistics

The descriptive statistics of age, height, weight and HGS for eight positions are summarized in Table 3.1. After applying exclusion criteria provided in Section 2.3.1, 165 persons were considered for the analysis. Of these, 21 are children (11 girls and 10 boys) and 144 adults (89 women and 55 men). The study population of men and women is divided into age groups by gender with 5-year intervals. No randomization was conducted for the test run.



**Figure 3.1:** Distribution of age by gender, number of participants shown per age category in absolute numbers. These numbers are split by children (boys and girls) and adults (men and women).

Figure 3.1 gives an indication of how the age categories of the study participants are distributed. The sample size is small for establishing own normative values for adults.

**Table 3.1: Descriptive statistics of demographic variables and HGS (kg),** summarized with mean, standard deviation (SD), minimum, quantiles, median and maximum.

	Mean	SD	Min	$Q_{25}$	$Q_{50}$	$Q_{75}$	Max
Boys (n = 10)							
Age	9.4	3.6	6	6	8	11	17
Height	140.3	18.9	120	126	132	154	173
Weight	31.2	13.3	16	22	28	38	59
Left, standing, 0 flex	16.8	10.8	7	9	14	18	42
Right, standing, 0 flex	14.6	6.7	8	10	12	16	30
Left, standing, 90 flex	13.7	7.2	6	9	10	18	28
Right, standing, 90 flex	16.3	9.4	7	11	14	19	40
Left, sitting, 0 flex	16.5	11.2	5	12	13	18	44
Right, sitting, 0 flex	16.7	9.6	10	12	14	16	42
Left, sitting, 90 flex	15.9	9.8	8	10	14	16	41
Right, sitting, 90 flex	16.6	9.7	8	10	14	18	41
Men (n = 55)							
Age	46.0	17.6	18	30	45	60	86
Height	177.9	5.9	162	174	179	182	188
Weight	77.9	13.6	53	70	76	83	118
Left, standing, 0 flex	43.3	9.2	19	36	44	50	62
Right, standing, 0 flex	46.7	10.0	21	40	46	52	68
Left, standing, 90 flex	42.3	8.2	20	38	43	48	60
Right, standing, 90 flex	45.6	9.2	21	39	46	51	67
Left, sitting, 0 flex	43.7	8.9	16	38	44	50	66
Right, sitting, 0 flex	46.3	9.5	22	40	46	52	68
Left, sitting, 90 flex	42.3	8.5	21	37	42	48	64
Right, sitting, 90 flex	45.7	9.5	21	38	46	51	66
Girls (n = 11)							
Age	11.7	3.6	6	9	12	14	17
Height	150.9	16.5	124	142	156	161	175
Weight	43.4	12.4	20	38	48	50	60
Left, standing, 0 flex	22.1	10.1	10	14	22	26	44
Right, standing, 0 flex	22.2	11.3	8	14	20	27	48
Left, standing, 90 flex	19.9	10.5	6	14	22	22	43
Right, standing, 90 flex	21.1	10.7	6	14	20	26	44
Left, sitting, 0 flex	20.4	8.9	10	14	20	24	40
Right, sitting, 0 flex	22.7	11.8	6	14	24	28	48
Left, sitting, 90 flex	20.5	10.1	6	16	22	24	42
Right, sitting, 90 flex	21.9	11.7	4	14	24	27	46
Women (n = 89)							
Age	42.7	14.7	19	30	40	56	74
Height	166.8	7.3	140	163	167	170	186
Weight	64.5	11.5	20	58	63	70	100
Left, standing, 0 flex	29.4	6.0	18	25	29	33	48
Right, standing, 0 flex	31.4	6.7	14	28	31	35	51
Left, standing, 90 flex	29.1	6.4	17	25	29	33	50
Right, standing, 90 flex	31.1	7.5	12	26	31	36	51
Left, sitting, 0 flex	29.6	6.7	17	25	28	33	51
Right, sitting, 0 flex	31.4	6.7	16	28	30	36	52
Left, sitting, 90 flex	29.1	6.6	17	24	28	32	48
Right, sitting, 90 flex	30.9	7.3	14	26	30	36	53

## 3.2 Analysis of Preferred Position

The preferred position is addressed in Tables 3.2 – 3.4. For men, only 47 of 55 recorded their preference. Table 3.2 shows the preferred position of the Jamar dynamometer by gender, Ta-

bles 3.3 and 3.4 show comparisons of the Jamar dynamometer positions.

**Table 3.2: Preferred position of the Jamar dynamometer by gender**, summarized with counts and percentage

	Boys		Men		Girls		Women	
	n	Percent	n	Percent	n	Percent	n	Percent
Preference	9		47		11		89	
... Left, standing, 0 flex	2	22%	4	9%	1	9%	10	11%
... Right, standing, 0 flex	1	11%	19	40%	0	0%	29	33%
... Left, standing, 90 flex	0	0%	0	0%	0	0%	4	4%
... Right, standing, 90 flex	1	11%	11	23%	2	18%	15	17%
... Left, sitting, 0 flex	1	11%	1	2%	2	18%	2	2%
... Right, sitting, 0 flex	1	11%	4	9%	3	27%	12	13%
... Left, sitting, 90 flex	1	11%	1	2%	0	0%	4	4%
... Right, sitting, 90 flex	2	22%	7	15%	3	27%	13	15%

Table 3.2 shows that position right, standing, 0 flex is favoured for both gender. In addition, the comparison of the positions shows a clear favouring of the positions 0 flex, right hand and standing. It is contrary to the recommendation made by the American Society of Hand Therapist (ASHT), which recommends the position seated, shoulder abducted, elbow flexed at 90 degrees.

The preferences from Table 3.2 were further split to see how frequently each position was preferred. In Table 3.3 the right hand is preferred in 123 cases and left hand in 33 cases. This shows that the right hand is preferred 3.7 times more often than the left. Furthermore, it seems that the participants prefer to stand rather than to sit and to keep the arms stretched rather than bent. A possible explanation for this could be that when the arm is stretched, the participant has to tense the muscles less to hold the dynamometer than when it is bent. This could be perceived as more comfortable. If we look at the confidence interval, we see that 0.5 is not included in any of the comparisons.

**Table 3.3: Univariate comparison of relative frequencies for preference of Jamar dynamometer position.** Shown proportions for flex, handedness and posture with 95% CI according to Wilson.

Prop. of Cond. 1 vs. Cond. 2	Cond. 1	Cond. 2	Fraction	Relative freq.	CI lwr	CI upr
0 flex vs. 90 flex	92	64	92 / 156	0.59	0.51	0.66
Right vs. Left	123	33	123 / 156	0.79	0.72	0.85
Standing vs. Sitting	99	57	99 / 156	0.63	0.56	0.71

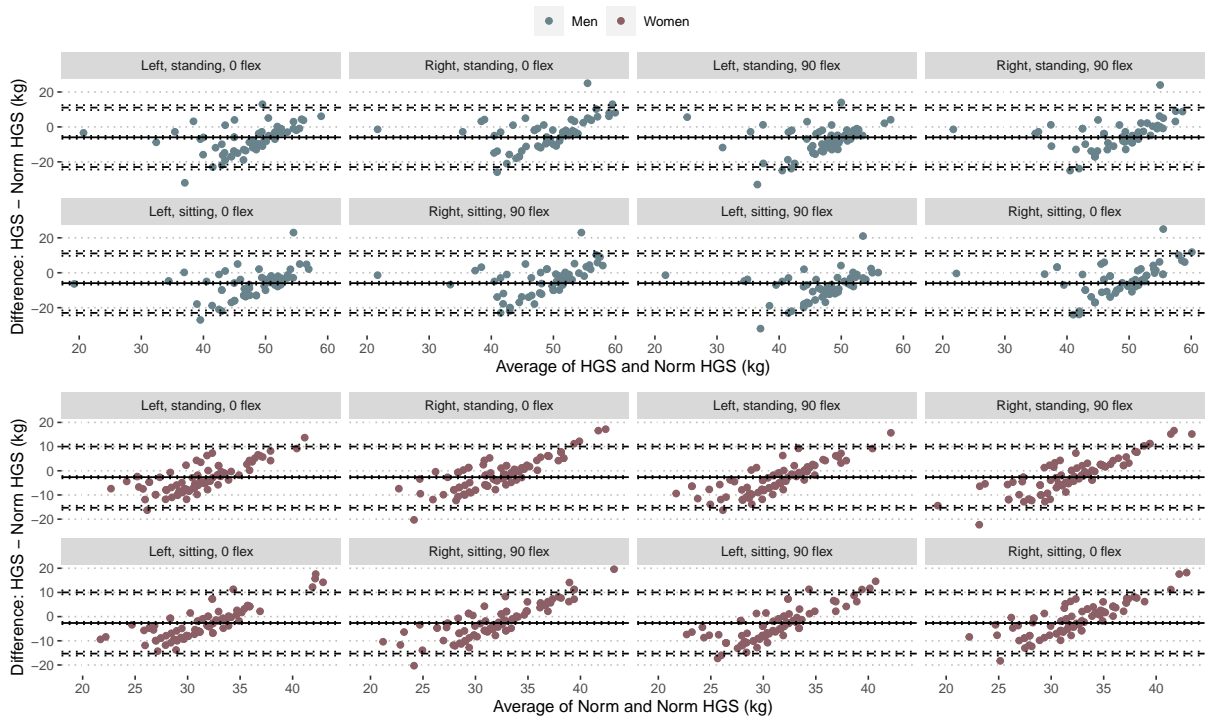
In addition, when looking at the Table 3.4 we see that standing, 0 flex is the most significantly preferred position for measuring HGS. Whereas no clear preference appears between the position standing, 90 flex versus sitting, 0 flex as well as between standing, 90 flex versus sitting 90 flex and sitting 0 flex versus sitting, 90 flex.

**Table 3.4: Comparisons of relative frequencies for preference of Jamar dynamometer position.** Shown proportions for flex, handedness and posture with 95% CI according to Wilson.

Prop. of Cond. 1 vs. Cond. 2	Cond. 1	Cond. 2	Fraction	Relative freq.	CI lwr	CI upr
standing, 0 flex vs. sitting, 0 flex	66	26	66 / 92	0.72	0.62	0.80
standing, 0 flex vs. standing, 90 flex	66	33	66 / 99	0.67	0.57	0.75
standing, 0 flex vs sitting 90 flex	66	31	66 / 97	0.68	0.58	0.76
standing, 90 flex vs sitting, 0 flex	33	26	33 / 59	0.56	0.43	0.68
standing, 90 flex vs sitting, 90 flex	33	31	33 / 64	0.52	0.40	0.63
sitting, 90 flex vs sitting, 0 flex	31	26	31 / 57	0.54	0.42	0.67

### 3.3 Validation of Existing Swiss Norms for Adults

Before calculating the SDS for the HGS, the Bland-Altman plot is used to see if there is a pattern between the norms and the measured HGS. If so, this should also be apparent after standardizing the HGS.



**Figure 3.2:** Bland-Altman plot, showing average differences of HGS and norms. The solid line represents the mean of difference of values between two measures (Bias). The dashed line define the limits of agreement (LoA). The dotted line represents the 95% confidence interval for each line. Note: different x and y scales for men and women.

The resulting Bland-Altman plot in Figure 3.2 shows a bias for men of -6 with 95% CI from -7 to -5. The corresponding lower LoA is -23 with 95% CI from -25 to -21 and the upper LoA is 12 with 95% CI from 9 to 13. For the women a bias of -2.6 with 95% CI from -4 to -2 has been estimated. The corresponding lower LoA is -16 with 95% CI from -17 to -14 and the upper LoA is 11

with 95% CI from 9 to 11. As the MID proposed by Bohannon (2019) range from 2.4 kg to 2.7 kg.

In order to validate the existing Swiss norms for adults on data from DOOD, the measured values of HGS were transformed into SDS of HGS as described in Section 2.4.3. In addition, SDS of maximal HGS, SDS of mean HGS and SDS of median HGS were computed. Then a one-sample t-test was conducted. Results of this test are shown in Table 3.5 for men and in Table 3.6 for women. In Figure 3.3 the distribution of the standardised HGS with the theoretical mean and its 95% CI grouped by men and women is shown.

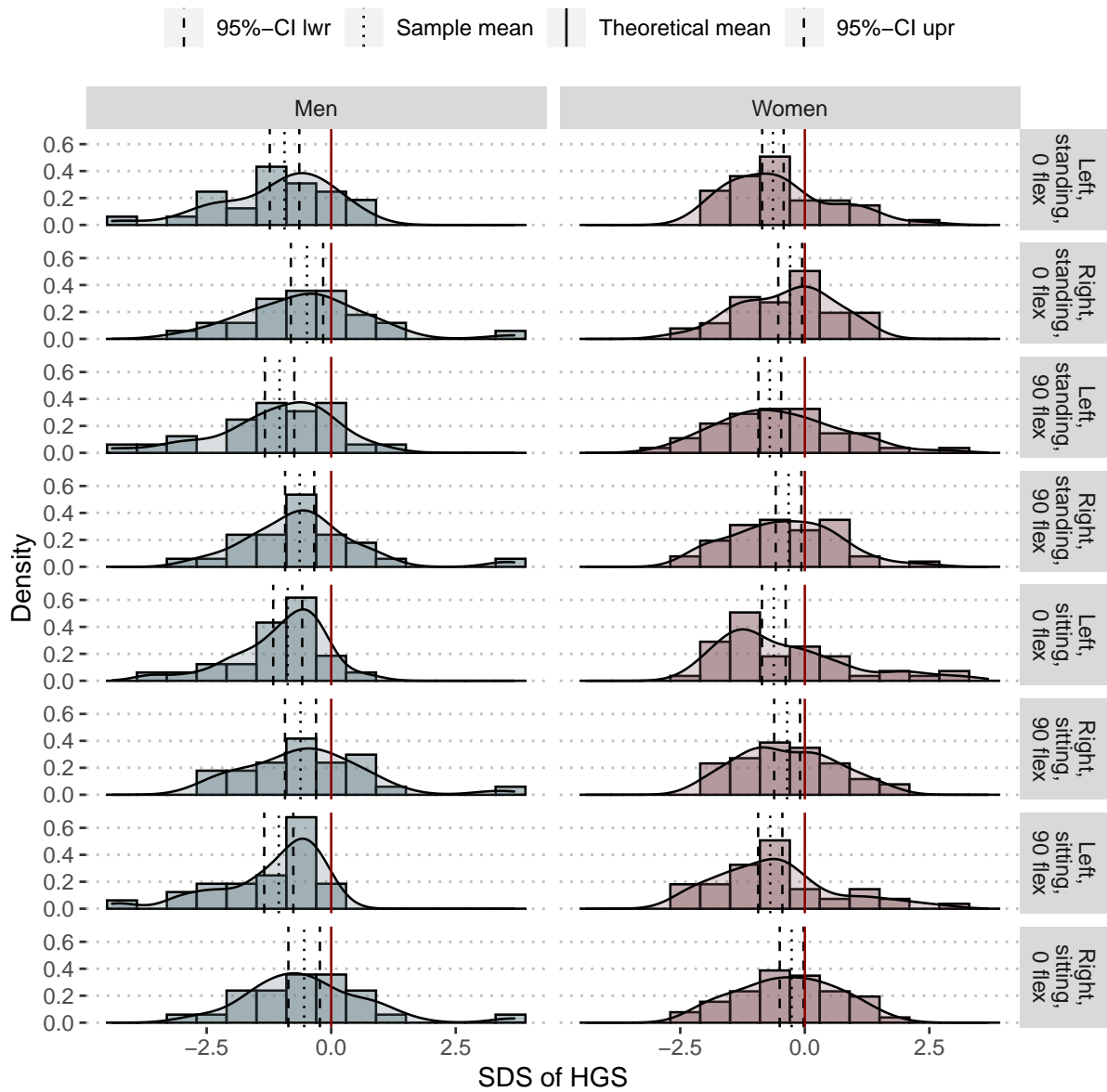
**Table 3.5: Analysis of SDS of HGS: One-sample t-test for men**, table gives T statistic, df, mean, SE, 95% CI for the difference and p-value.

Men (n =55)	T statistic	df	Mean	SD	CI lwr	CI upr	p-value
Left, standing, 0 flex	-6.20	54	-0.94	1.12	-1.24	-0.63	< 0.0001
Right, standing, 0 flex	-2.94	54	-0.49	1.23	-0.82	-0.15	0.0048
Left, standing, 90 flex	-6.89	54	-1.04	1.11	-1.34	-0.73	< 0.0001
Right, standing, 90 flex	-4.25	54	-0.63	1.10	-0.93	-0.33	< 0.0001
Left, sitting, 0 flex	-5.87	54	-0.87	1.10	-1.17	-0.57	< 0.0001
Right, sitting, 0 flex	-3.36	54	-0.54	1.20	-0.87	-0.22	0.0014
Left, sitting, 90 flex	-7.07	54	-1.05	1.10	-1.35	-0.75	< 0.0001
Right, sitting, 90 flex	-3.88	54	-0.62	1.18	-0.93	-0.30	0.0003
maximal HGS	-0.86	54	-0.13	1.12	-0.43	0.17	0.39
mean HGS	-5.37	54	-0.77	1.07	-1.06	-0.48	< 0.0001
median HGS	-5.01	54	-0.73	1.08	-1.03	-0.44	< 0.0001

**Table 3.6: Analysis of SDS of HGS: One-sample t-test for women**, table gives T statistic, df, mean, SE, 95% CI for the difference and p-value.

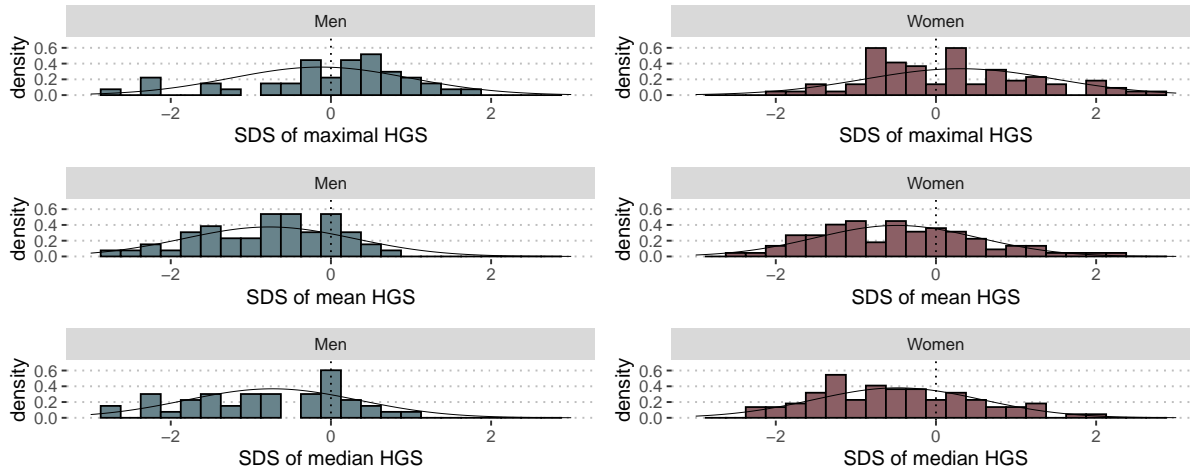
Women (n =89)	T statistic	df	Mean	SD	CI lwr	CI upr	p-value
Left, standing, 0 flex	-5.83	88	-0.64	1.04	-0.86	-0.42	< 0.0001
Right, standing, 0 flex	-2.41	88	-0.29	1.15	-0.54	-0.05	0.018
Left, standing, 90 flex	-6.03	88	-0.70	1.10	-0.93	-0.47	< 0.0001
Right, standing, 90 flex	-2.49	88	-0.33	1.24	-0.59	-0.07	0.015
Left, sitting, 0 flex	-5.14	88	-0.62	1.14	-0.86	-0.38	< 0.0001
Right, sitting, 0 flex	-2.17	88	-0.26	1.15	-0.51	-0.02	0.032
Left, sitting, 90 flex	-5.59	88	-0.69	1.17	-0.94	-0.45	< 0.0001
Right, sitting, 90 flex	-2.68	88	-0.36	1.25	-0.62	-0.09	0.0087
maximal HGS	2.37	88	0.30	1.19	0.05	0.55	0.02
mean HGS	-4.54	88	-0.49	1.01	-0.70	-0.27	< 0.0001
median HGS	-4.28	88	-0.48	1.05	-0.70	-0.26	< 0.0001

Table 3.5 shows that the results for the men are significant for all positions. The test statistic results in a significant p-value. Thus, indicating a deviation from the norm values. The negative estimates of the mean for each position indicate that the existing norm values are overly optimistic for the sample of men collected on the DOOD. If we consider only the SDS of max HGS, then we have no indication of the difference to the normative HGS values for men. However, this is not true for the SDS of mean and median HGS. In Table 3.6 the results for the women shows also that for all positions the test results are significant. This indicates a deviation from the norm values. If we consider only the SDS of max HGS, then the mean value is positive. So in this case, we can say that the norms are pessimistic for the sample of women collected at DOOD. The negative estimates of the mean for each position of SDS of mean HGS and SDS of median HGS indicate that the existing norm values are overly optimistic for the sample of women collected on the DOOD.



**Figure 3.3:** Distribution of the SDS of HGS, red solid line: theoretical mean of zero, dashed line: 95% CI and dotted line: sample mean

Analysis in Section 3.4 will show that SDS of mean HGS and SDS of median HGS are stable of the posture-elbow position. These results allow us to directly examine the SDS of mean HGS and median HGS. Mean and median reflects the HGS of a person much better than the maximum HGS. These results are also shown in Table 3.5 and Table 3.6. In addition, Figure 3.4 shows the distributions of SDS of maximum, mean and median HGS.



**Figure 3.4:** Distribution of SDS of the max HGS, mean HGS and median HGS. The x-axis shows the SDS of max, mean, and median HGS. Additionally, vertical dotted lines indicate the zero value.

The density curves show that the norm values are optimistic for men, while they are pessimistic for women when we consider the SDS of maximum HGS values. When looking at the SDS of mean HGS as well as at the median, the emerging conclusion is that the existing normative values are overly optimistic for both genders.

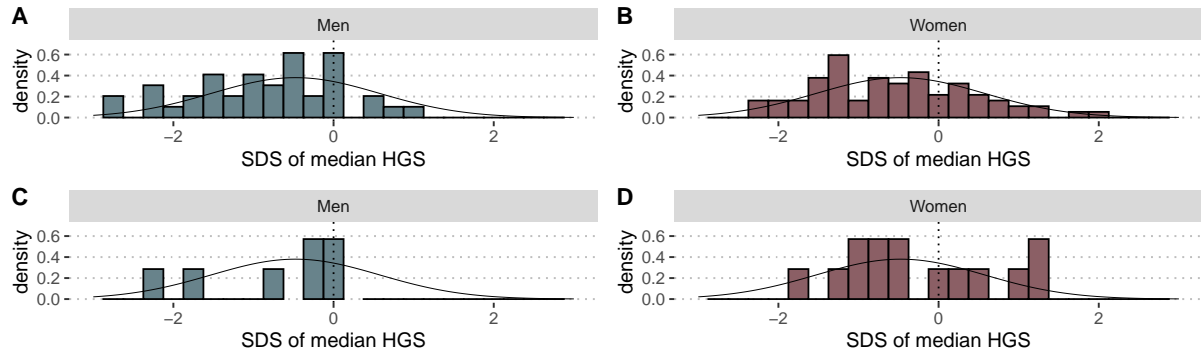
Inspired by Figure 2.1 in the mid-term presentation the question was asked whether measurements for adults below 60y and above 60y could be gathered together. We see in Figure 2.1 that, according to the normative values of the HGS, a decrease in strength can be expected from the age of 59y. For this reason, we evaluated the HGS values depending on these two age categories, up to 59y and  $\geq 60$ y. In Tables 3.7 and 3.8 the results of SDS of mean and median HGS for the men and women are shown. Once for the age group under 60y and once over 60y. For both genders the test statistic for  $\leq 60$ y group results in a significant p-value indicating a deviation from the norm value. Figure 3.5 shows the respective SDS of HGS distribution in a visual representation. The density curves show that the norm values tend to be optimistic for men and women, in  $< 60$ y group. 60y+ group is non significant due to small sample size.

**Table 3.7: Analysis of SDS of HGS: One-sample t-test for age category up to 59y and over 60y for men,** table gives T statistic, df, mean, SE, 95% CI for the difference and p-value.

Men	n	T statistic	df	Mean	SD	CI lwr	CI upr	p-value
mean HGS for age $< 60$ y	40	-6.26	39	-0.96	0.97	-1.27	-0.65	$< 0.0001$
median HGS for age $< 60$ y	40	-6.02	39	-0.92	0.97	-1.24	-0.61	$< 0.0001$
mean HGS for age 60y+	15	-0.88	14	-0.26	1.17	-0.91	0.38	0.4
median HGS for age 60y+	15	-0.69	14	-0.22	1.23	-0.90	0.46	0.5

**Table 3.8: Analysis of SDS of HGS: One-sample t-test for age category up to 59y and over 60y for women**, table gives T statistic, df, mean, SE, 95% CI for the difference and p-value.

Women	n	T statistic	df	Mean	SD	CI lwr	CI upr	p-value
mean HGS for age < 60y	75	-4.47	74	-0.53	1.03	-0.77	-0.29	< 0.0001
median HGS for age < 60y	75	-4.26	74	-0.52	1.07	-0.77	-0.28	< 0.0001
mean HGS for age 60y+	14	-1.03	13	-0.26	0.95	-0.81	0.29	0.32
median HGS for age 60y+	14	-0.86	13	-0.22	0.96	-0.77	0.33	0.41

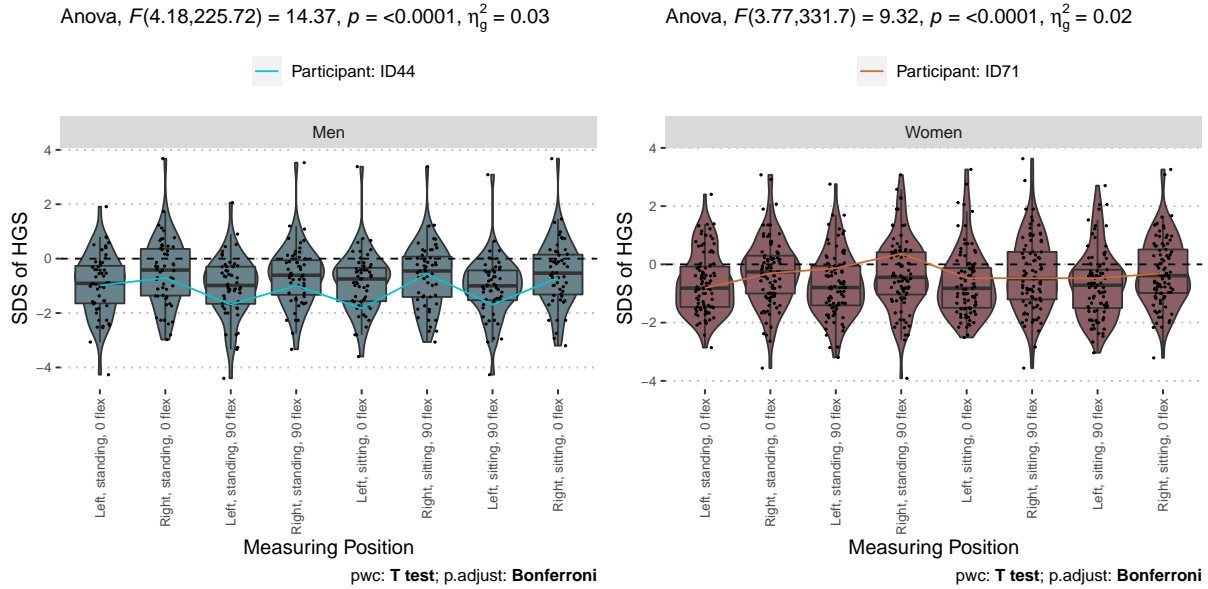


**Figure 3.5:** Distribution of SDS of median HGS: (A) men, age  $\leq 60y$ , (B) women, age  $\leq 60y$ , (C) men, age 60+ and (D) women, age 60+. The vertical dotted line indicates mean of zero.



### 3.4 Assessment Whether Handgrip Strength Values Are Stable Independent of the Posture-Elbow Position

To assess whether HGS values are stable independent of the posture-elbow position an ANOVA with repeated measures (rmANOVA) is conducted, since the same participants have been measured for the same outcome under different HGS positions.



**Figure 3.6:** Boxplot: SDS of HGS, for men and women

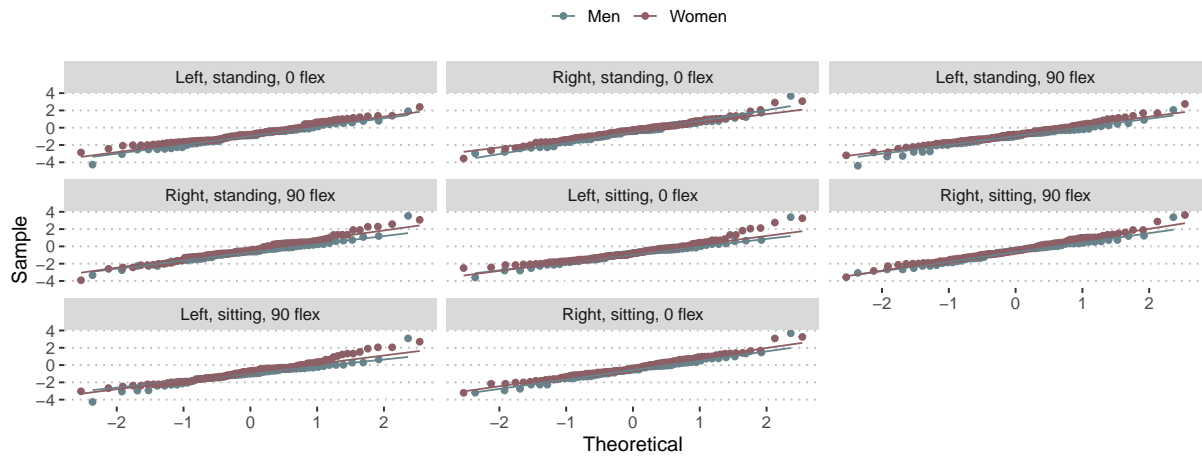
In order to use rmANOVA, some assumptions (see Section: 2.4.8 for details) needed to be checked. No extreme outliers for men and women were detected. Further, the assumption of normality was checked using the Shapiro-Wilk test and QQ-plot.

**Table 3.9: Test for normality**, according to Shapiro-Wilk for the SDS of the men's HGS data. Table gives the Position, Statistic and the p-value.

Position	Statistic	p-value
Left, standing, 0 flex	0.98	0.69
Right, standing, 0 flex	0.97	0.22
Left, standing, 90 flex	0.97	0.19
Right, standing, 90 flex	0.96	0.04
Left, sitting, 0 flex	0.95	0.016
Right, sitting, 90 flex	0.97	0.12
Left, sitting, 90 flex	0.94	0.008
Right, sitting, 0 flex	0.97	0.15

**Table 3.10: Test for normality**, according to Shapiro-Wilk for the SDS of the women's HGS data. Table gives the Position, Statistic and the p-value.

Position	Statistic	p-value
Left, standing, 0 flex	0.97	0.028
Right, standing, 0 flex	0.99	0.57
Left, standing, 90 flex	0.99	0.49
Right, standing, 90 flex	0.99	0.47
Left, sitting, 0 flex	0.94	0.0004
Right, sitting, 90 flex	0.99	0.43
Left, sitting, 90 flex	0.97	0.044
Right, sitting, 0 flex	0.98	0.25



**Figure 3.7:** QQ-Plot with reference line; SDS of HGS according to position and gender

The Shapiro-Wilk test shows that the distribution of the SDS of HGS positions do not significantly deviate from the normality with some minor exceptions. Based on this outcome, shown in Tables 3.9, 3.10 and considering the QQ-plot in Figure 3.7 we state for our analysis that the assumptions of normality is not severely violated. The assumption of sphericity is checked during the computation of the rmANOVA using the R function `anova_test` from the package `rstatix`.

**Table 3.11: Analysis of SDS of HGS: adjusted rmANOVA summary table for men using Greenhouse-Geisser correction ( $\hat{\epsilon} = 0.597$ )**

DFn: degree of freedom numerator, DFd: degree of freedom denominator, SSd: sum of squares numerator, SSd: sum of squares denominator, F: F-statistic, p-value, ges: generalized eta square

Effect	DFn	DFd	SSn	SSd	F	p-value	ges
(Intercept)	1.00	54.00	262.11	490.60	28.85	< 0.0001	0.32
Position	4.18	225.72	19.98	75.10	14.37	< 0.0001	0.03

**Table 3.12: Analysis of SDS of HGS: adjusted rmANOVA summary table for women using Greenhouse-Geisser correction ( $\hat{\epsilon} = 0.538$ )**

**DFn**: degree of freedom numerator, **DFd**: degree of freedom denominator, **SSn**: sum of squares numerator, **SSd**: sum of squares denominator, **F**: F-statistic, **p-value**, **ges**: generalized eta square

Effect	DFn	DFd	SSn	SSd	F	p-value	ges
(Intercept)	1.00	88.00	169.26	723.07	20.60	< 0.0001	0.15
Position	3.77	331.70	23.20	219.07	9.32	< 0.0001	0.02

The results of Mauchly's sphericity test indicate that the assumption of sphericity is violated. Mauchly's  $W = 0.177$ ,  $p\text{-value} < 0.0001$  for men and Mauchly's  $W = 0.124$ ,  $p\text{-value} < 0.0001$  for women. The significant value of these tests indicates that the assumption of sphericity is not met for the main effect. So we need to correct the F-ratios for these effects using the Greenhouse-Geisser adjustment for men with  $\epsilon = 0.597$  and for women with  $\epsilon = 0.538$ .

The results show that there is a significant effect between the SDS of the HGS and the different positions for men,  $F(4.18, 225.72) = 14.368$ ,  $p\text{-value} < 0.0001$ . In addition, it also shows a significant effect between the SDS of the HGS and the different positions for women,  $F(3.77, 331.7) = 9.321$ ,  $p\text{-value} < 0.0001$ . Based on this outcome, we decided to perform a post-hoc test to locate those specific differences in the measuring position of the Jamar dynamometer. Therefore, a Bonferroni corrected multiple pairwise t-test is performed between the levels of the position. The results of the post-hoc comparisons of the posture-elbow position in Table 3.13 (men) and in Table 3.14 (women) reveal that none of the pairwise comparisons are significantly different. In addition, Figure 3.6 visualises the data in a box and whiskers plot. The information of minimum, maximum, median and the inter-quartile range in a graphical representation is given.

**Table 3.13: Post-hoc comparison of the posture-elbow position for men**

Position 1	Position 2	Statistic	df	p-value	p-value (adj.)
Left, standing, 0 flex	Right, standing, 0 flex	-2.13	54	0.038	1.00
Left, standing, 0 flex	Left, standing, 90 flex	0.42	54	0.67	1.00
Left, standing, 0 flex	Right, standing, 90 flex	-1.30	54	0.2	1.00
Left, standing, 0 flex	Left, sitting, 0 flex	-0.30	54	0.76	1.00
Left, standing, 0 flex	Right, sitting, 90 flex	-1.37	54	0.18	1.00
Left, standing, 0 flex	Left, sitting, 90 flex	0.49	54	0.63	1.00
Left, standing, 0 flex	Right, sitting, 0 flex	-1.74	54	0.088	1.00
Right, standing, 0 flex	Left, standing, 90 flex	2.15	54	0.036	1.00
Right, standing, 0 flex	Right, standing, 90 flex	0.69	54	0.49	1.00
Right, standing, 0 flex	Left, sitting, 0 flex	1.79	54	0.079	1.00
Right, standing, 0 flex	Right, sitting, 90 flex	0.53	54	0.6	1.00
Right, standing, 0 flex	Left, sitting, 90 flex	2.86	54	0.006	0.17
Right, standing, 0 flex	Right, sitting, 0 flex	0.25	54	0.8	1.00
Left, standing, 90 flex	Right, standing, 90 flex	-1.93	54	0.059	1.00
Left, standing, 90 flex	Left, sitting, 0 flex	-0.70	54	0.49	1.00
Left, standing, 90 flex	Right, sitting, 90 flex	-1.87	54	0.067	1.00
Left, standing, 90 flex	Left, sitting, 90 flex	0.08	54	0.94	1.00
Left, standing, 90 flex	Right, sitting, 0 flex	-2.12	54	0.038	1.00
Right, standing, 90 flex	Left, sitting, 0 flex	1.32	54	0.19	1.00
Right, standing, 90 flex	Right, sitting, 90 flex	-0.08	54	0.94	1.00
Right, standing, 90 flex	Left, sitting, 90 flex	1.91	54	0.061	1.00
Right, standing, 90 flex	Right, sitting, 0 flex	-0.37	54	0.71	1.00
Left, sitting, 0 flex	Right, sitting, 90 flex	-1.40	54	0.17	1.00
Left, sitting, 0 flex	Left, sitting, 90 flex	0.94	54	0.35	1.00
Left, sitting, 0 flex	Right, sitting, 0 flex	-1.56	54	0.12	1.00
Right, sitting, 90 flex	Left, sitting, 90 flex	2.00	54	0.051	1.00
Right, sitting, 90 flex	Right, sitting, 0 flex	-0.32	54	0.75	1.00
Left, sitting, 90 flex	Right, sitting, 0 flex	-2.21	54	0.031	0.88

**Table 3.14: Post-hoc comparison** of the posture-elbow position for women

Position 1	Position 2	Statistic	df	p-value	p-value (adj.)
Left, standing, 0 flex	Right, standing, 0 flex	-2.14	88	0.035	0.98
Left, standing, 0 flex	Left, standing, 90 flex	0.39	88	0.7	1.00
Left, standing, 0 flex	Right, standing, 90 flex	-1.90	88	0.061	1.00
Left, standing, 0 flex	Left, sitting, 0 flex	-0.10	88	0.92	1.00
Left, standing, 0 flex	Right, sitting, 90 flex	-1.52	88	0.13	1.00
Left, standing, 0 flex	Left, sitting, 90 flex	0.30	88	0.76	1.00
Left, standing, 0 flex	Right, sitting, 0 flex	-2.23	88	0.028	0.79
Right, standing, 0 flex	Left, standing, 90 flex	2.39	88	0.019	0.53
Right, standing, 0 flex	Right, standing, 90 flex	0.18	88	0.86	1.00
Right, standing, 0 flex	Left, sitting, 0 flex	2.06	88	0.043	1.00
Right, standing, 0 flex	Right, sitting, 90 flex	0.33	88	0.74	1.00
Right, standing, 0 flex	Left, sitting, 90 flex	2.21	88	0.03	0.84
Right, standing, 0 flex	Right, sitting, 0 flex	-0.18	88	0.86	1.00
Left, standing, 90 flex	Right, standing, 90 flex	-2.42	88	0.018	0.50
Left, standing, 90 flex	Left, sitting, 0 flex	-0.49	88	0.62	1.00
Left, standing, 90 flex	Right, sitting, 90 flex	-1.87	88	0.064	1.00
Left, standing, 90 flex	Left, sitting, 90 flex	-0.06	88	0.96	1.00
Left, standing, 90 flex	Right, sitting, 0 flex	-2.54	88	0.013	0.36
Right, standing, 90 flex	Left, sitting, 0 flex	1.78	88	0.078	1.00
Right, standing, 90 flex	Right, sitting, 90 flex	0.17	88	0.87	1.00
Right, standing, 90 flex	Left, sitting, 90 flex	1.95	88	0.054	1.00
Right, standing, 90 flex	Right, sitting, 0 flex	-0.34	88	0.74	1.00
Left, sitting, 0 flex	Right, sitting, 90 flex	-1.50	88	0.14	1.00
Left, sitting, 0 flex	Left, sitting, 90 flex	0.43	88	0.67	1.00
Left, sitting, 0 flex	Right, sitting, 0 flex	-2.14	88	0.035	0.98
Right, sitting, 90 flex	Left, sitting, 90 flex	1.93	88	0.057	1.00
Right, sitting, 90 flex	Right, sitting, 0 flex	-0.51	88	0.61	1.00
Left, sitting, 90 flex	Right, sitting, 0 flex	-2.56	88	0.012	0.34

Since the post-hoc test after the Bonferroni correction turned out to be non-significant for each combination. We investigated whether the right-hand has an influence on the SDS of HGS. The results of the analysis is shown in Tables 3.15 and 3.16. For both genders, it can be seen that right-hand plays a significant role for the measurement of the SDS of HGS. Whereas the posture-elbow position: **Position4** (sitting/standing, 0°/90° flex) is statistically non-significant.

**Table 3.15: Analysis of SDS of HGS with two predictors (Position4 and Right-hand);** two-way rmANOVA, Position4 (sitting 0°, standing 0°, sitting 90°, standing 90°), for men

**DFn**: degree of freedom numerator, **DFd**: degree of freedom denominator, **SSn**: sum of squares numerator, **SSd**: sum of squares denominator, **F**: F-statistic, p-value, **ges**: generalized eta square

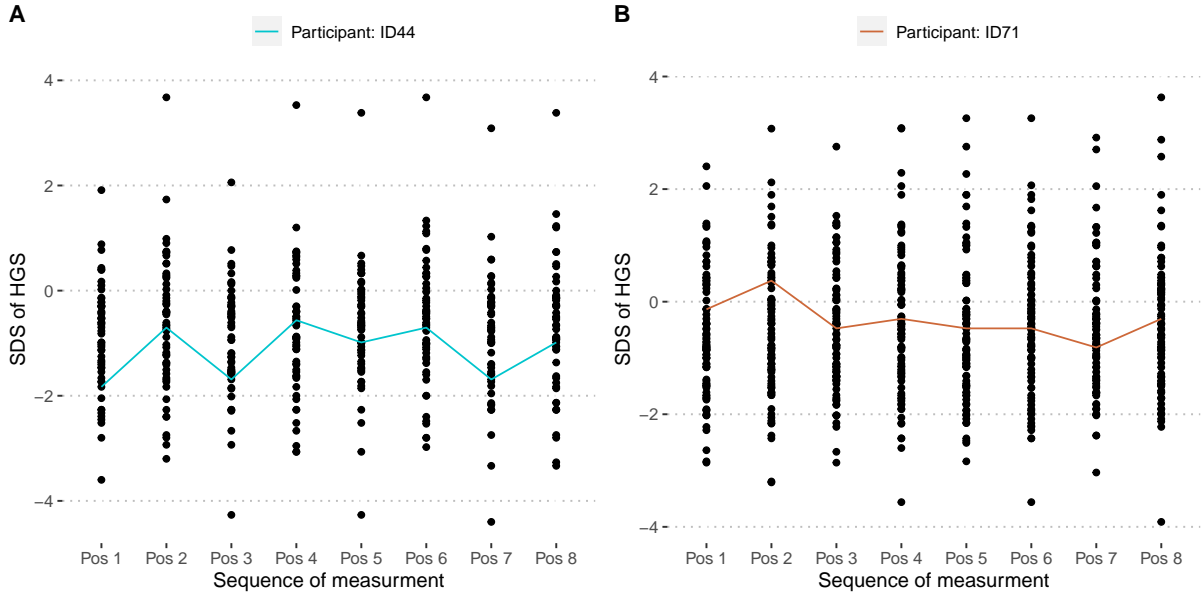
Effect	DFn	DFd	SSn	SSd	F	p-value	ges
Position4	3	435	1.71	565.93	0.44	0.72	0.00
Right-hand	1	435	18.03	565.93	13.86	0.0002	0.03

**Table 3.16: Analysis of SDS of HGS with two predictors (Position4 and Right-hand);** two-way rmANOVA, Position4 (sitting 0°, standing 0°, sitting 90°, standing 90°), for women

**DFn**: degree of freedom numerator, **DFd**: degree of freedom denominator, **SSn**: sum of squares numerator, **SSd**: sum of squares denominator, **F**: F-statistic, p-value, **ges**: generalized eta square

Effect	DFn	DFd	SSn	SSd	F	p-value	ges
Position4	3	707	0.80	942.18	0.20	0.9	0.00
Right-hand	1	707	22.37	942.18	16.79	< 0.0001	0.02

### Evaluation of Whether the Measurement Sequence Leads to Fatigue



**Figure 3.8:** Pattern of SDS of HGS obtained with Jamar dynamometer with respect to sequence of measurement, whether the sequence of measurement can represent fatigue; (A) men, (B) women.

To investigate whether repeated measurement leads to fatigue of the handgrip strength in the participant a linear mixed-effects model is used. Figure 3.8 shows the fatigue patterns of SDS of the HGS measurement ordered from the first measurement according to the dice to the last measurement. No deterministic association can be discerned for men and women. The result in Table 3.17 and Table 3.18 indicate that there is no evidence of fatigue due to sequence of measurement for men ( $p = 0.21$ ) and women ( $p = 0.25$ ).

**Table 3.17: Association between SDS of HGS and sequence of measurement in men:** Linear mixed-effects model

	Estimate	SE	df	t value	Pr(> t )
(Intercept)	-0.83	0.15	67	-5.54	< 0.0001
Sequence of measurement	0.01	0.01	385	1.25	0.21

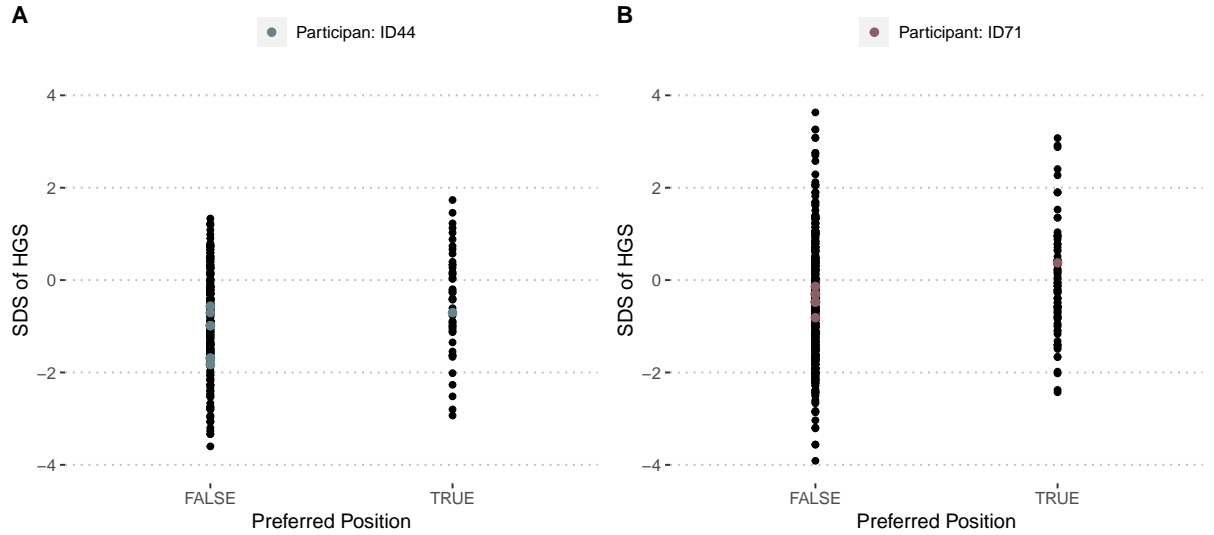
**Table 3.18: Association between SDS of HGS and sequence of measurement in women:** Linear mixed-effects model

	Estimate	SE	df	t value	Pr(> t )
(Intercept)	-0.54	0.12	124	-4.65	< 0.0001
Sequence of measurement	0.01	0.01	623	1.15	0.25

### 3.5 Exploration of Further Associations

#### 3.5.1 Association Between the Position Preferred and the SDS of HGS Measurement

We were also interested to investigate whether there is an association between the preferred positions and the SDS of HGS. According to Figure 3.9, a pattern emerges that the preferred position can lead to a higher HGS measurement for both men and women.



**Figure 3.9:** Pattern between position preferred and SDS of HGS; (A) men (B) women

**Table 3.19:** Association between SDS of HGS with sequence of measurement and preferred position in men; Linear mixed-effects Model

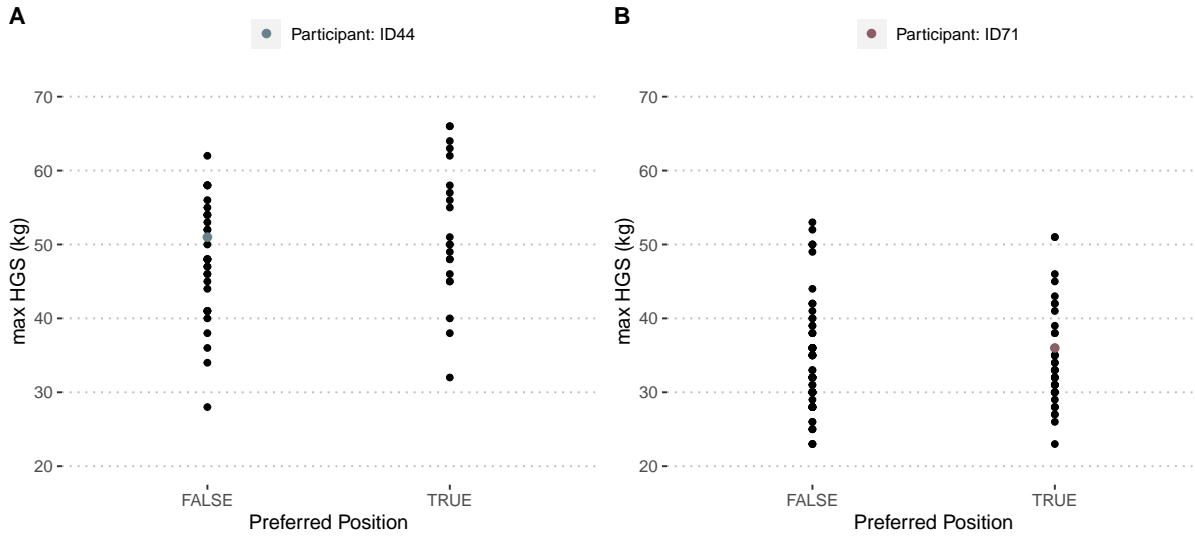
	Estimate	SE	df	t value	Pr(> t )
(Intercept)	-0.94	0.15	60	-6.49	< 0.0001
Sequence of easurement	0.01	0.01	329	1.26	0.21
Preferred position	0.40	0.08	329	5.28	< 0.0001

**Table 3.20:** Association between SDS of HGS with sequence of measurement and preferred position in women; Linear mixed-effects Model

	Estimate	SE	df	t value	Pr(> t )
(Intercept)	-0.64	0.12	123	-5.48	< 0.0001
Sequence of measurement	0.02	0.01	623	1.90	0.058
Preferred position	0.52	0.07	623	7.71	< 0.0001

The results of the analysis in Table 3.19 gives no indication that the sequence of measurement leads to lower SDS of HGS, which would correspond to fatigue. There is evidence that the preferred position of a participant leads to higher SDS of HGS values. The value of the intercept indicates that the norms are overoptimistic for men. Similar effects occur in women, shown in Table 3.20.

### 3.5.2 Association Between the Position Preferred and the max HGS Measurement



**Figure 3.10:** Association between preferred position and max HGS; (A) men (B) women

**Table 3.21:** Association between position preferred and max HGS for men and women; Two sample t-test; not preferred position = 0, preferred position = 1

Category	n	T value	df	Mean [0]	Mean [1]	SD	Diff HGS [0-1]	CI lwr	CI upr	p-value
Men	59	-1.47	34.55	48.34	51.86	18.37	-3.52	-8.37	1.34	0.15
Women	134	-0.54	90.79	33.25	33.91	14.20	-0.66	-3.10	1.77	0.59

**Table 3.22:** Association between position preferred and max HGS for men and women; Adjusted two sample t-test; not preferred position = 0, preferred position = 1

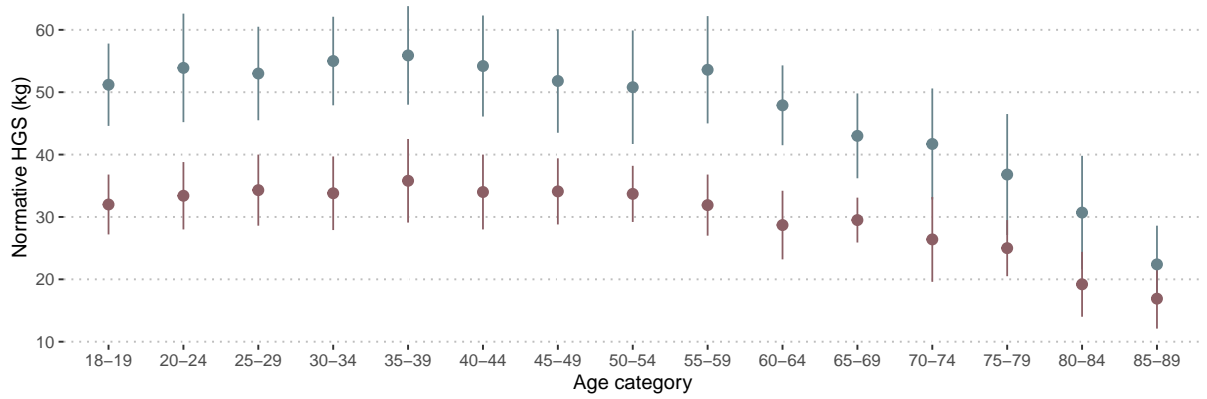
Category	n	T value	df	Mean [0]	Mean [1]	SD	Diff HGS [0-1]	CI lwr	CI upr	p-value
Men	47	-1.85	37.98	47.19	51.86	17.33	-4.66	-9.78	0.45	0.073
Women	89	0.91	84.62	35.30	33.91	14.37	1.38	-1.65	4.41	0.37

Two sample t-tests are performed for men and women to see if there are associations between preferred position and max HGS. Table 3.21 shows the result of these tests. There is no evidence that there is a difference in max HGS between preferred and not preferred position for men and women. In this test result the assumption that each participant is measured only once is violated. For this reason we adjust the data where only one measurement for each participant is considered. Thus, if a participant's max HGS is measured in both, preferred and non-preferred position, then only the preferred one is considered. The result of this adjusted test is shown in Table 3.22, resulting in the same conclusion as before.

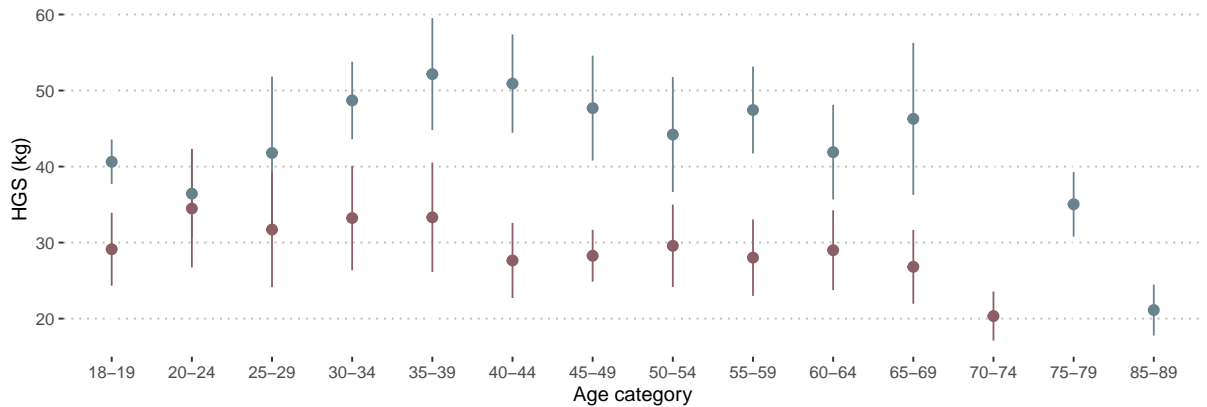
### 3.6 Evaluate Whether the Mean HGS Values of Men and Women Differ for the Respective Age Categories

At the mid-term presentation of this master project, the question was raised whether the two different norm values for men and women are necessary at all. It was argued that if one looks at the Figure 3.11, one could think that they are very similar, especially for people aged 60 and older. To evaluate this assumption statistically, a Welch t-test stratified by age categories was performed with the mean and SD from Werle et al. (2009). Moreover, the same test was conducted with the mean and SD from DOOD. The visual representation is shown in Figure 3.12.

The results of the Welch t-test based on mean, SD and n from Werle et al. (2009) is displayed in Table 3.23. It suggests that both groups, men and women, differ with regarding to the mean HGS value. For each age group, the difference of mean HGS values between men and women are significant. The test shows that it is indeed necessary to establish gender-specific norm values even for old people over 60y. The results of the Welch t-test based on Data from DOOD is displayed in Table 3.24. Here we get the same indication as before with the data from Werle.



**Figure 3.11:** Normative HGS mean and SD values from Werle et al. (2009). Only the dominant hand is considered.



**Figure 3.12:** HGS mean and SD from the data collected at the DOOD.





### 3.7 Computation of the Sample Size Required

Sample size computation are conducted according to the methods presented in Section 2.4.10. Tables 3.25 and 3.26 show the results of the sample size calculation for the MOE of 2.4 kg once for men and once for women. The sample size calculation with this MOE allows that the width of the 95% CI for the true mean in one direction does not exceed 2.4 kg. However, if more restriction is wanted, so that one decides that the deviation both downwards and upwards should be a maximum of 2.4 kg, then a larger sample is required. The amount  $n$  for each age category which would be necessary is shown in Table 3.27 for men and in Table 3.28 for women.

**Table 3.25: Computation of sample size ( $n$ ) based on 95% CI and MOE of 2.4 kg for men. Mean and SD taken from Werle.**

Age cat.	mean	SD	Z Score	MOE	$n$
18-19	51.20	6.60	1.96	2.40	30
20-24	53.90	8.70	1.96	2.40	51
25-29	53.00	7.50	1.96	2.40	38
30-34	55.00	7.10	1.96	2.40	34
35-39	55.90	7.90	1.96	2.40	42
40-44	54.20	8.10	1.96	2.40	44
45-49	51.80	8.30	1.96	2.40	46
50-54	50.80	9.10	1.96	2.40	56
55-59	53.60	8.60	1.96	2.40	50
60-64	47.90	6.40	1.96	2.40	28
65-69	43.00	6.80	1.96	2.40	31
70-74	41.70	8.90	1.96	2.40	53
75-79	36.80	9.70	1.96	2.40	63
80-84	30.70	9.10	1.96	2.40	56
85-89	22.40	6.20	1.96	2.40	26

**Table 3.26: Computation of sample size ( $n$ ) based on 95% CI and MOE of 2.4 kg for women. Mean and SD taken from Werle.**

Age cat.	mean	SD	Z Score	MOE	$n$
18-19	32.00	4.80	1.96	2.40	16
20-24	33.40	5.40	1.96	2.40	20
25-29	34.30	5.70	1.96	2.40	22
30-34	33.80	5.90	1.96	2.40	24
35-39	35.80	6.70	1.96	2.40	30
40-44	34.00	6.00	1.96	2.40	25
45-49	34.10	5.30	1.96	2.40	19
50-54	33.70	4.50	1.96	2.40	14
55-59	31.90	4.90	1.96	2.40	17
60-64	28.70	5.50	1.96	2.40	21
65-69	29.50	3.60	1.96	2.40	9
70-74	26.40	6.80	1.96	2.40	31
75-79	25.00	4.50	1.96	2.40	14
80-84	19.20	5.20	1.96	2.40	19
85-89	16.90	4.80	1.96	2.40	16

**Table 3.27: Computation of sample size ( $n$ )** based on 95% CI and MOE of 1.2 kg for men. Mean and SD taken from Werle.

Age cat.	mean	SD	Z Score	MOE	$n$
18-19	51.20	6.60	1.96	1.20	117
20-24	53.90	8.70	1.96	1.20	202
25-29	53.00	7.50	1.96	1.20	151
30-34	55.00	7.10	1.96	1.20	135
35-39	55.90	7.90	1.96	1.20	167
40-44	54.20	8.10	1.96	1.20	176
45-49	51.80	8.30	1.96	1.20	184
50-54	50.80	9.10	1.96	1.20	221
55-59	53.60	8.60	1.96	1.20	198
60-64	47.90	6.40	1.96	1.20	110
65-69	43.00	6.80	1.96	1.20	124
70-74	41.70	8.90	1.96	1.20	212
75-79	36.80	9.70	1.96	1.20	252
80-84	30.70	9.10	1.96	1.20	221
85-89	22.40	6.20	1.96	1.20	103

**Table 3.28: Computation of sample size ( $n$ )** based on 95% CI and MOE of 1.2 kg for women. Mean and SD taken from Werle.

Age cat.	mean	SD	Z Score	MOE	$n$
18-19	32.00	4.80	1.96	1.20	62
20-24	33.40	5.40	1.96	1.20	78
25-29	34.30	5.70	1.96	1.20	87
30-34	33.80	5.90	1.96	1.20	93
35-39	35.80	6.70	1.96	1.20	120
40-44	34.00	6.00	1.96	1.20	97
45-49	34.10	5.30	1.96	1.20	75
50-54	33.70	4.50	1.96	1.20	55
55-59	31.90	4.90	1.96	1.20	65
60-64	28.70	5.50	1.96	1.20	81
65-69	29.50	3.60	1.96	1.20	35
70-74	26.40	6.80	1.96	1.20	124
75-79	25.00	4.50	1.96	1.20	55
80-84	19.20	5.20	1.96	1.20	73
85-89	16.90	4.80	1.96	1.20	62

**Comparison of the Calculated Sample Size With That of [Werle et al. \(2009\)](#)**

The calculated sample size is approximately the same as the amount in [Werle et al. \(2009\)](#) if the width of the 95% CI is 4.8 kg. See Table 3.29 for the comparison. However, if one is more conservative and only allows a 95% CI width of 2.4 kg, then much more data is needed.

**Table 3.29: Comparison of sample sizes** from Werle et al. (2009) with computed sample sizes based on  $MOE^1 = 2.4$  kg and  $MOE^2 = 1.2$  kg.

Age cat.	mean	SD	Werle Men			Werle Women			MOE <sup>1</sup>	MOE <sup>2</sup>	
			MOE <sup>1</sup>	MOE <sup>2</sup>		MOE <sup>1</sup>	MOE <sup>2</sup>				
18-19	51.2	6.6	33	30	117	32	4.8	31	16	62	
20-24	53.9	8.7	29	51	202	33.4	5.4	31	20	78	
25-29	53	7.5	30	38	151	34.3	5.7	30	22	87	
30-34	55	7.1	28	34	135	33.8	5.9	30	24	93	
35-39	55.9	7.9	41	42	167	35.8	6.7	42	30	120	
40-44	54.2	8.1	37	44	176	34	6	39	25	97	
45-49	51.8	8.3	31	46	184	34.1	5.3	40	19	75	
50-54	50.8	9.1	40	56	221	33.7	4.5	34	14	55	
55-59	53.6	8.6	30	50	198	31.9	4.9	28	17	65	
60-64	47.9	6.4	33	28	110	28.7	5.5	30	21	81	
65-69	43	6.8	46	31	124	29.5	3.6	34	9	35	
70-74	41.7	8.9	33	53	212	26.4	6.8	27	31	124	
75-79	36.8	9.7	28	63	252	25	4.5	26	14	55	
80-84	30.7	9.1	29	56	221	19.2	5.2	32	19	73	
85-89	22.4	6.2	28	26	103	16.9	4.8	28	16	62	
Total			496	648	2573			482	297	1162	

## 3.8 Recommendations

The recommendations for children and adults are made on the basis of the literature review, our own analysis and the practical experience from DOOD. The aim is to recommend a position for measuring the HGS with the Jamar dynamometer, provide suggestions for the development of norms for children and adults, and provide some sample size recommendations.

### 3.8.1 Recommendations for the Optimal Posture-Elbow Position

Based on the analysis of the preferred position in Section 3.2, we recommend the following position: The participant stands with both legs hip-width straight on the floor, the shoulder is rotated neutrally, the elbow is extended i.e. bent at  $0^\circ$  and the forearm and wrist is in a neutral position. However, results of Section 3.5 indicate that we are flexible to use different positions.

### 3.8.2 Further Recommendations for the Design of the Experiment to Collect HGS Measurements for Development of Norms

Based on the literature review in Section 2.1 and the experience at the DOOD we recommend to place the handgrip width of the Jamar dynamometer on the second grip position from the inside. This will be suitable for most participants. When holding the Jamar dynamometer, the thumb should touch the index finger otherwise adjust the width of the device accordingly.

As soon as the participant is positioned correctly and is ready, the supervisor says "Squeeze" and after 3 seconds "Stop". During the experiment any verbal or visual encouragement should be avoided. The participant should hold the position until the measurement is read and written down by the supervisor. This is to prevent that the pointer of the readout is being changed when the dynamometer is removed.

If very reliable HGS measurements are needed, we recommend to record the results of two successive trials for each hand. It is not really necessary to take a rest between the measurements, but a short break of 15 seconds is recommended so that the procedure is the same for all participants. The average value of the two HGS measurements can then be used to develop norm values. This recommendations is based on the practical experience of DOOD.

### 3.8.3 Recommendations for the Sample Size

As discussed in the literature review, it is not easy to specify an appropriate sample size for the development of norm HGS values. Our recommendation is based on the results obtained from Section 3.7. Depending on how precise the median should be, we recommend a sample size of minimum 65 for a MOE of 2.4 kg or minimum 255 for a MOE of 1.2 kg for each age category and gender. This corresponds to a total study of  $15 \times 65 = 975$  respectively  $15 \times 255 = 3825$  for adults. Assuming similar sample sizes for children we would need a study with a total of  $8 \times 65 = 520$  respectively  $8 \times 255 = 2040$  for children. With the flexible design it should be possible to recruit enough children by visiting them at schools.



## Chapter 4

# Discussion

This study validated existing norms for the Swiss adult population provided by [Werle et al. \(2009\)](#) and found that the existing Swiss norms for adults are overly optimistic for both men ( $n = 55$ ) and women ( $n = 89$ ) participating in the experiment conducted on the DOOD (Section 3.3). We showed in Section 3.4 that there is no evidence that sequence of measurement leads to lower HGS values, which would indicate fatigue. In contrast to [Sousa-Santos and Amaral \(2017\)](#) and [Innes \(1999\)](#), our results show that not the variation in posture-elbow position but the right-hand (dominant hand) affects the HGS measurement. Further, we found in Section 3.2 that the posture-elbow position preferred is right, standing, zero degree flex which does not agree with the recommendation of the ASHT. Moreover, the results of Section 3.4 suggest that it is not mandatory to follow the recommendation by ASHT.

Since there is no evidence that preferred posture-elbow position leads to higher HGS values (Section 3.5), we are flexible to use different positions. If we can flexibly apply different posture-elbow positions, then the position can be adjusted to the physical ability of the participant without any disadvantage. In Section 3.8, we provided clear recommendations for the posture-elbow position and for the design of the experiment, which can be flexibly applied to adults and children. Moreover, we considered mean and SD of HGS from [Werle et al. \(2009\)](#), focused on the median and calculated the optimal sample size for each age category for both genders in Section 3.7. We demonstrated that the optimal sample size for each age category depends on the decision of how precisely the median should be estimated. We showed that at least 65 participants in each age category are needed if the length of 95% CI for the median of 4.8 kg is considered clinically appropriate. This validated the reliability of existing HGS Swiss norm from [Werle et al. \(2009\)](#) and provided a recommendation for an optimal sample size for the development of future HGS norms. Finally, this master thesis was written in R sweave in a reproducible manner and the R code is accessible to the general public.

On the DOOD mainly public health interested adults with unknown nationality participated. Therefore, the DOOD experiment provided a non-random sample obtained by convenience. Moreover, small sample sizes in each age category were collected. For this reason, our sample is insufficient to compute our own norms. Further, on the DOOD, we were limited to the volunteering participants. Therefore, we cannot claim that the sample is representative for the Swiss population. Nonetheless, the results of this study can serve as a stimulus to address the important goal of developing refined HGS norms for the Swiss population.

Following [Werle et al. \(2009\)](#) and [Mathiowetz et al. \(1986, 1985\)](#), we use the assumption of normality in each age category. However, the assumption of normality in each age category can be inappropriate. Therefore, future research should allow for distributional assumptions that are flexible enough to embrace other non-normal distributions.

To calculate the sample size in each age category, we rely on the mean and SD estimates of HGS from [Werle et al. \(2009\)](#). These HGS mean and SD estimates were obtained from small sample sizes. Therefore, we expect that mean and SD HGS estimates from [Werle et al. \(2009\)](#) are not reliable representatives of true values in the Swiss population in each age category. For this reason, a future study should consider more flexible statistical methods for construction of norms which are not based on mean and SD HGS estimates for each age category such as smoothing methods ([Gasser et al., 1996](#)) or quantiles fit by transformation model ([Hothorn et al., 2018](#); [Tamási and Hothorn, 2022](#)).

For the computation of sample sizes, we focus on the precision of the median. Whereas the median indicates the main HGS tendency, the extreme quantiles can be particularly important for the diagnostic process. Therefore, to guarantee reliability of extreme quantile estimates, future studies should include larger sample sizes in each age category.

This study validated existing norms for the Swiss adult population provided by [Werle et al. \(2009\)](#) and found that these norms are overly optimistic for HGS measurements of participants volunteering on the DOOD. These findings warn that the Swiss norms are possibly outdated and should be used with caution. Therefore, it might be worthwhile to conduct a new nationwide study to obtain refined norms.

Further, we clarified that sample sizes provided by [Werle et al. \(2009\)](#) are insufficient to provide reliable median quantile for HGS values in each age category if the length of 95% CI is fixed at 4.8 kg. Moreover, we provided concrete suggestions for appropriate sample sizes for both genders in each age category. This finding indicates that a new nationwide study should provide better sample sizes than [Werle et al. \(2009\)](#). Better sample sizes would lead to better HGS norms with more precise median and extreme quantiles. Such norms would be more reliable and better suited for the diagnostic process.

In addition, we provide evidence based recommendations for the measuring process and posture-elbow position that could easily be applied to adults and children. On the DOOD children and adults enjoyed taking HGS measurements. This indicates that the design of the experiment conducted at the DOOD could be easily implemented for children at schools. This design is more flexible than the ASHT design and can be an attractive option to collect enough HGS measurements for the development of reliable HGS norms for Swiss children. This would support a nationwide Swiss study, that would provide norms of HGS for each age category including adults and children. New norms for children and adults would assess muscle strength and general health of Swiss population in a non-invasive way.

All our results are computationally replicable. We provided open access to R code and data analysis online in the pdf-file provided on the [website](#) of the Master's program in Biostatistics. Moreover, we provided access to online form based on [Google Sheet](#), which considerably facilitates data collection. All these resources are accessible to everyone who is interested in developing future Swiss norms. Moreover, these resources facilitate the development of HGS norms for Swiss children and adults based on a playful but scientifically correct experiment to obtain HGS measurements. Such future HGS norms can help physicians and physiotherapists to reliably and non-invasively assess the muscle strength and health of Swiss populations in each age category for both children and adults. Furthermore, these future representative HGS norms for Swiss populations could prevent the development of muscular diseases (e.g. muscular dystrophy etc.) and thus actively contribute to the reduction of costs and overload of the health care system.



## Appendix A

# Review of the Hand Grip Strength Literature

In the subsequent pages, the details of the review of the literature of HGS are presented in tables.

<p>Grip strength reference values for Canadians aged 6 to 79: Canadian Health Measures Survey, 2007 to 2013 (Wong, Suzy L, 2016)</p>			<p>Handgrip strength and health in aging adults (McGrath et al., 2018)</p>	<p>Handgrip strength testing: a review of the literature (Immes, EV, 1999)</p>
What is measured	<ul style="list-style-type: none"> <li>- individual's grip strength measurements for right-hand and left-hand</li> </ul>	NA	<ul style="list-style-type: none"> <li>- review of the literature</li> </ul>	
How is it measured	<ul style="list-style-type: none"> <li>- twice on each hand, alternating</li> <li>- held in line with the forearm away from the body at the level of the thigh</li> </ul>	NA	<ul style="list-style-type: none"> <li>- many studies use standard testing position approved by American Society of Hand Therapist (ASHT)</li> <li>- sitting in a straight-backed chair with feet flat on the floor</li> <li>- common variation: standing, elbow extended rather than flexed to 90 degree</li> <li>- preferred to use the mean of three trials</li> <li>- other approaches were investigated one trial, two trial, etc.</li> <li>- all collected data had high test-retest reliability ICC &gt; .93</li> <li>- resting time 60 sec is not necessary; the differences in measurement are small</li> <li>- sample must be large, random and representative</li> <li>- normed groups for age and gender</li> </ul>	
Number of participants	<ul style="list-style-type: none"> <li>- 11'108 in total</li> <li>- 5'438 males and 5'670 females</li> </ul>	NA	<ul style="list-style-type: none"> <li>- this paper does not develop norms, but discuss the approach based on the computation of mean and standard deviation</li> <li>- split by gender and age group</li> </ul>	
How are norms established	<ul style="list-style-type: none"> <li>- quantile regression was used to develop reference equation for males and females</li> <li>- percentiles as a function of age, height and weight</li> </ul>	<ul style="list-style-type: none"> <li>- paper does not discuss any statistical method</li> </ul>	<ul style="list-style-type: none"> <li>- no statistical methods are applied for developing norms</li> <li>- mean and standard deviation are mentioned for the development</li> </ul>	
Which statistical method are applied	<ul style="list-style-type: none"> <li>- quantile regression/multiple regression</li> <li>- advantage of quantile regression it does not rely on distributional assumptions</li> </ul>	<ul style="list-style-type: none"> <li>- paper does not discuss any statistical method for establishing norms</li> </ul>		
How is age divided into categories	<ul style="list-style-type: none"> <li>- 6 to 11</li> <li>- 12 to 19</li> <li>- 20 to 39</li> <li>- 40 to 59</li> <li>- 60 to 79</li> </ul>	NA	NA	
How is strength development in people with increasing age	<ul style="list-style-type: none"> <li>- increases through childhood and adolescence</li> <li>- peak around age 40 to 44</li> <li>- afterwards decline: reference value higher for male than females</li> </ul>	<ul style="list-style-type: none"> <li>- declines in muscle mass and strength at approx. 4th decade of life</li> <li>- accelerate around 40 years of age</li> </ul>	NA	
Findings	<ul style="list-style-type: none"> <li>- difference between sexes were smaller during childhood than in adolescence and adulthood</li> <li>- right hand stronger than left hand</li> </ul>	<ul style="list-style-type: none"> <li>- article highlights evidence regarding handgrip strength and health</li> <li>- provide directions for future research</li> </ul>	<ul style="list-style-type: none"> <li>- very few subjects in each age/gender subgroup</li> <li>- no indication of what is an acceptable sample size</li> <li>- most sample sizes, when broken down into age and gender subgroups have 20-40 subjects</li> <li>- standing has been found to result in higher grip strengths than when sitting when using the same instrument</li> <li>- wrist position also affects grip strength, wrist flexion results in weaker grip strength than neutral or extended</li> <li>- participants fatigue is an issue when multiple maximum efforts are required in a short space of time</li> <li>- positive correlation between grip strength, bodyweight and height in healthy participants</li> <li>- there is disagreement regarding whether there is a consistent difference in grip strength between dominant and non-dominant hands</li> </ul>	

	Hand span influences optimal grip span in boys and girls aged 6 to 12 years (Romero et al., 2008)	Maximum grip strength in normal subjects from 20 to 64 years of age Hanten et al., 1999)	Hand Grip Strength: age and gender stratified normative data in a population-based study (Massy et al., 2011)
<b>What is measured</b>	<ul style="list-style-type: none"> <li>- determine if there is an optimal grip span for determining the max. handgrip strength in children from 6 to 12 and optimal grip span related to hand span</li> </ul>	<ul style="list-style-type: none"> <li>- alternating hand measure with 15 sec resting time and randomised start</li> </ul>	<ul style="list-style-type: none"> <li>- normative data, based on population</li> <li>- relationship between BMI and hand grip strength</li> </ul>
<b>How is it measured</b>	<ul style="list-style-type: none"> <li>- randomly tested on 10 occasions</li> <li>- using 5 different grip spans</li> <li>- allowing for 1 minute rest between</li> </ul>	NA	<ul style="list-style-type: none"> <li>- seated, elbow by their side</li> <li>- flexed to right angles</li> <li>- neutral wrist position</li> <li>- three measures</li> </ul>
<b>Number of participants</b>	<ul style="list-style-type: none"> <li>- 193 in total</li> <li>- 123 boys and 70 girls</li> </ul>	<ul style="list-style-type: none"> <li>- 1'182 in total</li> <li>- 553 males and 629 females</li> <li>- at least 49 individuals for each interval</li> </ul>	<ul style="list-style-type: none"> <li>- 2678 in total</li> <li>- 1366 males and 1312 females</li> <li>- recruited by telephone interviews</li> </ul>
<b>How are norms established</b>	<ul style="list-style-type: none"> <li>- does not focus on norms</li> <li>- investigate association between handspan and grip measure</li> </ul>	<ul style="list-style-type: none"> <li>- mean and standard deviation are used</li> <li>- splitted by gender and age category to establish norms</li> <li>- groups are at five-year intervals</li> </ul>	<ul style="list-style-type: none"> <li>- mean and standard deviation are used</li> <li>- splitted by gender and age category to establish norms</li> <li>- groups are at ten-year intervals</li> </ul>
<b>Which statistical method are applied</b>	<ul style="list-style-type: none"> <li>- hand span, grip strength and optimal grip span was obtained</li> <li>- for each hand span and gender by one-way ANOVA</li> </ul>	<ul style="list-style-type: none"> <li>- two parted t-test to determine dominant hand was stronger than non-dominant</li> <li>- two-way ANOVA to compare differences between GRIPs on right and left</li> </ul>	<ul style="list-style-type: none"> <li>- stratified by gender and age</li> </ul>
<b>How is age divided into categories</b>	NA	<ul style="list-style-type: none"> <li>- five year interval from age 20 to 64</li> </ul>	<ul style="list-style-type: none"> <li>- ten year interval from age 20 to 70</li> </ul>
<b>How is strength development in people with increasing age</b>	<ul style="list-style-type: none"> <li>- hand span and optimal grip span showed a significant linear association in children</li> </ul>	NA	NA
<b>Findings</b>	<ul style="list-style-type: none"> <li>- equation relating grip span as a function of hand span:</li> <li>- in boys is formulated as <math>y = x/4 + 0.44</math></li> <li>- in girls as <math>y = 0.3x - 0.52</math></li> <li>- x is the hand span (width between first and fifth fingers)</li> <li>- y is the optimal grip span</li> </ul>	<ul style="list-style-type: none"> <li>- combination of gender, handedness, age, and body height and/or weight explains only an additional 1% of the total variance in the GRIP</li> <li>- difficult to explain, why most left-handed are not stronger in their dominant hand</li> <li>- age has been reported as an important factor for grip strength in previous studies that showed a negative relationship between age and the grip strength for adults.</li> </ul>	<ul style="list-style-type: none"> <li>- higher hand grip strength was weakly related to higher BMI</li> <li>- for BMI smaller 30 and BMI higher 70 negatively related to higher BMI</li> </ul>

Grip and pinch strength: normative data for adults (Mathiowetz et al., 1985)			
Age- and gender-specific normative data of grip and pinch strength in a healthy adult Swiss population (Werte et al., 2009)			
The short-term reliability of grip strength measurement and the effects of posture and grip span (Watanabe et al., 2005)			
What is measured	NA	NA	- short-term reliability of grip strength measurement and the effects of posture and grip span
How is it measured	- seated, elbow flexed at 90 degree - three measures	- ASHT: seated, upright against the back of a chair shoulder adducted and neutrally rotated elbow flexed 90 degree	- measured twice, mean value was recorded - different approach one without resting and one with one min rest
Number of participants	- 628 in total - 310 males - 318 females	- 1023 in total	- 100 in total - 50 men - 50 women
How are norms established	- mean and standard deviation were calculated in each group splitted by gender and age category to establish norms - group are at 5-year intervals	- mean and standard deviation	does not focus on norms
Which statistical method are applied	mean and standard deviation	- paired t-test for dominant and non-dominant hand - ANOVA to detect differences between age groups, right and left hand	- does not focus on norms
How is age divided into categories	- five year interval of age from 20 to 75	- 15 age groups per gender of five year - 29 subjects in each category	NA
How is strength development in people with increasing age	- peak occurred in the age from 25 to 30 age group - grip strength of males improved in 14 to 24 year age groups - grip strength of women improved in 21 to 24 year age groups - relatively small difference between RH and LH	- peak between 30 and 35 year in men - peak between 40 in 44 in women	NA
Findings	- following recommendations are made: (1) standardized positioning (2) use average of three trials (3) calibration of the dynamometer (4) use same test instrument for pre- and post-testing	- curvilinear relation - repeated testing of grip strength showed a fatigue effect with a mean diff of 1.3 - 1.53 kg	- interval measurement with one minute - rest after each set

Differences in handgrip strength protocols to identify sarcopenia and frailty-a systematic review (Sousa-Santos et al., 2017)		Handgrip strength in old and oldest old Swiss adults-a cross-sectional study (Wearing et al., 2018)
<b>What is measured</b>	- systematic review  - AHST recommendation from 1981: measured seated with shoulders adducted, their elbows flexed to 90° and their forearms in neutral position using the Jamar dynamometer - jamar dynamometer presents high intra- and inter-individual reliability - most widely used - second handle position was the best position for the majority of the participants	- evaluate HGS in the Swiss-German population aged 75-99
<b>How is it measured</b>		- maximum values of the three trials was used
<b>Number of participants</b>	NA	- 244 in total - 88 men - 156 women
<b>How are norms established</b>	- statistical method for establishment of norms have not been compared by this review	- paper does not develop any norms
<b>Which statistical method are applied</b>	- statistical method for establishment of norms have not been compared by this review	- paper does not develop any norms
<b>How is age divided into categories</b>	NA	NA
<b>How is strength development in people with increasing age</b>	NA	- grip strength decrease with advancing age in both sexes - decline greater in men than women
<b>Findings</b>	- several factors have been shown to influence HGS values during measurement - influence of standing versus sitting posture: HGS values were evaluated, no significant differences were found by several studies - stronger grips strength measurement in the 90 degree elbow flexed position than in the fully extended position - encouragement and visual feedback had critical effects on HGS	- HGS was independently associated with age, height and ADL in men and women - men have significantly higher grip strength in all age groups than women



## Appendix B

# Computational Reproducibility

### B.1 Computational Details

This document was generated on Januar 26, 2023 at 10:24. R version and packages used to generate this report:

```
sessionInfo()

## R version 4.1.2 (2021-11-01)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib
##
## locale:
## [1] de_CH.UTF-8/de_CH.UTF-8/de_CH.UTF-8/C/de_CH.UTF-8/de_CH.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] lmerTest_3.1-3      lme4_1.1-27.1      Matrix_1.3-4
## [4] rstatix_0.7.0       BlandAltmanLeh_0.3.1 xtable_1.8-4
## [7] vtable_1.3.4        DescTools_0.99.45  ggpubr_0.4.0
## [10] kableExtra_1.3.4    forcats_0.5.1      stringr_1.4.0
## [13] dplyr_1.0.7         purrr_0.3.4        readr_2.1.2
## [16] tidyr_1.1.4         tibble_3.1.6       ggplot2_3.3.5
## [19] tidyverse_1.3.1     knitr_1.37
##
## loaded via a namespace (and not attached):
## [1] nlme_3.1-153        fs_1.5.2           lubridate_1.8.0
## [4] insight_0.18.6      webshot_0.5.2      httr_1.4.2
## [7] numDeriv_2016.8-1.1 tools_4.1.2        backports_1.4.1
## [10] sjlabelled_1.2.0    utf8_1.2.2         R6_2.5.1
## [13] DBI_1.1.2           colorspace_2.0-2   withr_2.5.0
## [16] gridExtra_2.3       tidyselect_1.1.2   Exact_3.1
## [19] compiler_4.1.2      cli_3.2.0          rvest_1.0.2
## [22] expm_0.999-6        xml2_1.3.3         labeling_0.4.2
## [25] scales_1.1.1        mvtnorm_1.1-3      proxy_0.4-26
## [28] systemfonts_1.0.4   digest_0.6.29      minqa_1.2.4
## [31] rmarkdown_2.11      svglite_2.1.0      pkgconfig_2.0.3
## [34] htmltools_0.5.2     dbplyr_2.1.1       fastmap_1.1.0
```

## [37] highr_0.9	rlang_1.0.2	readxl_1.3.1
## [40] rstudioapi_0.13	farver_2.1.0	generics_0.1.2
## [43] jsonlite_1.8.0	car_3.0-12	magrittr_2.0.3
## [46] Rcpp_1.0.8.3	munsell_0.5.0	fansi_1.0.2
## [49] abind_1.4-5	lifecycle_1.0.1	stringi_1.7.6
## [52] carData_3.0-5	MASS_7.3-54	rootSolve_1.8.2.3
## [55] grid_4.1.2	crayon_1.4.2	lmom_2.9
## [58] lattice_0.20-45	cowplot_1.1.1	haven_2.4.3
## [61] splines_4.1.2	hms_1.1.1	pillar_1.6.5
## [64] boot_1.3-28	gld_2.6.5	ggsignif_0.6.3
## [67] codetools_0.2-18	reprex_2.0.1	glue_1.6.2
## [70] evaluate_0.14	data.table_1.14.2	modelr_0.1.8
## [73] nloptr_2.0.0	vctrs_0.4.1	tzdb_0.2.0
## [76] cellranger_1.1.0	gtable_0.3.0	assertthat_0.2.1
## [79] xfun_0.29	broom_0.7.12	e1071_1.7-9
## [82] class_7.3-19	viridisLite_0.4.0	ellipsis_0.3.2



## B.2 R Code

### B.2.1 Main report file

#### Setup

```
# R Import data ####
#source("../code/01-DataPreparation.R")
#source("../code/02-DescriptiveStatistic.R")
#source("../code/03-00Dnorms.R")
source("../code/04-DataAnalysis.R") # Preparation for Data Analysis

# Libraries ####
require(xtable)          # to crate table with latex output
require(vtable)          # to crate summary table with latex output
# RQ1
require(BlandAltmanLeh) # Bland Altman

# RQ2
require(rstatix)          # Pipe-Friendly Framework for Basic Statistical Tests
require(lme4)             # Linear Mixed Model
require(lmerTest)         # provides p-values, anova and summary tables for lmer
```

Plot: HGS mean values with its sd from Werle et al. (2009)

```
# Plot 8: HGS values with its sd (Werle) ####

# mean HGS values from Werle with its sd values:

tmp <- dd_nms %>% filter(., category == "Men" | category == "Women")
# values taken from Werle and Canadian pater for children:
ggplot(data = tmp, aes(x = agecat, y = mean, ymin = mean - sd, ymax = mean + sd, col = category))+
  geom_pointrange()+
  #facet_wrap(~category, nrow = 2)+
  theme_pubclean()+
  xlab("Age category")+
  ylab("Normative grip strength (kg)")+
  scale_color_manual("category", values = c("Men" = "lightblue4", "Women" = "lightpink4"))+
  theme(legend.position = "none")+
  theme(axis.text = element_text(size = 8))

rm(list=c("tmp")) # remove tmp (temporary) dataset
```

Plot: Percentiles of HGS

```
# Plot 1: Percentile no Data ####

# Plot Percentiles using ggplot without data:
ggplot(data = dd_long_pct, aes(x = agecat, y = pct, color = pctcat,
                               group = pctcat))+
  #geom_point(size = .75, show.legend = T )+
  geom_line(show.legend = T)+
  ylim(0,70)+
  facet_wrap(~ category, scales = "free")+
  xlab("Age Category")+
  ylab("Handgrip Strength (kg)")+
  # Rename Legend and Axis:
  scale_color_manual("Quantile", values=c("indianred3","indianred2",
                                           "lightskyblue2","lightskyblue3","lightseagreen",
                                           "darkseagreen3","darkseagreen4"))+
  guides(linetype = "none")+
  theme_pubclean()+
```

```
theme(axis.text.x = element_text(angle = 0, vjust = 0.5, hjust=0.5),
      legend.text = element_text(size = 9),
      legend.key = element_rect(fill = "NA"))+
guides(colour = guide_legend(nrow = 1))
```

Plot: Percentiles of HGS with data

```
# Plot 2: Percentile with Data ####

# Plot Percentiles using ggplot with data:
ggplot()+
  # geom_point(data = dd_long_pct, aes(x = agecat, y = pct,
  #                                     color = pctcat, group = pctcat),
  #           size = 1.25, show.legend = FALSE, alpha = .02 )+
  geom_line(data = dd_long_pct, aes(x = agecat, y = pct, color = pctcat,
                                     group = pctcat), alpha = 0.5, show.legend = TRUE)+
  geom_jitter(data = dd_wide, aes(x = agecat, y = max),
             colour = "orange", size = 2.0, width = 0.15)+
  ylim(0,70)+
  facet_wrap(~ category, scales = "free")+
  xlab("Age Category")+
  ylab("Handgrip Strength (kg)")+
  # Rename Legend and Axis:
  scale_color_manual("Quantile", values=c("indianred3","indianred2","lightskyblue2",
                                           "lightskyblue3","lightseagreen","darkseagreen3",
                                           "darkseagreen4"))+

  theme_pubclean()+
  theme(axis.text.x = element_text(angle = 0, vjust = 0.5, hjust=0.5),
        legend.text = element_text(size = 9),
        legend.key = element_rect(fill = "NA"))+
  guides(linetype = "none",
        colour = guide_legend(nrow = 1))
```

Plot: Age Distribution

```
# Plot 3: Age Distribution ####
dd %>%
  ggplot(data = ., aes(x = agecat, fill = category))+
  geom_bar(position = "dodge", na.rm = TRUE)+
  geom_text(stat='count', aes(label=..count..), vjust=-1, cex = 2.5)+
  facet_wrap(category ~ ., scales = "free")+
  xlab("Age category")+
  ylab("Number of Participants")+
  ylim(0,15)+
  #scale_fill_grey()+
  scale_fill_manual("category", values = c("Boys" = "lightblue",
                                           "Girls" = "pink",
                                           "Men"="lightblue4",
                                           "Women"="lightpink4"))+

  theme_pubclean()+
  theme(legend.position = "none")+
  theme(axis.text.x = element_text(angle = 0, vjust = 0, hjust=0.5))+
  theme(axis.text = element_text(size = 8))
```

Table: Baseline characteristics and HGS measurment

```
# Table1: Baseline charact ####
table <- dd %>% dplyr::select(., Age, Height, Weight, Left_stand_0flex, Right_stand_0flex,
                             Left_stand_90flex, Right_stand_90flex, Left_sit_0flex, Right_sit_0flex,
                             Left_sit_90flex, Right_sit_90flex, category)

table$Height <- as.integer(table$Height)
```

```

table$Weight <- as.integer(table$Weight)

table.labs <- data.frame(var = c("Age", "Height", "Weight", "Left_stand_0flex",
                                "Right_stand_0flex", "Left_stand_90flex",
                                "Right_stand_90flex", "Left_sit_0flex", "Right_sit_0flex",
                                "Left_sit_90flex", "Right_sit_90flex", "category"),
                        labels = c("Age", "Height", "Weight", "Left, standing, 0 flex",
                                   "Right, standing, 0 flex", "Left, standing, 90 flex",
                                   "Right, standing, 90 flex", "Left, sitting, 0 flex",
                                   "Right, sitting, 0 flex", "Left, sitting, 90 flex",
                                   "Right, sitting, 90 flex", "Category"))

table1 <- sumtable(table,
  group = "category", group.test = FALSE, group.long = TRUE,
  title = "Physical characteristics and position preferences",
  anchor = "tab:table1",
  labels = table.labs,
  summ = c("mean(x)", "sd(x)", "min(x)",
            "pctile(x)[25]", "pctile(x)[50]", "pctile(x)[75]",
            "max(x)"),
  summ.names = c("Mean", "Std. Dev", "Min", "25%-Quantile", "50%-Quantile",
                 "75%-Quantile", "Max"),
  digits = 1, fixed.digits = TRUE,
  out = "csv")

colnames(table1) <- c("", "Mean", "SD", "Min", "$Q_{25}$", "$Q_{50}$",
"$Q_{75}$", "Max")

# add Sampe Size:
table1[1,1] <- paste0("Boys (n = ", sum(table$category == "Boys"), ")")
table1[14,1] <- paste0("Men (n = ", sum(table$category == "Men"), ")")
table1[27,1] <- paste0("Girls (n = ", sum(table$category == "Girls"), ")")
table1[40,1] <- paste0("Women (n = ", sum(table$category == "Women"), ")")

# Re-define label layout:
# Make header Bold:
bold <- function(x){
  paste("\bseries{" , x, "}", sep = "")
}

print(xtable(table1, align = "l|p{4cm}cccccc|"),
  hline.after=c(-1,1,12,14,25,27,38,40,51),
  include.rownames = FALSE, floating = FALSE,
  sanitize.colnames.function = bold,scalebox=0.80)

```

Table: Preferred position of the Jamar dynamometer by gender

```

# Table2: Preference Table ###
table <- dd %>% dplyr::select(., Preference, category)
table$Preference <- as.factor(table$Preference)
table$Preference <- factor(table$Preference,
  levels = c("Left, standing, 0 flex", "Right, standing, 0 flex",
            "Left, standing, 90 flex", "Right, standing, 90 flex",
            "Left, sitting, 0 flex", "Right, sitting, 0 flex",
            "Left, sitting, 90 flex", "Right, sitting, 90 flex"))

table.labs <- data.frame(var = c("Preference", "category"),
  labels = c("Preference", "Category"))

table2 <- sumtable(table,
  group = "category", group.test = FALSE, group.long = FALSE,
  title = "Position preferences of Jamar dynamometer",

```

```

    anchor = "tab:PreferenceTable",
    labels = table.labs,
    digits = 2, fixed.digits = TRUE,
    out = "csv")

bold <- function(x){
  paste("\\bfseries{" , x, "}", sep = "")
}

# Rename Header
colnames(table2) <- c("", "Boys", "", "Men", "", "Girls", "", "Women", "")
table2[1,] <-c(Variable = "", N = "n", Percent = "Percent",
  N = "n", Percent = "Percent", N = "n", Percent = "Percent", N = "n",
  Percent = "Percent")

print(xtable(table2, align = "l|p{4.5cm}cccccccc|"),
  hline.after=c(-1,1,10),
  include.rownames = FALSE, floating = FALSE,
  sanitize.colnames.function = bold,scalebox=0.90)

```

Table: Univariate comparison of the Jamar dynamometer position

```

# Table 3: Univariate Comp ####

# Create data with absolut number for each preferences:
flex0 <- nrow(filter(dd,grepl("0 flex",Preference))) -
  nrow(filter(dd, grepl("90 flex", Preference)))
flex90 <- nrow(filter(dd, grepl("90 flex", Preference)))
rHand <- nrow(filter(dd, grepl("Right", Preference)))
lHand <- nrow(filter(dd, grepl("Left", Preference)))
standing <- nrow(filter(dd, grepl("standing", Preference)))
sitting <- nrow(filter(dd, grepl("sitting", Preference)))

table_preference <- cbind(flex0, flex90, rHand, lHand, standing, sitting) %>%
  as.data.frame() %>%
  gather(key = "Position", value = "NoIndicaiton",
    flex0, flex90, rHand, lHand, standing, sitting)

# Calculate the proportions:
prop_0flex <- BinomCI(x = flex0,
  n = flex0 + flex90,
  conf.level = .95, method = "wilson") # Proportion for 0° flex
prop_90flex <- BinomCI(x = flex90,
  n = flex0 + flex90,
  conf.level = .95, method = "wilson") # Proportion for 90° flex

prop_rHand <- BinomCI(x = rHand,
  n = rHand + lHand,
  conf.level = .95, method = "wilson") # Proportion for Right hand
prop_lHand <- BinomCI(x = lHand,
  n = rHand + lHand,
  conf.level = .95, method = "wilson") # Proportion for Left hand

prop_standing <- BinomCI(x = standing,
  n = standing + sitting,
  conf.level = .95, method = "wilson") # Proportion for Standing

prop_sitting <- BinomCI(x = sitting,
  n = standing + sitting,
  conf.level = .95, method = "wilson") # Proportion for Sitting

```

```

# Porportion tablelle erstellen
# Var 1
Description <- c("0 flex vs. 90 flex",
                "Right vs. Left ",
                "Standing vs. Sitting")

# Var 2
n1 <- c(nrow(filter(dd,grepl("0 flex",Preference)))-nrow(filter(dd, grepl("90 flex", Preference))),
        nrow(filter(dd, grepl("Right", Preference))),
        nrow(filter(dd, grepl("standing", Preference)))
)

# Var 3
n2 <- c(nrow(filter(dd, grepl("90 flex", Preference))),
        nrow(filter(dd, grepl("Left", Preference))),
        nrow(filter(dd, grepl("sitting", Preference)))
)

absolut_prop <- c(paste(flex0,"/",flex90+flex0),
                  paste(rHand, "/", rHand+lHand),
                  paste(standing,"/", standing+sitting))

# DataFrame for the Table:
prop_table <- rbind(prop_0flex,prop_rHand,prop_standing) %>% as.data.frame() %>%
  cbind(Description,n1,n2, absolut_prop)

prop_table$est <- as.numeric(prop_table$est)
prop_table$lwr.ci <- as.numeric(prop_table$lwr.ci)
prop_table$upr.ci <- as.numeric(prop_table$upr.ci)

# rounding
prop_table <- prop_table %>%
  mutate_at(.vars = c("est", "lwr.ci", "upr.ci"),
            .funs = function(x){format(x = round(x,2))})

colnames(prop_table) <- c("Relative \nfreq. ", "CI lwr", "CI upr",
                          "Prop. of \nCond. 1 vs. Cond. 2", "Cond. 1", "Cond. 2", "Fraction")

# Reorder dataframe
prop_table <- prop_table[, c(4,5,6,7,1,2,3)]

table3 <- prop_table

bold <- function(x){paste0("\bseries{",{x},"")}}

print(xtable(table3,align = "l|p{6.0cm}p{1.5cm}p{1.5cm}p{1.7cm}p{1.7cm}p{1.0cm}p{1.0cm}|",
  floating = FALSE, include.rownames = FALSE,scalebox = 0.90, booktabs = FALSE,
  sanitize.colnames.function = bold, fixed = TRUE)

```

Table: Comparisons of relative frequencies for preference of Jamar dynamometer position

```

# Table 4: Multivariate Comp####
# Bivariat:

# a) standing 0 flex vs. sitting, 0 flex--> standing, 0 flex
# b) standing, 0 flex vs. standing, 90 flex --> standing, 0 flex
# c) standing, 0 flex vs. sitting, 90 flex --> standing, 0 flex
# d) standing 90 flex vs. sitting, 0 flex --> no sig. preference
# e) standing, 90 flex vs. sitting, 90 flex --> no sig. preference
# f) sitting, 0 flex vs sitting 90 flex --> no sig. preference

# standing, 0 flex vs. sitting, 0 flex
a <- BinomCI(x = nrow(filter(dd, grepl("standing, 0 flex", Preference))),

```

```

n = nrow(filter(dd, grepl("standing, 0 flex", Preference))) +
  nrow(filter(dd, grepl("sitting, 0 flex", Preference))),
method = "wilson")

# standing, 0 flex vs. standing, 90 flex
b <- BinomCI(x = nrow(filter(dd, grepl("standing, 0 flex", Preference))),
  n = nrow(filter(dd, grepl("standing, 0 flex", Preference))) +
    nrow(filter(dd, grepl("standing, 90 flex", Preference))),
method = "wilson")

# standing 0 flex vs sitting, 90 flex
c <- BinomCI(x = nrow(filter(dd, grepl("standing, 0 flex", Preference))),
  n = nrow(filter(dd, grepl("standing, 0 flex", Preference))) +
    nrow(filter(dd, grepl("sitting, 90 flex", Preference))),
method = "wilson")

# standing, 90 flex vs. sitting, 0 flex
d <- BinomCI(x = nrow(filter(dd, grepl("standing, 90 flex", Preference))),
  n = nrow(filter(dd, grepl("standing, 90 flex", Preference))) +
    nrow(filter(dd, grepl("sitting, 0 flex", Preference))),
method = "wilson")

# standing, 90 flex vs sitting, 90 flex
e <- BinomCI(x = nrow(filter(dd, grepl("standing, 90 flex", Preference))),
  n = nrow(filter(dd, grepl("sitting, 90 flex", Preference))) +
    nrow(filter(dd, grepl("standing, 90 flex", Preference))),
method = "wilson")

# sitting, 0 flex vs sitting, 90 flex
f <- BinomCI(x = nrow(filter(dd, grepl("sitting, 90 flex", Preference))),
  n = nrow(filter(dd, grepl("sitting, 90 flex", Preference))) +
    nrow(filter(dd, grepl("sitting, 0 flex", Preference))),
method = "wilson")

multi_pref <- rbind(a,b,c,d,e,f)
rm(a,b,c,d,e,f)

# Porportion table:
# Var 1
Description <- c("standing, 0 flex vs. sitting, 0 flex",
  "standing, 0 flex vs. standing, 90 flex",
  "standing, 0 flex vs sitting 90 flex",
  "standing, 90 flex vs sitting, 0 flex",
  "standing, 90 flex vs sitting, 90 flex",
  "sitting, 90 flex vs sitting, 0 flex")

# Var 2
n1 <- c(nrow(filter(dd, grepl("standing, 0 flex", Preference))),
  nrow(filter(dd, grepl("standing, 0 flex", Preference))),
  nrow(filter(dd, grepl("standing, 0 flex", Preference))),
  nrow(filter(dd, grepl("standing, 90 flex", Preference))),
  nrow(filter(dd, grepl("standing, 90 flex", Preference))),
  nrow(filter(dd, grepl("sitting, 90 flex", Preference)))
)

# Var 3
n2 <- c(nrow(filter(dd, grepl("sitting, 0 flex", Preference))),
  nrow(filter(dd, grepl("standing, 90 flex", Preference))),
  nrow(filter(dd, grepl("sitting, 90 flex", Preference))),
  nrow(filter(dd, grepl("sitting, 0 flex", Preference))),
  nrow(filter(dd, grepl("sitting, 90 flex", Preference))),
  nrow(filter(dd, grepl("sitting, 0 flex", Preference)))
)

```

```

absolut_prop <- c(paste(nrow(filter(dd, grepl("standing, 0 flex", Preference))),"/",
  nrow(filter(dd, grepl("standing, 0 flex", Preference)))+
  nrow(filter(dd, grepl("sitting, 0 flex", Preference)))),
  paste(nrow(filter(dd, grepl("standing, 0 flex", Preference))), "/",
  nrow(filter(dd, grepl("standing, 0 flex", Preference)))+
  nrow(filter(dd, grepl("standing, 90 flex", Preference)))),
  paste(nrow(filter(dd, grepl("standing, 0 flex", Preference))),"/",
  nrow(filter(dd, grepl("standing, 0 flex", Preference)))+
  nrow(filter(dd, grepl("sitting, 90 flex", Preference)))),
  paste(nrow(filter(dd, grepl("standing, 90 flex", Preference))),"/",
  nrow(filter(dd, grepl("standing, 90 flex", Preference)))+
  nrow(filter(dd, grepl("sitting, 0 flex", Preference)))),
  paste(nrow(filter(dd, grepl("standing, 90 flex", Preference))),"/",
  nrow(filter(dd, grepl("standing, 90 flex", Preference)))+
  nrow(filter(dd, grepl("sitting, 90 flex", Preference)))),
  paste(nrow(filter(dd, grepl("sitting, 90 flex", Preference))),"/",
  nrow(filter(dd, grepl("sitting, 90 flex", Preference)))+
  nrow(filter(dd, grepl("sitting, 0 flex", Preference))))
)

# DataFrame for the Table:
multi_pref <- multi_pref %>% as.data.frame() %>% cbind(Description,n1,n2, absolut_prop)

multi_pref$est <- as.numeric(multi_pref$est)
multi_pref$lwr.ci <- as.numeric(multi_pref$lwr.ci)
multi_pref$upr.ci <- as.numeric(multi_pref$upr.ci)

# rounding
multi_pref <- multi_pref %>%
  mutate_at(.vars = c("est", "lwr.ci", "upr.ci"),
    .funs = function(x){format(x = round(x,2))})

colnames(multi_pref) <- c("Relative freq.", "CI lwr", "CI upr",
  "Prop. of Cond. 1 vs. Cond. 2", "Cond. 1", "Cond. 2", "Fraction")

# Reorder dataframe
multi_pref <- multi_pref[, c(4,5,6,7,1,2,3)]

# HTML-Output:
# multi_pref %>%
#   kbl()%>%
#   kable_classic()%>%
#   kable_styling(bootstrap_options = c(),
#     full_width = TRUE,
#     position = "left",
#     font_size = 12)

# LaTeX-Output:
table4 <- multi_pref

bold <- function(x){paste0("\\bfseries{",{x},"}")}

print(xtable(table4,align = "l|p{6.0cm}p{1.5cm}p{1.5cm}p{1.7cm}p{1.7cm}p{1.0cm}p{1.0cm}|",
  floating = FALSE, include.rownames = FALSE,scalebox = 0.90, booktabs = FALSE,
  sanitize.colnames.function = bold, fixed = TRUE)

```

Preparation: Validation of Existing Swiss Norms for Adults

```
# >>> Preparation for RQ1: ####
# Validation of existing Swiss norms for adults

# Calculation of variables ####:

# SDS for max HGS:
dd_wide$maxSDS <- (dd_wide$max-dd_wide$mean)/dd_wide$sd

# SDS for mean HGS:
dd_wide$MeanHGS <- rowMeans(dd_wide[9:16]) # mean HGS of each participant
dd_wide$meanSDS <- (dd_wide$MeanHGS-dd_wide$mean)/dd_wide$sd

# SDS for median HGS:
dd_wide <- dd_wide %>%
  rowwise() %>%
  mutate(
    medianHGS = median(c(Left_stand_0flex, Right_stand_0flex,
                        Left_stand_90flex, Right_stand_90flex,
                        Left_sit_0flex, Right_sit_0flex,
                        Left_sit_90flex, Right_sit_90flex)
  ))
dd_wide$medianSDS <- (dd_wide$medianHGS-dd_wide$mean)/dd_wide$sd
# rowwise function changes the datatype, therefore set back to dataframe:
dd_wide <- data.frame(dd_wide)
```

Plot: Bland Altman

```
# Plot 5: Bland Altman ####

ba <- select(dd_long, ID, Description, order_ordinal, Position, HGS, mean, agecat, category)
ba <- ba %>% filter(., category == "Men" | category == "Women")
ba$diff <- ba$HGS-ba$mean # diff (Bias)
ba$avg <- (ba$HGS+ba$mean)/2 # average

# bland.altman.plot(group1 = ba$HGS, group2 = ba$mean, two = 1.96, mode = 1,
#                   graph.sys = "base", conf.int = 0.95, geom_count = FALSE)

ba.m <- ba %>% filter(., category == "Men")
bland.altman.stats.men <- bland.altman.stats(group1 = ba.m$HGS, group2 = ba.m$mean, two = 1.96)
ba.w <- ba %>% filter(., category == "Women")
bland.altman.stats.women <- bland.altman.stats(group1 = ba.w$HGS, group2 = ba.w$mean, two = 1.96)

ggarrange(
  ggplot(data = ba.m, aes(x=avg, y = diff, color = category))+
    geom_point()+
    facet_wrap( ~ Position ,
               # labeller = labeller(Position = label_wrap_gen(
               #   width = 5, multi_line = TRUE)),
               ncol = 4 )+
    theme_pubclean(base_size = 10)+
    theme(legend.position = "none")+
    xlab("Average of HGS and Norm HGS (kg)")+
    ylab("Difference: HGS - Norm HGS (kg)")+
    scale_color_manual("", values = c("Men"="lightblue4",
                                      "Women"="lightpink4"))+

  # bias with its CI
  geom_hline(yintercept = bland.altman.stats.men$CI.lines["mean.diff.ci.lower"],
             linetype = "dotted")+
  geom_hline(yintercept = bland.altman.stats.men$mean.diffs, linetype = "solid",
             color = "black", size = 0.5)+
  geom_hline(yintercept = bland.altman.stats.men$CI.lines["mean.diff.ci.upper"],
             linetype = "dotted")+

```



```

# LoA with its CI
geom_hline(yintercept = bland.altman.stats.men$CI.lines["lower.limit.ci.lower"],
  linetype = "dotted")+
geom_hline(yintercept = bland.altman.stats.men$lower.limit, linetype = "dashed",
  color = "black", size = 0.5)+
geom_hline(yintercept = bland.altman.stats.men$CI.lines["lower.limit.ci.upper"],
  linetype = "dotted")+
geom_hline(yintercept = bland.altman.stats.men$CI.lines["upper.limit.ci.lower"],
  linetype = "dotted")+
geom_hline(yintercept = bland.altman.stats.men$upper.limit, linetype = "dashed",
  color = "black", size = 0.5)+
geom_hline(yintercept = bland.altman.stats.men$CI.lines["upper.limit.ci.upper"],
  linetype = "dotted"),

ggplot(data = ba.w, aes(x=avg,y = diff, color = category))+
  geom_point()+
  facet_wrap( ~ Position ,
    # labeller = labeller(Position = label_wrap_gen(
    #   width = 5, multi_line = TRUE)),
    ncol = 4 )+
  theme_pubclean(base_size = 10)+
  theme(legend.position = "none")+
  xlab("Average of Norm and Norm HGS (kg)")+
  ylab("Difference: HGS - Norm HGS (kg)")+
  scale_color_manual("", values = c("Men"="lightblue4",
    "Women"="lightpink4")))+

# bias with its CI
geom_hline(yintercept = bland.altman.stats.women$CI.lines["mean.diff.ci.lower"],
  linetype = "dotted")+
geom_hline(yintercept = bland.altman.stats.women$mean.diffs, linetype = "solid",
  color = "black", size = 0.5)+
geom_hline(yintercept = bland.altman.stats.women$CI.lines["mean.diff.ci.upper"],
  linetype = "dotted")+

# LoA with its CI lwr
geom_hline(yintercept = bland.altman.stats.women$CI.lines["lower.limit.ci.lower"],
  linetype = "dotted")+
geom_hline(yintercept = bland.altman.stats.women$lower.limit, linetype = "dashed",
  color = "black", size = 0.5)+
geom_hline(yintercept = bland.altman.stats.women$CI.lines["lower.limit.ci.upper"],
  linetype = "dotted")+

# LoA with its CI upr
geom_hline(yintercept = bland.altman.stats.women$CI.lines["upper.limit.ci.lower"],
  linetype = "dotted")+
geom_hline(yintercept = bland.altman.stats.women$upper.limit, linetype = "dashed",
  color = "black", size = 0.5)+
geom_hline(yintercept = bland.altman.stats.women$CI.lines["upper.limit.ci.upper"],
  linetype = "dotted"),
  nrow = 2, common.legend = TRUE
)

rm(list=c("ba", "ba.m", "ba.w"))

```

Table: Analysis of SDS: One-sample T statistics for men

```

# Table 5: Validation norms for Men ####

# filter temporary (tmp) data with only men
tmp <- dd_wide %>% dplyr::select(category, Left_stand_0flex_std,
  Right_stand_0flex_std, Left_stand_90flex_std,
  Right_stand_90flex_std, Left_sit_0flex_std,
  Right_sit_0flex_std, Left_sit_90flex_std,
  Right_sit_90flex_std, maxSDS, meanSDS, medianSDS ) %>%
  filter(category == "Men")

```

```

# Conducting t Test for each position:
a <- t.test(x = tmp["Left_stand_0flex_std"], alternative = "two.sided")
b <- t.test(x = tmp["Right_stand_0flex_std"], alternative = "two.sided")
c <- t.test(x = tmp["Left_stand_90flex_std"], alternative = "two.sided")
d <- t.test(x = tmp["Right_stand_90flex_std"], alternative = "two.sided")
e <- t.test(x = tmp["Left_sit_0flex_std"], alternative = "two.sided")
f <- t.test(x = tmp["Right_sit_0flex_std"], alternative = "two.sided")
g <- t.test(x = tmp["Left_sit_90flex_std"], alternative = "two.sided")
h <- t.test(x = tmp["Right_sit_90flex_std"], alternative = "two.sided")
i <- t.test(x = tmp["maxSDS"], alternative = "two.sided")
j <- t.test(x = tmp["meanSDS"], alternative = "two.sided")
k <- t.test(x = tmp["medianSDS"], alternative = "two.sided")

# Generate DataFrame with the results of the tests:
table <- data.frame(rbind(unlist(a), unlist(b), unlist(c), unlist(d), unlist(e),
                          unlist(f), unlist(g), unlist(h), unlist(i), unlist(j), unlist(k)))

ttest <- table %>% select(., data.name, statistic.t, parameter.df, estimate.mean.of.x, stderr, conf.int1, conf.

# change variable to numeric variables:
for(i in 2:8){
  ttest[,i] <- as.numeric(ttest[,i])
}

# Caclulation of SD = SE*sqrt(n):=> stderr*sqrt(df+1)
ttest$SD <- ttest$stderr*sqrt(ttest$parameter.df+1)

# Round p-value
ttest$p.value.rounded <- sapply(ttest[,8], round.pValue)

# Rename Col.names
colnames(ttest) <- c(paste0("Men (n =", nrow(filter(dd_wide, category == "Men")), ")"),
                    "T statistic",
                    "df",
                    "Mean",
                    "SE",
                    "CI lwr",
                    "CI upr",
                    "p-value",
                    "SD",
                    "p-value (rounded)")

# Rename Positions:
ttest[,1] <- c("Left, standing, 0 flex",
              "Right, standing, 0 flex",
              "Left, standing, 90 flex",
              "Right, standing, 90 flex",
              "Left, sitting, 0 flex",
              "Right, sitting, 0 flex",
              "Left, sitting, 90 flex",
              "Right, sitting, 90 flex",
              "maximal HGS",
              "mean HGS",
              "median HGS")

# formate p-value to scientific notation:
ttest$p-value` <- format(signif(as.numeric(ttest$p-value`), 3), scientific = TRUE)

# HTML-Output:
# validationM <- kable(ttest,
#                       caption = (""),

```

```
#           digits = c(0,2,2,2,2,2,2,3,2,2))%>%
#   kable_classic_2()
#
# validationM

# LaTeX-Output:
# for presentation only: ttest[,c(1,4,9,6,7,10)]
table5 <- ttest[,c(1,2,3,4,9,6,7,10)]
table5$df <- as.integer(table5$df)
colnames(table5)[8] <- "p-value"

bold <- function(x){paste0("\\bfseries{",{x},"")}}

print(xtable(table5,
  align = "l|p{4.5cm}p{2.0cm}p{1.0cm}p{1.5cm}p{1.0cm}p{1.0cm}p{1.0cm}p{2.0cm}|",
  hline.after = c(-1,0,8,11),
  floating = FALSE, include.rownames = FALSE,scalebox = 0.85, booktabs = FALSE,
  sanitize.colnames.function = bold, fixed = TRUE)

rm(list=c("tmp"))
```

Table: Analysis of SDS: One-sample T statistics for women

```
# Table 6: Validation norms for Women ####

# Filter temporary (tmp) data with only women
tmp <- dd_wide %>% dplyr::select(category,Left_stand_0flex_std,
  Right_stand_0flex_std, Left_stand_90flex_std,
  Right_stand_90flex_std, Left_sit_0flex_std,
  Right_sit_0flex_std, Left_sit_90flex_std,
  Right_sit_90flex_std,maxSDS, meanSDS, medianSDS ) %>%
  filter(category == "Women")

# Conducting t Test for each position:
a <- t.test(x = tmp["Left_stand_0flex_std"], alternative = "two.sided")
b <- t.test(x = tmp["Right_stand_0flex_std"], alternative = "two.sided")
c <- t.test(x = tmp["Left_stand_90flex_std"], alternative = "two.sided")
d <- t.test(x = tmp["Right_stand_90flex_std"], alternative = "two.sided")
e <- t.test(x = tmp["Left_sit_0flex_std"], alternative = "two.sided")
f <- t.test(x = tmp["Right_sit_0flex_std"], alternative = "two.sided")
g <- t.test(x = tmp["Left_sit_90flex_std"], alternative = "two.sided")
h <- t.test(x = tmp["Right_sit_90flex_std"], alternative = "two.sided")
i <- t.test(x = tmp["maxSDS"], alternative = "two.sided")
j <- t.test(x = tmp["meanSDS"], alternative = "two.sided")
k <- t.test(x = tmp["medianSDS"], alternative = "two.sided")

# Generate DataFrame with the results of the tests:
table <- data.frame(rbind(unlist(a), unlist(b), unlist(c), unlist(d), unlist(e),
  unlist(f), unlist(g), unlist(h), unlist(i), unlist(j), unlist(k)))

ttest <- table %>%select(., data.name,statistic.t, parameter.df,
  estimate.mean.of.x, stderr,conf.int1, conf.int2, p.value)

# Change variable to numeric variables:
for(i in 2:8){
  ttest[,i] <- as.numeric(ttest[,i])
}

# Calculation of SD = SE*sqrt(n):=> stderr*sqrt(df+1)
ttest$SD <- ttest$stderr*sqrt(ttest$parameter.df+1)

# Round p-value
```

```

ttest$p.value.rounded <- sapply(ttest[,8], round.pValue)

# Rename Col.names
colnames(ttest) <- c(paste0("Women (n =", nrow(filter(dd_wide, category == "Women")), ")"),
  "T statistic",
  "df",
  "Mean",
  "SE",
  "CI lwr",
  "CI upr",
  "p-value",
  "SD",
  "p-value (rounded)")

# Rename Positions:
ttest[,1] <- c("Left, standing, 0 flex",
  "Right, standing, 0 flex",
  "Left, standing, 90 flex",
  "Right, standing, 90 flex",
  "Left, sitting, 0 flex",
  "Right, sitting, 0 flex",
  "Left, sitting, 90 flex",
  "Right, sitting, 90 flex",
  "maximal HGS",
  "mean HGS",
  "median HGS")

# formate p-value to scientific notation:
ttest$p-value` <- format(signif(as.numeric(ttest$p-value`),3), scientific = TRUE)

# HTML-Output:
# validationF <- kable(ttest, caption = (""), digits = c(0,2,2,2,2,2,2,3,2,2))%>%
#   kable_classic_2()
#
# validationF

# LaTeX-Output:
# for presentation only: ttest[,c(1,4,9,6,7,10)]
table6 <- ttest[,c(1,2,3,4,9,6,7,10)]
table6$df <- as.integer(table6$df)
colnames(table6)[8] <- "p-value"

bold <- function(x){paste0("\\bfseries{", {x}, "}")}

print(xtable(table6,
  align = "l|p{4.5cm}p{2.0cm}p{1.0cm}p{1.5cm}p{1.0cm}p{1.0cm}p{1.0cm}p{2.0cm}|"),
  hline.after = c(-1,0,8,11),
  floating = FALSE, include.rownames = FALSE, scalebox = .85, booktabs = FALSE,
  sanitize.colnames.function = bold, fixed = TRUE)

rm(list=c("tmp"))

```

Plot: Distribution SDS of the HGS

```

# Plot 4: HGS Distribution ###

# We are looking only for Men and Women:
tmpW <- dd_long %>%
  filter(., category == c("Women"))%>%
  group_by(category, Position) %>%
  summarise("mean" = mean(HGS_std),
    "sd" = sd(HGS_std),

```

```

"lwr" = mean(HGS_std)-(qnorm(p = .975, mean = 0, sd = 1)*sd(HGS_std)/sqrt(length(HGS_std))),
"upr" = mean(HGS_std)+(qnorm(p = .975, mean = 0, sd = 1)*sd(HGS_std)/sqrt(length(HGS_std))),
"mu" = 0)

tmpM <- dd_long %>%
  filter(., category == c("Men"))%>%
  group_by(category,Position) %>%
  summarise("mean" = mean(HGS_std),
    "sd" = sd(HGS_std),
    "lwr" = mean(HGS_std)-(qnorm(p = .975, mean = 0, sd = 1)*sd(HGS_std)/sqrt(length(HGS_std))),
    "upr" = mean(HGS_std)+(qnorm(p = .975, mean = 0, sd = 1)*sd(HGS_std)/sqrt(length(HGS_std))),
    "mu" = 0)

tmp <- rbind(tmpW,tmpM)
rm(list=c("tmpW","tmpM"))

tmp <- gather(tmp, key = "Measure", value = "value","mean", "lwr","upr", "mu")

ggplot()+
  geom_histogram(data = filter(dd_long,category == c("Men", "Women")),
    aes(x = HGS_std, y = ..density.., fill = category),
    binwidth = 0.6, alpha = 0.5, color = "black")+
  geom_density(data = filter(dd_long,category == c("Men", "Women")),
    aes(x = HGS_std, fill = category),
    alpha = 0.25)+
  facet_grid(Position ~ category,
    labeller = labeller(Position = label_wrap_gen(width = 10, multi_line = TRUE)))+
  #theme(strip.text.x = element_text(size = 8))+
  geom_vline(data = tmp,
    aes(xintercept = value,linetype = factor(Measure),
      col = factor(Measure)))+
  scale_fill_manual("", values = c("Boys" = "lightblue",
    "Girls" = "pink",
    "Men"="lightblue4",
    "Women"="lightpink4"))+
  scale_linetype_manual("", values = c(2,3,1,2),
    labels = c("95%-CI lwr",
      "Sample mean",
      "Theoretical mean",
      "95%-CI upr"))+
  scale_color_manual(values = c("black","black","darkred","black"))+
  theme(legend.position = "top", legend.key = element_rect(fill = "NA"))+
  labs(linetype = "")+
  xlab("SDS of HGS")+
  ylab("Density")+
  #xlim(-2.5,2.5)+
  guides(fill = "none", color = "none", linetype = "none")+
  theme_pubclean()

# scale_linetype_manual("", values = c(2,1,3,2),
#   labels = c("95%-CI lwr", expression(bar(x)),
#     expression(mu), "95%-CI upr"))

rm(list=c("tmp"))

```

Plot: maximal, mean and median SDS of HGS

```

# Plot 8: maximal, mean and median SDS of HGS ###

dd_wide <- data.frame(dd_wide)
tmpM <- dplyr::filter(dd_wide, dd_wide$category == "Men")
tmpW <- dplyr::filter(dd_wide, dd_wide$category == "Women")

```

```

# Visualisation of SDS of HGS for max, mean and median:

# SDS max HGS:
Vis.maxSDS.M <- ggplot(data = tmpM, aes(x = maxSDS, fill = category))+
  geom_histogram(aes(y = ..density..), bins = 25, color = "black")+
  geom_vline(xintercept = 0, lty = "dotted")+
  stat_function(fun = dnorm, args = list(mean = mean(tmpM$maxSDS), sd = sd(tmpM$maxSDS)),
    fill = tmpM$category, size = 0.25)+
  facet_grid(~category)+
  xlim(-3,3)+
  ylim(0,0.7)+
  theme_pubclean()+
  xlab("SDS of maximal HGS")+
  ylab("density")+
  scale_fill_manual("", values = c("Men" = "lightblue4", "Women" = "lightpink4"))+
  theme(legend.position = "none")

Vis.maxSDS.W <- ggplot(data = tmpW, aes(x = maxSDS, fill = category))+
  geom_histogram(aes(y = ..density..), bins = 25, color = "black")+
  geom_vline(xintercept = 0, lty = "dotted")+
  stat_function(fun = dnorm, args = list(mean = mean(tmpW$maxSDS), sd = sd(tmpW$maxSDS)),
    fill = tmpW$category, size = 0.25)+
  facet_grid(~category)+
  xlim(-3,3)+
  ylim(0,0.7)+
  theme_pubclean()+
  xlab("SDS of maximal HGS")+
  ylab("density")+
  scale_fill_manual("", values = c("Men" = "lightblue4", "Women" = "lightpink4"))+
  theme(legend.position = "none")

# SDS mean HGS:
Vis.meanSDS.M <- ggplot(data = tmpM, aes(x = meanSDS, fill = category))+
  geom_histogram(aes(y = ..density..), bins = 25, color = "black")+
  geom_vline(xintercept = 0, lty = "dotted")+
  stat_function(fun = dnorm, args = list(mean = mean(tmpM$meanSDS), sd = sd(tmpM$meanSDS)),
    fill = tmpM$category, size = 0.25)+
  facet_grid(~category)+
  xlim(-3,3)+
  ylim(0,0.7)+
  theme_pubclean()+
  xlab("SDS of mean HGS")+
  ylab("density")+
  scale_fill_manual("", values = c("Men" = "lightblue4", "Women" = "lightpink4"))+
  theme(legend.position = "none")

Vis.meanSDS.W <- ggplot(data = tmpW, aes(x = meanSDS, fill = category))+
  geom_histogram(aes(y = ..density..), bins = 25, color = "black")+
  geom_vline(xintercept = 0, lty = "dotted")+
  stat_function(fun = dnorm, args = list(mean = mean(tmpW$meanSDS), sd = sd(tmpW$meanSDS)),
    fill = tmpW$category, size = 0.25)+
  facet_grid(~category)+
  xlim(-3,3)+
  ylim(0,0.7)+
  theme_pubclean()+
  xlab("SDS of mean HGS")+
  ylab("density")+
  scale_fill_manual("", values = c("Men" = "lightblue4", "Women" = "lightpink4"))+
  theme(legend.position = "none")

# SDS median HGS:
Vis.medianSDS.M <- ggplot(data = tmpM, aes(x = medianSDS, fill = category))+
  geom_histogram(aes(y = ..density..), bins = 25, color = "black")+

```

```

geom_vline(xintercept = 0, lty = "dotted")+
stat_function(fun = dnorm, args = list(mean = mean(tmpM$medianSDS), sd = sd(tmpM$medianSDS)),
              fill = tmpM$category, size = 0.25)+
facet_grid(~category)+
xlim(-3,3)+
ylim(0,0.7)+
theme_pubclean()+
xlab("SDS of median HGS")+
ylab("density")+
scale_fill_manual("", values = c("Men" = "lightblue4", "Women" = "lightpink4"))+
theme(legend.position = "none")

Vis.medianSDS.W <- ggplot(data = tmpW, aes(x = medianSDS, fill = category))+
  geom_histogram(aes(y = ..density..), bins = 25, color = "black")+
  geom_vline(xintercept = 0, lty = "dotted")+
  stat_function(fun = dnorm, args = list(mean = mean(tmpW$medianSDS), sd = sd(tmpW$medianSDS)),
              fill = tmpW$category, size = 0.25)+
  facet_grid(~category)+
  xlim(-3,3)+
  ylim(0,0.7)+
  theme_pubclean()+
  xlab("SDS of median HGS")+
  ylab("density")+
  scale_fill_manual("", values = c("Men" = "lightblue4", "Women" = "lightpink4"))+
  theme(legend.position = "none")

ggarrange(Vis.maxSDS.M, Vis.maxSDS.W,
          Vis.meanSDS.M, Vis.meanSDS.W,
          Vis.medianSDS.M, Vis.medianSDS.W,
          ncol = 2, nrow = 3)

```

Table: Comparison up to 50 and over 60 for men

```

# Table 13: Comparison up to 50 and over 60 for Men ###

# One-sample t-Test for 18-59yr.:
# Men for mean and median
M.under60 <- tmpM %>% filter(., Age < 60)
a <- t.test(x = M.under60$meanSDS, alternative = "two.sided")
b <- t.test(x = M.under60$medianSDS, alternative = "two.sided")

# One-sample t-Test for over59yr.:
# Men for mean and median
M.over59 <- tmpM %>% filter(., Age > 59)
c <- t.test(x = M.over59$meanSDS, alternative = "two.sided")
d <- t.test(x = M.over59$medianSDS, alternative = "two.sided")

# Generate DataFrame with the results of the tests:
table <- data.frame(rbind(unlist(a), unlist(b), unlist(c), unlist(d)))

# add sample size as column:
df.n <- data.frame(n = c(nrow(M.under60), nrow(M.under60), nrow(M.over59), nrow(M.over59)),
                  data.name = c("M.under60$meanSDS", "M.under60$medianSDS", "M.over59$meanSDS",
                                "M.over59$medianSDS"))

table <- left_join(table, df.n, by = "data.name")

ttest <- table %>% select(., data.name, n, statistic.t, parameter.df,
                        estimate.mean.of.x, stderr, conf.int1, conf.int2, p.value)

# Change variable to numeric variables:
for(i in 3:9){

```

```

ttest[,i] <- as.numeric(ttest[,i])
}

# Calculation of SD = SE*sqrt(n):=> stderr*sqrt(df+1)
ttest$SD <- ttest$stderr*sqrt(ttest$parameter.df+1)

# Round p-value
ttest$p.value.rounded <- sapply(ttest$p.value, round.pValue)

# Rename Col.names
colnames(ttest) <- c("Men",
                    "n",
                    "T statistic",
                    "df",
                    "Mean",
                    "SE",
                    "CI lwr",
                    "CI upr",
                    "p-value",
                    "SD",
                    "p-value (rounded)")

# Rename Positions:
ttest[,1] <- c("mean HGS for age < 60y", "median HGS for age < 60y",
              "mean HGS for age 60y+", "median HGS for age 60y+")

# formate p-value to scientific notation:
ttest$p-value <- format(signif(as.numeric(ttest$p-value),3), scientific = TRUE)

# HTML-Output:
# validation <- kable(ttest, caption = (""), digits = c(0,2,2,2,2,2,2,3,2,2))%>%
#   kable_classic_2()
#
# validation

# LaTeX-Output:
# for presentation only: ttest[,c(1,4,9,6,7,10)]
table13 <- ttest[,c(1,2,3,4,5,10,7,8,11)]
table13$df <- as.integer(table13$df)
colnames(table13)[9] <- "p-value"

bold <- function(x){paste0("\\bfseries{",x,"}")}

print(xtable(table13,
              align = "l|p{5.5cm}p{1.0cm}p{2.0cm}p{1.0cm}p{1.5cm}p{1.0cm}p{1.0cm}p{1.0cm}p{1.5cm}|",
              hline.after = c(-1,0,2,4),
              floating = FALSE, include.rownames = FALSE, scalebox = .85, booktabs = FALSE,
              sanitize.colnames.function = bold, fixed = TRUE))

```

Table: Comparison up to 50 and over 60 for women

```

# Table 14: Comparison up to 50 and over 60 for Women ###

# One-sample t-Test for 18-59yr.:
# Women for mean and median
W.under60 <- tmpW %>% filter(., Age < 60)
a <- t.test(x = W.under60$meanSDS, alternative = "two.sided")
b <- t.test(x = W.under60$medianSDS, alternative = "two.sided")

# One-sample t-Test for over59yr.:
W.over59 <- tmpW %>% filter(., Age > 59)
c <- t.test(x = W.over59$meanSDS, alternative = "two.sided")
d <- t.test(x = W.over59$medianSDS, alternative = "two.sided")

```



```

# Generate DataFrame with the results of the tests:
table <- data.frame(rbind(unlist(a), unlist(b), unlist(c), unlist(d)))

# add sample size as column:
df.n <- data.frame(n = c(nrow(W.under60),nrow(W.under60),nrow(W.over59),nrow(W.over59)),
  data.name = c("W.under60$meanSDS", "W.under60$medianSDS", "W.over59$meanSDS",
"W.over59$medianSDS"))

table <- left_join(table, df.n, by = "data.name")

ttest <- table %>%select(., data.name, n, statistic.t, parameter.df,
  estimate.mean.of.x, stderr,conf.int1, conf.int2, p.value)

# Change variable to numeric variables:
for(i in 3:9){
ttest[,i] <- as.numeric(ttest[,i])
}

# Calculation of SD = SE*sqrt(n):=> stderr*sqrt(df+1)
ttest$SD <- ttest$stderr*sqrt(ttest$parameter.df+1)

# Round p-value
ttest$p.value.rounded <- sapply(ttest$p.value, round.pValue)

# Rename Col.names
colnames(ttest) <- c("Women",
  "n",
  "T statistic",
  "df",
  "Mean",
  "SE",
  "CI lwr",
  "CI upr",
  "p-value",
  "SD",
  "p-value (rounded)")

# Rename Positions:
ttest[,1] <- c("mean HGS for age < 60y", "median HGS for age < 60y",
  "mean HGS for age 60y+", "median HGS for age 60y+")

# formate p-value to scientific notation:
ttest$p-value <- format(signif(as.numeric(ttest$p-value`),3), scientific = TRUE)

# #HTML-Output:
# validation <- kable(ttest, caption = (""), digits = c(0,2,2,2,2,2,2,3,2,2))%>%
#   kable_classic_2()
#
# validation

# LaTeX-Output:
table14 <- ttest[,c(1,2,3,4,5,10,7,8,11)]
table14$df <- as.integer(table14$df)
colnames(table14)[9] <- "p-value"

bold <- function(x){paste0("\bseries{",{x},"")}}

print(xtable(table14,
  align = "l|p{5.5cm}p{1.0cm}p{2.0cm}p{1.0cm}p{1.5cm}p{1.0cm}p{1.0cm}p{1.0cm}p{1.5cm}|",
  hline.after = c(-1,0,2,4),
  floating = FALSE, include.rownames = FALSE,scalebox = .85, booktabs = FALSE,
  sanitize.colnames.function = bold, fixed = TRUE)

```

Plot: Comparison up to 50 and over 60

```
# Plot 9: Comparison up to 50 and over 60 ####

ggarrange(
  # Men under 60
  ggplot(data = M.under60,
    aes(x = medianSDS, fill = category)) +
    geom_histogram(aes(y = ..density..),
      bins = 25, color = "black") +
    geom_vline(xintercept = 0, lty = "dotted") +
    stat_function(fun = dnorm,
      args = list(mean = mean(tmpW$medianSDS),
        sd = sd(tmpW$medianSDS)),
      fill = tmpW$category, size = 0.25) +
    facet_grid(~category) +
    xlim(-3, 3) +
    ylim(0, 0.7) +
    theme_pubclean() +
    xlab("SDS of median HGS") +
    ylab("density") +
    scale_fill_manual("", values = c("Men" = "lightblue4",
      "Women" = "lightpink4")) +
    theme(legend.position = "none"),

  # Women under 60
  ggplot(data = W.under60, aes(x = medianSDS, fill = category)) +
    geom_histogram(aes(y = ..density..),
      bins = 25, color = "black") +
    geom_vline(xintercept = 0, lty = "dotted") +
    stat_function(fun = dnorm, args = list(mean = mean(tmpW$medianSDS),
      sd = sd(tmpW$medianSDS)),
      fill = tmpW$category, size = 0.25) +
    facet_grid(~category) +
    xlim(-3, 3) +
    ylim(0, 0.7) +
    theme_pubclean() +
    xlab("SDS of median HGS") +
    ylab("density") +
    scale_fill_manual("", values = c("Men" = "lightblue4",
      "Women" = "lightpink4")) +
    theme(legend.position = "none"),

  # Age category over 59
  # Median :
  # Men over 59
  ggplot(data = M.over59, aes(x = medianSDS, fill = category)) +
    geom_histogram(aes(y = ..density..),
      bins = 25, color = "black") +
    geom_vline(xintercept = 0, lty = "dotted") +
    stat_function(fun = dnorm, args = list(mean = mean(tmpW$medianSDS),
      sd = sd(tmpW$medianSDS)),
      fill = tmpW$category, size = 0.25) +
    facet_grid(~category) +
    xlim(-3, 3) +
    ylim(0, 0.7) +
    theme_pubclean() +
    xlab("SDS of median HGS") +
    ylab("density") +
    scale_fill_manual("", values = c("Men" = "lightblue4",
      "Women" = "lightpink4")) +
    theme(legend.position = "none"),
```

```

# Women over 59
ggplot(data = W.over59, aes(x = medianSDS, fill = category))+
  geom_histogram(aes(y = ..density..),
    bins = 25, color = "black")+
  geom_vline(xintercept = 0, lty = "dotted")+
  stat_function(fun = dnorm, args = list(mean = mean(tmpW$medianSDS),
    sd = sd(tmpW$medianSDS)),
    fill = tmpW$category, size = 0.25)+
  facet_grid(~category)+
  xlim(-3,3)+
  ylim(0,0.7)+
  theme_pubclean()+
  xlab("SDS of median HGS")+
  ylab("density")+
  scale_fill_manual("", values = c("Men" = "lightblue4", "Women" = "lightpink4"))+
  theme(legend.position = "none"),

labels = c("A", "B", "C", "D")

)

```

Preparation: Assessment Whether Handgrip Strength Values Are Stable Independent of the Posture-Elbow-Position

```

# >>> Preparation for RQ2 ####

# Filter the necessary Information for the Analysis
tmp <- dd_long %>% filter(category == "Men" | category == "Women")
tmpM <- dd_long %>% filter(category == "Men")
tmpW <- dd_long %>% filter(category == "Women")

```

Plot: Boxplot SDS of HGS, for men and women

```

# Plot 7: BoxPlot: SDS of HGS ####
res.aov.M1 <- anova_test(data = tmpM, dv = HGS_std, wid = ID, within = Position, effect.size = "ges", detailed = TRUE)
res.aov.W1 <- anova_test(data = tmpW, dv = HGS_std, wid = ID, within = Position, detailed = TRUE)

pwcM <- tmpM %>%
  pairwise_t_test(HGS_std ~ Position, paired = TRUE, p.adjust.method = "bonferroni")
pwcW <- tmpW %>%
  pairwise_t_test(HGS_std ~ Position, paired = TRUE, p.adjust.method = "bonferroni")

# Visualization
bxpM <- ggplot(data = tmpM, aes(x = Position, y = HGS_std))+
  geom_violin(fill = "lightblue4")+
  geom_boxplot(outlier.colour = NA, fill = "lightblue4")+
  geom_jitter(width = 0.15, size = 0.25)+
  geom_hline(yintercept = 0, lty = "dashed")+
  geom_path(data = filter(tmpM, ID == 44)[c(5,6,7,8,1,4,3,2),],
    aes(x = Position, y = HGS_std, group = ID, col = "Participant: ID44"))+
  scale_color_manual("", values = c("turquoise3"))+
  # geom_point(data = filter(tmpM, ID == 44)[c(5,6,7,8,1,2,3,2),],
  #   aes(x = Position, y = HGS_std, col = "blue"), size = 0.25)+
  facet_wrap(~category)+
  xlab("Measuring Position")+
  ylab("SDS of HGS")+
  #scale_fill_manual("category", values = c("Men" = "lightblue4"))+
  theme_pubclean()+
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))+
  theme(axis.text = element_text(size = 8))

bxpW <- ggplot(data = tmpW, aes(x = Position, y = HGS_std))+

```

```

geom_violin(fill = "lightpink4")+
geom_boxplot(outlier.colour = NA, fill = "lightpink4")+
geom_jitter(width = 0.15, size = 0.25)+
geom_hline(yintercept = 0, lty = "dashed")+
geom_path(data = filter(tmpW, ID == 71)[c(7,8,1,2,3,6,5,4),],
          aes(x = Position, y = HGS_std, group = ID, col = "Participant: ID71"))+
scale_color_manual("", values = c("sienna3"))+
#geom_point(data = filter(tmpW, ID == 71)[c(7,8,1,2,3,6,5,4),],
#           aes(x = Position, y = HGS_std, col = "orange"), size = 0.25)+
facet_wrap(~category)+
xlab("Measuring Position")+
ylab("SDS of HGS")+
#scale_fill_manual("category", values = c("Women" = "lightpink4"))+
theme_pubclean()+
theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))+
theme(axis.text = element_text(size = 8))

pwcM <- pwcM %>% add_xy_position(x = "Position")
pwcW <- pwcW %>% add_xy_position(x = "Position")

ggarrange(
  bxpM +
    #ylim(-5,5)+
    stat_pvalue_manual(filter(pwcM, p.adj.signif != "ns"),
                      label = "p.adj.signif")+
    labs(subtitle = get_test_label(res.aov.M1, detailed = TRUE),
         caption = get_pwc_label(pwcM)),

  bxpW +
    #ylim(-5,5)+
    stat_pvalue_manual(filter(pwcW, p.adj.signif != "ns"),
                      label = "p.adj.signif")+
    labs(subtitle = get_test_label(res.aov.W1, detailed = TRUE),
         caption = get_pwc_label(pwcW)),
  ncol = 2, legend = "top")

```

Table: Test for normality according to Shapiro-Wilk for the SDS of the men's HGS data

```

# Table 7: Shapiro-Wilk-Men####
table7 <- tmpM %>%
  group_by(Position) %>%
  shapiro_test(HGS_std) %>%
  mutate(Statistic = round(statistic,2)) %>%
  mutate("p-value" = lapply(p,round.pValue)) %>%
  select(., Position, Statistic, "p-value")
# table7 <- tmpM %>%
#   group_by(Position) %>%
#   shapiro_test(HGS_std) %>%
#   mutate(Statistic = round(statistic,2)) %>%
#   mutate("p-value" = round(p,2)) %>%
#   select(., Position, Statistic, "p-value")

#HTML-Output:
# table7 %>% kable() %>% kable_classic(full_width = FALSE, position = "float_left") %>%
#   footnote(general = " Shapiro-Wilk Test: SDS of HGS data of Men")

# LaTeX-Output:

#table6 <- ttest[,c(1,2,3,4,9,6,7,10)]

bold <- function(x){paste0("\\bfseries{",{x},"")}}

print(xtable(table7,align = "r|lrr|"),

```

```

floating = FALSE,
include.rownames = FALSE,
sanitize.colnames.function = bold,
booktabs = FALSE,
fixed = TRUE)
# hline.after = c(-1,0,8),
# floating = FALSE, include.rownames = FALSE, scalebox = .85, booktabs = FALSE,
# sanitize.colnames.function = bold, fixed = TRUE))

```

Table: Test for normality according to Shapiro-Wilk for the SDS of the women's HGS data

```

# Table 8: Shapiro-Wilk-Women ####
table8 <- tmpW %>%
  group_by(Position) %>%
  shapiro_test(HGS_std) %>%
  mutate(Statistic = round(statistic,2)) %>%
  mutate("p-value" = lapply(p,round.pValue)) %>%
  select(., Position, Statistic, "p-value")

#HTML-Output:
# table8 %>% kable() %>% kable_classic(full_width = FALSE, position = "float_left") %>%
# footnote(general = " Shapiro-Wilk Test: SDS of HGS data of Women")

# LaTeX-Output:

bold <- function(x){paste0("\\bfseries{",{x},"")}}

print(xtable(table8,align = "r|lrr|"),
      floating = FALSE,
      include.rownames = FALSE,
      sanitize.colnames.function = bold,
      booktabs = FALSE,
      fixed = TRUE)
# #align = "l|p{4.5cm}p{2.0cm}p{1.0cm}p{1.5cm}p{1.0cm}p{1.0cm}p{1.0cm}p{2.0cm}|",
# hline.after = c(-1,0,8),
# floating = FALSE, include.rownames = FALSE, scalebox = .85, booktabs = FALSE)

```

Plot: QQ-Plot with reference line

```

# Plot 6: QQ-Plot ####

ggplot(tmp, aes(sample = HGS_std, color = category))+
  facet_wrap(~Position)+
  geom_qq()+
  geom_qq_line(position = "identity")+
  theme_pubclean()+
  xlab("Theoretical")+
  ylab("Sample")+
  theme(legend.position = "top", legend.key = element_rect(fill = "NA"))+
  scale_color_manual("", values = c("Men"="lightblue4",
                                     "Women"="lightpink4"))

```

Table: Adjusted rmANOVA summary table for men using Greenhouse-Geisser correction

```

# Table 9: rmANOVA-Men ####

# dv:      dependent variable
# wid:     case/sample identifier
# within:  within-subjects factor/grouping variable
# effect.size = "ges" (generalized eta squared), "pes" (partial eta squared)

```

```

# If the test is significant than at least on position is different:

# Men

# ANOVA Table (type III tests)
res.aov.M1 <- anova_test(data = tmpM, dv = HGS_std, wid = ID, within = Position, effect.size = "ges", detailed = TRUE)

MauchlyTestM <- res.aov.M1$`Mauchly's Test for Sphericity`
SphericityCorrectionsM <- res.aov.M1$`Sphericity Corrections`

aovTable.M1 <- get_anova_table(res.aov.M1, correction = "GG")
aovTable.M1 <- aovTable.M1[, -c(8)]

# Rounding p-Value (if desired)
aovTable.M1$p <- lapply(aovTable.M1$p, round.pValue)

# Change Colnames:
colnames(aovTable.M1) <- c("Effect", "DFn", "DFd", "SSn", "SSd", "F", "p-value", "ges")

# Convert Data-structure
aovTable.M1$DFn <- round(as.numeric(aovTable.M1$DFn), 2)
aovTable.M1$DFd <- round(as.numeric(aovTable.M1$DFd), 2)

#aovTable.M1$p-value <- format(aovTable.M1$p-value, scientific = TRUE)

# # HTML Output:
# aovTable.M1 %>% kable() %>% kable_classic(full_width = FALSE, position = "float_left") %>%
# footnote(general = " rmANOVA table for Men")

# LaTeX-Output:
bold <- function(x){paste0("\\bfseries{", {x}, "}")}

print(xtable(aovTable.M1, align = "r|lrrrrrrr|"),
      floating = FALSE,
      include.rownames = FALSE,
      sanitize.colnames.function = bold,
      booktabs = FALSE,
      fixed = TRUE)
# #align = "l|p{4.5cm}p{2.0cm}p{1.0cm}p{1.5cm}p{1.0cm}p{1.0cm}p{1.0cm}p{2.0cm}|",
# #hline.after = c(-1, 0, 8),
# #floating = FALSE, include.rownames = FALSE, scalebox = .85, booktabs = FALSE)

```

Table: Adjuststed rmANOVA summary table for women using Greenhouse-Geisser correction

```

# Table 10: rmANOVA-Women ####

# dv:      dependent variable
# wid:     case/sample identifier
# within:  within-subjects factor/grouping variable
# effect.size = "ges" (generalized eta squared), "pes" (partial eta squared)

# If the test is significant than at least on position is different:

# ANOVA Table (type III tests)
res.aov.W1 <- anova_test(data = tmpW, dv = HGS_std, wid = ID, within = Position, detailed = TRUE)

MauchlyTestW <- res.aov.W1$`Mauchly's Test for Sphericity`
SphericityCorrectionsW <- res.aov.W1$`Sphericity Corrections`

aovTable.W1 <- get_anova_table(res.aov.W1, correction = "GG")
aovTable.W1 <- aovTable.W1[, -c(8)]

```

```

# Rounding p-Value
aovTable.W1$p <- lapply(aovTable.W1$p, round.pValue)

# Change Colnames:
colnames(aovTable.W1) <- c("Effect", "DFn", "DFd", "SSn", "SSd", "F", "p-value", "ges")

# Convert Data-structure
aovTable.W1$DFn <- round(as.numeric(aovTable.W1$DFn), 2)
aovTable.W1$DFd <- round(as.numeric(aovTable.W1$DFd), 2)
# aovTable.W1$p-value` <- format(aovTable.W1$p-value`, scientific = TRUE)

# # HTML Output:
# aovTable.W1 %>% kable() %>% kable_classic(full_width = FALSE, position = "left") %>%
# footnote(general = " rmANOVA table for Women")

# LaTeX-Output:
bold <- function(x){paste0("\\bfseries{", {x}, "}")}

print(xtable(aovTable.W1, align = "r|lrrrrrrr|",
  floating = FALSE,
  include.rownames = FALSE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE)
  # #align = "l|p{4.5cm}p{2.0cm}p{1.0cm}p{1.5cm}p{1.0cm}p{1.0cm}p{1.0cm}p{2.0cm}|",
  # hline.after = c(-1, 0, 8),
  # floating = FALSE, include.rownames = FALSE, scalebox = .85, booktabs = FALSE)

```

Table: Post-hoc comparison of the posture-elbow position for men

```

# Table 11: postHoc-Men ###
# pairwise Comparison :
pwcM <- tmpM %>%
  pairwise_t_test(HGS_std ~ Position, paired = TRUE, p.adjust.method = "bonferroni")

pwcM <- pwcM %>% select(., -c(.y., n1, n2))

# # HTML Output:

# pwcM %>%
# kable %>% kable_classic(full_width = FALSE, position = "float_left", font_size = 11) %>%
# footnote(general = "post-hoc analysis for men")

# LaTeX-Output:

colnames(pwcM) <- c("Position 1", "Position 2",
  "Statistic", "df", "p-value",
  "p-value \\ (adj.)",
  "p-value adj. \\ (signif.)")

pwcM$df <- as.integer(pwcM$df)
pwcM$p-value` <- sapply(pwcM$p-value`, round.pValue)
pwcM <- pwcM[, -c(7)]

bold <- function(x){paste0("\\bfseries{", {x}, "}")}

print(xtable(pwcM, align = "r|p{4.0cm}p{4.0cm}p{1.5cm}p{1cm}p{2cm}p{2cm}|",
  floating = FALSE,
  include.rownames = FALSE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,

```

```

fixed = TRUE,
scalebox = .65)
# #align = "l|p{4.5cm}p{2.0cm}p{1.0cm}p{1.5cm}p{1.0cm}p{1.0cm}p{1.0cm}p{2.0cm}|",
# #hline.after = c(-1,0,8),
# #floating = FALSE, include.rownames = FALSE, scalebox = .85, booktabs = FALSE)

```

Table: Post-hoc comparison of the posture-elbow position for women

```

# Table 12: postHoc-Women ####
# pairwise Comparison for Women:
pwcW <- tmpW %>%
  pairwise_t_test(HGS_std ~ Position, paired = TRUE, p.adjust.method = "bonferroni")

pwcW <- pwcW %>% select(., -c(.y., n1,n2))

# # HTML Output:

# pwcW %>%
#   kable %>% kable_classic(full_width = FALSE, position = "float_left", font_size = 11) %>%
#   footnote(general = "post-hoc analysis for men")

# LaTeX-Output:

colnames(pwcW) <- c("Position 1", "Position 2",
  "Statistic", "df", "p-value",
  "p-value \\ (adj.)",
  "p-value adj. \\ (signif.)")

pwcW$df <- as.integer(pwcW$df)
pwcW$p-value` <- sapply(pwcW$p-value`, round.pValue)
pwcW<- pwcW[,-c(7)]

bold <- function(x){paste0("\\bfseries{",{x},"")}}

print(xtable(pwcW,align = "r|p{4.0cm}p{4.0cm}p{1.5cm}p{1cm}p{2cm}p{2cm}|",
  floating = FALSE,
  include.rownames = FALSE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE,
  scalebox = .65)

```

Table: Analysis of SDS of HGS with two predictors (Position4 and Right-hand) for men

```

# Table: 28 ANOVA Handedness Men ####

tmpM <- dd_long %>% filter(category == "Men")

# Create new variable:
# Position4: Considering the Postion:
#   sitting, standing 90/0 without right and Left
# rechts: indicating which hand was used

tmpM$Position4 <- rep(0,length(tmpM$agecat)) # empty var.
tmpM$rechts <- tmpM$Position4 # empty var.

# indicate right or left
tmpM$rechts[grepl("Right", tmpM$Position)] <- 1
# indicate positions:
tmpM$Position4[grepl("standing, 0 flex", tmpM$Position)] <- 1
tmpM$Position4[grepl("standing, 90 flex", tmpM$Position)] <- 2
tmpM$Position4[grepl("sitting, 0 flex", tmpM$Position)] <- 3
tmpM$Position4[grepl("sitting, 90 flex", tmpM$Position)] <- 4

```



```

#neu
tmpM$Position4 <- factor(tmpM$Position4,
  levels = c("1","2","3","4"),
  labels = c("standing, 0 flex",
             "standing, 90 flex",
             "sitting, 0 flex",
             "sitting, 90 flex"))

tmpM$rechts <- factor(tmpM$rechts,
  levels = c("0","1"),
  labels = c("left-hand","right-hand"))

# Two-way ANOVA test
res.aov.M3 <- anova_test(HGS_std ~ Position4 + rechts,
  data = tmpM, effect.size = "ges", detailed = TRUE)

aovTable.M3 <- get_anova_table(res.aov.M3)
aovTable.M3 <- aovTable.M3[,-c(8)]

# Rounding p-value
aovTable.M3$p <- sapply(aovTable.M3$p, round.pValue)

# Change colnames:
colnames(aovTable.M3) <- c("Effect", "SSn", "SSd",
  "DFn", "DFd", "F", "p-value", "ges")

# Change rownames:
aovTable.M3$Effect[1] <- "Position4"
aovTable.M3$Effect[2] <- "Right-hand"

# Convert Data structure:
aovTable.M3$DFn <- as.integer(aovTable.M3$DFn)
aovTable.M3$DFd <- as.integer(aovTable.M3$DFd)

# Latex-Output:
bold <- function(x){paste0("\\bfseries{",{x},"}")}

#reorder
aovTable.M3 <- as.data.frame(aovTable.M3)
aovTable.M3 <- aovTable.M3[,c(1,4,5,2,3,6,7,8)]

print(xtable(aovTable.M3,align = "r|lrrrrrlr|"),
  floating = FALSE,
  include.rownames = FALSE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE)

```

Table: Analysis of SDS of HGS with two predictors (Position4 and Right-hand) for women

```

# Table: 29 ANOVA Handedness Women ####

tmpW <- dd_long %>% filter(category == "Women")

# Create new variable:
# Position4: Considering the Postion:
#   sitting, standing 90/0 without right and Left
# rechts: indicating which hand was used

tmpW$Position4 <- rep(0,length(tmpW$agecat)) # empty var.
tmpW$rechts <- tmpW$Position4 # empty var.

```

```

# indicate right or left
tmpW$rechts[grepl("Right", tmpW$Position)] <- 1
# indicate positions:
tmpW$Position4[grepl("standing, 0 flex", tmpW$Position)] <- 1
tmpW$Position4[grepl("standing, 90 flex", tmpW$Position)] <- 2
tmpW$Position4[grepl("sitting, 0 flex", tmpW$Position)] <- 3
tmpW$Position4[grepl("sitting, 90 flex", tmpW$Position)] <- 4

#neu
tmpW$Position4 <- factor(tmpW$Position4,
  levels = c("1", "2", "3", "4"),
  labels = c("standing, 0 flex",
    "standing, 90 flex",
    "sitting, 0 flex",
    "sitting, 90 flex"))

tmpW$rechts <- factor(tmpW$rechts,
  levels = c("0", "1"),
  labels = c("left-hand", "right-hand"))

# Two-way ANOVA test
res.aov.W3 <- anova_test(HGS_std ~ Position4 + rechts, data = tmpW, effect.size = "ges", detailed = TRUE)

aovTable.W3 <- get_anova_table(res.aov.W3)
aovTable.W3 <- aovTable.W3[, -c(8)]

# Rounding p-value
aovTable.W3$p <- sapply(aovTable.W3$p, round.pValue)

# Change colnames:
colnames(aovTable.W3) <- c("Effect", "SSn", "SSd",
  "DFn", "DFd", "F", "p-value", "ges")

# Change rownames:
aovTable.W3$Effect[1] <- "Position4"
aovTable.W3$Effect[2] <- "Right-hand"

# Convert Data structure:
aovTable.W3$DFn <- as.integer(aovTable.W3$DFn)
aovTable.W3$DFd <- as.integer(aovTable.W3$DFd)

# Latex-Output:
bold <- function(x){paste0("\\bfseries{", {x}, "}")}

#reorder
aovTable.W3 <- as.data.frame(aovTable.W3)
aovTable.W3 <- aovTable.W3[-c(3),] #rm intercation
aovTable.W3 <- aovTable.W3[, c(1, 4, 5, 2, 3, 6, 7, 8)]

print(xtable(aovTable.W3, align = "r|lrrrrrlr|"),
  floating = FALSE,
  include.rownames = FALSE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE)

```

Plot: Pattern of SDS of HGS obtained with Jamar dynamometer with respect to sequence of measurement

# Plot 10: Pattern Fatigue Measurement ####

ggarrange(

```

ggplot(data = tmpM, aes(x = as.factor(order_ordinal), y = HGS_std))+
  geom_point()+
  geom_path(data = filter(tmpM, ID == 44),
            aes(x = order_ordinal,
                y = HGS_std,
                group = ID,
                col = "Participant: ID44"))+
  scale_color_manual("", values = c("turquoise3"))+
  xlab("Sequence of measurment")+
  ylab("SDS of HGS")+
  scale_x_discrete(label = c(
    "Pos 1", "Pos 2", "Pos 3",
    "Pos 4", "Pos 5", "Pos 6",
    "Pos 7", "Pos 8"))+
  theme_pubclean(),

# Visualisation
ggplot(data = tmpW, aes(x = as.factor(order_ordinal), y = HGS_std))+
  geom_point()+
  geom_path(data = filter(tmpW, ID == 71),
            aes(x = order_ordinal,
                y = HGS_std, group = ID,
                col = "Participant: ID71"))+
  scale_color_manual("", values = c("sienna3"))+
  xlab("Sequence of measurment")+
  ylab("SDS of HGS")+
  scale_x_discrete(label = c(
    "Pos 1", "Pos 2", "Pos 3",
    "Pos 4", "Pos 5", "Pos 6",
    "Pos 7", "Pos 8"))+
  theme_pubclean(),
  nrow = 1, labels = c("A", "B")
# A: Men, B: Women
)

```

Table: Linear mixed-effects model, association between SDS of HGS and sequence of measurment in men

```

# Table 15: MixedModel-Men ###
# Mixed effect Model for men:
modMidexMod.M <- lmer(HGS_std ~ order_ordinal + (1|ID),
                      data = tmpM,
                      REML = FALSE)
SummaryMixedMod.M <- summary(modMidexMod.M)

table.mixedmod.M <- as.data.frame(SummaryMixedMod.M$coefficients) # Fixed effects
# HTML table:
# table.mixedmod.M %>% kable() %>% kable_classic()

# LaTeX table:

colnames(table.mixedmod.M) <- c("Estimate", "SE", "df", "t value", "Pr(>|t|)")
rownames(table.mixedmod.M) <- c("(Intercept)", "Sequence of measurement")

# Round p-values
table.mixedmod.M$df <- as.integer(table.mixedmod.M$df)

table.mixedmod.M[,5] <- sapply(table.mixedmod.M[,5], round.pValue)

bold <- function(x){paste0("\\bfseries{",x,"}")}

```

```
print(xtable(table.mixedmod.M,align = "|lp{1.5cm}p{1.cm}p{1.cm}p{1.5cm}p{1.5cm}|"),
      floating = FALSE,
      include.rownames = TRUE,
      sanitize.colnames.function = bold,
      booktabs = FALSE,
      fixed = TRUE,
      scalebox = .85)
```

Table: Linear mixed-effects model, association between SDS of HGS and sequence of measurment in women

```
# Table 16: MixedModel-Women ####
# Mixed effect Model for men:
modMidexMod.W <- lmer(HGS_std ~ order_ordinal + (1|ID),
                     data = tmpW,
                     REML = FALSE)
SummaryMixedMod.W <- summary(modMidexMod.W)

table.mixedmod.W <- as.data.frame(SummaryMixedMod.W$coefficients) # Fixed effects
# HTML table:
# table.mixedmod.W %>% kable() %>% kable_classic()
# LaTeX table:

colnames(table.mixedmod.W) <- c("Estimate", "SE", "df", "t value", "Pr(>|t|)")
rownames(table.mixedmod.W) <- c("(Intercept)", "Sequence of measurement")

# Round p-values
table.mixedmod.W$df <- as.integer(table.mixedmod.W$df)
table.mixedmod.W[,5] <- sapply(table.mixedmod.W[,5], round.pValue)

bold <- function(x){paste0("\\bfseries{",x,"}")}

print(xtable(table.mixedmod.W,align = "|lp{1.5cm}p{1.cm}p{1.cm}p{1.5cm}p{1.5cm}|"),
      floating = FALSE,
      include.rownames = TRUE,
      sanitize.colnames.function = bold,
      booktabs = FALSE,
      fixed = TRUE,
      scalebox = .85)
```

#### Preparation: Exploring Associations

```
# >>> Preparation RQ6 ####

tmp <- dd_long %>% filter(category == "Men" | category == "Women")

# remove participants which did not indicate their preferences:
tmp <- na.omit(tmp)

# Check if Position match with the indicated preference
tmp$PosMatchWithPref <- tmp$Preference == tmp$Position
tmp$PosMatchWithPref <- as.factor(tmp$PosMatchWithPref)

# Contains all the measurement without filtering for only the max HGS:
# used vor the visualisation
tmp.allHGS <- tmp
tmp.allHGS.m <- filter(tmp.allHGS, category == "Men")
tmp.allHGS.w <- filter(tmp.allHGS, category == "Women")

# Filter all the position where the max HGS were achieved:
tmp <- tmp %>% dplyr::group_by(.,ID) %>% filter(., HGS == max(HGS))
```

```
# Separate men and women:
tmpM <- tmp %>% filter(category == "Men")
tmpW <- tmp %>% filter(category == "Women")
```

Plot: Pattern between position preferred and SDS of HGS

```
# Plot 11: Association Position-SDS.HGS ####

ggarrange(
  ggplot(data = tmp.allHGS.m, aes(x = PosMatchWithPref, y = HGS_std))+
    geom_point()+
    geom_point(data = filter(tmp.allHGS.m, ID == 44),
      aes(x = PosMatchWithPref,
        y = HGS_std,
        col = "Participant: ID44"),
      #width = 0.03, height = 0.0,
      size = 2)+
    scale_colour_manual("", values = c("lightblue4"))+
    xlab("Preferred Position")+
    ylab("SDS of HGS")+
    ylim(-4,4)+
    theme_pubclean(),

  ggplot(data = tmp.allHGS.w, aes(x = PosMatchWithPref, y = HGS_std))+
    geom_point()+
    geom_point(data = filter(tmp.allHGS.w, ID == 71),
      aes(x = PosMatchWithPref,
        y = HGS_std,
        col = "Participant: ID71"),
      #width = 0.03, height = 0.0,
      size = 2)+
    scale_colour_manual("", values = c("lightpink4"))+
    xlab("Preferred Position")+
    ylab("SDS of HGS")+
    ylim(-4,4)+
    theme_pubclean(),
  labels = c("A", "B")
)
```

Table: Linear mixed-effects Model, Association between SDS of HGS with sequence of measurement and preferred position in men

```
# Table 17: MixedModel-Men ####

# Mixed effect Model for men:
modMidexMod.M <- lmer(HGS_std ~ order_ordinal + PosMatchWithPref + (1|ID),
  data = tmp.allHGS.m,
  REML = FALSE)
SummaryMixedMod.M <- summary(modMidexMod.M)

table.mixedmod.M <- as.data.frame(SummaryMixedMod.M$coefficients) # Fixed effects
# HTML table:
# table.mixedmod.M %>% kable() %>% kable_classic()

# LaTeX table:

colnames(table.mixedmod.M) <- c("Estimate", "SE", "df", "t value", "Pr(>|t|)")
rownames(table.mixedmod.M) <- c("(Intercept)", "Sequence of easurement", "Preferred position")

# Round p-values
table.mixedmod.M$df <- as.integer(table.mixedmod.M$df)
table.mixedmod.M[,5] <- sapply(table.mixedmod.M[,5], round.pValue)
```

```
bold <- function(x){paste0("\\bfseries{",{x},"")}}

print(xtable(table.mixedmod.M,align = "|lp{1.5cm}p{1.cm}p{1.cm}p{1.5cm}p{1.5cm}|",
  floating = FALSE,
  include.rownames = TRUE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE,
  scalebox = .85)
```

Table: Linear mixed-effects Model, Association between SDS of HGS with sequence of measurement and preferred position in women

```
# Table 18: MixedModel-Women ####

# Mixed effect Model for Women:
modMidexMod.W <- lmer(HGS_std ~ order_ordinal + PosMatchWithPref + (1|ID),
  data = tmp.allHGS.w,
  REML = FALSE)
SummaryMixedMod.W <- summary(modMidexMod.W)

SummaryMixedMod.W <- as.data.frame(SummaryMixedMod.W$coefficients) # Fixed effects
# HTML table:
# table.mixedmod.M %>% kable() %>% kable_classic()

# LaTeX table:

colnames(SummaryMixedMod.W) <- c("Estimate", "SE", "df", "t value", "Pr(>|t|)")
rownames(SummaryMixedMod.W) <- c("(Intercept)", "Sequence of measurement",
  "Preferred position")

# Round p-values
SummaryMixedMod.W$df <- as.integer(SummaryMixedMod.W$df)
SummaryMixedMod.W[,5] <- sapply(SummaryMixedMod.W[,5], round.pValue)

bold <- function(x){paste0("\\bfseries{",{x},"")}}

print(xtable(SummaryMixedMod.W,align = "|lp{1.5cm}p{1.cm}p{1.cm}p{1.5cm}p{1.5cm}|",
  floating = FALSE,
  include.rownames = TRUE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE,
  scalebox = .85)
```

Plot: Association between preferred position and max HGS

```
# Plot 12: Association Position-maxHGS ####

ggarrange(
  ggplot(data = tmpM,
    aes(x = PosMatchWithPref, y = max))+
    geom_point()+
    geom_point(data = filter(tmpM, ID == 44),
      aes(x = PosMatchWithPref,
        y = max,
        col = "Participant: ID44"),
      size = 2)+
    #geom_text(stat='count', aes(label=..count..), vjust=-1)+
    scale_colour_manual("", values = c("lightblue4"))+
    xlab("Preferred Position")+
```

```

    ylab("max HGS (kg)")+
    ylim(20,70)+
    theme_pubclean(),

ggplot(data = tmpW,
       aes(x = PosMatchWithPref, y = max))+
geom_point()+
geom_point(data = filter(tmpW, ID == 71),
          aes(x = PosMatchWithPref,
              y = max,
              col = "Participant: ID71"),
          size = 2)+
scale_colour_manual("", values = c("lightpink4"))+
xlab("Preferred Position")+
ylab("max HGS (kg)")+
ylim(20,70)+
theme_pubclean(),
labels = c("A", "B")
)

```

Table: Two sample t-test: Association between position preferred and max HGS for men and women

```

# Table 21: Two sample t-test - maxHGS with position preferred ####

# Convert data type:
# for men:
tmpM$PosMatchWithPref <- factor(tmpM$PosMatchWithPref,
                                levels = c("FALSE", "TRUE"),
                                labels = c(0,1))

# for women:
tmpW$PosMatchWithPref <- factor(tmpW$PosMatchWithPref,
                                levels = c("FALSE", "TRUE"),
                                labels = c(0,1))

a <- t.test(max ~ PosMatchWithPref, data = tmpM)
a$data.name <- "Men"

b <- t.test(max ~ PosMatchWithPref, data = tmpW)
b$data.name <- "Women"

# Generatate DataFrame
table <- data.frame(rbind(unlist(a), unlist(b)))

# add sample size as columns:
df.n <- data.frame(n = c(nrow(tmpM), nrow(tmpW)),
                   data.name = c("Men", "Women"))

table <- left_join(table, df.n, by = "data.name")

# calculation of SD:
table$SD <- as.numeric(table$stderr) * sqrt(as.numeric(table$n))

tab <- table %>% select(., data.name, n, statistic.t, parameter.df,
                      estimate.mean.in.group.0, estimate.mean.in.group.1, SD,
                      conf.int1, conf.int2, p.value)

# add diff in to table:
tab$diffPos <- as.numeric(tab$estimate.mean.in.group.0)-as.numeric(tab$estimate.mean.in.group.1)

```

```

# Round p.value
tab$p.value <- sapply(as.numeric(tab$p.value), round.pValue)

tab$statistic.t <- as.numeric(tab$statistic.t)
tab$parameter.df <- as.numeric(tab$parameter.df)
tab$estimate.mean.in.group.0 <- as.numeric(tab$estimate.mean.in.group.0)
tab$estimate.mean.in.group.1 <- as.numeric(tab$estimate.mean.in.group.1)
tab$SD <- as.numeric(tab$SD)
tab$conf.int1 <- as.numeric(tab$conf.int1)
tab$conf.int2 <- as.numeric(tab$conf.int2)
tab$diffPos <- as.numeric(tab$diffPos)

# Rename colnames
colnames(tab) <- c("Category", "n", "T value", "df", "Mean \\ [0]",
"Mean \\ [1]", "SD", "CI lwr", "CI upr", "p-value", "Diff HGS \\ [0-1]"
)

# HTML Output:
# tab %>% kable() %>% kable_classic_2()

# Latex Output:
bold <- function(x){paste0("\\bfseries{",x,"}")}

tab <- tab[,c(1,2,3,4,5,6,7,11,8,9,10)]

print(xtable(tab,
  align = "r|p{1.8cm}p{.8cm}p{1.6cm}p{.9cm}p{.9cm}p{.9cm}p{.9cm}p{.9cm}p{.9cm}p{.9cm}p{1.5cm}|",
  floating = FALSE,
  include.rownames = FALSE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE,
  sacebox = .15)

```

Table: Adjusted two sample t-test: Association between position preferred and max HGS for men and women

```

# Table 22: (adjusted) Two sample t-test - maxHGS with position preferred ####
# Get the data:
tmpM <- tmp %>% filter(category == "Men")
tmpW <- tmp %>% filter(category == "Women")

# Duplicates are removed:
ID.unique <- unique(tmpM$ID) # every entry once

unique.dat.M <- cbind(rep(NA, length(ID.unique)),
  rep(NA, length(ID.unique)))

# Loop will take for each participant only one entry:
# if max HGS was measured in preferred and not preferred pos
# than it will take only the position preferred:

for( i in 1:length(ID.unique)){
  pos <- ID.unique[i]
  Person.A <- tmpM$PosMatchWithPref[tmpM$ID == pos] #
  Person.B <- tmpM$max[tmpM$ID == pos]

  if (mean(as.integer(Person.A)) > 1){
    unique.dat.M[i,1] <- 1 # TRUE max HGS
    unique.dat.M[i,2] <- max(Person.B)
  }
}

```



```

else{
  unique.dat.M[i,1] <- 0 # FALSE max HGS
  unique.dat.M[i,2] <- max(Person.B)
}
}

# change colnames:
colnames(unique.dat.M) <- c("PosMatchWithPref", "max")

unique.dat.M <- as.data.frame(unique.dat.M)

# Conduct two sample ttest
table.M <- t.test(unique.dat.M$max ~ unique.dat.M$PosMatchWithPref)

## For Women
ID.unique <- unique(tmpW$ID) # every entry once

unique.dat.W <- cbind(rep(NA, length(ID.unique)), rep(NA, length(ID.unique)))

for( i in 1:length(ID.unique)){
  pos <- ID.unique[i]
  Person.A <- tmpW$PosMatchWithPref[tmpW$ID == pos]
  Person.B <- tmpW$max[tmpW$ID == pos]

  if (mean(as.integer(Person.A)) > 1){
    unique.dat.W[i,1] <- 1 # TRUE max HGS
    unique.dat.W[i,2] <- max(Person.B)
  }
  else{
    unique.dat.W[i,1] <- 0 # FALSE max HGS
    unique.dat.W[i,2] <- max(Person.B)
  }
}

# change colnames
colnames(unique.dat.W) <- c("PosMatchWithPref", "max")

unique.dat.W <- as.data.frame(unique.dat.W)

# Conduct two sample t-test:
table.W <- t.test(unique.dat.W$max ~ unique.dat.W$PosMatchWithPref)

# Generate DataFramed with the results:
table <- data.frame(rbind(unlist(table.M), unlist(table.W)))

# add sample size:
df.n <- data.frame(n = c(nrow(unique.dat.M), nrow(unique.dat.W)),
  data.name = c("unique.dat.M$max by unique.dat.M$PosMatchWithPref",
    "unique.dat.W$max by unique.dat.W$PosMatchWithPref"))

table <- left_join(table, df.n, by = "data.name")

# calculation of SD:
table$SD <- as.numeric(table$stderr) * sqrt(as.numeric(table$n))

tab <- table %>% select(., data.name, n, statistic.t, parameter.df,
  estimate.mean.in.group.0, estimate.mean.in.group.1, SD,
  conf.int1, conf.int2, p.value)

# add diff in to table:
tab$diffPos <- as.numeric(tab$estimate.mean.in.group.0)-as.numeric(tab$estimate.mean.in.group.1)

```

```

# Round p.value
tab$p.value <- sapply(as.numeric(tab$p.value), round.pValue)

tab$statistic.t <- as.numeric(tab$statistic.t)
tab$parameter.df <- as.numeric(tab$parameter.df)
tab$estimate.mean.in.group.0 <- as.numeric(tab$estimate.mean.in.group.0)
tab$estimate.mean.in.group.1 <- as.numeric(tab$estimate.mean.in.group.1)
tab$SD <- as.numeric(tab$SD)
tab$conf.int1 <- as.numeric(tab$conf.int1)
tab$conf.int2 <- as.numeric(tab$conf.int2)

# rename colnames
colnames(tab) <- c("Category", "n", "T value", "df", "Mean \\ [0]",
"Mean \\ [1]", "SD", "CI lwr", "CI upr", "p-value", "Diff HGS \\ [0-1]"
)

tab$Category[1] <- "Men"
tab$Category[2] <- "Women"

# #HTML Output:
# tab %>% kable() %>% kable_classic_2()

# Latex Output:
bold <- function(x){paste0("\\bfseries{",{x},"")}}

tab <- tab[,c(1,2,3,4,5,6,7,11,8,9,10)]

print(xtable(tab,
  align = "r|p{1.8cm}p{.8cm}p{1.6cm}p{.9cm}p{.9cm}p{.9cm}p{.9cm}p{.9cm}p{.9cm}p{.9cm}p{1.5cm}|",
  floating = FALSE,
  include.rownames = FALSE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE,
  sacebox = .15)

```

Plot: Normative HGS mean and SD values with its sd from Werle et al. (2009)

```

# Plot 13: HGS values with its sd (Werle) ####

# mean HGS values from Werle with its sd values:

tmp <- dd_nms %>% filter(. , category == "Men" | category == "Women")
# values taken from Werle and Canadian pater for children:
ggplot(data = tmp, aes(x = agecat, y = mean, ymin = mean - sd, ymax = mean + sd, col = category))+
  geom_pointrange()+
  #facet_wrap(~category, nrow = 2)+
  theme_pubclean()+
  xlab("Age category")+
  ylab("Normative HGS (kg)")+
  scale_color_manual("category", values = c("Men" = "lightblue4", "Women" = "lightpink4"))+
  theme(legend.position = "none")
  #theme(axis.text = element_text(size = 8))

rm(list=c("tmp")) # remove tmp (temporary) dataset

```

Plot: HGS mean and SD values from the data collected at the DOOD

```

# Plot 14: HGS values with its SD (DOOD) ####

tmp <- dd_long %>% filter(category == "Men" | category == "Women")

# DOOD:

```

```
summary <- tmp %>% group_by(., agecat, category) %>%
  summarise(
    count = n(),
    mean = mean(HGS, na.rm = TRUE),
    sd = sd(HGS, na.rm = TRUE)
  )

ggplot(data = summary, aes(x = agecat, y = mean, ymin = mean - sd, ymax = mean + sd, col = category)) +
  geom_pointrange() +
  #facet_wrap(~category, nrow = 2) +
  theme_pubclean() +
  xlab("Age category") +
  ylab("HGS (kg)") +
  scale_color_manual("category", values = c("Men" = "lightblue4", "Women" = "lightpink4")) +
  theme(legend.position = "none")
#theme(axis.text = element_text(size = 8))
```

Preparation: Evaluate Whether the Mean HGS Values of Men and Women Differ for the Respective Age Categories

```
# >>> Preparation MidTerm.Analysis ####
Werle <- dd_nms %>% select(., mean, sd, agecat, category) %>%
  filter(., category == "Men" | category == "Women")

# add sample size into dataFrame:
Werle <- cbind(Werle,
  n = c(33,29,30,28,41,37,31,40,30,33,46,33,28,29,28,
        31,31,30,30,42,39,40,34,28,30,34,27,26,32,28))

# create df Werle in wide format:
Men <- Werle %>% filter(., category == "Men") %>% select(., -c("category"))
colnames(Men) <- c("mean.Men", "sd.Men", "agecat", "n.Men")

Women <- Werle %>% filter(., category == "Women") %>% select(., -c("category"))
colnames(Women) <- c("mean.Women", "sd.Women", "agecat", "n.Women")

Werle_wide <- right_join(Men, Women, by = "agecat")[,c(3,1,2,4,5,6,7)]
```

Table: Welch two-sample t-test for the difference of mean HGS values between Men and Women from Werle

```
# Table 19: Welch t-test Werle ####
# see function in r.script: Functions.R

# Conduct two.sided Welch t-test:
# Gr1 = Men, Gr2 = Women
table <- mapply(FUN = twosided.welch.statistic,
  Werle_wide$mean.Men, Werle_wide$mean.Women,
  Werle_wide$sd.Men, Werle_wide$sd.Women,
  Werle_wide$n.Men, Werle_wide$n.Women)

colnames(table) <- c("18-19", "20-24", "25-29", "30-34",
  "35-39", "40-44", "45-49", "50-54",
  "55-59", "60-64", "65-69", "70-74",
  "75-79", "80-84", "85-89")

# transpose dataFrame
table <- t(table) %>% as.data.frame()

# add rownames als colvariable:
table$agecat <- c("18-19", "20-24", "25-29", "30-34",
  "35-39", "40-44", "45-49", "50-54",
```

```

      "55-59", "60-64", "65-69", "70-74",
      "75-79", "80-84", "85-89")
# add mean diff:
table$meanDiff <- as.numeric(table$mean.Gr1)-as.numeric(table$mean.Gr2)

# rename
colnames(table) <- c("mean(Men)", "mean(Women)", "SD(Men)", "SD(Women)",
  "n(Men)", "n(Women)", "T statistic", "df",
  "CI lwr", "CI upr", "p-value", "Age category", "Diff HGS (M-W)")

#round p-value
table$pvalue.rounderd <- sapply(table$p-value,round.pValue)
table$p-value <- format(signif(as.numeric(table$p-value),3), scientific = TRUE)

# Rounding
table$n(Men) <- as.integer(table$n(Men))
table$n(Women) <- as.integer(table$n(Women))
table$CI lwr <- floor(as.numeric(table$CI lwr))
table$CI lwr <- as.integer(table$CI lwr)
table$CI upr <- ceiling(as.numeric(table$CI upr))
table$CI upr <- as.integer(table$CI upr)
table$mean(Men) <- round(as.numeric(table$mean(Men)),1)
table$mean(Women) <- round(as.numeric(table$mean(Women)),1)
table$SD(Men) <- round(as.numeric(table$SD(Men)),1)
table$SD(Women) <- round(as.numeric(table$SD(Women)),1)

#HTML-Output
# kable(table) %>% kable_classic_2(full_width = F )

# Latex-Output:
table <- table %>% select(., -c("p-value"))
# reorder:
table <- table[,c(11, 1, 3, 5, 2, 4, 6, 7, 8, 12, 9, 10,13)]
colnames(table) <-c("Age cat.",
  "mean \\newline (M)","SD \\newline (M)","n \\newline (M)",
  "mean \\newline (W)","SD \\newline (W)","n \\newline (W)",
  "T value", "df", "Diff HGS \\newline (M-W)",
  "CI \\newline lwr", "CI \\newline upr",
  "p-value")

bold <- function(x){paste0("\\bfseries{",{x},"")}}

print(xtable(table,
  align = "r|p{.9cm}p{.8cm}p{.8cm}p{.8cm}p{.8cm}p{.8cm}p{.8cm}p{1.1cm}p{.8cm}p{1.4cm}p{.8cm}p{.8cm}",
  floating = FALSE,
  include.rownames = FALSE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE,
  sacebox = .15)

```

Plot: Welch two-sample t-test for the difference of mean HGS values between Men and Women from DOOD

```

tmp <- dd_long %>% filter(category == "Men" | category == "Women")

# mean HGS per agecat
meanHGS.Agecat <- tmp %>% group_by(agecat, category) %>% summarise_at(vars(HGS),list(meanHGS = mean))

```

```

# Calculate mean HGS for each participant:
tmp <- tmp %>% group_by(ID, agecat, category) %>% summarise_at(vars(HGS),list(meanHGS = mean))

# Sample size per each category:
n.tmp <- tmp %>% group_by(agecat, category) %>% count()

# Table 20: Welch t-test DOOD ####
agecat1819 <- tmp %>% filter(., agecat == "18-19")
agecat2024 <- tmp %>% filter(., agecat == "20-24")
agecat2529 <- tmp %>% filter(., agecat == "25-29")
agecat3034 <- tmp %>% filter(., agecat == "30-34")
agecat3539 <- tmp %>% filter(., agecat == "35-39")
agecat4044 <- tmp %>% filter(., agecat == "40-44")
agecat4549 <- tmp %>% filter(., agecat == "45-49")
agecat5054 <- tmp %>% filter(., agecat == "50-54")
agecat5559 <- tmp %>% filter(., agecat == "55-59")
agecat6064 <- tmp %>% filter(., agecat == "60-64")
agecat6569 <- tmp %>% filter(., agecat == "65-69")
agecat7074 <- tmp %>% filter(., agecat == "70-74")
agecat7579 <- tmp %>% filter(., agecat == "75-79")
agecat8084 <- tmp %>% filter(., agecat == "80-84")
agecat8589 <- tmp %>% filter(., agecat == "85-89")

# category = gendnder category
#a <- t.test(meanHGS ~ category, data = agecat1819, alternative = "two.sided", var.equal = FALSE)
b <- t.test(meanHGS ~ category, data = agecat2024, alternative = "two.sided", var.equal = FALSE)
c <- t.test(meanHGS ~ category, data = agecat2529, alternative = "two.sided", var.equal = FALSE)
d <- t.test(meanHGS ~ category, data = agecat3034, alternative = "two.sided", var.equal = FALSE)
e <- t.test(meanHGS ~ category, data = agecat3539, alternative = "two.sided", var.equal = FALSE)
f <- t.test(meanHGS ~ category, data = agecat4044, alternative = "two.sided", var.equal = FALSE)
g <- t.test(meanHGS ~ category, data = agecat4549, alternative = "two.sided", var.equal = FALSE)
h <- t.test(meanHGS ~ category, data = agecat5054, alternative = "two.sided", var.equal = FALSE)
i <- t.test(meanHGS ~ category, data = agecat5559, alternative = "two.sided", var.equal = FALSE)
j <- t.test(meanHGS ~ category, data = agecat6064, alternative = "two.sided", var.equal = FALSE)
k <- t.test(meanHGS ~ category, data = agecat6569, alternative = "two.sided", var.equal = FALSE)
#t.test(meanHGS ~ category, data = agecat7074, alternative = "two.sided", var.equal = FALSE)
#t.test(meanHGS ~ category, data = agecat7579, alternative = "two.sided", var.equal = FALSE)
#t.test(meanHGS ~ category, data = agecat8084, alternative = "two.sided", var.equal = FALSE)
#t.test(meanHGS ~ category, data = agecat8589, alternative = "two.sided", var.equal = FALSE)

# Generate DataFrame with the results of the tests:
table <- data.frame(rbind(unlist(b), unlist(c),
  unlist(d), unlist(e), unlist(f),
  unlist(g), unlist(h), unlist(i),
  unlist(j), unlist(k))
)

welch.ttest <- table %>%
  select(., data.name, statistic.t, parameter.df, estimate.mean.in.group.Men,
    estimate.mean.in.group.Women, stderr, conf.int1, conf.int2, p.value)

welch.ttest$data.name <- c("20-24", "25-29", "30-34",
  "35-39", "40-44", "45-49", "50-54",
  "55-59", "60-64", "65-69")

# change variable to numeric variables:
for(i in 2:9){
  welch.ttest[,i] <- as.numeric(welch.ttest[,i])
}

# Round p-value
welch.ttest$p.value.rounded <- sapply(welch.ttest[, "p.value"], round.pValue)

```

```

# Rename Col.names
colnames(welch.ttest) <- c("Age category", "T statistic", "df",
                          "Mean in Men", "Mean in Women", "SE",
                          "CI lwr", "CI upr", "p-value", "p-value (rounded)")

# formate p-value to scientific notation:
welch.ttest$p-value <- format(signif(as.numeric(welch.ttest$p-value),3), scientific = TRUE)

# to wide format:
# n
n.tmp <- spread(n.tmp, key = category, value = n)
colnames(n.tmp) <- c("Age category", "n (M)", "n (W)")
# Mean
mean.tmp <- tmp %>% group_by(agecat, category)%>%summarise(mean = mean(meanHGS))
mean.tmp <- spread(mean.tmp, key = category, value = mean)
colnames(mean.tmp) <- c("Age category", "mean (M)", "mean (W)")
# SD
SD.tmp <- tmp %>% group_by(agecat, category)%>%summarise(SD = SD(meanHGS))
SD.tmp <- spread(SD.tmp, key = category, value = SD)
colnames(SD.tmp) <- c("Age category", "SD (M)", "SD (W)")

# joint to data.frame
welch.ttest <- full_join(welch.ttest, n.tmp, by = "Age category")
welch.ttest <- full_join(welch.ttest, mean.tmp, by = "Age category")
welch.ttest <- full_join(welch.ttest, SD.tmp, by = "Age category")

# diff mean M-W
welch.ttest$diffMean <- welch.ttest$`mean (M)` - welch.ttest$`mean (W)`

welch.ttest <- welch.ttest[,c("Age category", "T statistic", "df",
                             "CI lwr", "CI upr", "p-value (rounded)",
                             "mean (M)", "mean (W)", "n (M)", "n (W)",
                             "SD (M)", "SD (W)", "diffMean")]

welch.ttest <- welch.ttest [c(11,1,2,3,4,5,6,7,8,9,10,12,13,14),]
welch.ttest <- welch.ttest[,c(1,7,11,9,8,12,10,2,3,13,4,5,6)]

# Rounding:
welch.ttest$n (M)` <- as.integer(welch.ttest$n (M)`)
welch.ttest$n (W)` <- as.integer(welch.ttest$n (W)`)
welch.ttest$CI lwr` <- floor(as.numeric(welch.ttest$CI lwr`))
welch.ttest$CI lwr` <- as.integer(welch.ttest$CI lwr`)
welch.ttest$CI upr` <- ceiling(as.numeric(welch.ttest$CI upr`))
welch.ttest$CI upr` <- as.integer(welch.ttest$CI upr`)
welch.ttest$`mean (M)` <- round(as.numeric(welch.ttest$`mean (M)`),1)
welch.ttest$`mean (W)` <- round(as.numeric(welch.ttest$`mean (W)`),1)
welch.ttest$SD (M)` <- round(as.numeric(welch.ttest$SD (M)`),1)
welch.ttest$SD (W)` <- round(as.numeric(welch.ttest$SD (W)`),1)

colnames(welch.ttest) <- c("Age cat.",
                          "mean \\newline (M)", "SD \\newline (M)", "n \\newline (M)",
                          "mean \\newline (W)", "SD \\newline (W)", "n \\newline (W)",
                          "T value", "df", "Diff HGS \\newline (M-W)",
                          "CI \\newline lwr", "CI \\newline upr",
                          "p-value")

#HTML-Output
# kable(welch.ttest) %>% kable_classic_2(full_width = F )

```

[illegible]

Preparation: Computation of the Sample Size Requirement

```
# >>> Preparation Sample Size Calc. #####

## Sample Size Calculation for HGS:
# Variable input:
# p-th CI: probabilities of the desired CI (e.g. 95%CI = 0.95)
# for the desired confidence level
# sigma: standard deviation (SD) of the outcome of interest
# MOE: margin of error (MOE) usually specified from a clinical/practical standpoint

sampleSize <- function(p, sigma, MOE){
  Z <- qnorm(p = 1-(1-p)/2)
  n <- ceiling((((Z*sigma)/MOE)^2)
  dat <- data.frame(Z,sigma, MOE,n)
  return(dat)
}

tmp <- dd_nms %>% select(., c("mean", "sd", "agecat", "category"))
tmp.M <- tmp %>% dplyr::filter(., category == "Men")
tmp.W <- tmp %>% dplyr::filter(., category == "Women")
```

Table: Computation of sample size (n) based on 95% CI and MOE of 2.4 kg for men

```
# Table 23: SampleSize.M (2xMOE)###
# Width(4.8)
# For Men
Sample.M <- sampleSize(p = 0.95, sigma = tmp.M$sd, MOE = 2.4)
n.M.2MOE <- Sample.M$n
Sample.M <- cbind(tmp.M, Sample.M)

# # HTML Output:
# Sample.M[,c(3,4,1,2,5,6,7,8)] %>% kbl() %>% kable_classic()

Sample.M <- Sample.M[,c(3,1,2,5,7,8)]

#Rounding:
Sample.M$Z <- round(Sample.M$Z, 2)
Sample.M$n <- as.integer(Sample.M$n)

colnames(Sample.M) <- c("Age cat.", "mean", "SD", "Z Score", "MOE", "$n$")

# Latex Output:
print(xtable(Sample.M, align = "r|p{1.2cm}p{1.1cm}p{1.1cm}p{1.1cm}p{1.1cm}p{1.1cm}|",
  floating = FALSE,
  include.rownames = FALSE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE,
```

```
NA.string="n.a.")
```

Table: Computation of sample size (n) based on 95% CI and MOE of 2.4 kg for women

```
# Table 24: SampleSize.Q (2xMOE)###

# For Women
Sample.W <- sampleSize(p = 0.95, sigma = tmp.W$sd, MOE = 2.4)
n.W.2MOE <- Sample.W$n
Sample.W <- cbind(tmp.W, Sample.W)

# # HTML Output:
# Sample.W[, c(3, 4, 1, 2, 5, 6, 7, 8)] %>% kbl() %>% kable_classic()

Sample.W <- Sample.W[, c(3, 1, 2, 5, 7, 8)]

# Rounding:
Sample.W$Z <- round(Sample.W$Z, 2)
Sample.W$n <- as.integer(Sample.W$n)

colnames(Sample.W) <- c("Age cat.", "mean", "SD", "Z Score", "MOE", "$n$")

# Latex Output:
print(xtable(Sample.W, align = "r|p{1.2cm}p{1.1cm}p{1.1cm}p{1.1cm}p{1.1cm}p{1.1cm}|",
  floating = FALSE,
  include.rownames = FALSE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE,
  NA.string="n.a.")
```

Table: Computation of sample size (n) based on 95% CI and MOE of 1.2 kg for men

```
# Width(2.4)

# Table 25: SampleSize.M (1xMOE)###

# For Men
Sample.M <- sampleSize(p = 0.95, sigma = tmp.M$sd, MOE = 1.2)
n.M.1MOE <- Sample.M$n
Sample.M <- cbind(tmp.M, Sample.M)

# # HTML Output:
# Sample.M[, c(3, 4, 1, 2, 5, 6, 7, 8)] %>% kbl() %>% kable_classic()

Sample.M <- Sample.M[, c(3, 1, 2, 5, 7, 8)]

# Rounding:
Sample.M$Z <- round(Sample.M$Z, 2)
Sample.M$n <- as.integer(Sample.M$n)

colnames(Sample.M) <- c("Age cat.", "mean", "SD", "Z Score", "MOE", "$n$")

# Latex Output:
print(xtable(Sample.M, align = "r|p{1.2cm}p{1.1cm}p{1.1cm}p{1.1cm}p{1.1cm}p{1.1cm}|",
  floating = FALSE,
  include.rownames = FALSE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE,
  NA.string="n.a.")
```

Table: Computation of sample size (n) based on 95% CI and MOE of 1.2 kg for women



```

# Table 26: SampleSize.W (1xMOE)####

# For Women
Sample.W <- sampleSize(p = 0.95, sigma = tmp.W$sd, MOE = 1.2)
n.W.1MOE <- Sample.W$n
Sample.W <- cbind(tmp.W, Sample.W)

# # HTML Output:
# Sample.W[, c(3, 4, 1, 2, 5, 6, 7, 8)] %>% kbl() %>% kable_classic()

Sample.W <- Sample.W[, c(3, 1, 2, 5, 7, 8)]

# Rounding:
Sample.W$Z <- round(Sample.W$Z, 2)
Sample.W$n <- as.integer(Sample.W$n)

colnames(Sample.W) <- c("Age cat.", "mean", "SD", "Z Score", "MOE", "$n$")

# Latex Output:
print(xtable(Sample.W, align = "r|p{1.2cm}p{1.1cm}p{1.1cm}p{1.1cm}p{1.1cm}p{1.1cm}|",
  floating = FALSE,
  include.rownames = FALSE,
  sanitize.colnames.function = bold,
  booktabs = FALSE,
  fixed = TRUE,
  NA.string = "n.a.")

```

Table: Comparison sample size from Werle et al. (2009) with computed sample size based on MOE of 4.8kg and 2.4 kg

```

# Table 27: Comparison of Sample Size ####

df.n <- data.frame(agecat = c("18-19", "20-24", "25-29", "30-34",
  "35-39", "40-44", "45-49", "50-54",
  "55-59", "60-64", "65-69", "70-74",
  "75-79", "80-84", "85-89"),
  means_men = as.numeric(c(51.2, 53.9, 53.0, 55.0, 55.9, 54.2,
    51.8, 50.8, 53.6, 47.9, 43.0, 41.7,
    36.8, 30.7, 22.4)),
  sds_men = as.numeric(c(6.6, 8.7, 7.5, 7.1, 7.9, 8.1, 8.3,
    9.1, 8.6, 6.4, 6.8, 8.9, 9.7, 9.1, 6.2)),
  means_women = as.numeric(c(32.0, 33.4, 34.3, 33.8, 35.8, 34.0,
    34.1, 33.7, 31.9, 28.7, 29.5, 26.4,
    25.0, 19.2, 16.9)),
  sds_women = as.numeric(c(4.8, 5.4, 5.7, 5.9, 6.7, 6.0, 5.3, 4.5,
    4.9, 5.5, 3.6, 6.8, 4.5, 5.2, 4.8)),
  n.M.Werle = as.integer(c(33, 29, 30, 28, 41, 37, 31, 40,
    30, 33, 46, 33, 28, 29, 28)),
  n.W.Werle = as.integer(c(31, 31, 30, 30, 42, 39, 40, 34,
    28, 30, 34, 27, 26, 32, 28)),
  n.M.2MOE = as.integer(n.M.2MOE),
  n.W.2MOE = as.integer(n.W.2MOE),
  n.M.1MOE = as.integer(n.M.1MOE),
  n.W.1MOE = as.integer(n.W.1MOE))

Total <- c("Total", "", "", "", "",
  sum(df.n$n.M.Werle), sum(df.n$n.W.Werle),
  sum(df.n$n.M.2MOE), sum(df.n$n.W.2MOE),
  sum(df.n$n.M.1MOE), sum(df.n$n.W.1MOE))

df.n <- rbind(df.n, Total)

```



```

# read the data and add age categories
get_data <- function(url) {
  vn <- c("Timestamp", "ID", "Age", "Gender", "Start")
  vn <- c(vn,
    apply(expand.grid(c("Left", "Right"),
      c("Oflex", "90flex"),
      c("stand", "sit")), 1,
      function(x) paste(x[c(1, 3, 2)], collapse = "_")))
  vn <- c(vn, "Preference", "Height", "Weight", "Chronic")
  df <- read_sheet(url)
  names(df) <- vn
  df$Gender <- factor(df$Gender, levels = c("Male", "Female"))
  df$Chronic <- factor(df$Chronic, levels = c("No", "Yes"))
  df$Start <- factor(df$Start, levels = 1:8)
  df$agecat <- cut(df$Age,
    breaks = c(5:17, 19, seq(from = 24, to = 86, by = 5), 89))
  df
}

dat <- get_data(url)
dat <- as.data.frame(dat)

# Data cleaning and data checking: ####
# change list in to variables:
dat$ID <- as.character(dat$ID)
dat$Left_stand_Oflex <- as.numeric(dat$Left_stand_Oflex)
dat$Right_stand_Oflex <- as.numeric(dat$Right_stand_Oflex)
dat$Right_stand_90flex <- as.numeric(dat$Right_stand_90flex)
dat$Left_stand_90flex <- as.numeric(dat$Left_stand_90flex)
dat$Right_stand_90flex <- as.numeric(dat$Right_stand_90flex)
dat$Left_sit_Oflex <- as.numeric(dat$Left_sit_Oflex)
dat$Right_sit_Oflex <- as.numeric(dat$Right_sit_Oflex)
dat$Left_sit_90flex <- as.numeric(dat$Left_sit_90flex)
dat$Right_sit_90flex <- as.numeric(dat$Right_sit_90flex)

## Corrections ####
dat[2, "Height"] <- 178 # HT in cm
dat <- dat[-c(33,34),] # remove 2 pseudo patients

# Check data types:
#str(dat)

# Save data as csv and rds
#write.csv(dat, file = "DOOD_raw.csv")
#saveRDS(object = dat, file = "DOOD_raw.rds")

```

code/02 Data Preparation.R:

```

#-----
# 02 Descriptive Statistic
# author: Vithersan Somasundaram
#
# Provides the code for cleaning the data
# data frame - dat: Contains the formatted raw data of the study
# data frame - dd: contains the formatted, cleaned data of the study according
# to the exclusion criteria
# -----

# Preparation ####

## Loading Libraries ####
require(tidyverse) # used for data wrangling

```

```

#library(table1)           # to describe baseline characteristics
#library(tableone)         # to describe baseline characteristics
require(kableExtra)        # create HTML/PDF tables
require(ggpubr)            # extension of ggplot2
require(DescTools)         # for descriptive statistics
require(vtable)           # Variable Table Function for sumtable

## Loading data ####
# Run this code only if new entries was made in the googleForms,
# requires authorisation of GoogleForms
# otherwise load cleaned data from the data folder

# source("../code/01-DataLoading.R")

# Latest version of the data:
dd <- read.csv("../data/D00D_raw.csv")

## Variable names ####
original_colnames <- c("ID", "Timestamp", "Study ID", "Age", "Gender", "Start",
  "Left, stand, 0 flex", "Right, stand, 0 flex", "Left, stand, 90 flex",
  "Right, stand, 90 flex", "Left, sit, 0 flex", "Right, sit, 0 flex",
  "Left, sit, 90 flex", "Right, sit, 90 flex",
  "Preference", "Height", "Weight", "Chronic",
  "Age category")

colnames(dd) <- c("ID", "Timestamp", "StudyID", "Age", "Gender", "Start", "Left_stand_0flex",
  "Right_stand_0flex", "Left_stand_90flex", "Right_stand_90flex",
  "Left_sit_0flex", "Right_sit_0flex", "Left_sit_90flex", "Right_sit_90flex",
  "Preference", "Height", "Weight", "Chronic", "agecat")

## Data formatting ####
# change 'int' to character:
dd$Start <- as.character(dd$Start)

# change 'chr' to factors:
dd$Gender <- as.factor(dd$Gender)
dd$Chronic <- as.factor(dd$Chronic)

# reorder the levels:
dd$agecat <- as.factor(dd$agecat)
dd$agecat <- factor(dd$agecat,
  levels = c(
    "(5,6]", "(6,7]", "(7,8]", "(8,9]", "(9,10]", "(10,11]", "(11,12]",
    "(12,13]", "(13,14]", "(14,15]", "(15,16]", "(16,17]", "(17,19]",
    "(19,24]", "(24,29]", "(29,34]", "(34,39]", "(39,44]", "(44,49]",
    "(49,54]", "(54,59]", "(59,64]", "(64,69]", "(69,74]", "(74,79]",
    "(79,84]", "(84,89]"),
  labels = c("6", "7", "8", "9", "10", "11", "12",
    "13", "14", "15", "16", "17", "18-19",
    "20-24", "25-29", "30-34", "35-39",
    "40-44", "45-49", "50-54", "55-59",
    "60-64", "65-69", "70-74", "75-79",
    "80-84", "85-89"))

# add new variable category with level (Men, Boys, Women, Girls)
dd <- dd %>% mutate(category = case_when(Age < 18 & Gender == "Male" ~ "Boys",
  Age > 17 & Gender == "Male" ~ "Men",
  Age < 18 & Gender == "Female" ~ "Girls",
  Age > 17 & Gender == "Female" ~ "Women"))

```

```

dd$category <- as.factor(dd$category)
dd$category <- factor(dd$category, levels = c("Boys", "Men", "Girls", "Women"))

# Apply Exclusion Criteria ###

# Exclude Participant according to the exclusion criteria:
dat <- dd # dat contains the whole data set without excluding participants

# Remove Participants with age < 6y:
dd <- dd %>% filter(., Age > 5)

# Exclude participants with chronic diseases or injuries
dd <- dd %>% filter(., Chronic == "No")

# Create new variable to distinguish between children and adults
dd <- dd %>% mutate(., gendercat = case_when(Age < 18 ~ "Children",
                                              Age > 17 ~ "Adults"))

write.csv(dd, "../DOOD_clean.csv", row.names = TRUE)

```

code/03 OOD norms.R:

```

#-----
# 03 OOD norms
# author: Vithersan Somasundaram
# based on the norm development from Fabio Barresi (04. march 2022)
# data frame - dd_nms is the merged dataset from (nms_boy, nms_girls, nms_men and nms_women):
# * contains mean and SD from Werle et al. (2009)
# * and Quantile values
#-----

# Function calc_norms ###

# Static plotting of norms without any contact to Google Forms

## means: mean vector
## sd: sd vector
## lwr: lower bound of age interval
## upr: upper bound of age interval [lwr, upr]
## pct: percentiles to calculate

calc_norms <- function(mean, sd, lwr, upr, pct =
  c(0.05, 0.1, 0.25, 0.5, 0.75, 0.9, 0.95)) {
  ## Calculation of the percentiles
  ps <- mapply(function(m, s) {
    p <- qnorm(pct, mean = m, sd = s)
    names(p) <- pct
    p
  },
  m = mean, s = sd, SIMPLIFY = FALSE)
  ## Create data frame with the percentiles
  df <- data.frame(mean = mean, sd = sd, lwr = lwr, upr = upr,
    pct = I(ps),
    agecat = factor(seq_along(mean),
      labels = paste0("(", lwr-1, ", ", upr, "]")))
  ## NOTE: fixed the line above
  df
}

# Function plot_norms_function ###
plot_norms <- function(norms, pagecat, phg, epsilon){
  ## pagecat: age category of a person

```

```

## phg: person's handgrp strength
## epsilon: widen the range of y-axis by epsilon value to see the highlghited point
nm <- do.call("rbind", norms$pct)
ps <- colnames(nm)
cols <- colorspace::diverge_hcl(length(ps), "Blue-Red2")
# cols <- c("deeppink", "orchid3", "royalblue1",
#           "cadetblue", "olivedrab3", "orange1", "indianred2")

plot.default(norms$agecat,
             norms$mean,
             type = "n",
             ylim = c(0,max(nm)+epsilon),
             xaxt = "n",
             xlab="Age",
             ylab="Handgrip Strength [kg]")
axis(1, at = as.numeric(norms$agecat),
     labels = levels(norms$agecat),
     las = 3,
     cex.axis = 0.75)

for (i in 1:7){
  lines(norms$agecat, nm[,i], col = cols[i], lwd = 2, lty = 1)
}
pos<-match(pagecat, norms$agecat)
points(norms$agecat[pos], phg, cex=1.25, col="black", pch=16)
legend("bottomright",
      legend = c("0.05", "0.10", "0.25", "0.50", "0.75", "0.90", "0.95"),
      ncol = 7,
      col = c(cols),
      lty = c(1),
      #ncol = 4,
      bty = "n",
      cex= .55)
}

# Calcluate Norms ####

# The values for the calculation of the norms for men ans women
# were taken from Werle. et al. (2009)
# and modified values from Wong. et. al. (2016) for boys and girls

# Calculate the relevant norms
## Men ####
means_men <- c(51.2, 53.9, 53.0, 55.0, 55.9, 54.2,
              51.8, 50.8, 53.6, 47.9, 43.0, 41.7, 36.8, 30.7, 22.4)
sds_men <- c(6.6, 8.7, 7.5, 7.1, 7.9, 8.1, 8.3,
            9.1, 8.6, 6.4, 6.8, 8.9, 9.7, 9.1, 6.2)
nms_men <- calc_norms(means_men, sds_men,
                    lwr = c(18, seq(20, 85, by = 5)),
                    upr = seq(19, 89, by = 5))

## Boys ####
means_boys <- c(8.0, 10.5, 13.1, 16.1, 19.0, 22.6, 26.5, 31.3,
              36.4, 41.4, 45.5, 48.4)
sds_boys <- c(1.9, 2.5, 2.9, 3.4, 3.8, 4.4, 5.0, 5.8, 6.5, 7.2,
            7.7, 7.9)
nms_boys <- calc_norms(means_boys, sds_boys,
                    lwr = seq(6, 17, by = 1),
                    upr = seq(6, 17, by = 1))

## Women ####

```

```

means_women <- c(32.0, 33.4, 34.3, 33.8, 35.8, 34.0, 34.1, 33.7,
                 31.9, 28.7, 29.5, 26.4, 25.0, 19.2, 16.9)
sds_women <- c(4.8, 5.4, 5.7, 5.9, 6.7, 6.0, 5.3, 4.5, 4.9, 5.5,
              3.6, 6.8, 4.5, 5.2, 4.8)
nms_women <- calc_norms(means_women, sds_women,
                       lwr = c(18, seq(20, 85, by = 5)),
                       upr = seq(19, 89, by = 5))

## Girls ####
means_girls <- c(6.9, 9.3, 11.8, 14.1, 16.8, 19.8, 22.8, 25.3,
                27.7, 29.3, 30.5, 31.3)
sds_girls <- c(2.6, 2.8, 3.0, 3.3, 3.6, 3.9, 4.3, 4.6, 4.9, 5.0, 5.2, 5.2)
nms_girls <- calc_norms(means_girls, sds_girls,
                       lwr = seq(6, 17, by = 1),
                       upr = seq(6, 17, by = 1))

# Create dataframe #####
# DataFrame with norms and percentiles
nms_men <- mutate(nms_men, category = rep("Men", nrow(nms_men)))
nms_boys <- mutate(nms_boys, category = rep("Boys", nrow(nms_boys)))
nms_women <- mutate(nms_women, category = rep("Women", nrow(nms_women)))
nms_girls <- mutate(nms_girls, category = rep("Girls", nrow(nms_girls)))
dd_nms <- rbind(nms_men, nms_boys, nms_women, nms_girls) # as data frame for all norms and gender
# remove subgroups of the df
#rm(list=c("nms_men", "nms_boys", "nms_women", "nms_girls"))

# rearrange agecat
dd_nms$agecat <- factor(dd_nms$agecat,
                      levels = c(
                        "(5,6]", "(6,7]", "(7,8]", "(8,9]", "(9,10]",
                        "(10,11]", "(11,12]", "(12,13]", "(13,14]",
                        "(14,15]", "(15,16]", "(16,17]", "(17,19]",
                        "(19,24]", "(24,29]", "(29,34]", "(34,39]",
                        "(39,44]", "(44,49]", "(49,54]", "(54,59]",
                        "(59,64]", "(64,69]", "(69,74]", "(74,79]",
                        "(79,84]", "(84,89]"),
                      labels = c("6", "7", "8", "9", "10", "11", "12",
                                "13", "14", "15", "16", "17", "18-19",
                                "20-24", "25-29", "30-34", "35-39",
                                "40-44", "45-49", "50-54", "55-59",
                                "60-64", "65-69", "70-74", "75-79",
                                "80-84", "85-89"))

# unlist pct:
dd_nms <- as.data.frame(matrix(unlist(dd_nms$pct), ncol=7, byrow = T)) %>%
  setNames(c("0.05", "0.10", "0.25", "0.50", "0.75", "0.90", "0.95")) %>%
  cbind(dd_nms) %>%
  subset(., select = -c(pct))

#write.csv(dd_nms, "../QuantileWerle.csv", row.names = TRUE)

```

code/04 Data Analysis.R:

```

#-----
# 04 Data Analysis
# author: Vithersan Somasundaram

# Preparation for the Data Analysis:
# Provides the code to merge norm data with Study data

```

```

# contains z-Transformation of the HGS data:
#   dd_long and dd_wide (longformat and wideformat)
#   dd_long_pct and dd_wide_pct contains in addition the determined percentile values
#   (only used: to generate percentile plots overlayed with data points)
#-----

# Preparation #####
## Import data #####
source("../code/02-DataPreparation.R")
source("../code/03-00Dnorms.R")
source("../code/Functions.R")

# rm single nms dat:
rm(list=c("nms_boys", "nms_girls", "nms_men", "nms_women"))
rm(list=c("means_boys", "means_girls", "means_women",
          "means_men", "sds_boys", "sds_girls",
          "sds_men", "sds_women"))

## new variables #####
# max : indicating the max HGS of each participant
# (used to plot percentile with max HGS points):
dd$max <- pmax(dd$Left_stand_0flex, dd$Right_stand_0flex, dd$Left_stand_90flex,
              dd$Right_stand_90flex, dd$Left_sit_0flex, dd$Right_sit_0flex,
              dd$Left_sit_90flex, dd$Right_sit_90)

# z-Transformation #####
# Z-Standardisation of the grip strength values
# Merge Dataframe of 00D with Dataframe of the norm Values:
# dd_long:      data from 00D with norm mean and sd
# dd_long_pct:  data from 00D with norm mean and sd incl. quantiles (0.05, 0.10, etc.)
# dd_long_pct used only for visualisation of the quantiles main data dd_long resp. dd_wide

dd_wide_pct <- merge(dd, subset(dd_nms, select = -c(lwr, upr)),
                    by = c("agecat", "category")) # with percentile
dd_wide <- merge(dd, subset(dd_nms, select = c(mean, sd, agecat, category)),
                 by = c("agecat", "category")) # with no percentile

# Calculation of z-Values for each position:
dd_wide <- dd_wide %>%
  mutate(Left_stand_0flex_std = (Left_stand_0flex - mean) / sd,
         Right_stand_0flex_std = (Right_stand_0flex - mean) / sd,
         Left_stand_90flex_std = (Left_stand_90flex - mean) / sd,
         Right_stand_90flex_std = (Right_stand_90flex - mean) / sd,
         Left_sit_0flex_std = (Left_sit_0flex - mean) / sd,
         Right_sit_0flex_std = (Right_sit_0flex - mean) / sd,
         Left_sit_90flex_std = (Left_sit_90flex - mean) / sd,
         Right_sit_90flex_std = (Right_sit_90flex - mean) / sd)

dd_wide_pct <- dd_wide_pct %>%
  mutate(Left_stand_0flex_std = (Left_stand_0flex - mean) / sd,
         Right_stand_0flex_std = (Right_stand_0flex - mean) / sd,
         Left_stand_90flex_std = (Left_stand_90flex - mean) / sd,
         Right_stand_90flex_std = (Right_stand_90flex - mean) / sd,
         Left_sit_0flex_std = (Left_sit_0flex - mean) / sd,
         Right_sit_0flex_std = (Right_sit_0flex - mean) / sd,
         Left_sit_90flex_std = (Left_sit_90flex - mean) / sd,
         Right_sit_90flex_std = (Right_sit_90flex - mean) / sd)

# From wide to long format #####
# Change dd_wide to dd_long (from wide to long format)

## Dataframe with quantiles: #####
dd_long_pct <- dd_wide_pct %>%

```



```

gather(.,key = "pctcat",value = "pct",
       "0.05","0.10","0.25","0.50","0.75","0.90","0.95")>%
gather(., key = "Position", value = "HGS",
       "Left_stand_0flex", "Right_stand_0flex", "Left_stand_90flex",
       "Right_stand_90flex", "Left_sit_0flex", "Right_sit_0flex",
       "Left_sit_90flex", "Right_sit_90flex") %>%
subset(., select = -c(Left_stand_0flex_std, Right_stand_0flex_std, Left_stand_90flex_std,
                      Right_stand_90flex_std, Left_sit_0flex_std, Right_sit_0flex_std,
                      Left_sit_90flex_std, Right_sit_90flex_std))

# filter df and rename with same key:
tmp_dd <- dd_wide_pct %>% dplyr::select(., "ID", "Left_stand_0flex_std",
                                       "Right_stand_0flex_std", "Left_stand_90flex_std",
                                       "Right_stand_90flex_std", "Left_sit_0flex_std",
                                       "Right_sit_0flex_std", "Left_sit_90flex_std",
                                       "Right_sit_90flex_std")

colnames(tmp_dd) <- c("ID", "Left_stand_0flex", "Right_stand_0flex",
                    "Left_stand_90flex", "Right_stand_90flex", "Left_sit_0flex",
                    "Right_sit_0flex", "Left_sit_90flex", "Right_sit_90flex")

tmp_dd <- tmp_dd %>% gather(., key = "Position",value = "HGS_std",
                          "Left_stand_0flex", "Right_stand_0flex", "Left_stand_90flex",
                          "Right_stand_90flex", "Left_sit_0flex", "Right_sit_0flex",
                          "Left_sit_90flex", "Right_sit_90flex")

# Merge both DataFrame together remove tmp:
dd_long_pct <- right_join(dd_long_pct,tmp_dd, by = c("ID", "Position"))
rm(list=c("tmp_dd"))

### DataFrame with no quantiles ###

### Distinguishing between the two measurement days ###
# First run: June
# Day of open Doors (DOOD) : July
dd_wide <- dd_wide %>%
  mutate(Description = case_when(
    startsWith(Timestamp,"2022-06") ~ "First run",
    startsWith(Timestamp,"2022-07") ~ "DOOD"
  ))

### Label the Measurement order at OOD ###
# Ordering the Measurement according
# to the order on the entry sheet:

# 1 : Left, standing, 0 flex
# 2 : Right, standing, 0 flex
# 3 : Left, sitting, 90 flex
# 4 : Right, sitting, 90 flex
# 5 : Left, sitting, 0 flex
# 6 : Right, sitting, 0 flex
# 7 : Left, sitting, 90 flex
# 8 : Right, sitting, 90 flex

dd_wide$Start <- as.numeric(dd_wide$Start)

dd_wide <- dd_wide %>%
  mutate(Pos1 = Start)%>%
  mutate(Pos2 = ifelse(Pos1 !=8, Pos1 + 1,1)) %>%
  mutate(Pos3 = ifelse(Pos2 !=8, Pos2 + 1,1)) %>%
  mutate(Pos4 = ifelse(Pos3 !=8, Pos3 + 1,1)) %>%
  mutate(Pos5 = ifelse(Pos4 !=8, Pos4 + 1,1)) %>%
  mutate(Pos6 = ifelse(Pos5 !=8, Pos5 + 1,1)) %>%

```

```

mutate(Pos7 = ifelse(Pos6 !=8, Pos6 + 1,1)) %>%
mutate(Pos8 = ifelse(Pos7 !=8, Pos7 + 1,1))

### Create Long Format: ###
# rm SDS Values:
dd_long <- subset(dd_wide, select = -c(Left_stand_Oflex_std, Right_stand_Oflex_std,
                                       Left_stand_90flex_std, Right_stand_90flex_std,
                                       Left_sit_Oflex_std, Right_sit_Oflex_std,
                                       Left_sit_90flex_std, Right_sit_90flex_std))

# rm HGS Values:
dd_long <- subset(dd_long, select = -c(Left_stand_Oflex, Right_stand_Oflex,
                                       Left_stand_90flex, Right_stand_90flex,
                                       Left_sit_Oflex, Right_sit_Oflex,
                                       Left_sit_90flex, Right_sit_90flex))

# put Position of measurement into long format:
# order : stands for the order of the HGS Measurement.
# Two variable is generated once in nominal scale and once in ordinal scale

dd_long <- dd_long %>%
  gather(., key = "order_nominal", value = "Position",
         "Pos1", "Pos2", "Pos3", "Pos4",
         "Pos5", "Pos6", "Pos7", "Pos8")

dd_long$order_ordinal <- as.integer(gsub(pattern = "Pos",
                                       replacement = "", x = dd_long$order_nominal))

dd_long$Position <- as.factor(dd_long$Position)
dd_long$Position <- factor(dd_long$Position,
                          labels = c("1" = "Left_stand_Oflex",
                                     "2" = "Right_stand_Oflex",
                                     "3" = "Left_stand_90flex",
                                     "4" = "Right_stand_90flex",
                                     "5" = "Left_sit_Oflex",
                                     "6" = "Right_sit_Oflex",
                                     "7" = "Left_sit_90flex",
                                     "8" = "Right_sit_90flex"))

# Insert HGS Value:
## Filter HGS value form long format
tmp <- dd_wide %>% select(., ID,
                        Left_stand_Oflex, Right_stand_Oflex,
                        Left_stand_90flex, Right_stand_90flex,
                        Left_sit_Oflex, Right_sit_Oflex,
                        Left_sit_90flex, Right_sit_90flex)

## Put in to long format
tmp <- tmp %>% gather(., key = "Position", value = "HGS",
                    Left_stand_Oflex, Right_stand_Oflex,
                    Left_stand_90flex, Right_stand_90flex,
                    Left_sit_Oflex, Right_sit_Oflex,
                    Left_sit_90flex, Right_sit_90flex)

dd_long <- right_join(dd_long, tmp, by = c("ID", "Position"))

# Insert SDS Value:
tmp <- dd_wide %>% select(., ID,
                        Left_stand_Oflex_std, Right_stand_Oflex_std,
                        Left_stand_90flex_std, Right_stand_90flex_std,
                        Left_sit_Oflex_std, Right_sit_Oflex_std,
                        Left_sit_90flex_std, Right_sit_90flex_std)

# rename
colnames(tmp) <- c("ID",
                  "Left_stand_Oflex", "Right_stand_Oflex",
                  "Left_stand_90flex", "Right_stand_90flex",

```

```

        "Left_sit_0flex", "Right_sit_0flex",
        "Left_sit_90flex", "Right_sit_90flex")

tmp <- tmp %>% gather(., key = "Position", value = "HGS_std",
                    "Left_stand_0flex", "Right_stand_0flex", "Left_stand_90flex",
                    "Right_stand_90flex", "Left_sit_0flex", "Right_sit_0flex",
                    "Left_sit_90flex", "Right_sit_90flex")

dd_long <- right_join(dd_long, tmp, by = c("ID", "Position"))
rm(list=c("tmp"))

# Correct the order of the factor variable:
dd_long$Position <- as.factor(dd_long$Position)
dd_long$Position <- factor(dd_long$Position,
                          levels = c("Left_stand_0flex", "Right_stand_0flex",
                                       "Left_stand_90flex", "Right_stand_90flex",
                                       "Left_sit_0flex", "Right_sit_90flex",
                                       "Left_sit_90flex", "Right_sit_0flex"),
                          labels = c("Left, standing, 0 flex", "Right, standing, 0 flex",
                                       "Left, standing, 90 flex", "Right, standing, 90 flex",
                                       "Left, sitting, 0 flex", "Right, sitting, 90 flex",
                                       "Left, sitting, 90 flex", "Right, sitting, 0 flex"))

# Formation of dd_long_pct and dd_wide_pct ####
# change 'chr' variable to factor
dd_long_pct$pctcat <- as.factor(dd_long_pct$pctcat)
dd_long_pct$pctcat <- factor(dd_long_pct$pctcat,
                            levels = c("0.05", "0.10", "0.25", "0.50", "0.75", "0.90", "0.95"),
                            labels = c("5th", "10th", "25th", "50th", "75th", "90th", "95th"))

# change to Factor variables
dd_long_pct$category <- as.factor(dd_long_pct$category)
dd_long_pct$category <- factor(dd_long_pct$category,
                              levels = c("Boys", "Men", "Girls", "Women"))
dd_long_pct$Position <- as.factor(dd_long_pct$Position)
dd_long_pct$Position <- factor(dd_long_pct$Position,
                              levels = c("Left_stand_0flex", "Right_stand_0flex",
                                           "Left_stand_90flex", "Right_stand_90flex",
                                           "Left_sit_0flex", "Right_sit_90flex",
                                           "Left_sit_90flex", "Right_sit_0flex"),
                              labels = c("Left, standing, 0 flex", "Right, standing, 0 flex",
                                           "Left, standing, 90 flex", "Right, standing, 90 flex",
                                           "Left, sitting, 0 flex", "Right, sitting, 90 flex",
                                           "Left, sitting, 90 flex", "Right, sitting, 0 flex"))

dd_wide_pct$category <- as.factor(dd_wide_pct$category)
dd_wide_pct$category <- factor(dd_wide_pct$category,
                              levels = c("Boys", "Men", "Girls", "Women"))

# Save data frame as csv and rds

# write.csv(dd_long, "../data/HGS.longformat.csv", row.names = FALSE)
# write.csv(dd_wide, "../data/HGS.wideformat.csv", row.names = FALSE)
# write.csv(dd_long_pct, "../data/HGSpct.longformat.csv", row.names = FALSE)
# write.csv(dd_wide_pct, "../data/HGSpct.wideformat.csv", row.names = FALSE)

```

code/05 Functions.R:

```

# Function for Rounding p-value ####
# two significant digit e.g. p = 0.43 pr 0.057
# if 0.001 < p-value > 0.0001 round to one significant digit
# else p < 0.0001

```

```

# example: sapply(dat[,8], round.pValue)

round.pValue <- function(x) {
  if (x < 0.0001) {
    pval <- "< 0.0001"
  } else if (x <= 0.001 && x >= 0.0001){
    pval <- format(signif(x,digits = 1), scientific = FALSE)
  } else {
    pval <- format(signif(x, digits = 2), scientific = FALSE)
  }
  return(pval)
}

# two.sided Welch test: ####
# Variable information:
# x1: represents the sample mean of Group 1
# x2: represents the sample mean of Group 2
# sd1: represents the SD of the Group 1
# sd2: represents the SD of the Group 2
# n1: number of the sample observations in Group 1
# n2: number of the sample observations in Group 2

twosided.welch.statistic <- function(x1, x2, sd1, sd2, n1, n2){
  # t.statistic
  numerator <- x1-x2
  denominator <- sqrt((sd1^2/n1)+(sd2^2/n2))
  t <- numerator / denominator
  # df
  df.numerator <- ((sd1^2/n1)+(sd2^2/n2))^2
  df.denominator <- ((sd1^4/(n1^2*(n1-1)))+(sd2^4/(n2^2*(n2-1))))
  df <- df.numerator/df.denominator
  # 95%-CI
  CI.lwr <- (x1-x2) - qt(0.975, df = df) * sqrt((sd1^2/n1)+(sd2^2/n2))
  CI.upr <- (x1-x2) + qt(0.975, df = df) * sqrt((sd1^2/n1)+(sd2^2/n2))
  # p-value
  # left tailed : p = cdf(t-score)
  # right tailed: p = 1 - cdf(t-score)
  # two-tailed: p = 2 * cdf(- |t-score|) or 2-2*cdf(t-score)
  p.value <- 2 * pt(-abs(t), df = df)

  # return output
  table <- data.frame(mean.Gr1 = x1, mean.Gr2 = x2,
                      sd.G1 = sd1, sd.G2 = sd2,
                      n1 = n1, n2 = n2,
                      t = t, df = df,
                      CI.lwr, CI.upr,
                      p.value)

  return(table)
}

```

## B.3 Data

The collected raw data of the test run is stored as `TestRun_dat.rds`. The raw data, from test run and DOOD which is saved as `DOOD_raw.csv`. After applying the exclusion criteria the cleaned data was saved as `DOOD_clean.csv`. In the process of data input, curation and preparation as explained in Section 2.4.4. The dataset `DOOD_clean.csv` and `QuantileWerle.csv` were merged together. The latter contains the mean and SD HGS values from Werle et al. (2009) with its quantile values. Afterwards, the data were stored as csv-files in long format as (`HGS.longformat.csv`) and wide format as (`HGS.wideformat.csv`). These datasets were used in Section 3 for the analysis of the research questions. In addition, (`HGSpct.longformat.csv`) and

(HGSpct.wideformat.csv) datasets were generated which contain additionally the quantile values. The data set HGSpct.longformat.csv was used to generate the Figure [2.2](#) and [2.6](#).



# Bibliography

- Abdi, H. (2010). The Greenhouse-Geisser correction. *Encyclopedia of Research Design*, 1(1):544–548. [19](#)
- Andri et al., S. (2022). *DescTools: Tools for Descriptive Statistics*. R package version 0.99.45. [16](#)
- Bates, D., Mächler, M., Bolker, B., and Walker, S. (2015). Fitting linear mixed-effects models using lme4. *Journal of Statistical Software*, 67(1):1–48. [16](#), [20](#)
- Begley, C. G. and Ioannidis, J. P. (2015). Reproducibility in science: improving the standard for basic and preclinical research. *Circulation research*, 116(1):116–126. [2](#)
- Bland, J. M. and Altman, D. (1986). Statistical methods for assessing agreement between two methods of clinical measurement. *The Lancet*, 327(8476):307–310. [12](#)
- Bobos, P., Nazari, G., Lu, Z., and MacDermid, J. C. (2020). Measurement properties of the hand grip strength assessment: A systematic review with meta-analysis. *Archives of Physical Medicine and Rehabilitation*, 101(3):553–565. [3](#), [21](#)
- Bohannon, R. W. (2008). Hand-grip dynamometry predicts future outcomes in aging adults. *Journal of Geriatric Physical Therapy*, 31(1):3–10. [1](#), [4](#)
- Bohannon, R. W. (2019). Minimal clinically important difference for grip strength: A systematic review. *Journal of Physical Therapy Science*, 31(1):75–78. [3](#), [27](#)
- Bohannon, R. W., Peolsson, A., Massy-Westropp, N., Desrosiers, J., and Bear-Lehman, J. (2006). Reference values for adult grip strength measured with a Jamar dynamometer: A descriptive meta-analysis. *Physiotherapy*, 92(1):11–15. [1](#), [4](#)
- Brown, H. and Prescott, R. (2015). *Applied Mixed Models in Medicine*. John Wiley & Sons. [20](#)
- Dalgaard, P. (2020). *Introductory Statistics with R*. Springer. [11](#)
- Das, K. R. and Imon, A. (2016). A brief review of tests for normality. *American Journal of Theoretical and Applied Statistics*, 5(1):5–12. [18](#)
- España-Romero, V., Artero, E. G., Santaliestra-Pasias, A. M., Gutierrez, A., Castillo, M. J., and Ruiz, J. R. (2008). Hand span influences optimal grip span in boys and girls aged 6 to 12 years. *The Journal of Hand Surgery*, 33(3):378–384. [3](#), [4](#)
- Gasser, T., Molinari, L., and Roos, M. (1996). Methodology for the establishment of growth standards. *Hormone Research in Paediatrics*, 45(Suppl. 2):2–7. [46](#)
- Hanten, W. P., Chen, W.-Y., Austin, A. A., Brooks, R. E., Carter, H. C., Law, C. A., Morgan, M. K., Sanders, D. J., Swan, C. A., and Vanderslice, A. L. (1999). Maximum grip strength in normal subjects from 20 to 64 years of age. *Journal of Hand Therapy*, 12(3):193–200. [2](#), [3](#), [4](#)
- Hanusz, Z. and Tarasińska, J. (2015). Normalization of the Kolmogorov-Smirnov and Shapiro-Wilk tests of normality. *Biometrical Letters*, 52(2):85–93. [18](#)
- Härkönen, R., Harju, R., and Alaranta, H. (1993). Accuracy of the Jamar dynamometer. *Journal of Hand Therapy*, 6(4):259–262. [1](#)
- Hothorn, T., Möst, L., and Bühlmann, P. (2018). Most likely transformations. *Scandinavian Journal of Statistics*, 45(1):110–134. [46](#)
- Huntington-Klein, N. (2022). *vtable: Variable Table for Variable Documentation*. R package version 1.3.4. [16](#)

- Innes, E. (1999). Handgrip strength testing: A review of the literature. *Australian Occupational Therapy Journal*, 46(3):120–140. [1](#), [2](#), [3](#), [4](#), [45](#)
- Kassambara, A. (2021). *rstatix: Pipe-Friendly Framework for Basic Statistical Tests*. R package version 0.7.0. [16](#)
- Kuzala, E. A. and Vargo, M. C. (1992). The relationship between elbow position and grip strength. *The American Journal of Occupational Therapy*, 46(6):509–512. [1](#)
- Kuznetsova, A., Brockhoff, P. B., and Christensen, R. H. B. (2017). lmerTest package: Tests in linear mixed effects models. *Journal of Statistical Software*, 82(13):1–26. [16](#)
- Lehnert, B. (2015). *BlandAltmanLeh: Plots (Slightly Extended) Bland-Altman Plots*. R package version 0.3.1. [16](#)
- Leong, D. P., Teo, K. K., Rangarajan, S., Lopez-Jaramillo, P., Avezum Jr, A., Orlandini, A., Seron, P., Ahmed, S. H., Rosengren, A., Kelishadi, R., et al. (2015). Prognostic value of grip strength: Findings from the prospective urban rural epidemiology (pure) study. *The Lancet*, 386(9990):266–273. [1](#)
- Leps, J. and Smilauer, P. (2020). *Biostatistics With R: An Introductory Guide for Field Biologists*. Cambridge University Press. [11](#), [19](#)
- Massy-Westropp, N. M., Gill, T. K., Taylor, A. W., Bohannon, R. W., and Hill, C. L. (2011). Hand grip strength: Age and gender stratified normative data in a population-based study. *BMC Research Notes*, 4(1):1–5. [2](#), [3](#), [4](#)
- Mathiowetz, V., Kashman, N., Volland, G., Weber, K., Dowe, M., Rogers, S., et al. (1985). Grip and pinch strength: Normative data for adults. *Archives of Physical Medicine Rehabilitation*, 66(2):69–74. [1](#), [2](#), [3](#), [4](#), [45](#)
- Mathiowetz, V., Wiemer, D. M., and Federman, S. M. (1986). Grip and pinch strength: norms for 6-to 19-year-olds. *The American Journal of Occupational Therapy*, 40(10):705–711. [1](#), [45](#)
- McGrath, R. P., Kraemer, W. J., Snih, S. A., and Peterson, M. D. (2018). Handgrip strength and health in aging adults. *Sports Medicine*, 48(9):1993–2000. [3](#)
- National Academies of Sciences, Engineering, and Medicine and others (2019). *Reproducibility and Replicability in Science*. The National Academies Press. [2](#)
- Park, E., Cho, M., and Ki, C.-S. (2009). Correct use of repeated measures analysis of variance. *The Korean Journal of Laboratory Medicine*, 29(1):1–9. [19](#)
- Peters, M. J., van Nes, S. I., Vanhoutte, E. K., Bakkers, M., van Doorn, P. A., Merckies, I. S., Faber, C. G., and group, P. S. (2011). Revised normative values for grip strength with the Jamar dynamometer. *Journal of the Peripheral Nervous System*, 16(1):47–50. [1](#)
- Potter, K., Hagen, H., Kerren, A., and Dannenmann, P. (2006). Methods for presenting statistical information: The box plot. In *VLUDS*, pages 97–106. Citeseer. [12](#)
- R Core Team (2021). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria. [14](#), [16](#)
- Roberts, H. C., Denison, H. J., Martin, H. J., Patel, H. P., Syddall, H., Cooper, C., and Sayer, A. A. (2011). A review of the measurement of grip strength in clinical and epidemiological studies: Towards a standardised approach. *Age and Ageing*, 40(4):423–429. [1](#)
- Shapiro, S. S. and Wilk, M. B. (1965). An analysis of variance test for normality (complete samples). *Biometrika*, 52(3/4):591–611. [18](#)
- Shiratori, A. P., Iop, R. d. R., Borges Júnior, N. G., Domenech, S. C., and Gevaerd, M. d. S. (2014). Evaluation protocols of hand grip strength in individuals with rheumatoid arthritis: A systematic review. *Revista Brasileira de Reumatologia*, 54:140–147. [1](#)
- Smith, D. A. and Lukens, S. A. (1983). Stress effects of isometric contraction in occupational therapy. *The Occupational Therapy Journal of Research*, 3(4):222–242. [4](#)
- Sousa-Santos, A. and Amaral, T. (2017). Journal of hand therapy differences in handgrip strength protocols to identify sarcopenia and frailty - a systematic review. *BMC Geriatrics*, 17(1):1–21. [1](#), [3](#), [7](#), [45](#)



- Soysal, P., Hurst, C., Demurtas, J., Firth, J., Howden, R., Yang, L., Tully, M. A., Koyanagi, A., Ilie, P. C., López-Sánchez, G. F., et al. (2021). Handgrip strength and health outcomes: Umbrella review of systematic reviews with meta-analyses of observational studies. *Journal of Sport and Health Science*, 10(3):290–295. [1](#)
- Stahel, W. (2013). *Statistische Datenanalyse: Eine Einführung Für Naturwissenschaftler*. Springer-Verlag. [11](#)
- Tamási, B. and Hothorn, T. (2022). tramm: Mixed-effects transformation models using template model builder. *R Journal*, pages Epub-ahead. [46](#)
- Trossman, P. B. and Li, P.-W. (1989). The effect of the duration of intertrial rest periods on isometric grip strength performance in young adults. *The Occupational Therapy Journal of Research*, 9(6):362–378. [1](#), [4](#)
- Tukey, J. W. (1977). Exploratory data analysis Addison-Wesley. *Reading, MA*, 688:581–582. [11](#)
- Watanabe, T., Owashi, K., Kanauchi, Y., Mura, N., Takahara, M., and Ogino, T. (2005). The short-term reliability of grip strength measurement and the effects of posture and grip span. *The Journal of Hand Surgery*, 30(3):603–609. [3](#)
- Wearing, J., Konings, P., Stokes, M., and de Bruin, E. D. (2018). Handgrip strength in old and oldest old Swiss adults—a cross-sectional study. *BMC Geriatrics*, 18(1):1–9. [3](#), [4](#)
- Werle, S., Goldhahn, J., Drerup, S., Simmen, B. R., Sprott, H., and Herren, D. (2009). Age- and gender-specific normative data of grip and pinch strength in a healthy adult Swiss population. *Journal of Hand Surgery (European Volume)*, 34(1):76–84. [1](#), [2](#), [3](#), [4](#), [5](#), [13](#), [38](#), [41](#), [42](#), [45](#), [46](#), [55](#), [88](#), [95](#), [106](#)
- Wickham, H. (2016). *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York. [16](#)
- Wilson, E. B. (1927). Probable inference, the law of succession, and statistical inference. *Journal of the American Statistical Association*, 22(158):209–212. [16](#)
- Wong, S. L. (2016). Grip strength reference values for Canadians aged 6 to 79: Canadian health measures survey, 2007 to 2013. *Health Reports*, 27(10):3. [2](#), [3](#), [5](#)

