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ANALYZING SENSOR BASED HUMAN ACTIVITY DATA USING TIME SERIES SEGMENTATION TO DETERMINE SLEEP DURATION

by

YOGESH DEEPAK LAD

A THESIS

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ABSTRACT

Sleep is the most important thing to rest our brain and body. A lack of sleep has adverse effects on overall personal health and may lead to a variety of health disorders. According to Data from the Center for disease control and prevention in the United States of America, there is a formidable increase in the number of people suffering from sleep disorders like insomnia, sleep apnea, hypersomnia and many more. Sleep disorders can be avoided by assessing an individual's activity over a period of time to determine the sleep pattern and duration. The sleep pattern and duration can be determined for an individual with the help of commercially available fitness devices such as Fitbit, Nike, Apple, and many others, which are activity trackers with accelerometer sensors. But these devices determine sleep duration from a "Proprietary Algorithm", which processes the movement sensor data. Due to the proprietary nature, in a long-term study, the developer of the algorithm could update and make changes to the algorithm without revealing the details of the update to the user. This affects the measures reported by the algorithm. Hence to determine correct and reliable sleep duration, an Algorithm is developed by directly analyzing the actigraphy signals using time series segmentation. The study was done on a group of 20 healthy Undergraduate students from Missouri University of Science and Technology, whose daily physical activities were recorded using the GENEActiv accelerometer wristwatch worn on the non-dominant wrist. In this thesis, an open source algorithm has been developed using the daily physical activity data to estimate the sleep duration for any individual.

Keywords: Actigraphy, GENEActiv, Sleep, Data Analysis, Time series segmentation, Physical Activity, Algorithm

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1. INTRODUCTION

1.1. BACKGROUND

Sleep is required and necessary to rest the brain and body. It plays an important role in maintaining good physical health and wellness throughout our lives. Sleep also plays a crucial role in helping the brain work adequately and efficiently. Getting the right amount of sleep helps in improving one's problem-solving skills and improves one's learning capability. On the contrary, sleep deprivation has adverse effects on a person's health and life in several different ways [1].

In recent times, sleep deprivation has been a common problem. Sleep deprivation is caused to an individual if he or she gets less sleep than required for normal functioning of the body. However, normal differs across individuals. According to the article in Medical News Today by Kathleen Davis FNP [2] sleep deprivation has many adverse effects on the human body system.

Some of the effects include but not limited to:

- The weakening of the immune system
- Respiratory diseases
- High risk of Diabetes
- Risk of cardiovascular disease
- Hormone production
- Depression
- Obesity

The usual cause of sleep deprivation [1] are sleep disorders like insomnia, sleep apnea, Restless Leg Syndrome (RLS), and primary hypersomnia. According to the American Sleep Association (ASA) [3], "Sleep Disorders represent some of the most challenging medical conditions and affect 1 in 3 people at some stage of their lives." According to the Centers of Disease Control and Prevention (CDC) [4] 50-70 million US adults suffer from a sleep disorder and 37.9% of people reported unintentionally falling asleep during the day at least once, in the preceding month. Furthermore, 4.7% proclaim that they nod off or fell asleep while driving at least once in the preceding month. In addition, drowsy driving due to inappropriate sleep accounted for nearly 1,550 fatalities

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and 40,000 non-fatal injuries reported annually in the United States of America. According to CDC [4], Insomnia is the most prevalent sleep disorder, with short-term issues reported by 30% adults and chronic insomnia affecting 10% of all adults in the U.S. Out of 25 million U.S. adults having obstructive sleep apnea, 9-21% in women; 24-31% in men. In addition, 100,000 deaths are caused each year in US hospitals due to medical errors and sleep deprivation.

Further, statistics shown in the study by The RAND Corporation [5] reveals that lack of sleep has a big impact on the nation's economy. The study states that the United States of America sustains economic losses up to $411 billion dollars per year (2.28% of its GDP) due to lack of sleep. It has been observed that lack of productivity is in part due to lack of sleep. In the United States, 1.2 million working days are lost annually due to lack of sleep. In addition, lack of sleep leads to 13% higher mortality risk. The statistics show that the problem of not obtaining adequate sleep is a serious one and cannot be ignored. In order to prevent it, an accurate sleep pattern assessment and determining the sleep duration of an individual should be done to find the causes and severity of the sleep disorders.

There are different methods in which sleep pattern can be assessed, like questionnaires, actigraphy, polysomnography and multiple sleep latency test. Among all the methods mentioned, Actigraphy is an instrumental method where the evaluation is done through human activity and movement measurement.

Actigraphy is recorded and measured continuously with the help of a small device called Actigraph (wrist-worn accelerometer). An accelerometer is an electromechanical device which measures the acceleration forces of the body. Moreover, an actigraph is generally a lightweight portable device, which is normally the size of a wristwatch. It is worn mostly on the hip, belts, ankles, arms, wrist and other body movement collection points of interests. As the actigraph records and detects the movement of an individual, in recent times wrist actigraphy have been widely employed for assessing the sleep pattern of an individual over a continuous period of time [6]. In order to determine the sleep pattern and sleep duration for an individual in the long term, developing an automatic sleep scoring algorithm that is cost-efficient and easily available is important. It is through the development of such an algorithm that small changes in an individual activity

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and sleep patterns can be assessed. This capability to assess the small variability on an individual basis would prove useful to any long-term study that seeks to assess habitual patterns for individuals and a possible correlation between activity and sleep patterns.

1.2. MOTIVATION AND SCOPE.

The sleep pattern and sleep duration can be determined for an individual with the help of commercially available fitness devices which are in the form of a wristwatch or by examining the person in a sleep laboratory. Some of the well-known companies like Fitbit, Nike, Apple, Samsung, Nokia, Garmin and many others make fitness devices. These devices do direct analysis on the data collected and display the summary of each day which includes sleep duration, deep sleep duration, a number of steps walked throughout the day and other useful information to turn an individual into a healthier human being. The summary data can be used by an individual to change their behavior towards leading a healthier life. Thus, by presenting an individual with their activity and sleep, then they can be proactive in making better decisions. These decisions include going to bed at an earlier time, walking more to meet physical activity goals, duration of activity and other key activity summary information. The following Figure 1.1 shows the working of a commercially available fitness device [7].

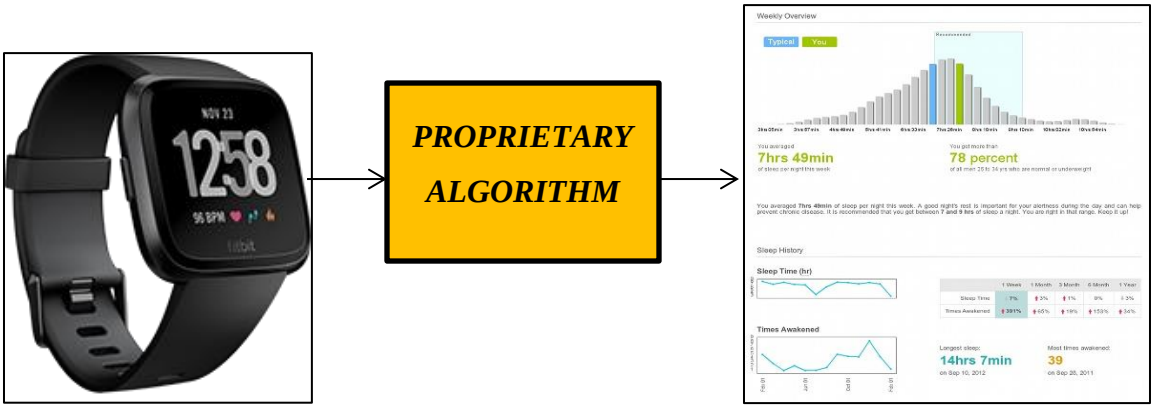

Figure 1.1. Working of Commercially Available Fitness Devices

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But these devices though useful and informative, use a “Proprietary algorithm” to analyze their data. Proprietary algorithms are the algorithm developed by the company to achieve a specific goal. The company has sole rights, trademarks, and often have a patent(s) associated with the algorithm. The company does not reveal what and how they are analyzing the accelerometer data with the algorithm which makes it difficult to understand how the data is analyzed, summarized, and presented to the end user. Moreover, whether the results of the analyzed data are appropriate for changing the individual’s daily habits to lead a healthier life. In addition, the measures determined by the device are affected if there is any update provided for the algorithm by the manufacturer during a long-term study. This makes it unreliable to use these devices for analyzing the sleep pattern and to have reliable sleep duration of the individual over a long-term study.

On the other hand, the sleep centers help in determining sleep duration and sleep pattern of the person by performing a sleep study in a lab. In this sleep study, a technologist places different sensors or electrodes on the person’s body and records different types of sensor data (heart and breathing rates, body movements, eye movements and many others) while the person is asleep. The data collected from the sleep study is analyzed by the technologist and then later evaluated by a doctor. Depending upon the results the doctor recommends a change in daily activities to lead a healthier life.

Thus, it is necessary to have an algorithm where the individual can be assessed in a more open environment, knows how the analysis takes place in the device and have reliable results regarding the common sleep measures. The sleep measures include sleep duration, activity, and so forth.

The algorithm would help in knowing how a person’s sleep pattern and sleep duration differs from day to day. It has remained an elusive correlation in the literature that sleep and more importantly, lack of sleep can impact the cognitive performance of the individuals.

Cognitive performance [8]– [10] is the capability of the person in utilizing the knowledge acquired by the mental process to perform a certain action. Furthermore, with the help of results from the Algorithm, we could find the relation between the sleep

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pattern and sleep duration of an individual with that of the cognitive performance, which according to the literature remains an elusive correlation due to lack of long-term studies and complexities involved with sleep. By determining the sleep pattern and sleep duration of an individual with that of the previous night we can examine the performance of the individual for the following day and continue this study for a long term to see if an individual's unique sleep patterns and rhythm, variations, and other key characteristics information can be tied down.

1.3. LITERATURE REVIEW

1.3.1. The Emergence of Actigraphy. The early research in actigraphy data analysis involved using a piezoelectric transducer to record wrist activity, (D. J Mullaney et al., 1980) [11] used the piezoelectric transducer to record the actigraphy data of the participants in his sleep study to determine their total sleep time. They also recorded the activity of the brain with Electroencephalography (EEG), the activity of skeletal muscles with electromyography (EMG) and eye movement with the help of Electrooculography (EOG). Each recorded activity which was then scored into two states: sleep state and wake state. The research study by (D. J Mullaney et al., 1980) [11] showed that the actigraphy overestimated the total sleep time (TST) by 15 minutes using the Rechtschaffen and Kales model [12]. The overestimation was due to the actigraphy interpreting very low-frequency movement as sleep despite the person being awake in the bed, which is a clear drawback of using accelerometers, which only record movement information. Thus, small movements or periods of low mobility have the potential to misclassifying an individual in the sleep state. Furthermore, despite the overestimation of the sleep duration on an average by 15 minutes with respect to EEG it still has the benefit of being low in cost and individual does not have to be monitored in the sleep lab, which is often an uncomfortable situation. Thus, the research showed that Actigraphy is more convenient to use and can be a reliable method to be used for clinical purposes. The cost-benefit of the actigraphy can be increased further, by developing algorithms which can improve the scoring of sleep and give more reliable sleep duration.

Keeping this in mind (Webster et al., 1982) [13] developed the first automatic sleep scoring algorithm. The study measured the participant's wrist activity with the help

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of a piezoceramic transducer, which was digitized to identify the sleep and wake states of an individual. This digitized activity signal was then scored using an automatic scoring program which was a combination of ten different mathematically formulated algorithms to identify the sleep/wake states with that of the EEG. Both the scores agreed 94.46% of the time. (Webster et al.. 1982) [13] also collected data and recorded specific movement functions using a wearable microprocessor-based digital activity monitor. The automatic scoring program devised by them also scored the newly collected data, obtained from the wearable microprocessor-based digital activity monitor which agreed 93.4% with the EEG regarding the sleep duration measure. The study (Webster et al.. 1982) [13] indicated that the data from the wrist activity can be digitized and scored using an automatic scoring program with the help of the computer with negligible loss in the accuracy of sleep duration. The automatic scoring program was 5 to 10 times less costly as compared to EEG scoring and could compute the score in seconds. Furthermore, the use of an all-digital system is a fast, accurate and a cost-efficient method to monitor sleep using wrist activity data in an ambulatory environment. Unlike EEG which required electrodes to be placed throughout the human body mostly the scalp, a digital activity monitor is comfortable and appropriate as it is a non-intrusive sensor. This research led to the advancement and development to improve the automatic sleep scoring algorithm.

1.3.2. Early Research in Automatic Sleep-Scoring Systems. (Sadeh et. Al, 1989) [14] used an automatic scoring procedure on actigraphy data to discriminate between sleep and wake states and validate it against the Polysomnography (PSG) recordings. Polysomnography (PSG) is a type of test similar to EEG, conducted during sleep for the purpose of detecting sleep disorders in an individual. The automatic scoring procedure developed by (Sadeh et. Al, 1989)[14] has the following attributes: handled large data sets, correctly classified sleep-wake states and accurately estimated the sleep efficiency. Sleep efficiency is the ratio of time an individual is asleep at night to that of the total time the individual has spent in the bed. To classify the sleep and wake states correctly an optimal discriminant function [15] was developed from the accelerometer data. Further, the automatic scoring procedure correctly differentiated between the individuals from a normal population and an individual belonging to a group of insomniacs and individuals with sleep apnea. The procedure could also correctly identify

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the severity of sleep apnea by using the actigraphy/accelerometer data alone. The study concluded that the actigraphy recordings can be used for initial large-scale screening studies and in studies of the clinical nature. An actigraph can be used as a tool for assessing the problems or issues of sleep, obtaining clinical data from physical activity data, and differentiating sleep and wake states for patients in bed. But the study needed to have more improvement in the sleep scoring procedure to achieve the clinical standards.

(Cole et al., 1992) [16] developed an automatic scoring algorithm for distinguishing sleep and wakefulness states based on data collected from wrist activity via an accelerometer. The method was a replicate of the Webster's algorithm [13], with (Cole et al., 1992) rescaling the Webster's algorithm to attain a high accuracy for identifying the sleep and wake state. The accuracy obtained from wrist activity to distinguish sleep and wake state was 88% accurate with that of the polysomnography (PSG) in a mixed sample of subjects. The research study found that it is easier to record multiple night sleep recordings using a wrist activity as compared to Polysomnography due to its convenience, non-intrusive nature, and cost efficiency. Furthermore, the study stated that in spite of night sleep variability in humans, the actigraph can be used as a device to identify the sleep and wake states by recording multiple nights in order to improve the accuracy. With the growing popularity of using actigraphy in sleep studies, the research focus now turned towards its validation and actigraphy specifications

1.3.3. Actigraphy Validation Techniques and Methodological Issues.

(Sadeh et. Al, 1994) [17] developed and validated a new sleep-wake scoring algorithm for the miniature wrist actigraph (AMA-32, Ambulatory Monitoring, Inc. Ardsley, NY) and assessed the different methodological issues of actigraphy placement. The results of the algorithm were compared with the Polysomnography readings (PSG). The non-dominant hand and dominant hand scoring agreed 91%-93% with that of PSG's sleep/wake period durations. The activity levels from the dominant and non-dominant hand differed during the sleep and wake period. The study suggested methodological issues of the variation in the device sensitivity with regards to movements. The methodological issues include correct use of actigraphy and its artifacts which are not addressed properly in clinical research. To identify artifacts related to breathing motion during sleep, the use of twin wrist actigraphy is helpful. This study involved a group of

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subjects ranging from 10-25 years of age. In order to expand the research and involve other age groups (Sadeh et. al, 1995) [18] further expanded his work in the field of actigraphy by examining the validity of actigraphy in the assessment of sleep-wake patterns of infants. In this research study instead of using the PSG as a means for validation, an observation method was selected where the infant was observed continuously by an expert to examine and score the movement of an infant during sleep. This study also used the miniature wrist actigraph (AMA-32, Ambulatory Monitoring, Inc. Ardsley, NY), which was attached to the infant's ankle in order to collect the activity data. In order to assess the sleep and wake pattern of the actigraphy data, an automatic scoring algorithm was developed and validated with the observer scoring. The use of experts is common practice and PSG itself is a form of expert-based translations where the signal is marked to define different states of sleep, based on various signal properties. Results showed that the automatic sleep scoring algorithm and the observer scoring agreed 95.3% of the time. The research specifically stated that while examining the infant with actigraphy data, the data first should be structured and cleaned using a program [14, 19] to apply an automatic scoring algorithm. Otherwise, the actigraph can lead to confusing results with an infant being identified as sleeping due to very low-frequency movements. This research concluded by stating that actigraphy can be used for assessing the sleep-wake patterns for an infant in order to determine whether the infant has any disorder development in the early phase of life like breathing difficulties, problems in sleeping, and others. Since actigraphy can be used for long-term sleep studies, further research is required for doing longitudinal studies to assess the maturational pattern in different types of infants. Moreover, research should be done to know if actigraphy can be used as a tool to evaluate the clinical interventions.

In a review study, (Sadeh et. al, 1995) [20] examined the previously available experimental actigraphy data to find its potential clinical and research use in the field of sleep medicine. The review was divided into three different parts, with the first part focused on the methods which were used for assessing the validity and reliability of actigraphic sleep assessment. The second part focused on actigraphic experimental and clinical methods in sleep medicine. Lastly, the third part discussed the issues related to methodology in a sleep-wake study using actigraphy. The review stated that the

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actigraphy had methodological issues which include actigraphy reliability and validity in assessing the sleep and wake patterns, uniform use of units of measurement, placement of actigraphic device, artifacts like sleeping surface, moving bed partner, a mattress and also individual differences between the participants demographic information like age, gender, and others. However, can be mastered with further research related to actigraphy placement, improving the recording of ambulatory movements, and with further research in automatic scoring algorithms. Based on the review study (Sadeh et. al, 1995) [20] stated that actigraphy can be used in assessing the sleep disorders as it is one of the most cost-efficient methods for long-term assessment of sleep. Actigraphy, can differentiate between the sleep and wake states in a person lying in the bed and can assess sleep and wake patterns in patients suffering from sleep disorders. This review then helped other researchers to make improvement in the sleep study research using actigraphy.

Actigraphy has gained popularity in sleep study research, (Clete A. Khushida et al, 2001) [21] obtained common sleep measures from actigraphy like total sleep time (sleep duration), sleep efficiency (measure of mobility during sleep. E.g. tossing & turning), and wakefulness (amount of time spent active). These sleep measures were then validated with Polysomnography (PSG) recordings and subjective questionnaires. The methodology involved sleep disordered patients, whose actigraphic and PSG data was used to calculate the sensitivity, specificity and accuracy measure for a 30 sec time period or epoch. The results of the study stated that the sleep measures like total sleep time and sleep efficiency from the PSG data had high significance with the combination of actigraphy and subjective data. The research study concluded that in order to determine the total sleep duration and sleep efficiency in sleep-disordered subjects, the use of subjective data is more beneficial than the actigraphic data. This is because when the sleep measures for the combined data of actigraphy and subjective data were not statistically significantly different from the PSG data. The research results showed that it is more beneficial to use a subjective data rather than the actigraphy data for a person's sleep duration.

1.3.4. Reviewing the Role of Actigraphy in Sleep Medicines. In the (Sadeh et. Al, 2002) [22] study mention effectiveness, dependability, and restrictions for identifying the sleep and wake patterns using actigraphy. The study mentioned that actigraphy has

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been declared as a reliable method in order to determine sleep and wake disorders and also to differentiate between different clinical groups. The research also states that there are pitfalls related to actigraphy, for example actigraphy cannot distinguish between patients having long periods of low activity or one who is active in sleep. There is no validation available for scoring algorithms, devices or clinical groups. Further, using automatic scoring algorithms by ignoring artifacts lead to inaccurate results. The authors of (Sadeh et. al, 2002) gave recommendations in order to overcome the pitfalls mentioned to improve future research and clinical studies which involves the use of actigraphy. The pitfalls mentioned were then used in the future research in order to improve the results. (Luciane de Souza et. al, 2003) [23] in their paper have the main objective, which was to assess the similarity between Polysomnography (PSG) and formerly proposed an algorithm of Cole et al. (1992) and Sadeh et al. (1994) in order to analyze the actigraphy recordings. The per minute agreeance between the algorithms and PSG was evaluated by calculating the sensitivity, specificity, and accuracy with regards to sleep duration and other sleep measures. The calculation of specificity and sensitivity gave more information about the similarity between the two algorithms. The similarity of the sleep parameters like sleep latency, sleep efficiency, total sleep time and intermediate awakening calculated from the two algorithms was compared with the PSG by Bland and Altman technique. Bland and Altman developed a technique to estimate the similarity within a sample on the basis of the mean difference between two systems from each subject [24,25]. The research study stated that the Bland and Altman's technique is a powerful technique, which showed that actigraphy overestimated all the sleep parameters and underestimated the awakening for each subject. The study provided information on the advantages and drawbacks of actigraphy, in addition, stated that the extent of similarity between the actigraphy and PSG should be decided by the researcher which might influence their research study.

1.3.5. Wrist Activity Monitor. (G.Jean-Louis et. Al, 2001) [26] determined sleep-wake states from the nighttime wrist movement by using different motion-quantifying algorithms and was compared with the Polysomnography (PSG) readings. The study involved healthy adults wearing commercially available wrist activity monitor Actillume I (Ambulatory Monitoring, Inc. Ardsley, NY) and Mini Motionlogger

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(Ambulatory Monitoring, Inc. Ardsley, NY), in addition, PSG recordings were done simultaneously with Somnostar digital polysomnography (SensorMedics, Yorba Linda, CA) to compare the results from the wrist activity monitors. The study involved estimating the sleep and wake states from nighttime wrist movements with five different actigraphy modalities and comparing the results with the Polysomnography (PSG) readings. All the five modalities agreed with the PSG readings with a range of 91.4%-96.5% agreement, the Proportional Integrating Mode (PIM) from the Mini Motionlogger (Ambulatory Monitoring, Inc. Ardsley, NY) performed the best (96.5%) to differentiate between the sleep and the wake states. This research showed that the commercially available actigraphic device can be used for sleep study research. The sleep and wake states can be distinguished by recording the wrist activity data of an individual.

In another research study related to wrist activity monitor (Lotojonen et al. 2003) [27] differentiated the sleep and wake states during bedtime and naptime using an online activity monitoring device Vivago WristCare (IST International Security Technology Oy, Helsinki, Finland) and actigraphy (ActiWatch, Cambridge Neurotechnology, AW4). The result was calculated using two previously developed scoring algorithm by Jean-Louis et al. (1996) [28] and Sadeh et. Al (1994) [17] and tested against the PSG recordings. Both the devices Vivago WristCare and Actiwatch showed similar performance when tested against Polysomnography (PSG). On the other hand for the nap-time analysis, the results were compared with each other (Vivago WristCare and Actiwatch) which showed similar results. (Lotojonen et al. 2003) [27] concluded by stating that the Vivago WristCare which is a physical activity monitoring device and a security device used by elderly people can be used for determining the sleep and wake states in long-term sleep study as it showed similar performance with actigraphy.

Since actigraph devices were available commercially in different types of configurations, (Kathleen Benson et al. 2004) [29] in the research study compared two commercially available actigraphy devices with different manufacturer, hardware, firmware and PC software: Actiwatch L(Mini-Mitter Co., Inc, Bend, Ore) and Basic Mini Motionlogger (Ambulatory Monitoring, Inc, Ardsley, NY) to assess the performance in deriving measures of sleep. The results showed that the Mini Motionlogger when set to high sensitivity resulted in more total sleep time, less wake after sleep onset time and

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greater sleep efficiency as compared to the Actiwatch L. Furthermore, when the sensitivity was set to low the Mini Motionlogger resulted in higher wake after sleep onset as compared to Actiwatch L. The study showed that when the sensitivity was set to medium both the device had similarity in their performance. The purpose of the study was to compare the results of devices with each other and find if we have equivalent results despite different configurations (hardware and software) for both the devices. The author concluded by stating that for the selection of commercial actigraph device other specific characteristics like cost, memory, weight, interface, and output measures should be taken into consideration. In addition, the authors stated that the sleep measures like sleep latency, total sleep time, wake after sleep onset, sleep efficiency obtained from the actigraph devices cannot be validated without the PSG recordings. The research showed the necessity of using PSG data to validate the results from the actigraphy device.

Keeping this research in mind and the necessity to validate the sleep measures from the commercially available actigraphy device with the polysomnography (PSG) recordings, (Lorenzo Tonetti et al. 2008) [30] in the research study compared two commercially available actigraphy with that of the PSG recordings in a population of healthy subjects. The study involved the subjects wearing commercially available actigraphs: Basic Mini-Motionlogger (MML; Ambulatory Monitoring, Inc., Ardsley, New York, USA) and Actiwatch (AW; Cambridge Neurotechnology Ltd, Cambridge, UK) with parallel PSG recording. Both the actigraph devices and polysomnography (PSG) gave sleep measures: sleep onset latency, total sleep time, wake after sleep onset, and sleep efficiency. The comparison of sleep measures from the two actigraph devices and polysomnography resulted in the Sleep onset latency being underestimated by both the actigraph devices while having similar performances with other measures of sleep. (Lorenzo Tonetti et al. 2008) [30] concluded that both the commercially available actigraph devices can be used for measuring the sleep measures except for Sleep Onset Latency (SOL) and a limitation of obtaining results for healthy population only. The research study showed that the commercially available actigraphs have good performance when compared to PSG and can be used for assessing sleep and wake states. This led to an increase in the use of commercially available actigraphs in sleep research study.

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(Allison R. Weiss et. al, 2010) [31] also used a commercially available device used for measuring core physical activity to estimate sleep. The devices used for the study were: Sleepwatch (Ambulatory Monitoring, Inc., Ardsley, NY), Actiwatch (Respironics, Pittsburgh, PA) and Actical (Respironics, Pittsburgh, PA) in addition Polysomnography (PSG) recordings were also recorded for result comparison. All the three devices overestimated the total sleep time with regards to the PSG recordings, this is due to the inability of actigraphy to correctly detect the wake-up periods in a subject that is not moving much. The study showed that the Actical device which is used for specifically measuring core physical activity gave strong results of total sleep time in correlation with the other actigraphy devices (Actiwatch and Sleepwatch). (Allison R. Weiss et. al, 2010) [31] thus concluded that using a physical activity measurement device in sleep research, it helps in knowing a distinct sleep and physical activity statistics for each participant which will result in knowing their health behaviors.

1.3.6. Probabilistic & Statistical Distribution Models in Actigraphy.

(Andrew S.P Lim et. al, 2011) [32] developed a model using actigraphy data to assess fragments of human rest and active patterns using a probabilistic state transition model. The study states that actigraphy has more advantages over polysomnography to assess the rest and activity pattern in an individual. The advantages of the actigraphy include it is a non-invasive/intrusive method and has the ability to record activity on a long-term basis, that can be used in an open environment and has the ability to interpret the behavior of the individual. The fragmentation of rest differs with the individual's age, sex, and Body Mass Index (BMI). The probabilistic model developed in the research study is cost efficient, can be effortlessly implemented in analyzing data and has the ability to be implemented in exhaustive clinical studies.

In (A. Domingues et. al 2012) [33] the author developed a model for describing the different states in actigraphy data based on three statistical distribution: Exponential, Rayleigh, and Gaussian. The study stated that by utilizing the parameters and weights of combination model of the three distributions it can be seen that the sleep and the wake are a different statistical distribution which was then used to distinguish between two states. The research showed that the sleep and wake states can be differentiated by examining the statistical properties like the distribution of the states. The results obtained from the

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model were not lucid to determine the best mixture distribution and more research is required to improve the distribution models.

1.3.7. Use of Actigraphy Signals. As actigraphy records the data of activity for each subject by recording the signals. (Cristina Crespo et al. 2012) [34] developed an algorithm to identify the activity and rest periods by using the actigraphy signals in order to correctly identify the ambulatory blood pressure monitoring parameters. The algorithm developed in the study uses morphological processing of actigraphy signals, adaptive rank-order filters, and rank-order decision logic. The algorithm performance was around 94% when tested on the dominant and non-dominant hand of 104 subjects. The previously developed algorithms like Sadeh et. Al (1995) [20], Cole et. Al (1992) [16] was specifically used for studying sleep disorders where they are highly sensitive to numerous wake periods during an individual's sleep. This drawback is overcome by the algorithm developed for identifying the sleep and rest cycle with respect to the ambulatory blood pressure monitoring and assessment related to cardiovascular risk. The proposed algorithm is not highly sensitive and ignores the short periods of transition between the rest and activity period. The algorithm in spite of the high performance should be validated with the differently available algorithm in order to be used for clinical applications. Specifically characterizing the performance of the algorithm with different population would help in the more detailed examination of the algorithm developed.

The actigraph device records signal with different features which are then used for analyzing the human activity. In the research study by (Mohammed A. Khabou et al. 2013) [35], they used 63 common features which are already used in actigraphy data analysis to find the best performers from them [36]. To find the best features the study used two algorithms: entropy minimization and add-one feature, among which the add-one feature algorithm performed better. On the selection of the best features, a class prototype was generated using K-means and min-max clustering algorithms for classifying the actigraphy signals into five different activities like standing, lying down, sitting at a desk and jogging on the treadmill. The algorithm performed with a classification accuracy of 95%-100% by using only 1-5 features. The model needs more improvement by using a more refined classifier to get a more accurate classification. In

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order to achieve more accurate classification a study (D.Martin-Martinez et. Al, 2014) [37], proposed methodology to determine the sleep and wake periods automatically by analyzing the actigraphy signals. The design parameters for the actigraphy signal are automatically set by first estimating the binary classification (sleep and wake states) by using the expectation-maximization algorithm. Secondly, the previously determined binary classification is refined using an iterative linear classifier for better determination of the two states. This methodology had a general application and was able to identify few minutes of multiple rest intervals.

(Matthew William Driller et al. 2017) [38] studied device placement to measure sleep by wearing an actigraphy device on the dominant and non-dominant wrist. The study measured different sleep measures like total sleep time, total time in bed, sleep efficiency, sleep latency, wake after sleep onset, sleep onset time and wake time for both the writs to measure sleep. The results showed that there was no notable difference between any of the sleep measures which proved that the actigraphy device can be worn on any wrist to analyze the actigraphy data. Further, this research gave an insight that the actigraphy device placement does not matter to determine the accurate sleep measures. So, the device placement is up to the researcher and the individual on which wrist to opt for recording the activity. The device should be placed on the wrist which is more comfortable for the user. Till now the wrist activity was monitored to record the person movement. To take the research a step further (Kelsie M.Full et.al 2018) [39] validated hip and wrist-borne physical activity accelerometer devices used for recording the physical activity data with polysomnography (PSG). The physical activity accelerometer device (GT3X+ Actigraph, LLC, Pensacola, FL) measured the sleep measures like total sleep time, sleep efficiency and wake after sleep onset time and was compared to the sleep measure data of the polysomnography (PSG) recordings. The results showed that there was no significant difference between the sleep measures determined by the accelerometer and the polysomnography (PSG) which proved that the physical activity accelerometers can be used for determining viable sleep measures.

The literature review thus encourages to develop an algorithm that automatically identifies the Sleep and Wake states of a person using the activity signals alone for assessing the sleep pattern and sleep duration. The previous studies do not include

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research where the algorithm is developed by directly analyzing the activity signals recorded by the actigraph. This encourages to develop an algorithm which can analyze actigraphy signals recorded using the actigraphic device for all types of user and not too focused to a specific group of users. The algorithm developed in the thesis is an open source and can be used for determining sleep duration in a preliminary long-term sleep study. The working of the algorithm involves directly analyzing the actigraphy signals for each individual involved in the study over a 24-hour duration by using Changepoint detection and Z-scoring to determine the sleep duration.

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2. METHODOLOGY

This section will describe the methodology used to develop the algorithm for determining the sleep duration of participants in detail. The methodology uses a combination of preprocessing accelerometer data, statistical change point, threshold classification, and time series segmentation. The following Figure 2.1. shows a flowchart of the important steps involved in developing the methodology:

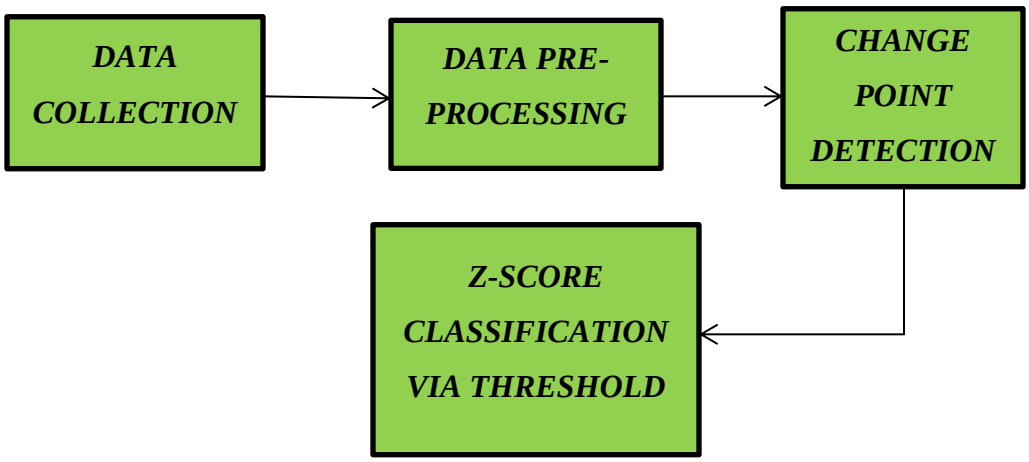

Figure 2.1. Flowchart of the Methodology

2.1. DATA DETAILS

The data for the experiment was collected using the GENEActiv Original smartwatch [40]. This smartwatch consists of an accelerometer which is used to measure the human activities. The GENEActiv was specifically chosen for the research because it has the advantage of collecting raw data. This feature is not provided by any other manufacturer. Thus, it provides the benefit of using the unfiltered data, so that researchers can reuse the data anytime in the future for comparison. It also gives the flexibility of using different tools and statistical packages to analyze the data. Lastly, GENEActiv is an

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open source giving more benefit for researchers. Figure 2.2 illustrates a GENEActiv smartwatch [41].

Figure 2.2. GENEActiv Original made by Activinsights

The raw accelerometer data was recorded at a sampling frequency rate of 60 Hz but was downsampled to one-minute aggregates. These aggregates are the sum of signals beyond the sensing threshold of the accelerometer device, refer to GENEActiv watch for details regarding these sensing thresholds [41]. These one-minute aggregates show the daily activity of the person in all types of environments as it captures mobility throughout the entire day. The data collection was done for the Fall 2016 semester and Spring 2017 semester across 28 participants which included 5218 days. All the participants were healthy Undergraduate students both males and females from the Missouri University of Science and Technology. The student participants were all between 18-20 years of age. The watch was worn on the non-dominant wrist for all participants. The watch was charged once a month for 5 hours for each participant, which resulted in loss of days' worth of data for the individual due to charging. The data collected include mean acceleration in the x, y, and z-direction, sum vector magnitude, near body temperature and light exposure for each participant [40]. These measures will be fully described in the proceeding section of this document.

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2.2. DATA DETAILS

The GENEActiv watch records 10 different data, which were aggregated to per minute sums for each participant. For this thesis, the focus was solely on the feature of sum vector magnitude (SVM) which is the summation of the magnitude of acceleration along all the three axes (x, y, and z) together. This helps in knowing the magnitude of the movement in all the direction without using a feature of each axes separately. Table 2.1 shows the 10 different features that are recorded by the GENEActiv watch.

Table 2.1. Data Set Features

Features	Description
x_m	Mean of acceleration in the X direction (x)
y_m	Mean of acceleration in the Y direction (y)
z_m	Mean of acceleration in the Z direction (z)
lux_m	Mean light level
temp_m	Mean temperature
SVM	sum of vector magnitudes (SVMgs = $[(x^2 + y^2 + z^2)^{1/2} - 1g]$)
x_p	The standard deviation in the X direction
y_p	The standard deviation in the Y direction
z_p	The standard deviation in the Z direction
lux_p	Peak light level

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2.3. ALGORITHM

To develop the algorithm for determining the sleep duration from sleep, data is first collected and converted into suitable file format required for doing the analysis. All the converted data files undergo data pre-processing which involves cleaning & prepping the data files along with data filtering using a Butterworth filter to remove the extreme high and low-frequency data points. The filtering process sought to remove all data related to frequencies not commonly observed in human activity. Further, we segment the filtered time series data into 1440 minutes, which contains a full 24-hour segment of data from noon to the next day's noon. Next, change point detection analysis is applied and z-score is then used to create a clear threshold value to classify activity signals as sleep or activity. This threshold results in a determination of the sleep duration of a person based on their activity captured by the one-minute aggregates of accelerometer data. This process is discussed in detail in the proceeding sections.

2.4. DATA COLLECTION AND CONVERSION

The data recorded for each participant in the GENEActiv wrist-worn accelerometer is transferred to the Desktop/Laptop using the GENEActiv software platform [42]. Initially, the files are in binary (.bin) format which is then converted using the Data Converter tab of the GENEActiv software to a comma separated (.csv) file format for the purpose of analysis. The epoch length during the conversion of the binary file to comma separated file is set to 60 seconds. The comma separated file (.csv) has all the features mentioned above in Table 1.1 for each minute. The sum vector magnitude is created for each epoch and the gravitational force (1g) is subtracted. The comma separated value (.csv) file having all the features of table 1.1. for each minute is then used for doing further analysis. The GENEActiv watch has been previously used in a variety of activity and sleep research [43-45].

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2.5. DATA PRE-PROCESSING

2.5.1. Data Preparation. The first stage of data pre-processing involves the data preparation of the data collected for each participant. The data collected from the watch was not clean and structured i.e. it did not have the same start-time and end-time for all the participants, which makes the analysis difficult.

In order to make it structured, the data had to be cleaned, especially in regard to the start-time and end-time. This is because each participant picks up their respective watch at different times of the day at the initial start of a collection and during the charging periods. The goal of structuring the data is to have complete days of activity information that have the same start-time and end-time, which will make the analysis easier. In this thesis, the start-time for a day of data considered from 12:00 pm to 11:59 am on the following day. This was achieved by writing a program script as shown in Appendix, in the RStudio environment using the R package [46].

The data cleaning assured that each participant had complete days of data i.e. 1440 minutes. The start- time (12:00:00 pm) and end-time (11:59:00 am) was specifically chosen to ensure the analysis considers the most common time most people sleep. Hence, this time block was chosen with the hopes that it would capture the full time in bed for any person. It should be noted that not all people sleep during this time block. Thus, some days resulted in the sleep period extending beyond this time block or beginning with sleep into the afternoon. Inconsistent Participants

After cleaning all the data files, it was compiled into one file containing all the participants with complete days of data using the ‘readbulk’ package of the CRAN-R project [47]. The final data file consisted of 1160 days of data across 20 participants. Figure 2.3 illustrates the activity pattern of a participant after preparing the dataset:

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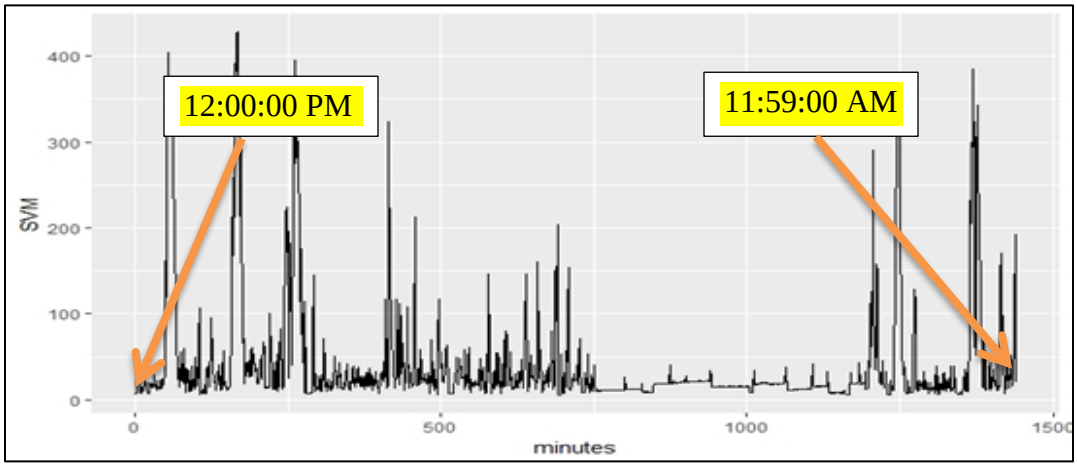

Figure 2.3 Typical Unfiltered Activity Graph of a Participant

2.5.2. Data Filtering. After the data preparation, the second stage of the data pre-processing involves filtering actigraphy signals. As per the research study by Redmond and Hegge [48], a voluntary human movement does not exceed 3-4 Hz, on another hand, an involuntary movement like tremor or shivering does not exceed 5 Hz. To remove frequencies that are outside of this human movement frequency range from the dataset. The data was filtered. The filtering process results in a smoother representation of the signal. A bandpass filter has the ability to remove the high and low frequencies from a recorded signal. Thus, a low bandpass Butterworth filter is used to remove the low frequency and attenuate the high-frequency noise from the actigraphy signals. The data filtering helps to have the frequency response as flat as possible to distinguish between the sleep and wake state. This also allows the focus of exploration of the activity data common to human activity.

For this analysis, the low pass Butterworth filter with order 3 was used for filtering out the high-frequency points of the Sum Vector Magnitude (SVM) feature for further analysis. The Sum Vector Magnitude (SVM) is specifically used to analyze the data as it is a vector magnitude of acceleration in all the directions (x, y, and z). This helps in knowing the magnitude of the wrist movement in all the direction without using a feature of each axes separately in the analysis.

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To generate and apply the Butterworth filter for the data, the Signal package from the CRAN-R project [49] in the R studio environment was used. From the 'signal' package, to generate the Butterworth filter, 'butter' function was used. Further, the 'filtfilt' function was used to apply the generated Butterworth filter to smooth the data. The 'filtfilt' function uses a forward and a reverse pass to filter the signal using the generated filter to get a square magnitude response in the process. Mathematically, according to the [55] the square magnitude response of the Nth order Butterworth filter is represented as,

$$|H(w)|^2 = \frac{1}{1+\left(\frac{w}{w_c}\right)^{2N}} \quad (1)$$

Where,

w_c is the cut-off frequency, which in this case is set to 0.04, and

w is the frequency of the original signal that will be processed

The cut-off frequency of 0.04 is selected to eliminate the frequencies greater than 0.04 Hz, further for digital filters the cut-off frequency should be between 0 and 1.

The figure 2.4 below represents an unfiltered signal of the SVM data:

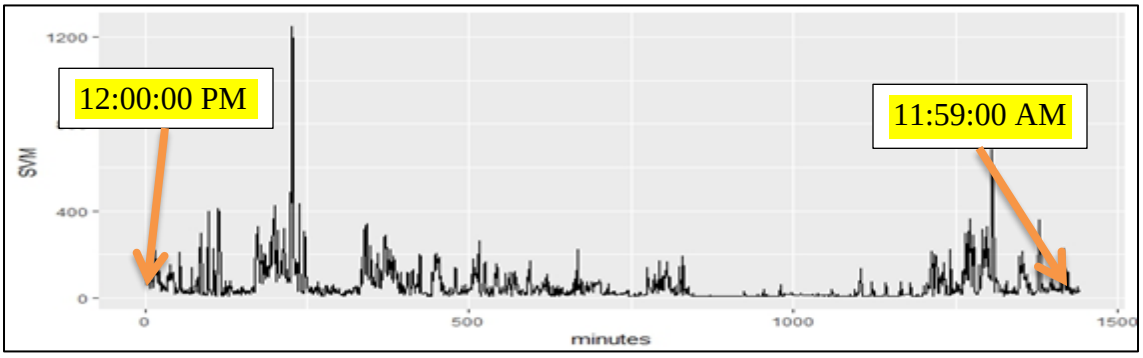

Figure 2.4. Unfiltered Signal of Sum Vector Magnitude (SVM)

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Once we apply the Butterworth filter to the SVM data we get a smoother activity signal with less fine-grained variation to be used for further analysis. The Figure 2.5 below shows the filtered signal which we get after applying the filter:

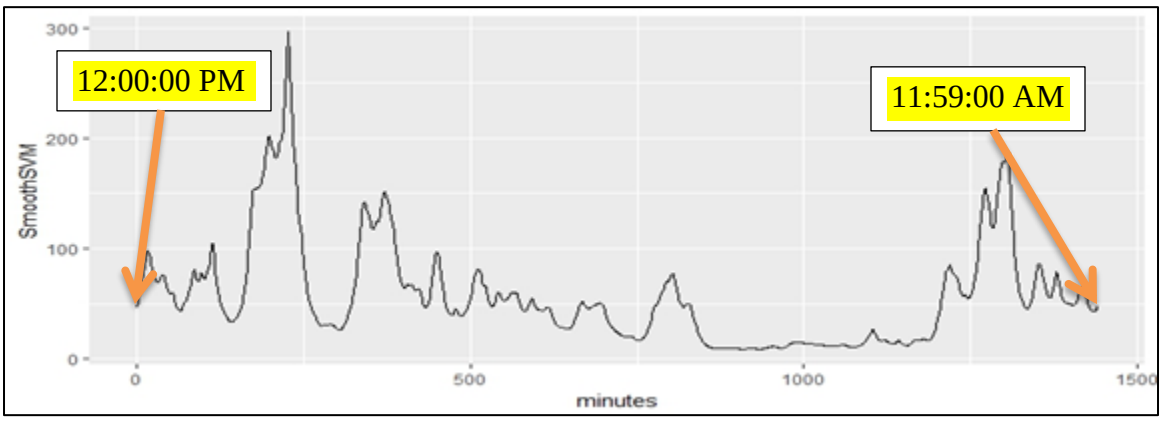

Figure 2.5. Applying Butterworth Filter on Sum Vector Magnitude(SVM)

2.6. TIME SERIES SEGMENTATION

This section discusses the application of the statistical Change Point Detection in detail to the cleaned and filtered human activity signals. The human activity involves multiple sections of high and low levels of activity all throughout the day, which is the reason that draws attention to assess the change in variance. That is when people are sleeping their movements are less frequent and less intense than when they are awake and active. The main aim of this methodology is to identify the positions of the change point by assessing the change in variance.

To make the reader easily understand the concept of detecting the change point by assessing the variance, it is necessary to summarize and represent it mathematically. The methodology uses the concept of detecting changes in variance by assuming no consistency in the probability of false alarm or mean as developed in (Douglas M. Hawkins and K. D. Zamba, 2005 [50]). The methodology as developed in [50] is summarized as below:

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For a step change to be detected from one specified in-control level to some other specified out of control level in a normally distributed data, can be represented by the change point formulation as shown below:

Let X_i be the sequence of two samples of data following a normal distribution:

$$X_i \sim \begin{cases} N(\mu_1, \sigma_1), & \text{if } i \le \tau \\ N(\mu_2, \sigma_2), & \text{if } i > \tau \end{cases} \quad (2)$$

Where τ is the change point, while the remaining variables are mean and standard deviations μ_1, σ_1 respectively.

Now, consider X_i a sequence of datapoints for a given dataset, which would follow the equation of change point model as shown in Equation (2). Considering there are 'n' data points accumulated, the statistical summary for $0 \le i < k \le n$ is explained as below:

$$\bar{X}_{i,k} = \sum_{j=i+1}^{k} \frac{X_j}{(k-i)} \quad (3)$$

The Equation (3) calculates the mean by taking a sample (i to k) from the total sequence of data points.

$$V_{i,k} = \sum_{j=i+1}^{k} (X_j - \bar{X}_{i,k})^2 \quad (4)$$

The Equation (4) calculates the difference of the point from the mean for the interval i to k.

Now, if a change point is considered at τ = k we now have two samples, then the remaining parameters are calculated for both the samples i.e. between the sequence 0 to k and k to n:

$$\hat{\mu}_1 = \bar{X}_{0,k} \quad (5)$$

Where Equation (5) calculates mean for the sequence 0 to k

$$\hat{\mu}_2 = \bar{X}_{k,n} \quad (6)$$

Equation (6) calculates mean for the sequence k to n

$$\hat{\sigma}_1^2 = V_{0,k} / (k-1) \quad (7)$$

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Equation (7) calculates the variance for the sequence 0 to k

$$\hat{\sigma}_2^2 = V_{k,n} / (n-k-1) \qquad (8)$$

Equation (8) calculates the variance for the sequence k to n

The equation (5),(6),(7), and (8) are calculated to find the unknown parameters - mean and variance $\hat{\mu}_1, \hat{\mu}_2, \hat{\sigma}_1^2$ and $\hat{\sigma}_2^2$ respectively. Thus, the variance is determined depending on the mean.

The variance for the sequence from 0 to n is calculated by adding the 0 to k and k to n variance:

$$\sigma^2 = (V_{o,k} + V_{k,n}) / (n-2) \qquad (9)$$

Further, to test the equality of variance using the standard deviations calculated in equation (7), (8) and (9), the likelihood ratio test statistic is applied. The likelihood ratio test statistic compares the goodness of fit for two statistical models. The likelihood ratio is calculated to understand the likeliness of the data under one model than the other. The likelihood ratio can be compared to the critical value to decide whether the model should be rejected or accepted.

The likelihood ratio test statistics is determined using (Bartlett and Kendall (1946), Bartlett (1937), Bartlett (1955)).

$$G_{k,n} = \left[(k-1) \ln\left(\frac{\hat{\sigma}^2}{\hat{\sigma}_1^2}\right) + (n-k-1) \ln\left(\frac{\hat{\sigma}^2}{\hat{\sigma}_2^2}\right) \right] / C \qquad (10)$$

Where,

C = Bartlett correction factor

$$C = 1 + \left[(k-1)^{-1} + (n-k-1)^{-1} - (n-2)^{-1} \right] / 3$$

The 'C' is used for adjusting the degree of freedom as the variance is estimated by calculating the mean.

$G_{k,n}$ is represented in the form of F-ratio to test the equality of variance. It is a two-sided statistical hypothesis of the variance between two samples of data. If the ratio is equal, then the

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variance is always equal to 1. As F-ratio is represented as F = $\frac{\hat{\sigma}_2^2}{\hat{\sigma}_1^2}$, then the equation (10) represents as below:

$$G_{k,n} = \frac{\left[(k-1)\ln\{k-1+(n-k-1)F\}+(n-k-1)\ln\{(k-1)F^{-1}+n-k-1\}-(n-2)\ln(n-2)\right]}{C}$$

The $G_{k,n}$ values go on increasing considerably above or below 1, increasing the size of the distribution. A large value of this ratio of variance would show the distribution variance are unequal which would help in detecting a significant statistical change in the distribution.

Thus, to determine the change in the variance without knowing the change point (τ) at first, the Generalized likelihood ratio test is used. The Generalized likelihood ratio test is given by maximizing the value of $G_{k,n}$ across all the possible values of k where the range of k>1. We can define the Generalized likelihood ratio test statistic to determine the change in the variance when the change point is unknown:

$$G_{\max,n} = \max_{2 \le k \le n-2} G_{k,n} \qquad (11)$$

To summarize the procedure for determining the step change when the change point is unknown, the following steps should be followed:

- $G_{\max,n}$ which is the generalized likelihood ratio is computed for a shift in the variance at some unknown previous time after having added all the n observations to the total data set.
- If $G_{\max,n} \le h_n$, where h_n is denoted as some suitable control limit which is user-defined. If the condition is satisfied then there is no variance shift leaving the process intact
- If $G_{\max,n} > h_n$, then there is a shift in the variance

The Generalized likelihood ratio concept is applied in the methodology for identifying the sleep/wake states by assessing the variance in the activity signal recorded for each individual participant wearing the watch.

For performing the change point detection analysis, the ‘changepoint’ package was used from the CRAN-R project [51] and implemented it in the RStudio environment.

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The changepoint package follows the same procedure for assessing the variance as developed in [50]. Further, the data points with a change in variance were identified using the function 'cpt.var' from the 'changepoint' package, by using the 'PELT' method. The PELT algorithm which has similarity with the segment neighborhood algorithm is used for providing the exact segmentation of the change points. The PELT algorithm is more computationally efficient as it uses pruning and dynamic programming. It has the ability to detect change point as the data set increases, with the change points being spread and not confined to one area of the segment. The PELT algorithm is represented mathematically to make it clearer for the reader [52].

PELT ALGORITHM: This algorithm is similar to the Optical Partitioning or OP method [52] but is more computationally efficient and has the ability to find the global minimum of the cost function. The global minimum of the cost function is calculated by:

$$\sum_{i=1}^{m+1}[C(y_{(\tau i-1+1):\tau i})+\beta] \tag{12}$$

The PELT algorithm improves its computational efficiency by pruning. Pruning eliminates the values of change points (τ) that can never attain the minima. The minimization is calculated at each iteration with the following equation:

$$F(\tau^*)=\min_{0\le\tau<\tau^*}[F(\tau)+C(y_{(\tau+1):\tau^*})+\beta] \tag{13}$$

Where τ*=1…n

The condition under which the pruning can be done is proved in the following theorem:

Theorem:

Assume that when a change point is introduced in a sequence of observation, the cost C of the sequence reduces. There exists a constant K such that for all t<s<T,

$$C(y_{(t+1):s})+C(y_{(s+1):T})+K\le C(y_{(t+1):T}) \tag{14}$$

Then, if

$$F(t)+C(y_{(t+1):s})+K\ge F(s) \tag{15}$$

holds at a future time T>s, t can never be the optimal last changepoint prior to T.

The condition in the theorem for a changepoint, t, is removed which are not relevant for obtaining the final change points which helps improve the computational efficiency.

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The pseudo code for the PELT algorithm is given in the Appendix. The code demonstrates that at each step the changepoint which satisfied the condition is removed from the following iteration.

After the PELT algorithm is applied, a new vector is created to include the first and the last point of the sequence to find the maximum difference between all the breakpoints. Further, we mark the sleep period identified by the change point as red and wake period as black. The points between the two numbers giving the maximum difference between the change point are the sleep period and the rest is the wake period. The outliers present in the sleep period detected by the change point analysis are identified by the boxplot. The points lying on the periphery of the boxplot which is in fact wake are detected as sleep, are converted back to wake. Once the filtering of data and changepoint detection is completed, Z-scoring is applied.

2.7. Z-SCORING

This section discusses the Z-score, which is the preceding step before determining the sleep duration. Z-score is a value which helps determine whether the value obtained from the analysis is useful for the dataset. In order to apply the z-score, a predetermined value is selected by the statistician and values above or below the z-score are eliminated from the dataset as an outlier. This will determine the cutoff point, threshold, to classify activity data as belonging to the sleep period or is considered to be wake activity.
In this case, a point is considered as an outlier if the Z- the score is less than 1.96 or has less than 95% confidence interval, in the sleep period identified by the Change Point Detection analysis. This level can be adjusted by the researcher. After the scoring completion, the data is binarized to represent the sleep and wake periods in the data set with 1 being wake and 0 being sleep. This was done to clearly determine the sleep and wake periods of the participant. The z-score was calculated mathematically as:

$$\text{Z-score} = \frac{\mathbf{F_{SVM}} - Mean(F_{SVMred})}{SD(F_{SVMred})} \tag{16}$$

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Where,

Filtered SVM data = F_{SVM}

Mean of Filtered SVM data corresponding to non-active periods = Mean(F_{SVMred})

Standard Deviation of Filtered SVM data corresponding to non-active periods = SD(F_{SVMred})

After eliminating the outliers and determining the z-score we can now determine the sleep duration of the person with the sleep start time and wake time.

2.8. SLEEP DURATION

This section discusses how to determine the sleep duration once the data set was structured and filtered. For determining the sleep duration in a particular day, the binarized results of change point detection were used, where '0' being sleep and '1' being awake. The maximum sequence of continuous '0' was considered as sleep duration for each day and participant.

In addition, the sleep start and the wake time was determined for each participant. While determining, the sleep duration, we eliminate the days where the participants sleep all day (1440 minutes) or who doesn't sleep at all (0 minutes) and stays awake. The participants result with 1440 minutes of sleep as the accelerometer device sensor might have been stuck at a lower frequency. This may result in the actigraphy showing a long period of sleep duration. The sleep duration obtained from our method was compared with the GENEActiv Macro [53-54] in order to determine the accuracy of the results obtained.

The following Figure 2.6 shows the visualizations after applying change point detection analysis and z-scoring for a participant in the data set.

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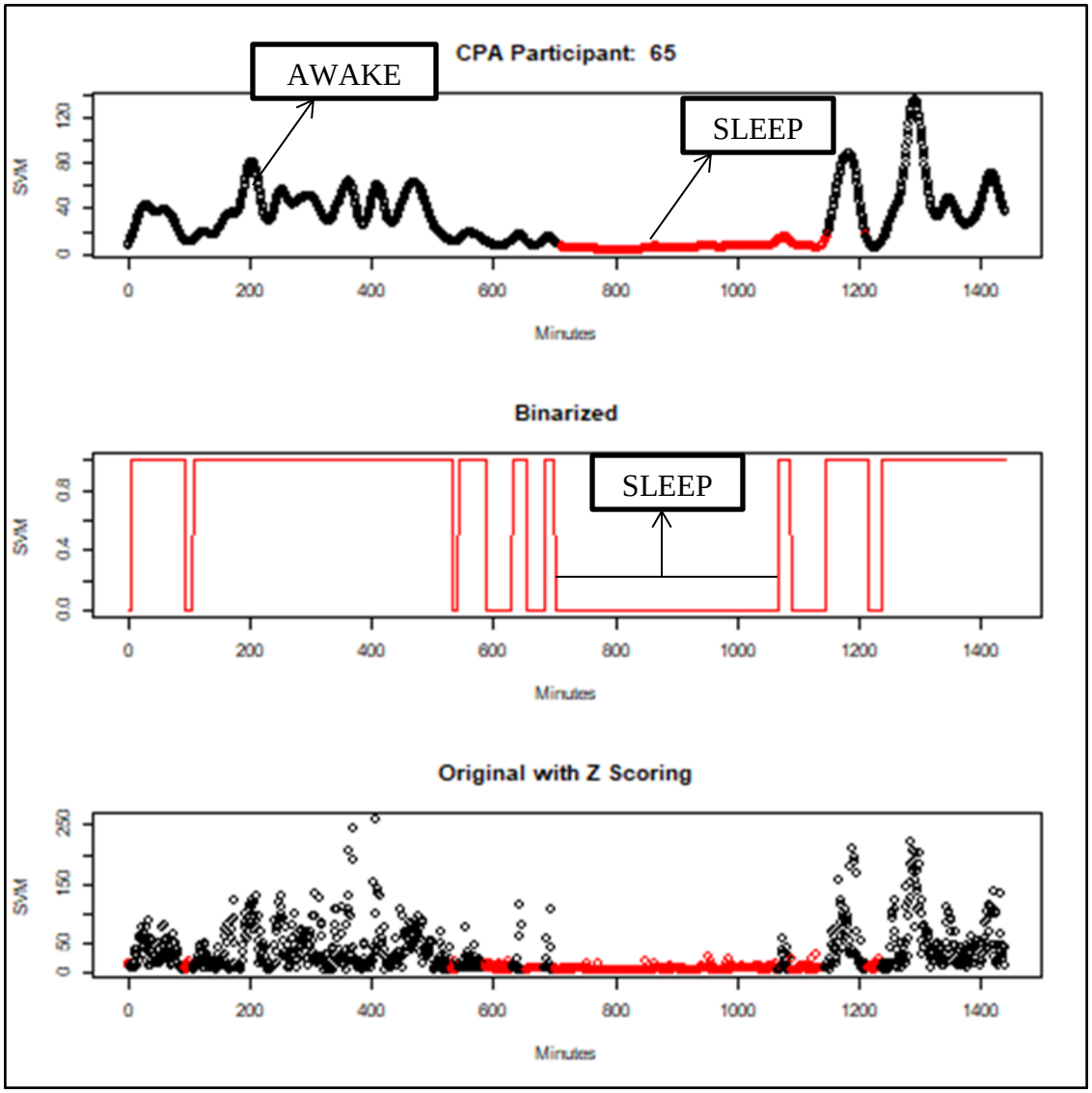

Figure 2.6. Change Point Detection Analysis Results for a Single Day

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3. RESULTS

This section highlights the analysis of the actigraphy signals. Furthermore, this section seeks to illustrate the sleep scoring algorithm previously outlined in the methodology section of the document.

All the analysis was done in the R studio environment. Before analyzing the results, participants with the highly inconsistent data were removed from the dataset in an effort to have a reliable analysis of actigraphy signals and proposed methodology. The highly inconsistent data consisted of long periods of wake or sleep states in an individual. Such type of activity pattern is not found in a normal healthy human activity and is suspected to have been caused by faulty sensing. These faulty sensing periods can occur when the sensor is momentarily stuck. The Figure 3.1. Below illustrates one of the participants with inconsistent data:

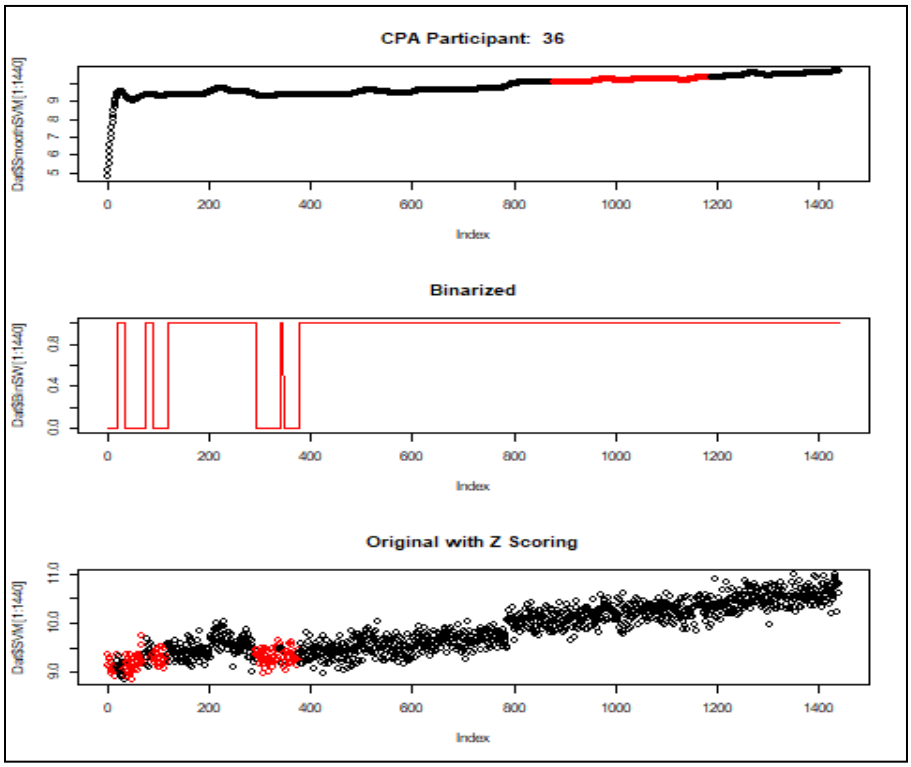

Figure 3.1. Participant with Inconsistent Physical Activity Data

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From the above Figure 3.1., it is seen that the recording of the activity signal from the sensor is highly inconsistent. This is because the sensor might have been stuck at a higher frequency, thereby recording a high-frequency signal even when the person is not in an active state. Another reason for the inconsistency may be due to the participant not wearing the watch continuously resulting in a very low activity being recorded. Activity pattern recorded in such an inconsistent manner cannot be considered for determining the sleep duration of the participant and were excluded from the analysis. After removing the inconsistent participants, the final data set consisted of 1160 days of data for 20 participants. Once, the participants with inconsistent data were removed, sleep duration was determined using the methodology as explained in Section 2 of this document. As given in the methodology section that Sum Vector Magnitude (SVM) is the only feature used for determining the sleep duration. Thus, it is the only one examined for inconsistency. The other individual sensor data like acceleration in x, y, and z direction is not considered during analysis or for its inconsistency in recording the activity data. The results of the algorithm were validated against the sleep duration from GENEActiv Macro [49].

The main purpose of the analysis was to increase the agreeance of sleep duration, i.e. reduce the average difference of sleep duration from the Algorithm and GENEActiv Macro. This was done by adjusting different parameters and finding the best results. The following subsection describes the analysis in detail:

3.1. ANALYSIS-1

The first part of the analysis involved testing different orders of the Butterworth filter. The Butterworth filter order helps in getting a flat frequency response. Higher the filter order more the flat frequency response. By testing the different order of Butterworth filter, the best order which would help differentiate the sleep and wake was order 3. Selection of the best filter order was done by inspecting the data visually and testing different orders of the filter. The order 3 of the Butterworth filter gave the best flat frequency response. Further, the change point was also able to differentiate between the sleep and wake states accurately as compared to other orders.

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Once the order was decided, the critical values were tested while analyzing the data. The critical values help to discriminate between two groups in a dataset by comparing the test results with the critical values. In this case, the Z-scores was calculated and tested with a critical value to determine the sleep duration. For the reader to understand the critical value more clearly it is explained with the help of the following Figure 3.2.:

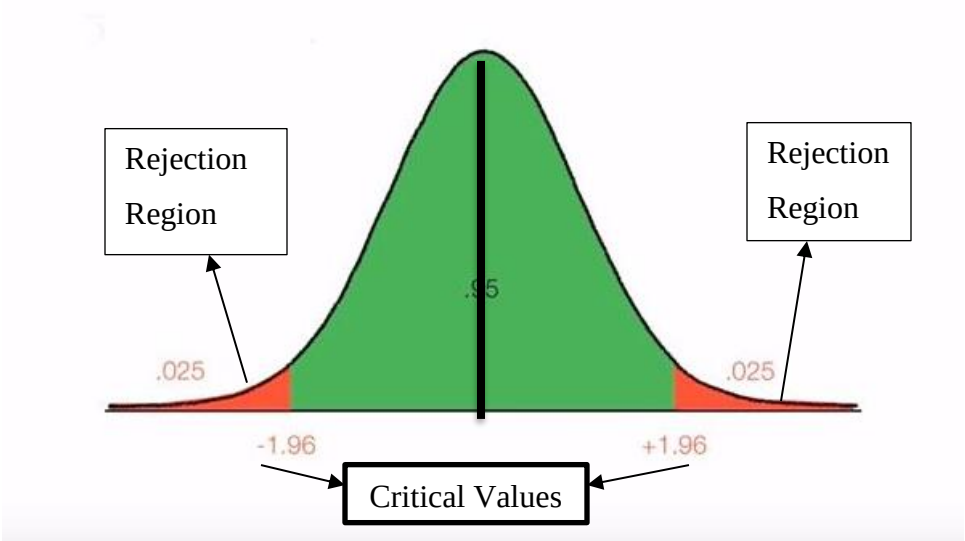

Figure 3.2. Normally Distributed Data with Different Regions

The critical values are the boundary of the rejection region in the given distribution. The above Figure 3.2. shows the critical values 1.96 which are the boundaries of the rejection region. The red regions on both sides of the distribution are the rejection regions. The green region tells us that, if the Z-score lies within this region then it has 95% probability that the results determined as sleep is in fact sleep. If the Z-score lies within the rejection region then the null hypothesis is rejected, and that point has a low probability of being sleep. The researcher himself decides how much data should be considered for determining the sleep. The researcher sets these critical values

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himself. Keeping this in mind different critical values were considered to analyze the average difference between the sleep duration of the algorithm and the GENEActiv Macro. The following Table 3.1. Summarizes the results of different critical values:

Table 3.1. Results for Different Critical Values

Critical Values	Confidence Interval (%)	Alpha	Sample size	Average Duration Difference
1.96	95	0.05	1160	60.93
1.75	92	0.08	1160	41.96
1.65	90	0.1	1160	31.38
1.45	85	0.15	1160	8.96

From the above Table 3.1., the results show that the average difference between the sleep duration from the algorithm and GENEActiv Macro reduces as we reduce the critical values. The lesser the confidence interval more is the agreeance between the sleep duration of the algorithm and GENEActiv Macro. For a critical value of 1.45 and having a confidence interval of 85%, the Algorithm overestimated the sleep duration from the GENEActiv Macro by only 8.96 minutes. This tells that as the critical value or in simpler words a threshold value for the recorded signal is reduced more amount of the sleep period is captured. Further, the average difference between the sleep duration from the Algorithm and GENEActiv Macro is reduced. As the critical value of 1.45 gave the least average sleep duration difference, further analysis was done using this critical value. The following Table 3.2. shows the best results in the sleep duration and Table 3.3. shows the worst results of sleep duration when compared with GENEActiv Macro:

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Table 3.2. Best Results of GENEActiv Macro and Algorithm

Date	Participant	Day	Algorithm Duration (mins)	Macro Duration (mins)
10/31/2016	21	Monday	367	387
3/22/2017	32	Wednesday	336	320
3/31/2017	32	Friday	236	236
2/17/2017	34	Friday	444	458
2/23/2017	40	Thursday	370	384
3/1/2017	42	Wednesday	340	340
3/28/2017	46	Tuesday	348	336
1/21/2017	47	Saturday	204	201

Table 3.3. Worst Results of GENEActiv Macro and Algorithm

Date	Participant	Day	Algorithm Duration (mins)	Macro Duration (mins)
3/29/2017	50	Wednesday	870	525
11/27/2017	55	Monday	414	226
11/30/2017	55	Thursday	78	261
9/16/2017	57	Saturday	1137	407
9/11/2017	59	Monday	605	286
9/15/2017	60	Friday	775	358
9/6/2017	65	Wednesday	383	723
9/30/2017	67	Saturday	990	389

3.2. ANALYSIS-2

Further, to inspect the results visually, a plot of the sleep duration from the GENEActiv Macro and algorithm was plotted. The following Figure 3.3. shows the plot below:

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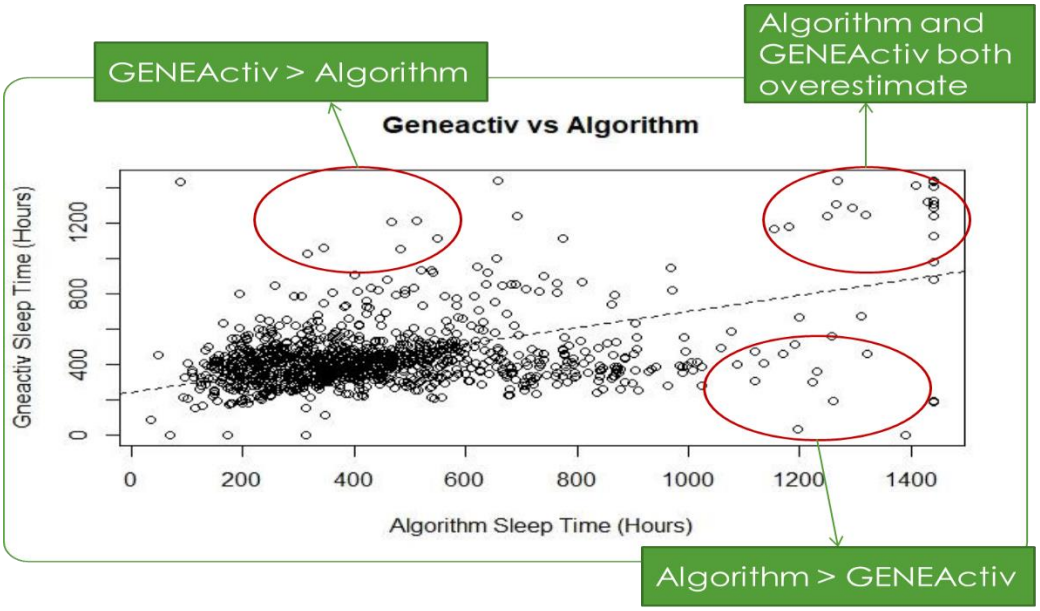

Figure 3.3. Comparison of Sleep Duration from GENEActiv vs Algorithm

The above Figure 3.3. shows that there are outliers in the results obtained for the sleep duration. The outliers are mostly the higher sleep durations. In order to remove the outliers, an assumption was made that a normal healthy person sleeps for 8 hours (480 minutes) per day. All the days which has slept more than 8 hours of the day should be removed. For this, sleep duration was incrementally reduced, and four different data sets were created as follows:

- Firstly, removing days with more than or equal to 1400 minutes of sleep
- Secondly, removing days with more than or equal to 1200 minutes of sleep
- Thirdly, removing days with more than or equal to 800 minutes of sleep
- Lastly, removing days with more than 480 minutes of sleep

By incrementally eliminating the days with the respective sleep duration, as shown above, the sample size automatically goes on decreasing. Further, to have in-depth analysis, the four newly created data sets were again tested with the critical value as shown in table 3.2. For the purpose of explanation, results of only one critical value i.e. 1.45 is shown and explained. The analysis of the other critical values as shown in table

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3.2. are summarized in the Appendix B. The following Table 3.4. summarizes the results of the different sample size used:

Table 3.4. Standard Error and P-value for Different Sample Sizes

Original Sample Size	Duration (d) removed (mins)	Final Sample Size	y=mx+b	Standard Error	P-Value	Conclusion	Average Duration Difference
1160	0	1160	240.93x+0.46	0.0198	0.3982	Accept Null Hypothesis	8.96
1160	d>1400	1124	343.39x+0.19	0.0212	0.53	Accept Null Hypothesis	5.16
1160	d>1200	1112	356.66x+0.1566	0.0218	0.9519	Accept Null Hypothesis	0.46*
1160	d>800	1042	332.27x+0.2282	0.0285	7.37E-07	Reject Null Hypothesis	33.33*
1160	d>480	774	327.93x+0.2362	0.0471	2.20E-16	Reject Null Hypothesis	88.33*

*- sleep duration of algorithm underestimates from the sleep duration of GENEActiv Macro

From the above Table 3.4., it is seen that the agreeance in the sleep duration from the GENEActiv Macro and algorithm increases as we reduce the sample size by only a few data points. This shows that as the outliers are removed from the data the average difference of the sleep duration goes on decreasing. But this comes with a tradeoff, as we

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reduce the sample size by eliminating the days the standard error goes on increasing. Additionally, as we reduce the sample size by eliminating sleep duration of more than 20 hours, the algorithm starts to underestimate the sleep duration from the GENEActiv Macro.

To summarize the analysis, the Algorithm cannot perform accurately for all the sample sizes. In order to improve its performance, there has to be a tradeoff for losing the data in order to get more information about the individual's sleep duration. This is done by making assumptions about eliminating the outliers, adjusting different parameters, and reducing the sample size.

Further, every individual has his own sleep pattern, which makes it difficult for the algorithm to detect the sleep duration accurately for each one of them. In addition, the analysis is focused solely on the sleep duration because it helps us determine the sleep pattern of the person. It also tells us the days where an individual sleep more and days where he sleeps lesss. Further, it also helps in determining whether a person follows the same pattern for a longer period of time or changes frequently. For example, the following Figure 3.4. shows the sleep duration in percentage for each day of the week:

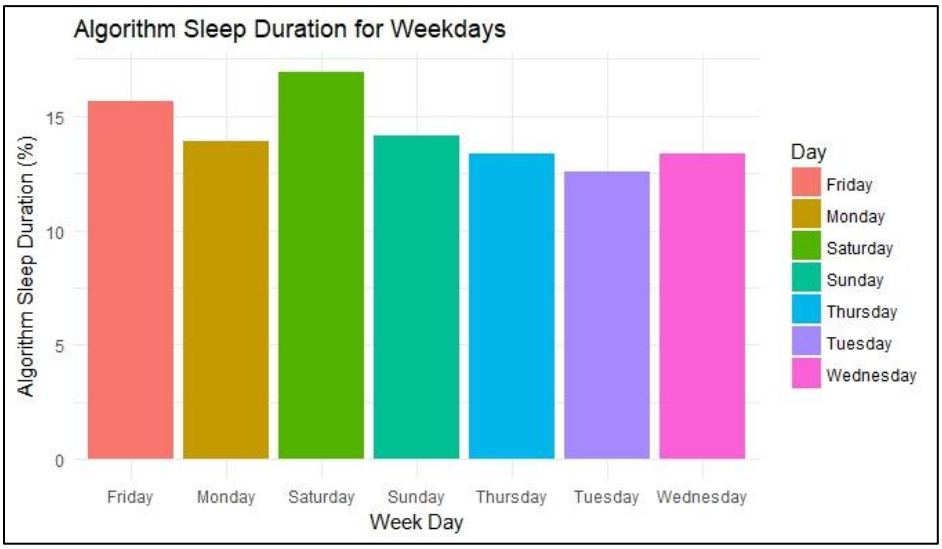

Figure 3.4. Sleep Duration for Each Weekday According to Algorithm

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The Figure 3.4. shows us that the all participants sleep more on Saturday followed by Friday.

To get more insight into the sleep duration for each participant, refer Appendix for plots of various participants to illustrate differences in duration of sleep throughout the week. The participants 57 and 67 are not visualized as both the participants had more than 8 hours of sleep.

Lastly, the GENEActiv Macro has been used in previous research studies which makes it reliable validation method for testing the performance of the algorithm. So, for example, if the sleep duration between the Algorithm and GENEActiv Macro agrees more it can be assumed that the algorithm performs better. The below Table 3.5. shows the mean difference between the sleep duration for each participant.

Table 3.5. Sleep Duration for each Participant

Participant	Algorithm	GENEActiv Macro
21	314	413.4
22	283.8	435.625
24	326.6	394.8125
32	281.6	395.4643
34	299	327.6364
40	297.8	445.1081
42	311.5	403.8974
44	303.5	384.8049
46	366	631.7561
47	312.6	340.6049
50	418.3	401.0833
55	287.8	316.359
59	413.1	287.8667

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Table 3.5. Sleep Duration for each Participant (contd.)

Participant	Algorithm	GENEActiv Macro
60	226	384.48
63	408.4	333.9583
65	369	423.8816
71	327.1	359.1154
74	266.7	451.6842

It can be seen from the Table 3.5. that the participants 71, 50, 55, 24, 32 and 47 have close agreeance with the sleep duration from the algorithm and GENEActiv Macro. While the other participants sleep duration is either overestimated or underestimated. This brings us to the conclusion that no algorithm can determine the exact sleep duration as every person has different activity pattern.

3.3. ANALYSIS-3

ANOVA Analysis

Further to test the results, ANOVA analysis was used. The ANOVA analysis was done for the data set without the outliers. The linear function of ANOVA gives us great insights into the results. The first plot shows the residual vs fitted for the sleep duration from Algorithm and GENEActiv Macro. The residual vs fitted plot is shown below in Figure 3.5. tells us that the data is evenly spread with no real dominant slope and no increasing or decreasing spread is observed. Further, the error is evenly distributed above and below by almost the same amount.

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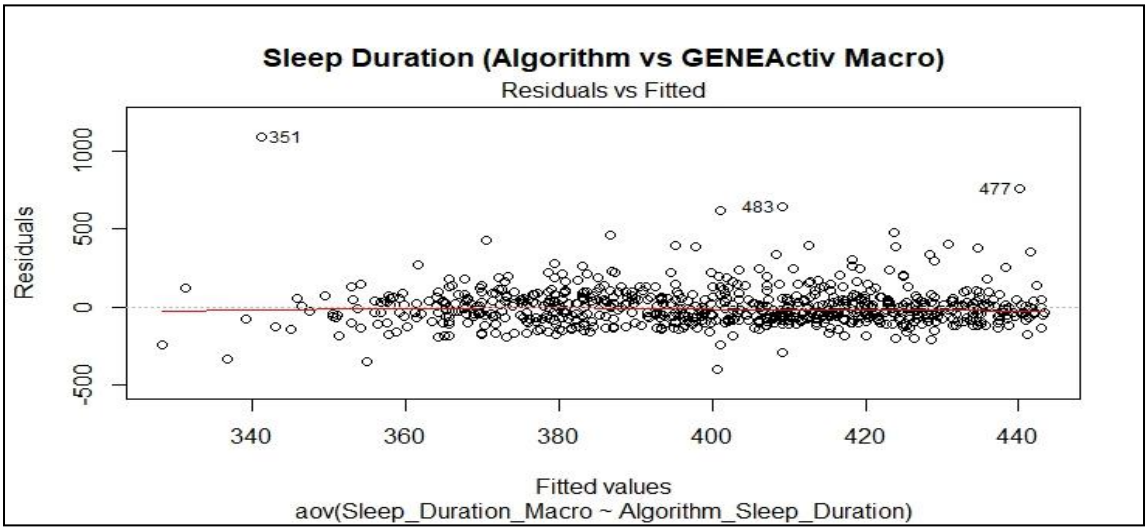

Figure 3.5. Residual vs Fitted Values of Sleep Duration

The next plot, normal QQ plot states whether the samples are coming from the same distribution or not. In our case, as shown below in Figure 3.6. the QQ plot shows that the positive side seems to differ, and the sleep duration of the algorithm is generally higher than expected when compared to GENEActiv Macro. They are still some outliers that influence the distribution.

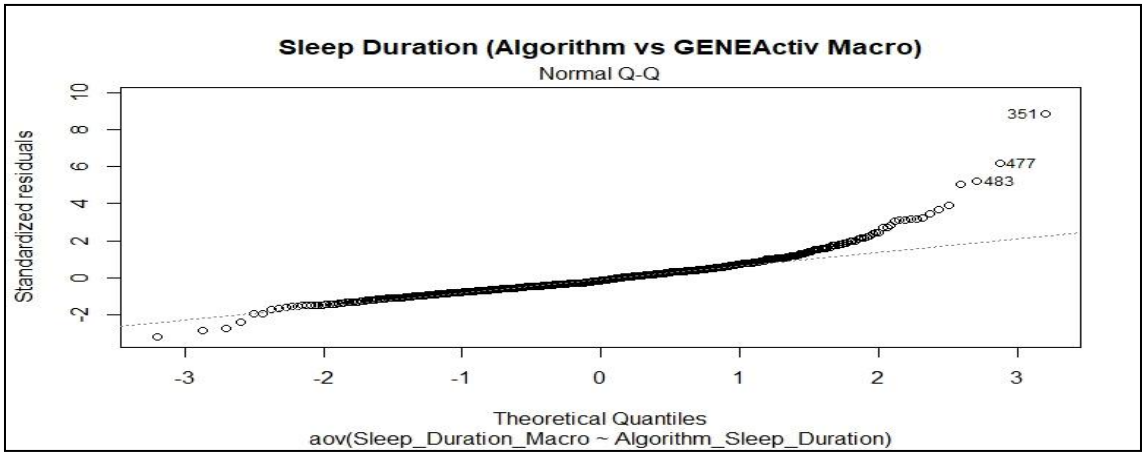

Figure 3.6. Normal Q-Q Plot for Sleep Duration

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Next, we plot the scale-location plot as shown below in Figure 3.7. The plot shows a horizontal line which shows that the variance is equal throughout the two samples. The below Figure 3.7. shows the Scale location plot:

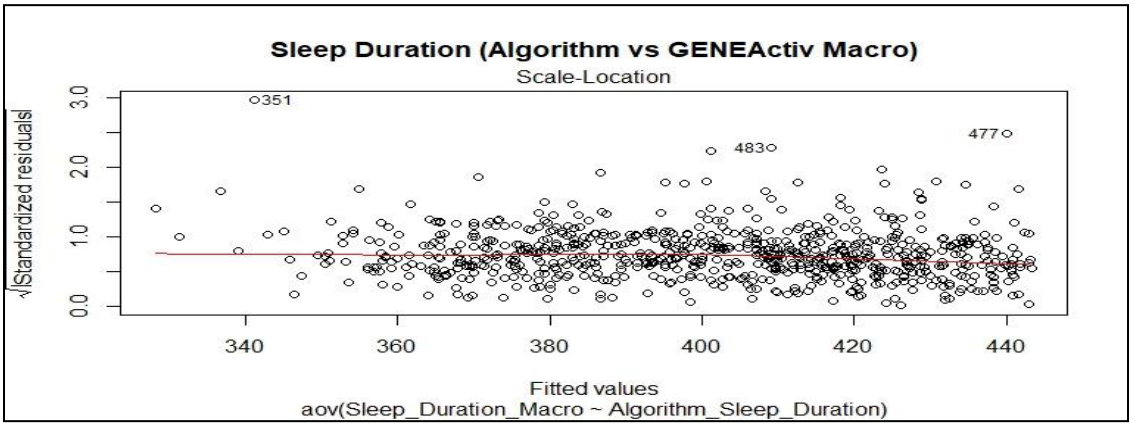

Figure 3.7. Scale Location for the Sleep Duration

The residual vs leverage plot as shown below shows that there are few outliers that might be dominating the estimate of the linear model. These outliers might be throwing the estimate of the coefficient off. The Figure 3.8. below show the residuals vs leverage plot:

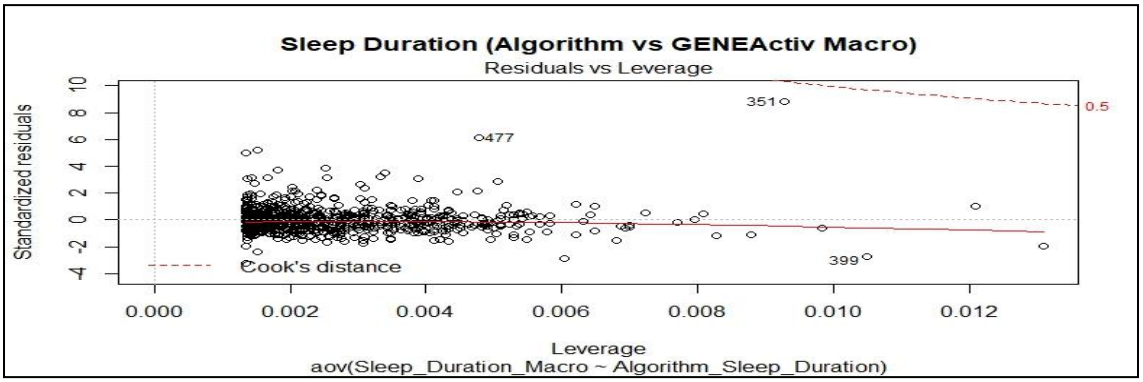

Figure 3.8. Residuals vs Leverage Plot for Sleep Duration

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The results show that the sleep duration from the GENEActiv Macro and the Algorithm have close agreeance with each other on an average. The ANOVA results also state that as the higher sleep duration are eliminated from the data set, the agreeance increases.

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4. CONCLUSION

4.1. DISCUSSION

In this thesis, an Algorithm is developed for determining the sleep duration of a person using sensor-based physical wrist activity data. The algorithm used the physical activity signals recorded by the GENEActiv wrist-worn accelerometer device. The physical activity signals were analyzed, and the sleep duration was determined for 20 individual participants over a period of 1160 days, after removing participants with highly inconsistent physical activity data. In addition, the Butterworth filter filtered out the data and eliminated the low-frequency noise from the signal and attenuated the high-frequency points.

The algorithm was developed using the Statistical method of Changepoint detection and Z-scoring as the threshold/ cutoff between the two classifications of sleep and wake. Further, the sleep duration was determined by first identifying the sleep and wake states using the Changepoint detection and then scoring the exact sleep duration of the participants using the Z-scoring. The Z-score was tested against the threshold value selected by the researcher. The sleep duration obtained from the algorithm was then validated with sleep duration resulted from the GENEActiv Macro. The results show that the sleep duration was overestimated by 8 minutes on an average by the algorithm with that of the sleep duration from the GENEActiv Macro. The parameters used for obtaining this result were Butterworth filter of order 3 and the threshold value of 1.45.

The algorithm developed in this thesis is an open source and can be applied for determining sleep duration in long-term sleep research studies. It is robust and performed well for different participants in the dataset. Unlike the previous algorithms as explained in the literature, the algorithm developed in this thesis directly analyzes the activity signal to determine the sleep duration of the person.

Despite the algorithm having the ability to determine the sleep duration, there are some limitations to this process. The results of the analysis as described in section 3, it can be seen that it is difficult to determine the sleep duration by examining the physical activity of the person recorded by an actigraphic device. A physical activity involves various high and low-frequency movements. In this thesis, the signals recorded by the

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actigraphic device are analyzed directly. This makes it difficult for differentiating different activities. For instance, when the signals are analyzed, the low-level frequency movements like sitting, taking a nap, writing, etc. are considered as the person sleeping. This is because the value of the frequency signal is very low and almost equal to a person sleeping. On the other hand, sometimes a person moves frequently while sleeping, which causes some high-frequency movement in the signal recorded. Thus, the signals of high frequency are recorded by the actigraphic device in spite of the person sleeping. This makes it difficult to determine the exact sleep duration for each day in the dataset. Further, each person has different sleeping habits and patterns, which makes it tricky to find the exact sleep duration for each person.

4.2. FUTURE WORK

This research can be used as a baseline for developing other sophisticated models and algorithms related to automatic sleep scoring. The sophisticated models include developing Deep Nets to identify different movements from the activity signal. Further, this research can be further expanded by relating the sleep duration of the person with his cognitive performance. The cognitive performance includes the person's ability to think critically, daily activities, working, driving etc. By doing so we can come to know how a person performs the following day by knowing the sleep duration from the previous night. This indeed would help us get activity pattern of the person with his cognitive performance.

Polysomnography (PSG) is a well know validation test used in sleep studies, the sleep duration from the PSG should be validated with the sleep duration of the Algorithm for testing the performance. This validation would help in knowing in more detail about the performance of the algorithm developed and what further improvements might be needed to improve the performance.

Also, other parameters like the critical frequency of the Butterworth filter and penalty for detecting change point should also be tested to improve the results. Analyzing and testing these parameters is important as it would tell which parameters have the most effect on the algorithm and parameters needed to be removed.

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APPENDIX

1. The following code is used for finding the sleep duration of any individual using Changepoint detection and Z-scoring. Please refer to the code comments for an explanation of each step.

Code:

```
print(" Sleep Duration Algorithm: Ivan G. Guardiola and Yogesh Lad")
print("LOADING ALL LIBRARIES FOR PROCESSING")
library(mmand);library(ggplot2);library(lattice);library(zoo);library(caret)
library(changepoint);library(e1071);library(dplyr);library(lubridate)
library(cluster);library(foreign);library(progress)
library(ecp);library(mvtnorm);library(zoo);library(mmand);library(changepoint)
library(BreakoutDetection);library(TTR);library(Mcomp);library(lattice)
library(MASS);library(smoother);library(signal);library(ppls);library(plyr)
################################################################################
################################################################################
#############

#Data cleaning and structuring
getwd()
wd<-setwd("C:/Users/guardiolai/Desktop/Sleep/")#set Working directory

list.files(wd)
dat03<-read.csv("CASB050_left wrist_034190_2017-04-13 14-10-34.csv", header =
TRUE)#read one minute CSV actigraphy data
head(dat03)


#create two new columns with date and time separated for easier segmentation
dat03$tmsp<-as.POSIXct(dat03$TimeStamp ,format = "%Y-%m-%d %H:%M",
tz="UTC")
```

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```
head(dat03)
Data<-dat03[-1]
head(Data)


#Determine first day of date
firstinst<-as.POSIXct(head(Data$tmsp,n=1),format= "%Y-%m-%d %H:%M",tz="UTC")
lastinst<-as.POSIXct(tail(Data$tmsp, n=1),format="%Y-%m-%d %H:%M",tz="UTC")
paste("Start Date: ", firstinst, " End Date: ", lastinst)

class(Data$tmsp)
lastinst

library(lubridate)

# if the first day starts before noon then start date is same day at noon
#else if the first data starts after noon then beginning date is the next day at noon
if (hour(firstinst)<12){
  startdate<-as.POSIXct(paste(as.Date(firstinst)," 12:00"),format= "%Y-%m-%d
%H:%M",tz="UTC")
}else{
  startdate<-as.POSIXct(paste(as.Date(firstinst)+days(1)," 12:00"),format= "%Y-%m-%d
%H:%M",tz="UTC")
}
#similarly this must be done for the enddate

if (hour(lastinst)<12){
  enddate<-as.POSIXct(paste(as.Date(lastinst)-days(1)," 12:00"),format= "%Y-%m-%d
%H:%M",tz="UTC")

}else{
```

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```
 enddate<-as.POSIXct(paste(as.Date(lastinst)," 12:00"),format= "%Y-%m-%d
%H:%M",tz="UTC")
}
paste("New Start Date: ", startdate, " New End Date: ", enddate)

#Determine number of days in the data
n_days<-abs(round(as.numeric(difftime(startdate ,enddate , units = c("days"))),digits=0))
#create sequence of startdates
seqStart<-seq(startdate, by= "day", length.out = n_days)
seqStart
seqEnd<-seq(startdate+days(1)-minutes(1), by="day", length.out = n_days)
seqEnd
#check if the number of start end dates are the same
paste("Are the number of start and end dates the same?
",length(seqStart)==length(seqEnd))
paste("This file contains ", n_days, " days of complete data." )

#plot all days of data SVM
tmp_list <- list() # create temporary list

for (i in 1:n_days)#loop through number of days
{
 print(paste("Proc day:", i))

 print(paste("Length of Day " ,i," is: ", length(subset(Data, tmsp >= seqStart[i] & tmsp
<=seqEnd[i])$SVM), "day:",seqStart[i],seqEnd[i]))
 tmp_list[[i]] <- subset(Data, tmsp >= seqStart[i] & tmsp <=seqEnd[i])$SVM}


dataDout <- data.frame(tmp_list) #creates data frame with only SVM as columns for
respective night date as names
```

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```
names(dataDout) <- paste0(as.Date(seqEnd)) #names columns as datasets

#plot all days together
require(ggplot2)
require(reshape2)
dataDout$Time<-1:1440
df <- melt(dataDout ,  id.vars = 'Time', variable.name = 'Nights')
ggplot(df, aes(Time,value)) + geom_line(aes(colour = Nights)) #all on one graph
ggplot(df, aes(Time,value)) + geom_line() + facet_grid(Nights ~ .) #all on separate
panels

#create a column of participant name this column is "Participant"

ParticipantNum<-50#assign participant number here

#segment all data for all days that are complete
ComData<-subset(Data,tmsp>=head(seqStart,n=1)& tmsp<=tail(seqEnd,n=1))
head(ComData, n=3)
tail(ComData,n=3)
#export data for all complete dates
#naming convention is as: Participant ID, x,y,z and magnitude- (Timestamp,
x_m,y_m,z_m, SVM )
ComData$Participant<-rep.int(ParticipantNum,length(ComData$SVM))

head(ComData,n=3)
writeDat<-ComData[,c(13,12,1,2,3,4,6,7,8,9,10,11)] #organizing column order
head(writeDat)

# Write CSV in R
write.csv(writeDat, file = "CASB_050_03.csv",row.names=FALSE) #name output file
```

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```
#########################################################################
#########################################################################
#

#Combining all the output files after cleaning the data and making one data frame
library(readbulk)
fulldat <- read_bulk(directory = "C:/Users/Yogesh/Downloads/",subdirectories =
FALSE,verbose = TRUE)
names(fulldat)
head(fulldat)

#########################################################################
#########################################################################
#

print("READING ALL DATA")
Dat<-read.csv("C:/Users/Yogesh/Downloads/CASB_sleepdata-Spring.csv",
header=TRUE)#read csv file
head(Dat)
AllDat <- Dat[,c(-1,-2,-17)]#Deleting unwanted columns
head(AllDat)
AllDat<-AllDat[!(AllDat$Participant==36),]#removing inconsistent participant
participants<-unique(AllDat$Participant) #determine the set of participants in the data
print(paste0("Data contains ", length(participants)," participants for processing"))
datafile<-data.frame()

#########################################################################
#########################################################################
#
#Change Point Detection Analysis
##### start of processing all participants
```

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```
P=1;
for(P in 1:length(participants)){
  print(paste0("Processing Participant: ",participants[P]))
  Dat<-AllDat[AllDat$Participant==participants[P],]
  print(head(Dat))
  LL<-length(Dat$Participant) # determines the length of a column this is the total
number of observations in the column
  print("CHECKING DATA")
  print(paste0("Is the data divisible by 1440: ", base::ifelse(LL%%1440==0," YES ", "
NO "))) #checks we have complete data
  print("SETTING UP PRELIMINARIES")
  Inc<-seq(1,LL,by=1440) #Creates the sequence for i increments
  N_day<-LL/1440 # determines the number of complete days of data accross all
participants
  print(paste0("Number of complete days of data: ", N_day))
  pb <- progress_bar$new(total =N_day) #progress bar set up
  n=1 #initiate progress bar
  print("FILTERING RAW DATA: DERIVING SMOOTHER")
  W<-.04
  b1 <- butter(2, W)
  Dat$SmoothSVM<- filtfilt(b1, Dat$SVM)
  histogram(Dat$SmoothSVM)


##########################################################################
######################
  #Looping through the entire day to find the sleep duration
  print("BEGINNING CHANGE-POINT ANALYSIS")
  i<-NULL
  for(i in 1:N_day){
    if(i<N_day){
```

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```
    Sys.sleep(n/N_day) #update progress bar
    n = n+1 #increment the progress bar counter
    x <-seq(1:1441) #x vector for plots
    y <-seq(1:1106)
    pb$tick() #generate tick for progress bar
    a<-Inc[[i]]
    b<-Inc[[i+1]]-1
    day <-Dat$SmoothSVM[a:b] # attain entire day of data
    res<-cpt.var(day,penalty="AIC",pen.value=0.001,method="PELT") #attain vhange in
variance
    pp<-c(0,cpts(res),1440)#creating a variable to store a vector so to include 0 and 1440
    breakp <-pp[c(which.max(diff(pp)),which.max(diff(pp))+1)] #obtains max diff
between all breakpoints
    cols <-c(rep("black", times=breakp[[1]]),rep("red",times=breakp[[2]]-breakp[[1]]),
rep("black", times=1440-breakp[[2]]))
   }
 }
 #Adding a new column named group to the original data frame
 Dat$group <- with(data = Dat,cols)
 #Dat$BinaryCP <- ifelse(Dat$group=="black",0,1)
 #plot(Dat$SmoothSVM[1:1440],col=Dat$group, main = "Change point analysis")
 outsDat<-boxplot.stats(Dat$SmoothSVM[Dat$group=="red"])$out #determines the
outliers in the red sleep group
 for(j in 1:length(Dat$SVM)){
  if(Dat$group[j]=="red"&& Dat$SmoothSVM[j] %in%
outsDat==TRUE){Dat$group[j]<-"black" }}
 print("\nFILTERING COMPLETED")
 #plot(Dat$SmoothSVM[1:1440],col=Dat$group, main = "Change point analysis")

 print("BEGINNING SCORING")
```

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```
  Dat$Z_S<-(Dat$SmoothSVM-
mean(Dat$SmoothSVM[Dat$group=="red"]))/sd(Dat$SmoothSVM[Dat$group=="red"])
#generate z scores
  #Desired Confidence Interval          Z Score
  #90% 95% 99%        1.645 1.96 2.576
  Dat$Fgroup<-ifelse(Dat$Z_S<1.45,"red","black")
  Dat$BinSW<-ifelse(Dat$Z_S<1.45,0,1)
  print("END SCORING")

  #### plot for checking
  print("PRINTING PLOTS FOR VISUAL INSPECTION")
  plot.new()
  par(mfrow=c(3,1))
  plot(Dat$SmoothSVM[1:1440],col=Dat$group, main = paste0("CPA Participant:  ",
participants[P]),xlab = "Minutes",ylab = "SVM")
  plot(Dat$BinSW[1:1440], col=Dat$Fgroup,main="Binarized", type="l",xlab =
"Minutes",ylab = "SVM")
  plot(Dat$SVM[1:1440], col=Dat$Fgroup, main="Original with Z Scoring",xlab =
"Minutes",ylab = "SVM")

  print("DETERMINING SLEEP MEASURES")
  nameP<-paste0("C:/Users/Yogesh/Downloads/Plots",participants[P],".png" )
  dev.copy(png,nameP)
  dev.off()

  DFSleep<-data.frame(Dat) #creates new data frame for results

  print(paste0("Participant",participants[P]," has been processed."))
  #bring this code into the for loop to create output for each participant.
  Outname<-paste0("OutDatParticipant", participants[P],".csv")
  write.csv(DFSleep, file = Outname)
```

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```
 #rm(DFOut,Dat,DFSleep,i,j)
}

##########################################################################
##########################################################################

#Combining all the output files
library(readbulk)
fulldat <- read_bulk(directory = "C:/Users/Yogesh/Downloads/Sleep data
frame",subdirectories = FALSE,verbose = TRUE)
names(fulldat)
head(fulldat)
final_data <- fulldat[,c(-1,-2,-7,-21)]
final_data <-
final_data[,c("TimeStamp","X_m","Y_m","Z_m","Lux_m","Temp_m","SVM","X_std","
Y_std","Z_std","Lux_p","Participant","SmoothSVM","group","Z_S","Fgroup","BinSW")
]
head(final_data)
write.csv(final_data,"Final_Sleep_df.csv")
##########################################################################
##########################################################################

#Reading the data obtained from Change point and Z-scoring
rle_dat <- read.csv("Final_Sleep_df.csv",header=TRUE)
head(rle_dat)
rle_dat <- rle_dat[,-1]#removing the unwanted column
rle_dat$Date <- as.Date(rle_dat$TimeStamp)#converting timestamp to date
head(rle_dat)
#Determing the sleep duration
k<-NULL
LL<-length(rle_dat$BinSW)
```

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```
Inc<-seq(1,LL,by=1440) #Creates the sequence for k increments
N_day<-(LL/1440)
new_dat <- data.frame()
for(k in 1:N_day){
   if(k<N_day){
   a<-Inc[[k]]
   print(a)
   b<-Inc[[k+1]]-1
   print(b)
   max_rle <- rle(rle_dat$BinSW[a:b])
   #print(max_rle)
   if(max_rle$lengths==1440&&max_rle$values==1){
     new_dat[k,2]<-0
     new_dat[k,1] <- rle_dat$TimeStamp[[a]]
     new_dat[k,3] <- rle_dat$Participant[[a]]
   }else{
   myruns <- max(max_rle$lengths[max_rle$values==0])#finding the max sequence of
zeros
   h <- ifelse(myruns<1440,myruns,1440)#replacing lengths equal to 1440 with 1440
   print(paste0("Duration "  ,h))#printing the max duration
   #adding values in the newdataframe
   new_dat[k,1] <- rle_dat$TimeStamp[[a]]
   new_dat[k,2] <- h
   new_dat[k,3] <- rle_dat$Participant[[a]]
   }
  }
}
colnames(new_dat) <- c("Date","Algorithm_Sleep_Duration","Participant")#renaming
the columns for new_dat
new_dat$Date <- as.Date(new_dat$Date)#converting the timestamp to date
new_dat$Day <- weekdays(as.Date(new_dat$Date))
```

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```
head(new_dat)
new_dat <- new_dat[,c("Participant","Date","Day","Algorithm_Sleep_Duration")]
head(new_dat)

#Validation Dataset
library(dplyr)
summary <- read.csv("SummaryStats.csv",header = TRUE)
sum <- summary%>%arrange(PartNo)#arranging the summary data by participant
sum$Day <- as.character(sum$Day)#converting the timestamp to string format
class(sum$Day)
x <- sum$Day
sum$Date <- substr(x,10,20)#extracting the date by mentioning the character number
sum$Date <- as.Date(sum$Date)#Date format
class(sum$Date)

#Changing the column names for the MACRO summary dataset
colnames(sum)[colnames(sum)=="PartNo"]<-"Participant"
colnames(sum)[colnames(sum)=="Sleep.time"]<-"Sleep_Duration_Macro"
colnames(sum)[colnames(sum)=="Sleep.Efficiency"]<-"Sleep_Efficiency_Macro"

summary_final <- sum[,c("Date","Participant","Sleep_Duration_Macro")]#arranging the
columns
#merging dataframes
tf <- merge(new_dat, summary_final, by=c("Date","Participant"), all = TRUE)
tf <- unique(tf)
total_data <- tf %>% arrange(Participant)#arrange the data frame with participant
number
head(total_data)
#new data frame by removing NA's
total_data <- total_data[complete.cases(total_data), ]#removing NAs
head(total_data)
```

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```
hist(new_dat$Algorithm_Sleep_Duration, main = "Algorithm Sleep Duration",xlab =
"Sleep Duration")#histograms
hist(summary$Sleep.time, main = "GENEActiv Macro Sleep Duration",xlab = "Sleep
Duration")#histograms
write.csv(total_data,"Sleep_Validation.csv")#writing the csv file
##############################################################################
##############################################################################

#Results
#t-test for the whole sample
t.test(total_data$Algorithm_Sleep_Duration,total_data$Sleep_Duration_Macro) #t-test

##############################################################################
##############################################################################
#Analysis without outliers
#Analysis by removing days with 1440 minutes of sleep
remove_1400 <- total_data[!(total_data$Algorithm_Sleep_Duration>=1400),]
analysis_1400 <- lm(Sleep_Duration_Macro~Algorithm_Sleep_Duration,data =
remove_1400)
summary(analysis_1400)
summary(analysis_1400)$coefficients[, "Std. Error"]
t.test(remove_1400$Algorithm_Sleep_Duration,remove_1400$Sleep_Duration_Macro)
#t-test


#Analysis by removing with 1200 minutes of sleep
remove_1200 <- total_data[!(total_data$Algorithm_Sleep_Duration>=1200),]
analysis_1200 <- lm(Sleep_Duration_Macro~Algorithm_Sleep_Duration,data =
remove_1200)
summary(analysis_1200)
summary(analysis_1200)$coefficients[, "Std. Error"]
```

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```
t.test(remove_1200$Algorithm_Sleep_Duration,remove_1200$Sleep_Duration_Macro)
#t-test


#Analysis by removing with 800 minutes of sleep
remove_800 <- total_data[!(total_data$Algorithm_Sleep_Duration>=800),]
analysis_800 <- lm(Sleep_Duration_Macro~Algorithm_Sleep_Duration,data =
remove_800)
summary(analysis_800)
summary(analysis_800)$coefficients[, "Std. Error"]
t.test(remove_800$Algorithm_Sleep_Duration,remove_800$Sleep_Duration_Macro) #t-
test


#Analysis by removing with greater than 480 minutes of sleep
remove_480 <- total_data[!(total_data$Algorithm_Sleep_Duration>480),]
analysis_480 <- lm(Sleep_Duration_Macro~Algorithm_Sleep_Duration,data =
remove_480)
summary(analysis_480)
summary(analysis_480)$coefficients[, "Std. Error"]
t.test(remove_480$Algorithm_Sleep_Duration,remove_480$Sleep_Duration_Macro) #t-
test

##########################################################################
##########################################################################

#Comaprison of GENEActiv and Algorithm for outliers and without outliers
#Analysis of the whole sample
anova_outlier <- aov(Sleep_Duration_Macro~Algorithm_Sleep_Duration,data =
total_data)
```

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```
analysis_outlier <- lm(Sleep_Duration_Macro~Algorithm_Sleep_Duration,data =
total_data)
msum <- summary(analysis_outlier)
summary(analysis_outlier)$coefficients[, "Std. Error"]
pval = pf(msum$fstatistic[1], msum$fstatistic[2], msum$fstatistic[3], lower.tail=FALSE)
rsq = summary(analysis_outlier)$r.squared
plot(total_data$Algorithm_Sleep_Duration,total_data$Sleep_Duration_Macro,main="Ge
neactiv vs Algorithm",xlab="Algorithm Sleep Time (Hours)",ylab="Gneactiv Sleep Time
(Hours)")
abline(anova_outlier$coefficients,lty=2)
mtext(paste("r-squared:", signif(rsq,3), "\np:", signif(pval,3)),1,line=3.5,at=7.5)


#Analysis without outlier
anova_wdoutlier <- aov(Sleep_Duration_Macro~Algorithm_Sleep_Duration, data =
remove_480)
analysis_wdoutlier <- lm(Sleep_Duration_Macro~Algorithm_Sleep_Duration,data =
remove_480)
msum_wdoutlier <- summary(analysis_wdoutlier)
summary(analysis_wdoutlier)$coefficients[, "Std. Error"]
pval_wdoutlier = pf(msum_wdoutlier$fstatistic[1], msum_wdoutlier$fstatistic[2],
msum_wdoutlier$fstatistic[3], lower.tail=FALSE)
rsq_wdoutlier = summary(analysis_wdoutlier)$r.squared
plot(remove_480$Algorithm_Sleep_Duration,remove_480$Sleep_Duration_Macro,main
="Geneactiv vs Algorithm",xlab="Algorithm Sleep Time (Hours)",ylab="Gneactiv Sleep
Time (Hours)")
abline(anova_wdoutlier$coefficients,lty=2)
mtext(paste("r-squared:", signif(rsq_wdoutlier,3), "\np:",
signif(pval_wdoutlier,3)),1,line=3.5,at=7.5)
```

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```
#########################################################################
#########################################################################
#ANOVA analysis
#ANOVA analysis of Sleep duration from algorithm and MACRO with 8 hours of sleep
analysis <- aov(Sleep_Duration_Macro~Algorithm_Sleep_Duration, data = remove_480)
summary(analysis)
plot(analysis, which =1, main = "Sleep Duration (Algorithm vs GENEActiv Macro)")
plot(analysis, which =2,  main = "Sleep Duration (Algorithm vs GENEActiv Macro)")
plot(analysis, which =3,  main = "Sleep Duration (Algorithm vs GENEActiv Macro)")
plot(analysis, which =5,  main = "Sleep Duration (Algorithm vs GENEActiv Macro)")

#ANOVA analysis of Sleep duration from algorithm and MACRO for complete data
analysis2 <- aov(Sleep_Duration_Macro~Algorithm_Sleep_Duration, data = total_data)
summary(analysis2)
plot(analysis2, which =1, main = "Sleep Duration (Algorithm vs GENEActiv Macro)")
plot(analysis2, which =2,  main = "Sleep Duration (Algorithm vs GENEActiv Macro)")
plot(analysis2, which =3,  main = "Sleep Duration (Algorithm vs GENEActiv Macro)")
plot(analysis2, which =5,  main = "Sleep Duration (Algorithm vs GENEActiv Macro)")

#Plotting the difference for sleep duration for each day
remove_480$Participant <- as.factor(remove_480$Participant)#converting to factors
class(remove_480$Participant)
remove_480$Day <- as.factor(remove_480$Day)#converting to factors
class(remove_480$Day)
analysis_hsd <- aov(Algorithm_Sleep_Duration~Participant, data = remove_480)
plot(TukeyHSD(analysis_hsd))

#########################################################################
#########################################################################
```

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```
#mean difference between each participant sleep duration
table_A_480 <- aggregate(Algorithm_Sleep_Duration ~ Participant, data=remove_480,
mean)
table_M_480 <- aggregate(Sleep_Duration_Macro ~ Participant, data=remove_480,
mean)

table_A_800 <- aggregate(Algorithm_Sleep_Duration ~ Participant, data=remove_800,
mean)
table_M_800 <- aggregate(Sleep_Duration_Macro ~ Participant, data=remove_800,
mean)

table_A_1200 <- aggregate(Algorithm_Sleep_Duration ~ Participant,
data=remove_1200, mean)
table_M_1200 <- aggregate(Sleep_Duration_Macro ~ Participant, data=remove_1200,
mean)

table_A_1400 <- aggregate(Algorithm_Sleep_Duration ~ Participant,
data=remove_1400, mean)
table_M_1400 <- aggregate(Sleep_Duration_Macro ~ Participant, data=remove_1400,
mean)

table_A_total_data <- aggregate(Algorithm_Sleep_Duration ~ Participant,
data=total_data, mean)
table_M_total_data <- aggregate(Sleep_Duration_Macro ~ Participant, data=total_data,
mean)

##############################################################################
##############################################################################
```

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```
#subsetting data by participant (Change the particiapnt number for plotting different participants)
part <- remove_480[remove_480$Participant==21,]
#Distribution of the sleep duration throughout the week for all the participant
#calculating the total duration of sleep for each day of the week
weekday_dat <- aggregate(part$Algorithm_Sleep_Duration, by=list(Day=part$Day), FUN=sum)
#finding the sum of all the days
weekday_dat$Totalsum <- sum(part$Algorithm_Sleep_Duration)
#calculating the percentage
weekday_dat$Percent <- (weekday_dat$x/weekday_dat$Totalsum)*100
#plotting the graph for each weekday
ggplot(data=weekday_dat, aes(x = Day, y=Percent, fill=Day))+geom_bar(stat = "identity")+ggtitle(label = "Algorithm Sleep Duration for Weekdays")+theme_minimal()+xlab("Week Day")+ylab("Algorithm Sleep Duration (%)")
```

##
##

2. PELT Algorithm as given in [52]

PELT Method

Input: A set of data of the form, $(y_1, y_2, \ldots, y_n)$ where y_i belongs to R

A measure of fit C(.) dependent on the data

A penalty constant β which does not depend on the number or location of changepoints.

A constant K that statisfies equation (13) in section 2 of the thesis.

Initialise: Let n= length of the data and set F(0) = -β, cp(0) =NULL, $R_1=\{0\}$

Iterate for τ = 1,…..,n

1. Calculate $F(\tau^*) = \min_{0 \le \tau < \tau^*}[F(\tau) + C(y_{(\tau+1):\tau^*}) + \beta]$.

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2. Let $\tau^1 = \arg\{\min_{\tau \in R_{\tau^*}}[F(\tau) + C(y_{(\tau+1):\tau^*}) + \beta]\}$
3. Set $cp(\tau^*) = [cp(\tau^1), \tau^1]$
4. Set $R_{\tau^*+1} = \{\tau^* \cap \{\tau \in R_{\tau^*} : F(\tau) + C(y_{\tau+1:\tau^*}) + K < F(\tau^*)\}\}$

Output: the change point recorded in cp(n).

3. The below tables are for different critical values used in the Analysis Section in section 3 of the thesis:

Table-1 Average sleep duration difference for different sample size for critical value of 1.96

Critical Values	Confidence Interval (%)	Alpha	Sample size	Average Duration Difference
1.96	95	0.05	1160	60.93
1.96	95	0.05	1122	56.87
1.96	95	0.05	1101	45.96
1.96	95	0.05	1000	0.05
1.96	95	0.05	682	52.15*

Table-2 Average sleep duration difference for different sample size for critical value of 1.75

Critical Values	Confidence Interval (%)	Alpha	Sample size	Average Duration Difference
1.75	92	0.08	1160	41.96
1.75	92	0.08	1123	38.11
1.75	92	0.08	1106	29.7
1.75	92	0.08	1021	9*
1.75	92	0.08	725	63 *

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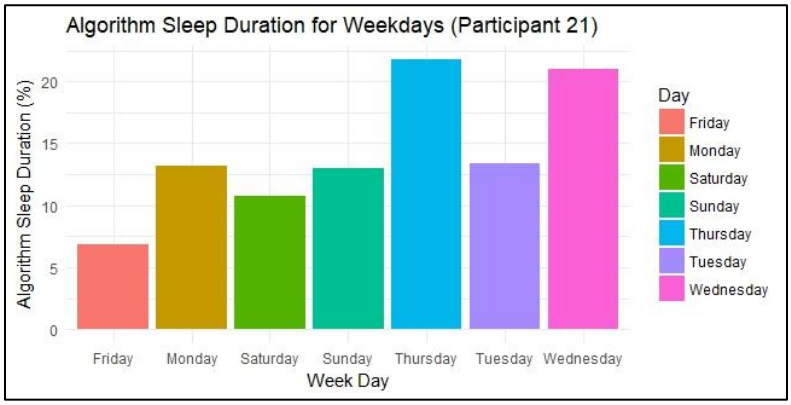
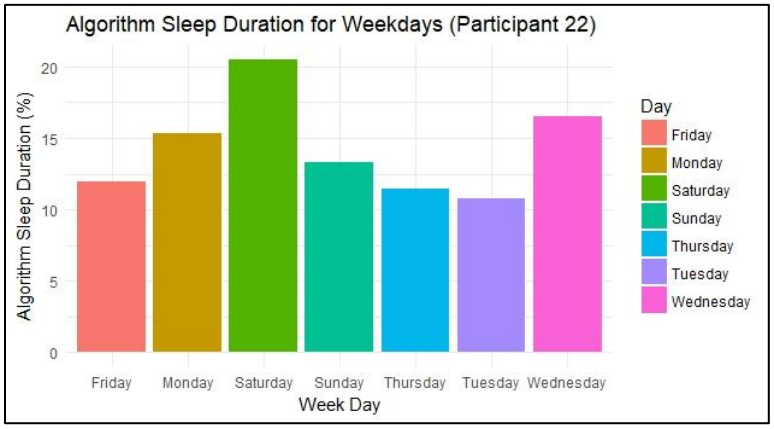
Table-1 Average sleep duration difference for different sample size for critical value of 1.65

Critical Values	Confidence Interval (%)	Alpha	Sample size	Average Duration Difference
1.65	90	0.1	1160	31.38
1.65	90	0.1	1124	28.3
1.65	90	0.1	1108	20.12
1.65	90	0.1	1030	16*
1.65	90	0.1	743	69*

4. Plots for each participant for critical value of 1.45 for each day of the week





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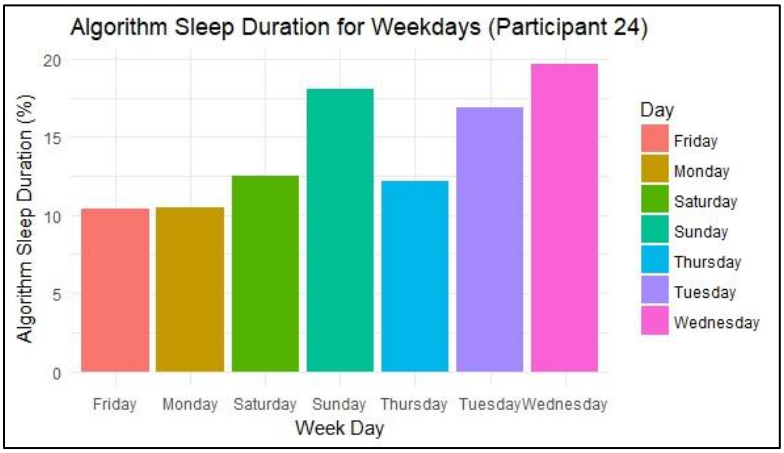

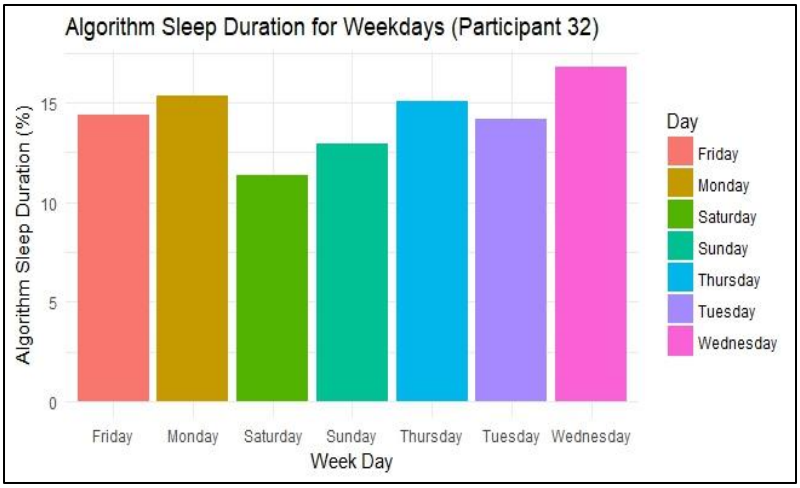

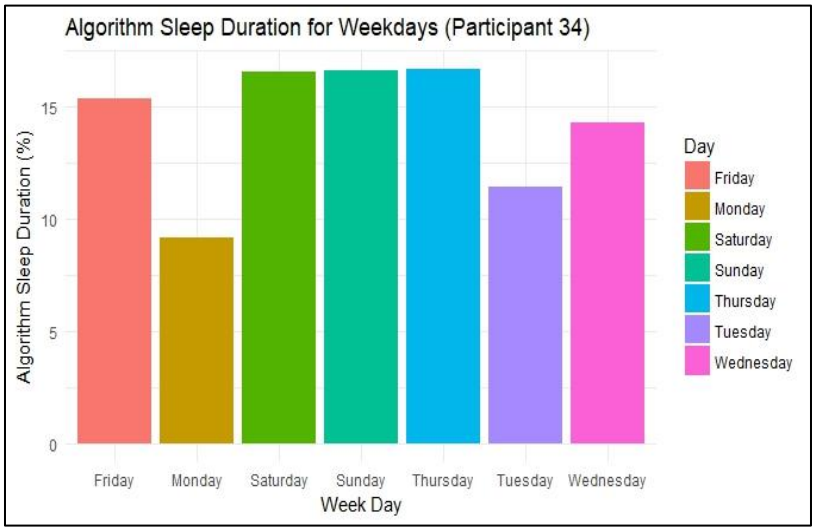

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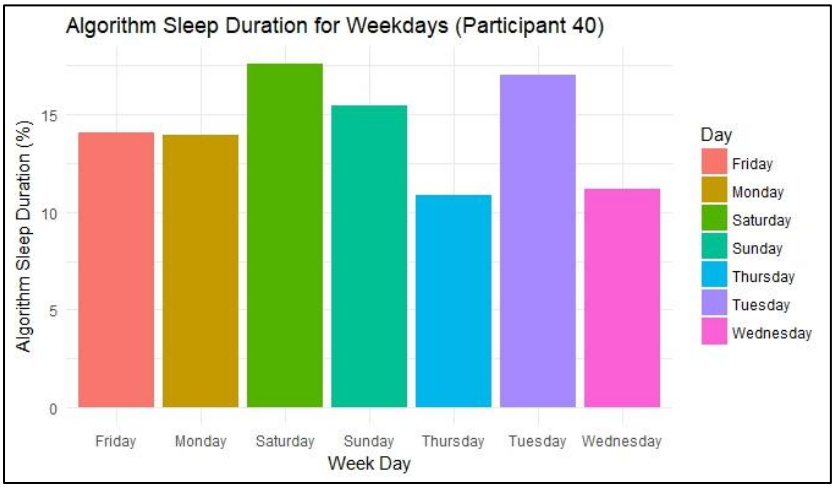

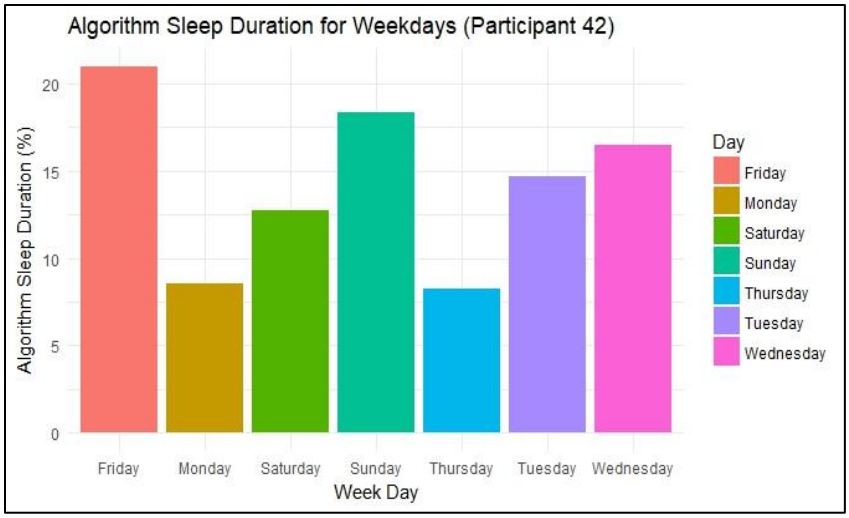

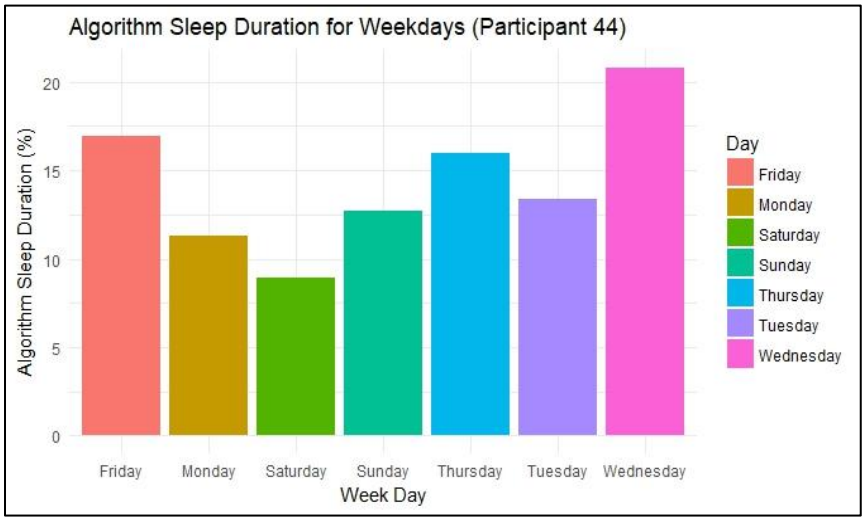

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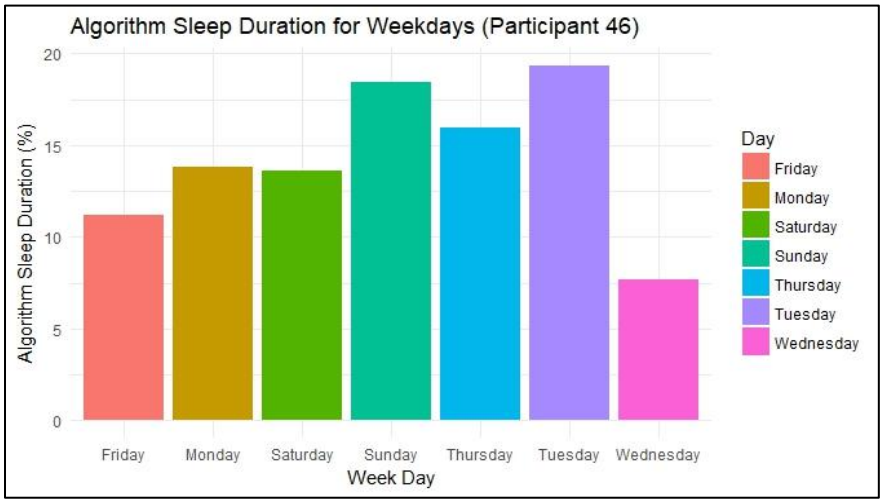

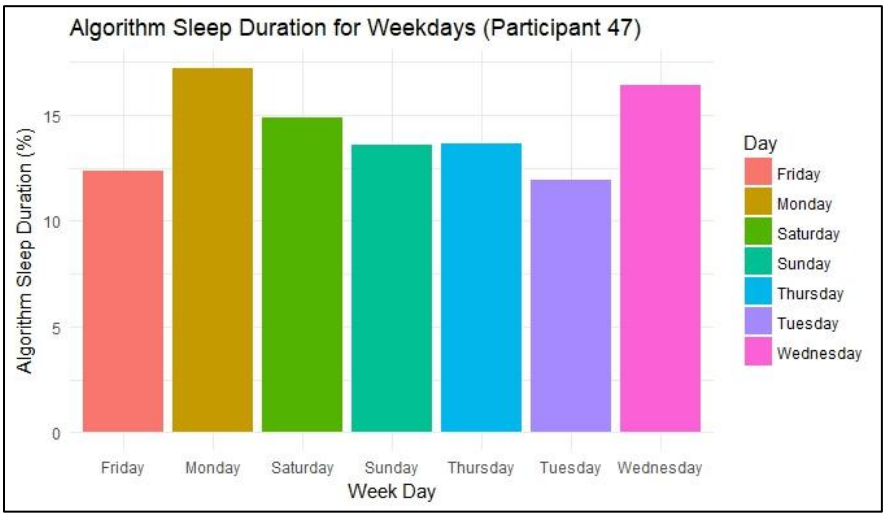

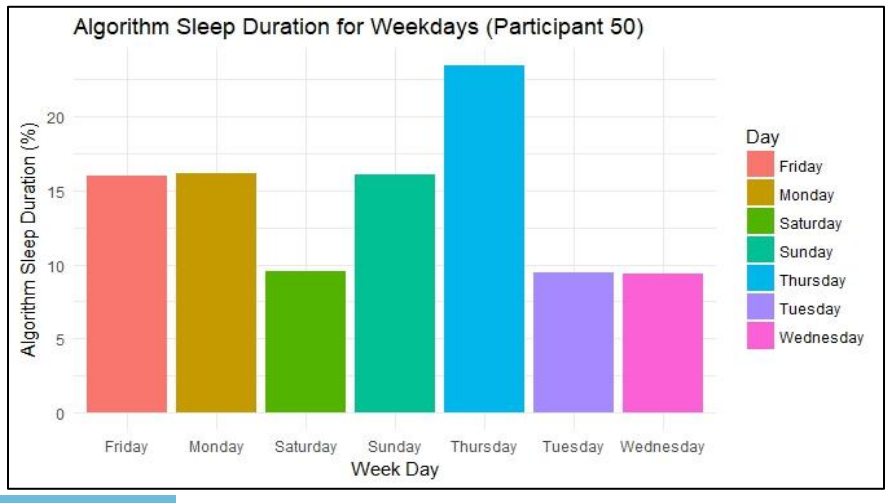

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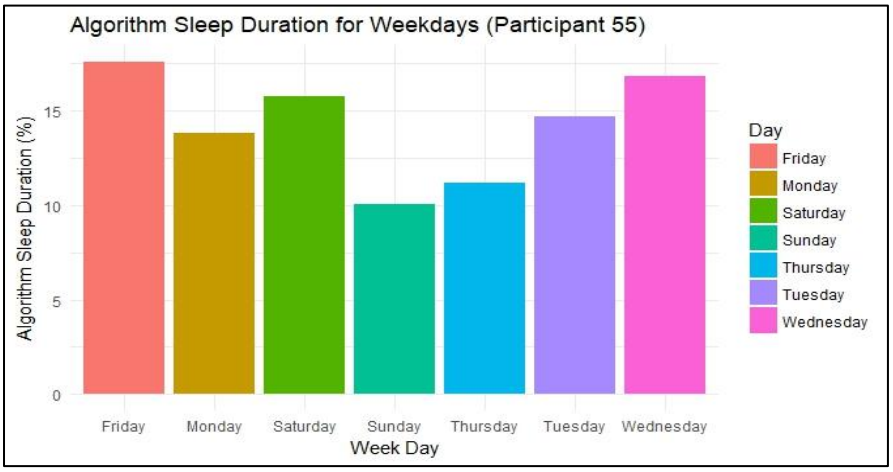

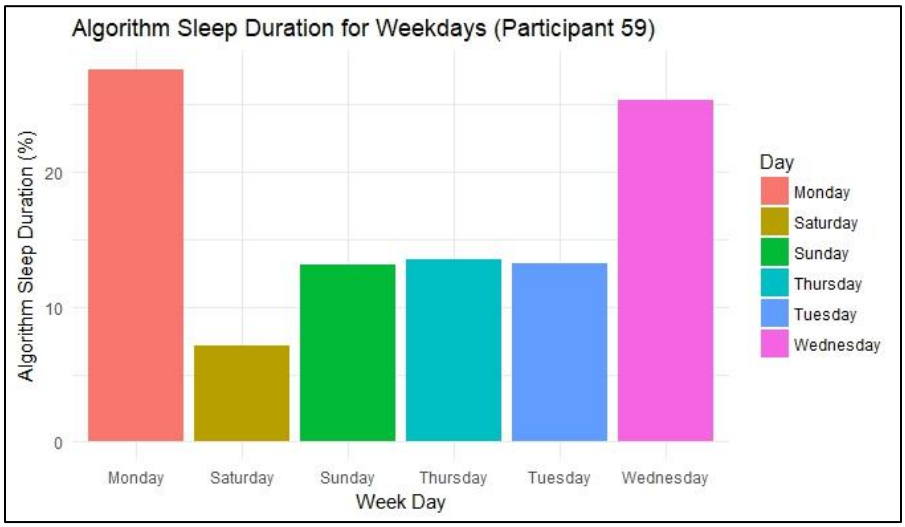

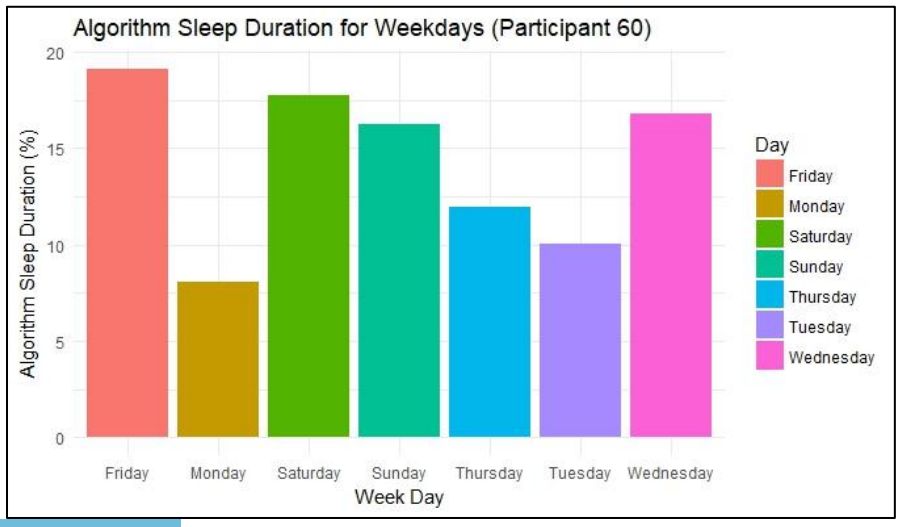

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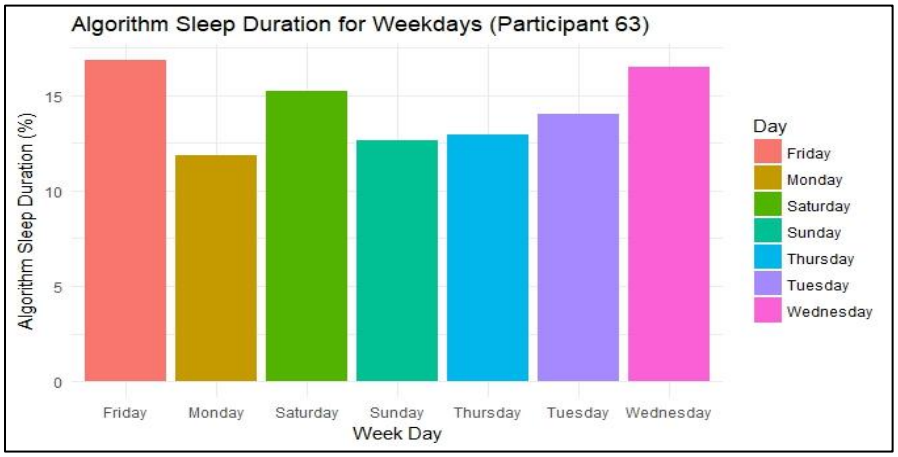

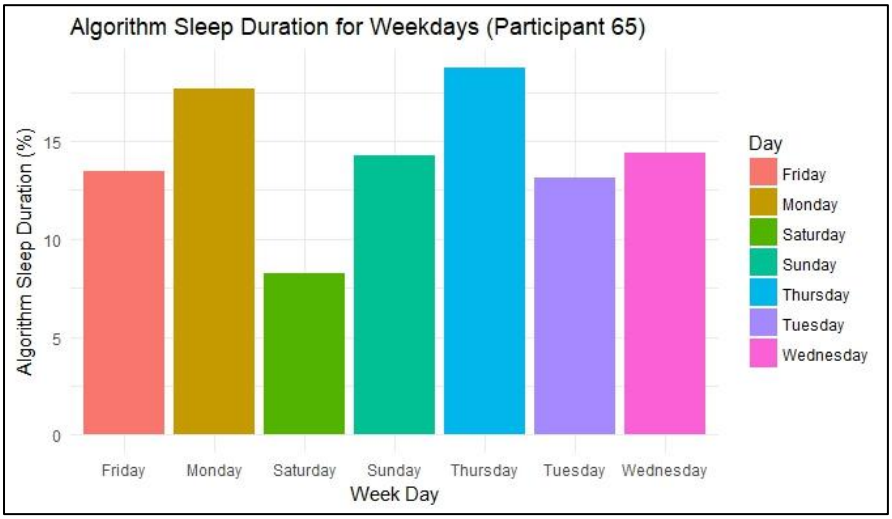

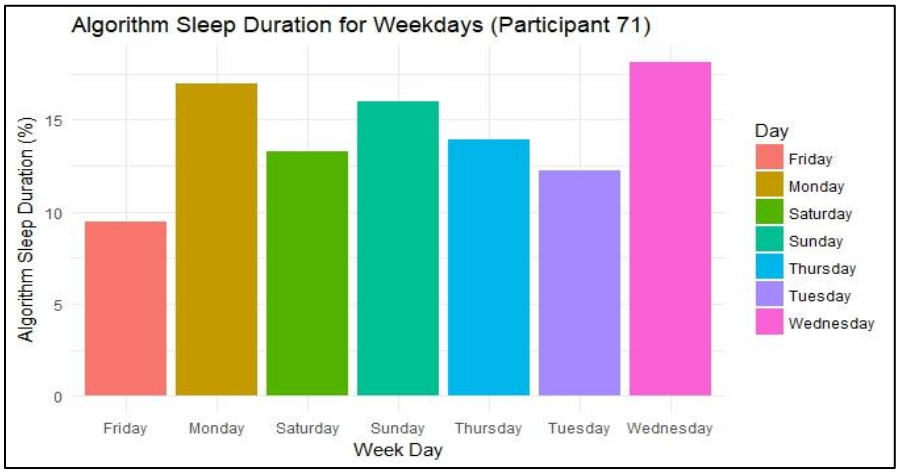

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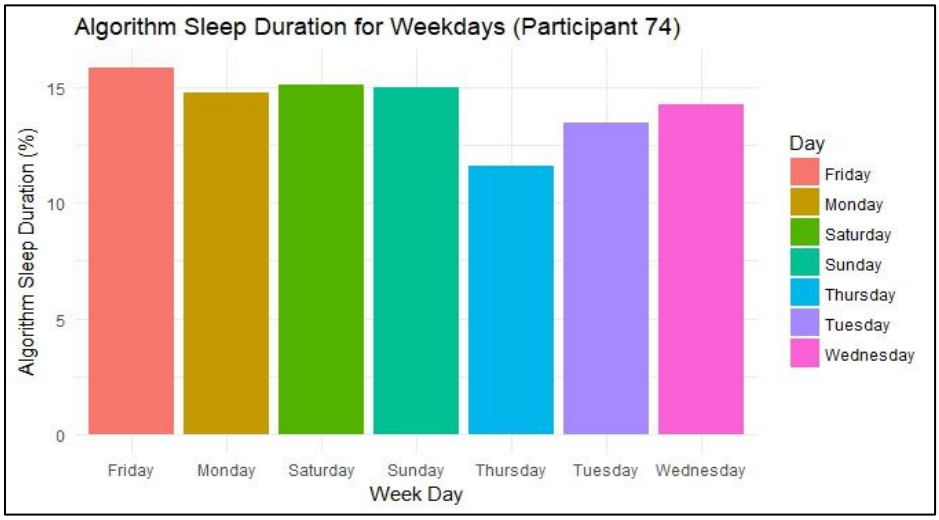

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