The Effects of Social Interaction on Heart-Rate Variability

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This research article intends to prove whether social psychology and human interaction can indeed affect heart-rate variability. We conducted a study in which two subjects worked both individually and cooperatively on a Jenga based game. This article begins by providing a brief overview of the modern research that's taken place regarding heart-rate variability. We then discuss a step by step solution of the methods we deployed to be able to analyze our data successfully. What we found is that that social interaction does elicit a positive response in time-domain, function-domain, and non-linear metrics, including but not limited to RMSSD and LF/HF values.

INTRODUCTION

Heart-Rate Variability has been studied for decades as a means of determining cardiovascular diseases. Poor heart-rate variability has been linked in numerous research studies as a determinant in poor cardiovascular health, vascular disease, various cognitive impairments, and mental disorders, among other factors. (Pham, Lau, Chen, & Makowski, 2021). The determination of whether a heart is healthy versus poor would be mathematically impossible to devise. Such an equation that could calculate oscillations in heart-beats or IBI (inter-beat) interval data simply does not exist. Thus, taking one factor such as the stability of a heart is not enough to identify ectopic beats. (Acar, Malik, Hemingway, & Savelieva, 2000) However, open-source software has given us the capability to simulate a heart beat-by-beat and determine different measurements and variability of data. We can analyze sets of raw data and determine similarities in heart-rate variability such as time-domain and frequency-domain analysis, even going so far as determining correlations between nonlinear data with Poincaré plots.

Time-domain and frequency-domain analysis are two methods commonly used in research of heart-rate variability. Although one may consider high values of heart-rate variability to be accurate, such is not the case. Several reasons exist as to the invalidity of data, including the fact that several pathological conditions can yield high values of HRV. (Shaffer & Ginsberg, 2017). Not every method works for the data collected. Should you decide to calculate relative frequency between signals, you may consider using frequency-domain techniques such as the ratio of standard deviation correlation amongst two subjects. (SD1/SD2). Likewise, non-linear correlations can quantify unpredictability and and complexity in a series of IBIs. (Shaffer & Ginsberg, 2017).

Context is crucial when interpreting relative heart-rate variability measurements. It's important to consider several factors such as recording length, sampling frequency, and background of participants in your study, among other factors (Shaffer & Ginsberg, 2017). With open-source software and a host of programming languages, it's never been easier to detect valid correlations in our data sets.

Many studies have involved the application of machine learning, wearable devices, and artificial intelligence to gather pertinent information related to ECG and "IBI" (Inter-Beat) Interval Data. Going further, some studies have even attempted to entirely mitigate the manual quantification and analysis of ECG data. (Acar et al., 2000).

With the technology advancements and ability to correlate sets of data, the question that now comes up regards which type of data affect heart-rate variability. One can use ECG Actiheart to collect pertinent information and intelligently analyze it in an effort to determine various metrics related to human trust. In the case of this article, we analyze the effects of human social psychology on heart-rate variability data. One such study concluded that social interaction is important for psychological wellbeing and overall life satisfaction. Thus increase in activity of the vagus nerve, measured by heart-rate variability plays an important roll in our day-to-day lives. (Shahrestani, Stewart, Quintana, Hickie, & Guastella, 2015). The results in this study hope to prove similar results, however no assumptions should be made as to the nature of the data collected in this experiment since both participants could have the possibility of experiencing similar outcomes in either the individual and cooperative game modes.

Further, this article encompasses a study based off the usage of Neurokit2, and the Python Programming Language. Neurokit2 is an open-source and python driven framework for processing neurophysiological signal data. (Makowski et al., 2021a). The option of using custom processing pipelines is available, which allows an individual to fine tune neurokit function methods to their usage. Several research studies have utilized the power of processing pipelines including that of (Frasch, 2022), where data sets were used in conjunction with Neurokit to determine applications of sleep physiology. As with standard HRV computation, neurokit also includes statistical based methods, as mentioned under time-domain and frequency analysis. If you'd like to calculate the standard deviation or mean of sets of data, two relatively simple calculations, you can easily use Neurokit and Python to accomplish this task.

Although this study is strictly based on heart-rate variability data, you can also perform functions with electrodermal activity (EDA), Respiratory Rate Variability (RRV), Electroculography (EOG), among other physiological measurments.

METHODS

Participants

A total of twelve participants were recruited from our local institution. Six trials were conducted in which two people par-

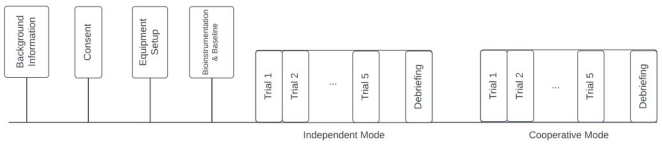


Figure 1. Experiment Analysis

ticipated per each consecutive trial. We made sure each group of participants did not know each other, without telling them. Additionally, we used second trial results since data was most concise and clean. Participants were briefed on the experiment, while being allowed to introduce each other. Consent was also gathered amongst each participant.

Experimental Procedure

This experiment starts by having both participants consent to our study, as previously noted. For our model, we use Jenga, a popular game built on the concept of stacking and removing blocks continuously, until an unstable structure results. Participants are first asked to wear an ECG Actiheart, which is synced to the device and quantifies data such as Heart Rate Variability (HRV), as well as cardiac electrodermal activity (EDA).

ECG Actiheart setup is simple. The first step involves connecting the device to the computer and syncing it by doing a signal test. A signal test allows the ECG R-Wave to be tested to confirm good skin contact of the electrodes. It's recommended to do this before all recordings to maintain accuracy. Once the signal test is loaded onto the device, participants are instructed to wear it and sit still for a total of 5 minutes so as to not disturb readings. Once the signal test is complete, we verify whether it passed or failed in the Actiheart window. Pass indicates it's safe to upload full waveform mode. Full waveform mode provides readings of ECG, BPM, IBI, and body position throughout a recording. Finally, once this mode is uploaded, participants are instructed to secure the device onto their chest. Refer to fig 5. for a model of the entire experiment

Data Analysis

HRV has become a relatively convenient way to determine cardiovascular abnormalities, among other relevant theories. Although the initial phase of the project simply entailed briefing our participants and having them complete both trial modes, the secondary phase entails complex theories of signal processing, thus preventing an ordinary user from being able to understand the inner workings of our data. However, to make it easier to understand, Python, a popular and user-friendly programming language, as well as Neurokit2, an open-source python package that's designated towards both novice and advanced users, are used as the main framework in this project. Before discussing further, let's refer to fig 2 for a model overview of how participant data is quantified accordingly.

As you can see, the data we collected is stored on our local computer under the RAW format. We'll then convert it into a pandas dataframe, that being a two-dimensional and mutable data structure. The bulk of this article entails talking about a vast amount of neurokit routines, including but not limited to trimming data, applying a band pass filter, which will be discussed further on, cleaning ECG signals, and finding QRST peaks, among several other routines

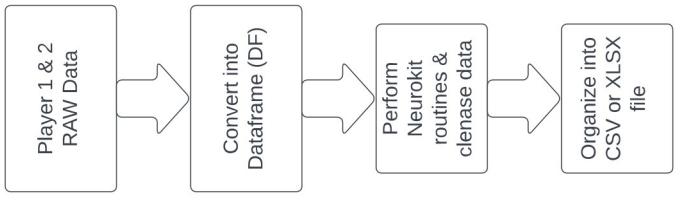


Figure 2. Data Analysis Model

Preprocessing Techniques

Before implementing Neurokit, we need to load our cardiac data into an IDE by defining preprocessing functions relative to where the data is stored on the disk. For the purpose of this experiment, we'll define a function called load_data() and use the open() method to direct the software to our local file(s). Data from the first participant and the second participant are stored in a mutable object and passed through as a variable for our dataframe analysis. If one wanted to void the complexity of creating separate functions to load data, Neurokit provides a data() function that can allow us to easily obtain data files such as JSON and TXT locally or from a known web address. The bio_process() function allows us to use process different types of signals using signal specific pipelines, however for this article, we'll use a custom processing pipeline to clean our data.

HRV Analysis

The data has been successfully processed as a dataframe and loaded into memory. Now we can apply a host of neurokit function methods in order to clean our data. The most common being ECG _clean(), can let us define a sampling rate up to 1024 Hz and allow us to get a better view of oscillations. If one would like to generate x amount of seconds of ECG signal, the ecg_simulation() method is available for our analysis. You can simulate an infinite amount of possibilities between defining a duration, sampling rate, and heart_rate. Below is a snippet of code defining a simulation

```
# Generate 15 seconds of ECG signal (recorded at 250
    samples / second)
ecg = nk.ecg_simulate(duration=15,
    sampling_rate=250, heart_rate=70)

# Process it
signals, info = nk.ecg_process(ecg,
    sampling_rate=250)

# Visualise the processing
nk.ecg_plot(signals, sampling_rate=250)
```

Before we proceed to discussing Neurokit in-depth, it's important to analyze how the data was segmented between individual and cooperative game modes.

Segmenting Data

Although time-domain and function-domain results were obtained with Neurokit, one issue that was faced was having to properly segment the data between individual and cooperative game modes. First, we obtained the estimate between the amount of data sets in each vector, by using the len() function in Python to obtain an estimate of ten million rows. Note that each data point in the vector is calculated in seconds. In theory, it is possible to compare the twenty-four hour time values we obtained per each trial for player one and player two, versus the raw data.

By analyzing the initial start of the export versus the start time of the trial, we could take the estimate between those two values, multiply it by sixty seconds, and then multiply by one-thousand twenty-four samples. Note that one-thousand twenty-four samples arrive in sixty seconds. The calculation obtained is the vector point inside the RAW data.

We can use the CAT command in Linux in order to take each vector point from the start and end of each trial and output it into a separate text file. CAT allows us to concatenate files and print them on the standard output. Below is the command used in order to initiate this process.

```
cat EXHSTX_ECG.txt | awk 'NR >=2150400 && NR
    <=2273280' > OUTPUT
```

Let "X" refer to each player data. The first numerical entry is a starting theoretical value inside of the vector and our last entry is defined as our desired ending value of the vector. We output the exact data to a file called OUTPUT for later use.

Signal Filtering

Neurokit comes with a multitude of signal filtering options that can be implemented. We can distort the signal by using signal_distort() function, where we modify the amplitude, frequency, and linear drift of our data. The essence of this is to add noise and artifacts to the data. In the case of this project, we utilized the default signal filtering option, as listed below

```
# cleans
nk.signal_filter(clean_signalP1, sampling_rate=1024,
    lowcut = 10, highcut = 48)
nk.signal_filter(clean_signalP2, sampling_rate=1024,
    lowcut = 10, highcut = 48)
```

If one wanted too, any amount of lowcut and or highcut could be specified until exact results are obtained. In our case, it was recommended to use a low value of 10 and a high value of 48. One more available option we could use is the detrending feature, whereby data can be removed from the baseline drift or trend.

Locating peaks in ECG Data

Locating various types of peaks, including P, Q, R, S, and T waves, can be made relatively simple. After loading data using the data() method, we can use ecg_peaks() to determine various types of peaks from our graphs. Unfiltered results are accepted, however in our case we use a set of filtered data for optimal results, as mentioned previously. For our project, we aim to detect R-Peaks in our data, which are classifed as the local maxima in each set of graphs. the ecg_peaks() function is used, however Neurokit2 also provides a low level function method called findpeaks that explicitly detects R peak waves in our data.

HRV Time-Domain Indices

HRV Time-Domain indices help quantify several attributes according to the measurement of IBI's (Interbeat Interval). It is possible to describe this metric using 24 hours, short term (ST, 5 min), and ultra-short term (UST < 5 min) (Shaffer & Ginsberg, 2017). A number of relevant parameters are described in the table below

Time-Domain Parameters	Description
MeanNN	Mean of the RR intervals
SDNN	Standard Dev. of RR intervals
SDANN1, SDANN2, SDANN5	STDEV of avg RR intervals
SDNNI1, SDNNI2, SDNNI5	Mean of STDEV of RR intervals
RMSSD	Root Mean Square of RR int. diff.

As you will notice, the two most important parameters to take into consideration are the mean and the standard deviation of RR successive intervals. Later in the results section, both these statistics will be quantified amongst both player 1 and player 2, both individually and cooperatively. Additionally, if one wanted to quantify a host of other statistics, the Neurokit documentation contains a more extensive list of such.

SDNN vs SDAN

In the table above, it was mentioned that SDNN is the standard deviation of successive RR intervals. Accordingly, one can consider it a measure of overall variability, and or total power of a system. Since the SDNN is a measure of the power of a total regulation system, 24 hour recordings provide more accuracy as opposed to short-term or ultra short-term recordings. Epochs for SDAN measurements are computed on a short-term scale, approximately 5 minutes. Thus, SDNN does not equate to SDAN measurements since it is calculated using 5 minutes segments instead of an entire 24 hours interval. It's valid to assume SDAN measurements don't provide any additional useful information in contrast to SDNN measurements. (Shaffer, McCraty, & Zerr, 2014)

SDNN Index

The SDNN Index is an important computation when it comes to calculating the mean of the standard deviation of RR success intervals. To compute the indices from 1,2, and 5, calculate exactly two-hundred and eighty-eight segments from five minute intervals in a 24 hour record. Then, calculate the standard deviation of N intervals contained in each five minute segment. (Shaffer et al., 2014). If the data provided is too short, no computation is performed.

RMSSD

RMSSD is computed using the square root of the mean of the sum of successive differences between adjacent RR intervals. (Makowski et al., 2021b). RMSSD and SD1, that being the standard deviation perpendicular to the line of identity, are

equal to each other. Both RMSSD and SD1 are considered to be calculated with short-term, beat-to-beat variability, , and thus should not be used as separate heart-rate variability metrics (Ciccone et al., 2017). However, other research has proposed various ultra-short time periods, from a minimum of 10 seconds to a maximum of 60 seconds.

pNNx

PNN20 & PNN50 are more commonly used heart-rate variability measures designed to calculate the proportion of RR intervals, greater than 20 milliseconds (ms) or greater than that of 50 ms. PNN50 was founded by a team of researchers in 1984, and shortly thereafter, exact threshold measurements were able to be computed. (Mietus, Peng, Henry, Goldsmith, & Goldberger, 2002).

HF and LF

With time-domain analysis of heart-rate variability having been discussed, this article turns its attention towards frequency-domain analysis. In contrast to time-domain, where we measure the variability of a system, frequency analysis involves a technique in which one determines how much of a signal lies within one or more frequency bands. We begin by focusing on the difference between HF and LF frequencies. High-Frequency (HF) thresholds involve a range of Hertz (HZ) between 0.15 and 40, whereas Low-Frequency (LF) thresholds involve a range of Hertz (HZ) between 0.04 to 0.15 Hz. The recommended minima for both HF and LF signals is classified between 1, 2, and 5 minutes (Makowski et al., 2021b). Further, both HF and LF can potentially be classified as a ratio of each other, called the LF/HF Ratio, however, the scientific community has heavily debated whether or not these two separate measurements can be mathematically computed. (Billman, 2013).

Nonlinear Indices and the Poincaré Plot

In contrast to time-domain methods where variability of the system is measured, non-linear indices measure quality, scaling, and correlation properties of signals, or rather the unpredictability, fractability, and complexity of a signal (Godoy, 2016). The Poincaré Plot is a geometrical technique that has the ability to quantify two data points in a time series (Satti et al., 2019). To put it more simply, it is a graphical representation of each NN interval plotted against the previous NN interval (Makowski et al., 2021b). Relevant non-linear parameters that can be plotted with a Poincaré model are listed below

Non-Linear Parameters	Description
SD1	STDEV perpendicular to the line of identity
SD2	STDEV along line identity (long-term HRV)
SD1/SD2	Ratio of SD1 to SD2. (long-term HRV)

RESULTS

Individual Mode | Time-Domain Estimates

Following below is a table indicating relevant R-R time-domain data for player 1 and player 2 in the individual game mode. Note that the experiment this article describes is in regards to the second round conducted on participants.

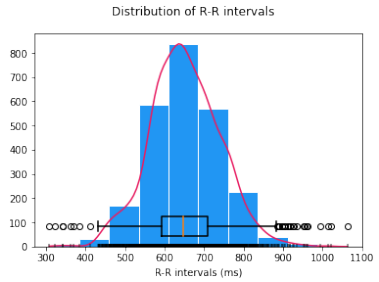
Table 1. *Player 1 | Individual R-R Data*

Trial	1	2	3	4
Mean	678.03	637.92	658.27	662.26
SDNN	75.78	75.43	95.91	55.5
RMSSD	49.74	45.12	53.34	29.07
SDSD	49.78	45.15	53.38	29.13

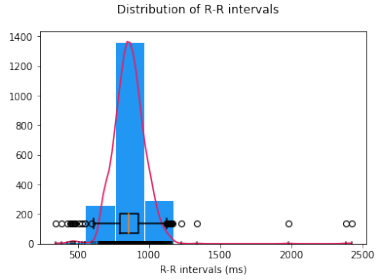
Trial	1	2	3	4
Mean	889.81	853.26	859.76	895.99
SDNN	102.6	67.8	111.71	130.07
RMSSD	87.25	57.53	73.02	133.07
SDSD	87.31	57.66	73.12	133.58

RMSSD is the best indicator of parasympathetic activity in the heart (Minarini, 2020). The parasympathetic activity invokes "rest" conditions whereas the sympathetic nervous system activates a "fight or flight" response. (Tindle & Tadi, 2021). Note that these values correlate with individual game mode data. SDNN is a measure of tracking physiological stress over time, as it can capture cardiac variability difference within individuals (Altini, 2018). In regards to player 2, we see a trend in which their SDNN value increases exponentially upon moving to trial 4. It is possible to conclude that the stress levels of player 2 increased significantly throughout the course of at least one trial, including that of player 1.

SDNN values give us insight into the autonomic nervous system (ANS), that of which regulates heart rate and blood pressure, among other factors. (Gordan, Gwathmey, & Xie, 2015). High SDNN values for player 2 correlate with RMSSD values in that player 2 likely faced an abundance of stress and high blood pressure as the trials progressed. We again notice that player 1 had almost the same effect in at least once instance during each consecutive trial.



(a) Player 1



(b) Player 2

Figure 3. Distribution of R-R Intervals | COOP trial 4

Individual Mode | Frequency Domain Estimates

The HF band correlates with RMSSD and PnnX time domain measures. Thus, a low HF band may indicate stress, panic, and or anxiety. (Shaffer & Ginsberg, 2017). For player 1, we found a relatively constant HF band whereas with player 2 there was a stark increase in the level of HF that occurred especially as the trials progressed. Our theory validates the values obtained from the RMSSD data as well as our PNN20, PNN50, and PNN80 data. LF tends to ellicit heavy breathing in individuals (Shaffer & Ginsberg, 2017). Thus, anything such as exercise can elicit a response where increased heart rate and blood pressure occur as a response to one's breathing rhythms. Player 1 experienced a sharp increase in the LF band between trial 3 and 4. Likewise, player 2 experienced a sharp LF increase between trial 1 and 2. Given these scenarios, it's fair to assume that in at least one instance, both players experienced an intense reaction, likely when the blocks fell and their trial ended.

Individual Mode | Non-Linear Estimates

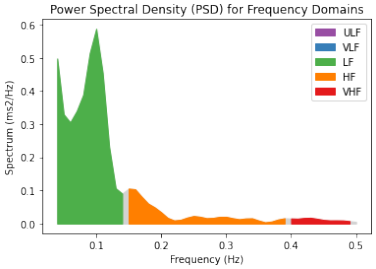
As previously noted, Poincaré plots take a sequence of R-R intervals and plot every R-R interval against it's prior interval. (Shaffer & Ginsberg, 2017). Much research has been done as to how to better quantitatively measure descriptors that are not linearly dependent. (Brennan, Palaniswami, & Kamen, 2001). However, two of the most widely used methods this article implemented involve determining whether the shape of the plot is elliptical or not, as well as measuring both SD1 and SD2 correlation coefficients, excluding their respective ratios. SD1 is defined as a mass of points perpendicular to the line of identity (Brennan et al., 2001), whereas SD2 was simply measured along the line of identity. Both players exhibited normal elliptical plots with data falling along the 45° line of identity. Since the ratio of SD1/SD2 is heavily correlated with the ratio of LF/HF, and has had its accuracy heavily debated in research such as that of (Billman, 2013), this article does not include these calculations.

Cooperative Mode | Time Domain Estimates

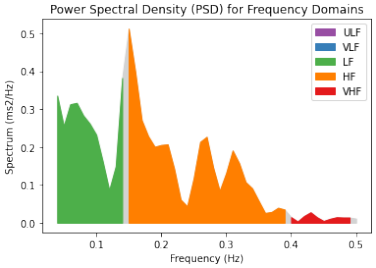
We found that the overall RMSSD values between both players was significantly decreased in comparison to that of the individual game mode. The SDNN values for both player 1 and player 2 were also overall significantly decreased, although at first player 2 seemed to elicit almost the same reaction values as that of the individual game mode. We can conclude that the social aspect of working together on what could be considered a mildly frustrating task likely improved player 2's overall values considerably

Cooperative Mode | Function Domain Estimates

For the function domain estimates in cooperative mode, HF and LF values differed from what was first expected. LF values went up significantly while HF values remained almost minuscule and constant among both players. It's been noted that the ratio of LF to HF is relatively innacurate, however one theory we have is that the data discovered for player 2 may have been incorrectly segmented or computed at the start of trial 1 and or 2.



(a) Player 1



(b) Player 2

Figure 4. Frequency data for both participants | Individual Trial 4

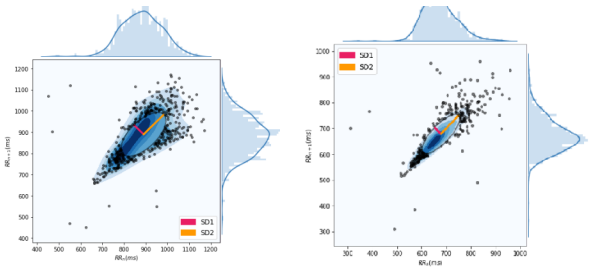


Figure 5. Poincaré Estimates for Player 1 and 2 | Individual Trial 1, Respectively

Cooperative Mode | Nonlinear Estimates

The same theory arises as to why the ellipse was deformed for player 2 given that the subjects data was perhaps incorrectly segmented at trial 1. However, SD2 met the line of identity at the 45° angle and the plots of SD1 were disbursed correctly.

Table 2. *Player 1 | Cooperative R-R Data*

Trial	1	2	3	4
Mean	652.29	655.74	667.90	680.29
SDNN	57.14	96.51	33.89	15.54
RMSSD	48.27	50.24	34.20	56.20
SDSD	48.27	50.26	34.26	56.30

Trial	1	2	3	4
Mean	865.60	873.82	856.33	855.88
SDNN	57.76	40.28	0.661821	33.21
RMSSD	117.14	127.32	47.81	62.70
SDSD	117.17	127.41	47.93	62.85

CONCLUSION

We found that social psychology does indeed elicit a positive response regardless of gender or age. Our theory was

proven correct by the data we were able to decipher from our subjects including that of RMSSD time-domain and LF HF function data. Retrospectively, our time-domain, function-domain, and non-linear estimates proved that interacting with other humans, even on complex tasks, does activate different parts of the heart and can likely mitigate different types of mental conditions, panic, anxiety, and vascular disease.

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