Comparison of Two Filtering Methods for Heart Rate Variability Analysis

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Abstract. Heart diseases are amongst the most common causes of death in the industrialized world. Since the cardiological system is very complex and hard to capture in its entirety, researchers are looking for indicators of its health. A promising one is the heart rate variability (HRV), i.e., the variation of the time intervals between two heartbeats. It reflects physiological processes, which influence the rhythm of the heart. An approach by researchers is a visualization tool, the Poincaré plot, to analyse HRV. Numerous data models exist in order to automatically quantify Poincaré plots.

To extract as much information as possible from Poincaré plots, it has to be filtered from artefacts and outliers before applying the data models.

The goal of this work is to test the influence of two different filtering methods on the Poincaré plot quantification methods.

A test case was constructed were a database with healthy heart rates and one with pathological heart rates were filtered with the two methods. Thereafter two Poincaré plot measures were evaluated using the filtered data sets. Afterwards the differences between these data sets were statistically examined.

It can be concluded that the fully automated filtering via clustering shows no large drawbacks compared to the traditional method of ECG annotation based filtering for HRV-analysis via Poincaré plots.

Introduction

According to a report by the European Society of Cardiology, heart failure is a leading cause of death in the EU and is on the rise due to an increasing age of the population [1]. Since an early diagnosis of heart conditions leads to more successful treatments, researchers look for markers of heart diseases [2].

More than 30 years ago HRV was introduced as such a method [3]. HRV is the variation of the time interval between consecutive heartbeats. It highly depends on the extrinsic regulation of the heart rate, i.e., the time interval between two beats, and reflects changes in the balance of the different regulatory systems, including the autonomous nervous system [3].

Studies show a connection between the balance of the autonomic nervous system measured with HRV and cardiovascular diseases [4].

In studies of HRV, both time- and frequency-domain measures are typically used by practitioners and researchers [3]. Since the influences of the generation of beats are also non-linear [5], a visualization tool originating in chaos theory, the Poincaré plot and models to quantify it, have become popular tools to analyse HRV in the last 20 years [6].

The data basis of most HRV-measures, including the Poincaré plot used in this work, consists of so called RR-Intervals. These are the time distances between two consecutive R-peaks in an ECG Signal, as shown in Figure 1.

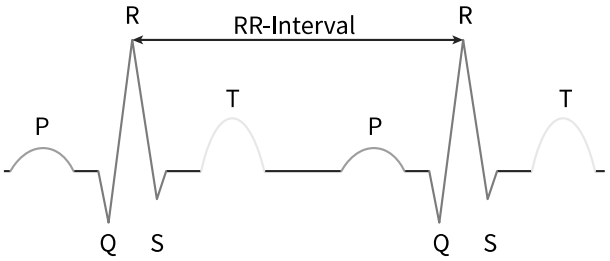

Figure 1: An ECG signal of two heart beats and the corresponding RR-interval.

Since hardly any ECG recording is ever without any artefacts or outliers (due to movement or ectopic beats, i.e., irregular heart beats) the signal has to be filtered to improve the information density of the Poincaré plots and the corresponding HRV-measures [7].

In most cases, this is done based on ECG annotations, where each heartbeat in the ECG signal is labelled, e.g. as a normal beat or as a premature beat. These annotations are either created manually by a physician, automatically by a computer, or semi-automatically, where the computer output is reviewed manually. All beats not labelled as normal are filtered out.Since the creation of annotations is a very time consuming task, which can only be done by trained personal, fully automatic methods should be considered. One of these approaches is to find artifices and outliers via clustering algorithms and filter these out. The question we examine in this work is, what the impact of the two filter methods is on HRV analysis via Poincaré plots.

1 Methods & Models

1.1 Poincaré plot

As mentioned beforehand Poincaré plots are a visualization tool for heart rate data. They are constructed as follows.

Given a data set of N RR-intervals $\{RR_1, \dots, RR_N\}$ a Poincaré plot is defined as the following mapping:

$$R \to R \times R$$
$$\{RR_1, \dots, RR_N\} \mapsto$$
$$\{(RR_1, RR_2), (RR_2, RR_3), \dots, (RR_{N-1}, RR_N)\}$$

A typical Poincaré plot of a non-pathological, 2 hour-long, unfiltered heart rate recording is shown in Figure 2.

1.2 Filtering via cluster algorithms

Clustering is defined as the grouping of data points based on similarities between these points [8]. Which similarity is measured depends on the used data, in our case we cluster based on the distances of the points in the Poincaré plot.

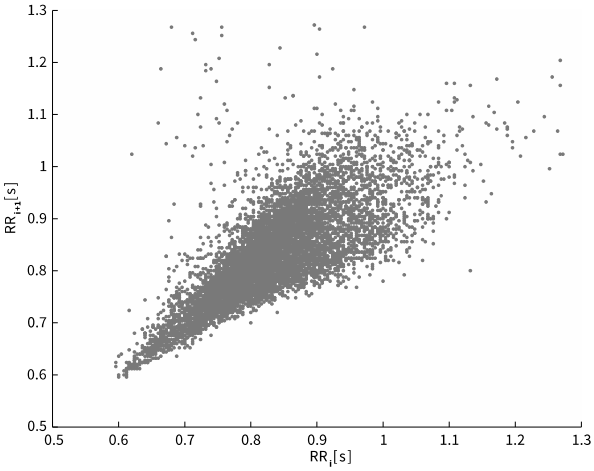

Figure 2: Unfiltered Poincare plot of a non-pathological 2 hour-long heart rate recording.

After considering different algorithms (k-means, single linkage and mean-shift), we chose the DBSCAN-Algorithm, because it does not require an a-priori number of clusters and shows a high robustness against noise. DBSCAN stands for Density-Based Spatial Clustering of Applications with Noise and was proposed by Ester et al. in [9].

The algorithm needs the parameters ε and *MinPts* as inputs, where ε is a neighbourhood threshold and *MinPts* is the minimum number of points a cluster consists of. DBSCAN distinguishes three types of data points:

- *Core points:* These have *MinPts* or more different points in their ε-environment.
- *Density reachable points:* These have at least one other data point in their ε-environment, but less than *MinPts*.
- *Noise:* These are neither core points nor density reachable points.

The following pseudo code describes the algorithm:

```
function=DBSCAN(D,ε , MinPts)
for (all unvisited points P in dataset D)
   mark P as visited
   N=getNeighboringPoints(P,ε)
   if(sizeof(N) < MinPts)
     mark P as noise
   else
     C = next cluster
     add P to cluster C
     for (P' in N)
       if(P' is not a member of any cluster)
         recursiveExpandCluster(P',C,ε ,
   MinPts)
       end
     end
    end
end
end

function=recursiveExpandCluster(P,C,ε
,MinPts)
  add P to cluster C
  if(P is not visited)
    mark P as visited
    N = getNeighbors(P,ε)
    if(sizeof(N) >= MinPts)
      for{ P' in N}
        if(P' is not member of any cluster)
          recursiveExpandClus-
ter(P',C,ε,MinPts)
        end
      end
    end
  end
end
```

One of the difficulties lies in the choice of ε. If it is too small, the algorithm overclusters, i.e., it separates visibly connected clusters, or it underclusters if ε is too large, i.e., it merges visibly unconnected clusters.

Therefore, we applied a refinement of DBSCAN, the Ensemble-DBSCAN (EDBSCAN) proposed by Xia et al. in [10].

This algorithm runs DBSCAN r-times iterating ε equidistantly from ε_{min} to ε_{max}, with:

$$\varepsilon_{min} := D_4^{mean} - \frac{D_4^{mean} - D_4^{min}}{8},$$
$$\varepsilon_{max} := D_4^{mean} + \frac{D_4^{max} - D_4^{mean}}{8}$$

The variable D_4 stands for the set of distances between the data points and their fourth nearest neighbour, D_4^{mean} is its mean value and D_4^{min} and D_4^{max} are the minimal and maximal value of the set. The result of every iteration is saved in the co-association matrix A, by adding 1 to each entry $A_{i,j}$, if the i-th and the j-th data point are in the same cluster and 0 otherwise. After all iterations the co-association matrix is normalized via element-wise division by r.

The final clusters are then constructed by using a voting method, described in the following pseudo code:

```
assign first data point to first cluster
for (all other points of D)
  calculate A_max := max_{j=1,...,i-1} A_{i,j}
  if(A_max < 0.5)
    assign current point to a new cluster
  else
    assign current point to cluster
ofD(k),
    whereA_{i,k} = A_max
  end
end
```

Afterwards, clusters with less data points than a given threshold are considered as noise. The threshold for this categorization is set so that clusters consisting of presumably non-pathological extrasystoles are ignored. Therefore, a number of 10 extrasystoles per hour is used as a threshold, based on the findings in [11], [12].

The sinusoidal beat cluster was then chosen as the one closest to the mean value of $\{RR_1, \ldots, RR_N\}$. To reduce assignment errors a correction by adding a small shift of 0.01 seconds to both coordinates of the mean was implemented.

This can be justified by the following reasons. First, most of the errors occur because of arrhythmias with a shorter RR-interval length. Therefore, these beats move the mean closer to zero, away from the actual sinus beats. Second, no case was observed were the mean value was above the sinusoidal cluster, which would be the case for very atypical heart rates of a high amount of single slow beats in connection with a very fast sinus beat. Third, the small shift of 0.01 seconds only slightly alters the mean value, but enough to prohibit most of the incorrect assignments.

1.3 Deleting points of a Poincaré plot

Since Poincaré plots represent the relation between two consecutive beats, the filtering can not be done by deleting one beat interval in $RR_x := \{RR_1, \dots, RR_{N-1}\}$ and the same in $RR_y := \{RR_2, \dots, RR_N\}$, but the preceding one in RR_x and the following one in RR_y has to be deleted as well, as shown in Figure 3 [7].

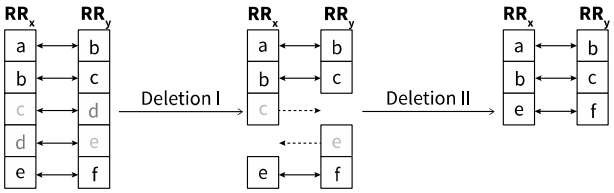

Figure 3: Deletion of the incorrect RR-interval "d" (Deletion I) and the corresponding counterparts "c" in RR_x and "e" in RR_y (Deletion II).

1.4 Poincaré plot measures

Different methods exist to automatically quantify Poincaré plots. In this work the following were used.

Ellipse Fitting Method.

The commonly used method to quantify Poincaré plots is the ellipse fitting method [13]. For this method an ellipse is fitted to the Poincaré plot, as shown in figure 4. The center of the ellipse is the mean value of the RR-intervals, the length of the major axis (*SD2*) is the standard deviation in the direction of the line of identity and the length of the minor axis (*SD1*) is the standard deviation perpendicular to the line of identity. The values *SD1*, *SD2* and their ratio are used as Poincaré plot measurements.

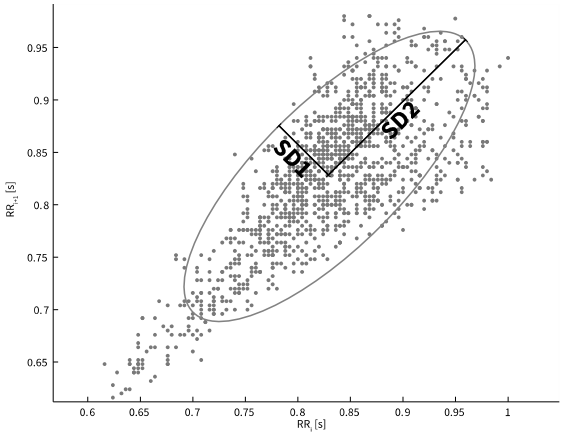

Figure 4: The ellipse fitting method to measure Poincaré plots.

Longitudinal-Transversal Measure.

Another method to quantify Poincare plots was proposed by Toichi et al. in [14]. It consists of the measurement of the Poincaré plot's maximal extension in the direction of the line of identity (L) and perpendicular to it (T), as shown in Figure 5. Their ratio is used as an additional measure.

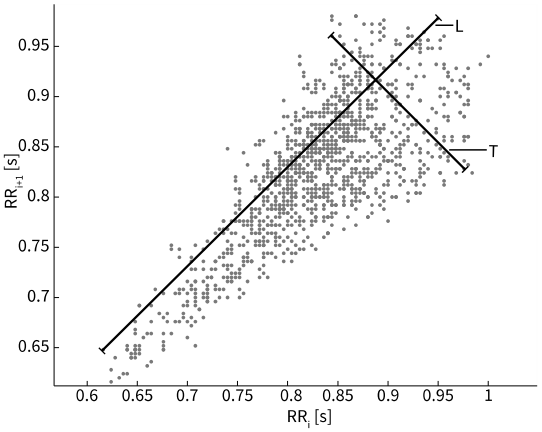

Figure 5: Longitudinal (L) and transversal (T) measurements of a Poincaré plot.

2 Data and Tests

2.1 Data

All data used to test the indices were taken from Physionet.org [15], a free-access, on-line archive of physiological signals. Physionet.org guarantees that all data have been fully anonymised, and may be used without further institutional review board approval.

To create a control group, the *Normal Sinus Rhythm RR Interval Database* was used. It consists of 54 ECG recordings, each one approximately 24 hours long. It contains semi-automatically annotated heart rate data of subjects with normal sinus rhythm (30 men, aged 28.5 to 76, and 24 women, aged 58 to 73) digitized at a sample frequency of 128 Hz [15].

For pathological heart rate data the *Massachusetts Institute of Technology (MIT) - Boston's Beth Israel Hospital (BIH) Arrhythmia Database* was used. It contains 48 half-hour recordings, sampled with a frequency of 360 Hz, from 47 subjects (25 men aged 32 to 89 years and 22 women aged 23 to 89 years) [16]. It consists of a set of randomly chosen recordings and 25 recordings especially chosen to include examples of uncommon but clinically important arrhythmias recorded at the BIH Arrhythmia Laboratory [16], all annotated manually.

2.2 Test procedure

For both data sets 1500 data points were taken from the middle of all recordings. These were filtered either according to the semi-automatic annotations as provided by Physionet, i.e., excluding all beats, which are not labeled as normal, or filtered via clustering, where only the sinusoidal cluster, i.e., the cluster consisting of the regular beats, is retained for analysis. The first 1000 data points were taken from these filtered points, in order to create a baseline, because after the filtering the recordings had different amount of data points. Afterwards their Poincaré plot measures were calculated.

To test if the measures show significant differences between the non-pathological and the pathological data set, a Wilcoxon rank sum test was applied to calculate the p-value, as recommended in [17], since most of the results were not normally distributed.

A test outcome was declared significant for $\rho < 0.05$ and very significant for $\rho < 0.01$.

3 Results

The results of the Wilcoxon rank sum test are shown in Table 1, with significant differences are marked with * and highly significant differences with **.

	Annotation Filtering	Cluster Filtering
SD1	0.8789	<0.01**
SD2	0.0149*	0.0564
SD1/SD2	0.0288*	<0.01**
L	0.0187 *	0. 1290
T	0. 5953	0. 1962
L/T	0. 3210	<0.01**

Table 1: The p-values of differences between pathological and non-pathological data sets of different Poincaré plot measures, either filtered via clustering or via annotations.

The ellipse fitting measures *SD2*, and *SD1/SD2* have significant differences for pathological and non-pathological heart rate data filtered with annotations. Of the longitudinal-transversal measures only *L* shows significant differences for the same data sets.

Data filtered via clustering have very significant differences for the two ellipse fitting measures *SD1* and *SD1/SD2*. These data sets have also very significantly different longitudinal-transversal measure *L/T*.

The following tables show the parameters of distribution for data filtered via annotations, see Table 2, and based on clustering, see Table 3. The first value is the median value of the measure for all recordings in this data set and the following two values describe the central range, i.e. they are the 2.5th and 97.5th percentiles.

	Non-Pathological Data	Pathological Data
SD1	0.0288, (0.0113, 1.6299)	0.0290, (0.0113, 0.2172)
SD2	0.0865, (0.0236, 1.5946)	0.0589, (0.0204, 0.3944)
SD1/SD2	0.3554, (0.1358, 1.2175)	0.5618, (0.1696, 1.5005)
L	0.6933, (0.1991 32.8089)	0.5003, (0.2609, 1.7208)
T	0.5359, (0.0710, 64.5699)	0.4639, (0.1034 2.2881)
L/T	1.2444, (0.5082, 4.7220)	0.9605, (0.6488, 3.5580)

Table 2. Parameters of distributions (median, 2.5th and 97.5th percentile) of data filtered via annotations.

	Non-Pathological Data	Pathological Data
SD1	0.0184, (0.0078, 0.1313)	0.0249, (0.0113, 0.1729)
SD2	0.0743, (0.0230, 0.1856)	0.0544, (0.0188, 0.1592)
SD1/SD2	0.2527, (0.1089, 0.8478)	0.5354, (0.1925, 1.6819)
L	0.4558, (0.1428, 1.0422)	0.3564, (0.1319, 0.9899)
T	0.1933, (0.0599, 0.7737)	0.2157, (0.0661, 0.9868)
L/T	2.0893 (1.2270, 4.7136)	1.3403, (0.6908, 3.1703)

Table 3. Parameters of distributions (median, 2.5th and 97.5th percentile) of data filtered via clustering.

4 Discussion

No instances were found in literature, where Poincaré plots were filtered via clustering. If mentioned at all the filtering was done either manually or semi-automatically.

A visual comparison of the data sets showed that both filtering methods could not find every outlier, but data filtered via annotations had a higher rate of unfiltered outliers, which also had a greater distance to the rest of the points, compared to the unfiltered outliers after cluster based filtering.

Therefore, Table 1 could be interpreted as an indicator for a higher sensitivity of the ellipse fitting method to outliers, which also reduce the differences between pathological and non-pathological data sets.

Comparing Table 2 and 3 one sees, that data filtered via annotations has larger 95th percentiles for *SD1*, *SD2*, *L* and *T*. This is also due to a higher number of outliers and their larger distances for these data.

The Ellipse fitting measures indicate in Table 2 and Table 3 wider but shorter Poincaré plots for pathological heart rate data filtered via annotations. The same is true for the longitudinal measures in Table 3. This behaviour is in accordance to the traditional interpretation of Poincaré plot shapes [18].

5 Conclusion

The fully automated filtering via clustering shows no drawbacks compared to the traditional method of ECG annotation based filtering for HRV analysis via Poincaré plots. This is done with a largely reduced effort in contrast to the annotation based filtering method.

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