Efficiency of Different Heartbeat Detection Methods by Using Alternative Noise Reduction Algorithms

Marcus Vollmer^{1,2}, Jader Alexander Giraldo Guzmán^{1,2}

¹ Institute of Bioinformatics, University Medicine Greifswald, Germany
² DZHK (German Centre for Cardiovascular Research), partner site Greifswald, Germany

Abstract

Motivation: ECG noise reduction is an essential step in the ECG preprocessing pipeline. In particular, the quality of beat detection can be affected by several artifacts. The variety of available methods ranges from filter-based techniques (e.g. Butterworth or FIR), signal decomposition (e.g. wavelets) to neural networks (Cycle-GAN).

Methods: 12-lead resting ECGs from the SFB/TR19 study on inflammatory dilated cardiomyopathy (n=704) and from the Study of Health in Pomerania (n=17,717) were preprocessed with 14 different methods to evaluate the accuracy of heartbeat detection methods in relation to the chosen method for preprocessing. Open source signal libraries (neurokit2, py-ecg-detectors, WFDB among others) with 34 detectors were evaluated. Sensitivity and Positive Predictive Values (PPV) were computed for each combination of preprocessing and detection method in a train/test scheme. Annotations were corrected for fixed delays and scored at a tolerance of 50 ms.

Results and conclusion: Eplimited performed best, regardless of the chosen preprocessing method. For diseased ECGs, in Kalidas2017 it was seen an improvement in performance from 0.713 to 0.876 and from 0.778 to 0.879 for PPV and sensitivity respectively. Best results can be achieved with ECG leads V3, V5 and V6.

1. Introduction

Ultrasound and Electrocardiography (ECG) are the most non-invasive techniques used to perform the diagnosis of cardiac diseases [1]. However, ECG is the first, possibly cheapest option to identify electrical anomalies in the heart – for example in the case of Atrial Fibrillation (AF) which is the most common cardiac arrhythmia. However, it is estimated that approximately 33% of the population remains undiagnosed, since in the early stage of this condition, events occur at random and are self-terminating [2]. In order to make an accurate diagnosis with ECGs, it is usually necessary to use pre-processing methods to remove noise caused by the power line interference, motion artifacts, thermal noise, etc., before actually analyzing the heart rhythm or ECG delinearization (e.g., [3]). Information extracted from ECGs for diagnosis of cardiac arrhythmia includes the computation of the segments and intervals and their variability, or the analysis of P-QRS-T waves. This is usually processed separately: methodologies are divided into methods for noise reduction and methods for detecting patterns in the recordings or characterizing heart health (e.g., [4] for a review of methods). Our study focuses on the detection of heart beats in relation to the chosen preprocessing method. Respectively, we are searching for the best combination of the methods to suppress noise and beat detection methods in order to increase the accuracy in diagnostic tasks.

2. Methods

2.1. Preprocessing methods

We applied 14 different methods to preprocess the ECGs: Corcodan [5] includes four steps: spike removal, low-pass Butterworth filter (60Hz cutoff), baseline drift removal using local linear estimates, substraction of trimmed average. From Neurokit2 [6] we applied: Neurokit (default) (high-pass 5th order Butterworth filter with $0.5 \,\mathrm{Hz}$ cutoff, 50 Hz powerline removal), pantompkins1985 (1st order Butterworth filters, bandpass cutoffs 5 Hz and 15 Hz [7]), hamilton2002 (1st order Butterworth filter, bandpass cutoffs 8 Hz and 16 Hz [8]), biosppy (FIR filter, cutoffs 3 Hz and 45 Hz [9]), elgendi2010 (2nd order Butterworth filter, bandpass cutoffs 8 Hz and 20 Hz [10]), engzeemod2012 (4th order Butterworth filter, bandstop cutoffs of 48 Hz and 52 Hz [11]). Two additional 5th order Butterworth filter were applied with Scipy.signal, bandpass cutoffs frequencies 3 Hz-20 Hz and 0.05 Hz-42 Hz respectively. We further used three wavelet denoising methods (Haar, Daubechies 4, Symlets 8): pywt was used for 1-D stationary wavelet transform using the Haar function (with detail coefficients at the 2nd level of decomposition). From skimage.restoration we utilized the denoise_wavelet function with BayesShrink method to estimate the soft wavelet threshold for every single wavelet sub-band with 3 levels of wavelet decomposition of wavelets db4 and sym8. As a representative of newly emerging techniques, we make use of a Cycle-GAN [12]. This method performs a blind ECG restoration by the application of the cycleconsistent generative adversarial networks for noise-free ECG recovery. For this application two Self-ONNs are used as generator and discriminator. While the generator is used to learn how to transform the corrupted segment (with noise) to a clean one, on the other hand the discriminator is used to learn how to transform a clean segment to a corrupted one and will be discarded after training in order to maximize the adversarial loss functions. We used a pretrained GAN from the authors which works on normalized data. For the scaled version, called Cycleganscaled, the 5th and 95th quantiles of the raw ECG were used for a scaling factor in order to reconstruct the amplitude of the original signal.

2.2. QRS detection methods

The following open source packages and methods were used for heart beat detection. Neurokit2 (0.1.4.1) [6]: Pan-Tompkins (1985), Nabian (2018), Zong (2003), Gamboa (2008), Martinez (2003), Rodrigues (2021), BioSPPY, Kalidas (2017), Christov (2004), Elgendi (2010), ProMac, Hamilton (2002). Py-ecg-detectors (1.3.2) [13]: Hamilton, Christov, Engelse and Zeelenberg, Pan-Tompkins, Stationary Wavelet Transform (Kalidas and Tamil), Elgendi, FIR matched filter, Zong (wqrs). WFDB for Python (4.0.0) [14, 15]: XQRS, XQRS+learn, xqrs_detect, xqrs_detect+learn, gqrs_detect. Eplimited (eplimited 1.1 for R) [16]: eplimited without scaling; scaled amplitude using a factor of 1000; scaled using the 10% and 97.5% quantiles of the raw ECG. As we noticed that Eplimited do not annotate beats till second 7.5, our methodology for Eplimited was: downsampling to 200 Hz, concatenation of the mirrored signals, generation of annotations, and shifting back beat annotations by 7.5 s. ECG2RR (0.1.0) [17]: LSTM-based detector ecg2rr, ecg2rr (threshold=300 ms). C-LABPL [18]: a Pan-Tompkins adaptation. WTdelineator [19]: waveletbased ECG delineation.

2.3. Data description & evaluation

12-lead resting ECGs of 10s length were used from the following sources: The SFB/TR19 study on inflammatory dilated cardiomyopathy [20] includes 704 ECGs from patients included at the study centre Greifswald, Germany. The recordings contain various cardiac arrhythmia, e.g., 113 AFIB, 66 AVB, 63 LAA, 110 LBBB. The Study of Health in Pomerania (SHIP) includes two individual cohorts with follow-up examinations [21]: SHIP-START cohort (START-0: n=3546 ECGs, START-1: n=3274, START-2: n=2314, START-3: n=1713) and SHIP-TREND cohort (TREND-0: n=4386, TREND-1: n=2484).

For finding the best combinations of preprocessing and beat detection methods we extracted the positive predictive value and the sensitivity from the resulting annotations in each lead and recording. In the following we divided the dataset into training: 60% of SFB/TR19 + SHIP-START (n=11,269), and testing: 40% of SFB/TR19 + SHIP-TREND (n=7,152). Testing data was used to prove stability of the chosen combinations. To derive the individual true positive, false negative, and false positive numbers, reference annotations were needed. For SFB/TR19 we used automated and manually screened annotations that are stored in Philips SierraECG XML files. For SHIP data, reference annotations were built using a silver standard: All annotations generated for the same recording were Gauss-filtered with a standard deviation (sd) of 100 ms, summed and filtered a second time with sd of $50 \,\mathrm{ms}$. The resulting wave was then normalized by to 0 and 1 and peaks were identified. Peak locations above the threshold of 0.5 were regarded as the true beat locations. By pairwise comparison of annotations with the created reference taking a tolerance of 10 ms, 25 ms, 50 ms, 100 msinto account, we counted FN, FP, TP + multiple matches within the central part of the ECG (first to the ninth second). We also searched for systematic shifts of annotations are corrected for it. Thereafter results were aggregated by the computation of average sensitivity and positive predictive values (PPV). Individual PPVs were set to 0% and sensitivity was set to 100% if no beat was detected or if an error was reported during the detection. A ranking of combinations was made on the average sum of PPV with Sensitivity.

3. Results & Conclusion

Table 1 and Figures 1 and 2 are showing the PPV and Sensitivity at 50 ms tolerance. Table 1 shows the best six detectors with the best two combinations in comparison with applying the detectors on the raw ECGs in the training set. Even though we did not change the internal preprocessing of the detector, we were able to improve the performance of certain beat detection methods through the transfer of already preprocessed data, especially in diseased ECGs - with a remarkable improvement in the Neurokit2 method: Kalidas2017 improved PPV from 71.3% to 87.2%, Sensitivity from 77.8% to 87.5% when using BioSPPy preprocessing. Best results were achieved with Eplimited. Figure 1 shows, that good performance can be achieved with any preprocessing method. Figure 2 shows the best performing leads: V3, V5, V6. WFDBs learning options do increase the senstivity of lead III, aVF and aVL. Furthermore, we see potential to improve the performance by adjusting the parameters of either the preprocessing methods or the internal preprocessing function of the detectors.

Funding & Acknowledgements

MV and JAGG acknowledge funding by the DZHK-Excellence Grant on advancing digital aspects (Postdoc-Startup), funding ID: 81X3400110. SFB/TR19 received funding from Deutsche Forschungsgemeinschaft (DFG), project number 5486135. The Study of Health in Pomerania is part of the Community Medicine Research Network of the University Medicine Greifswald, which was funded by the German Federal Ministry for Education and Research, the Ministry for Education, Research and Cultural

Table 1. Best 6 detectors on raw data with best 2 preprocessing combinations					
		Healthy cohort		Diseased cohort	
		Train	Test	Train	Test
		SHIP-START	SHIP-TREND	60% SFB	40% SFB
Preprocessing	Detector	PPV/Sens	PPV/Sens	PPV/Sens	PPV/Sens
raw	eplimited quantile-scaled	.956 / .962	.972 / .979	.930 / .943	.931 / .941
corcodan		.957 / .963	.975 / .983	.932 / .946	.932 / .942
biosppy		.955 / .962	.973 / .983	.920 / .933	.918 / .928
raw	nk2::kalidas2017	.930 / .940	.967 / .970	.715 / .784	.713 / .778
biosppy		.954 / .953	.975 / .974	.893 / .898	.872 / .875
neurokit		.955 / .954	.975 / .974	.893 / .898	.876 / .879
raw	wfdb4::xqrs	.941 / .953	.975 / .971	.854 / .874	.842 / .860
corcodan		.941 / .953	.975 / .971	.854 / .874	.843 / .860
neurokit		.941 / .954	.975 / .964	.865 / .884	.852 / .868
raw	nk2::neurokit	.954 / .950	.973 / .972	.779 / .738	.768 / .730
corcodan		.954 / .952	.973 / .974	.795 / .765	.786 / .756
biosppy		.948 / .952	.971 / .974	.796 / .802	.780 / .784
raw	wfdb4::xqrs_detect+learn	.941 / .953	.965 / .976	.854 / .874	.842 / .860
corcodan		.941 / .953	.965 / .975	.854 / .874	.843 / .860
neurokit		.941 / .954	.964 / .975	.865 / .883	.852 / .868
raw	wfdb4::xqrs+learn	.941 / .953	.965 / .975	.854 / .874	.842 / .860
corcodan		.941 / .953	.964 / .975	.854 / .874	.843 / .860
neurokit		.941 / .954	.964 / .975	.865 / .884	.852 / .868

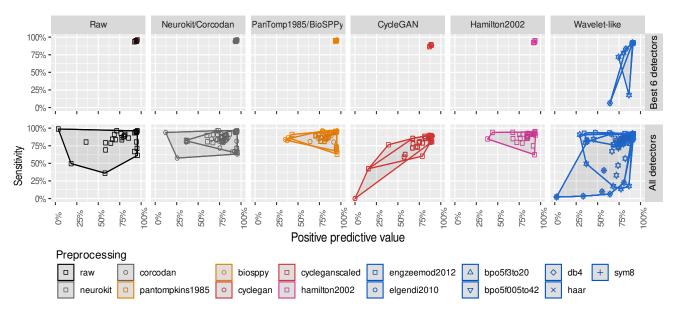


Figure 1. Average PPV and Sensitivity of testing records at 50 ms tolerance displayed for all detectors (bottom) in comparison to the best 6 detectors (top) with convex hull of each preprocessing methods. The methods for preprocessing are grouped by the common visual representation of the resulting waveform.

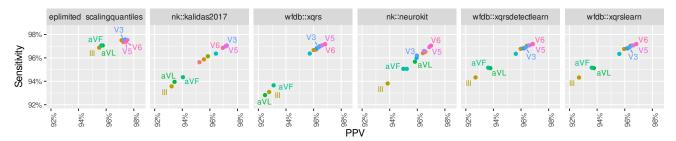


Figure 2. Average lead-wise performance of the best six detection methods across the best four preprocessing techniques (raw, Corcodan, BioSSPy, Neurokit).

Affairs, and the Ministry for Social Affairs of the State Mecklenburg-Western Pomerania, Germany.

References

- Maganti K, Rigolin VH, Sarano ME, Bonow RO. Valvular heart disease: Diagnosis and management. Mayo Clinic Proceedings 2010;85(5):483–500.
- [2] Cotter PE, Martin PJ, Ring L, Warburton EA, Belham Mark fand Pugh PJ. Incidence of atrial fibrillation detected by implantable loop recorders in unexplained stroke. Neurology 2013;80(17):1546–1550.
- [3] Tejedor J, García CA, Márquez DG, Raya R, Otero A. Multiple Physiological Signals Fusion Techniques for Improving Heartbeat Detection: A Review. Sensors 2019; 19(21):4708.
- [4] Tripathi PM, Kumar A, Komaragiri R, Kumar M. A Review on Computational Methods for Denoising and Detecting ECG Signals to Detect Cardiovascular Diseases. Archives of Computational Methods in Engineering 2021;1–40.
- [5] Sodmann PF, Vollmer M, Kaderali L. Segment, Perceive and Classify-Multitask Learning of the Electrocardiogram in a Single Neural Network. In 2021 Computing in Cardiology (CinC), volume 48. 2021; 1–4.
- [6] Makowski D, Pham T, Lau ZJ, Brammer JC, Lespinasse F, Pham H, Schölzel C, Chen SHA. NeuroKit2: A Python Toolbox for Neurophysiological Signal Processing. Behavior Research Methods 2021;53(4):1689–1696.
- [7] Pan J, Tompkins WJ. A Real-Time QRS Detection Algorithm. IEEE transactions on biomedical engineering 1985; 32(3):230–236.
- [8] Hamilton PS, Tompkins WJ. Quantitative Investigation of QRS Detection Rules Using the MIT/BIH Arrhythmia Database. IEEE transactions on biomedical engineering 1986;33(12):1157–1165.
- [9] Carreiras C, Alves AP, Lourenço A, Canento F, Silva H, Fred A, et al. BioSPPy: Biosignal Processing in Python, 2015-2022. URL https://github.com/ PIA-Group/BioSPPy.
- [10] Elgendi M, Jonkman M, De Boer F. Frequency Bands Effects on QRS Detection. In Biosignals 2010 Proceedings of the 3rd International Conference on Bio-inpsired Systems and Signal Processing, volume 1. 2010; 428–431.
- [11] Engelse WA, Zeelenberg C. A Single Scan Algorithm for

QRS-Detection and Feature Extraction. Computers in cardiology 1979;6:37–42.

- [12] Kiranyaz S, Devecioglu OC, Ince T, Malik J, Chowdhury M, Hamid T, Mazhar R, Khandakar A, Tahir A, Rahman T, et al. Blind ECG Restoration by Operational Cycle-GANs. arXiv preprint arXiv220200589 2022;.
- [13] Porr B, Howell L, Stournaras I, Nir Y. Popular ECG R Peak Detectors Written in Python (1.2.0). Database: Zenodo [Internet], 2022. URL https://doi.org/10.5281/ zenodo.5919190.
- [14] Xie C, McCullum L, Johnson A, Pollard T, Gow B, MoodyB. Waveform Database Software Package (WFDB) for Python. PhysioNet, 2022.
- [15] Goldberger AL, Amaral LA, Glass L, Hausdorff JM, Ivanov PC, Mark RG, Mietus JE, Moody GB, Peng CK, Stanley HE. PhysioBank, PhysioToolkit, and PhysioNet: Components of a New Research Resource for Complex Physiologic Signals. Circulation 2000;101(23):e215–e220.
- [16] Hamilton PS. Open Source ECG Analysis Software Documentation. Computers in cardiology 2002;101–104.
- [17] Laitala J, Jiang M, Syrjälä E, Naeini EK, Airola A, Rahmani AM, Dutt ND, Liljeberg P. Robust ECG R-Peak Detection Using LSTM. In Proceedings of the 35th Annual ACM Symposium on Applied Computing. Association for Computing Machinery, 2020; 1104–1111.
- [18] Sznajder M, Łukowska M. Python Online and Offline ECG QRS Detector Based on the Pan-Tomkins Algorithm (v1.1.0). Database: Zenodo [Internet], 2017. URL https: //doi.org/10.5281/zenodo.826614.
- [19] Ledezma CA. WTdelineator, 2018. URL https:// github.com/caledezma/WTdelineator.
- [20] Angelow A, Weitmann K, Schmidt M, Schwedler S, Vogt H, Havemann C, Staudt A, Felix S, Stangl K, Klingel K, et al. The German Transregional Collaborative Research Centre 'Inflammatory Cardiomyopathy – Molecular Pathogenesis and Therapy'. Cardiology 2009;113(3):222–230.
- [21] Völzke H, Schössow J, Schmidt CO, Jürgens C, Richter A, Werner A, Werner N, Radke D, Teumer A, Ittermann T, et al. Cohort Profile Update: The Study of Health in Pomerania (SHIP). International Journal of Epidemiology 2022;.

Address for correspondence:

Marcus Vollmer / marcus.vollmer@uni-greifswald.de Institute of Bioinformatics / University Medicine Greifswald Felix-Hausdorff-Str. 8 / 17475 Greifswald / Germany