LU electrocardiography database: a new open-access validation tool for delineation algorithms

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Abstract

We report a new Lobachevsky University database (LUDB) of ECG signals that contains 200 samples of 10-second 12-lead electrocardiograms (ECG) from different subjects. The boundaries of the ECG signal complexes are manually annotated by cardiologists for all samples and independently for each lead. The database is representative of a variety of signal morphologies. In addition, all records have an attributed diagnosis. These features make LUDB a promising tool for validating ECG delineation algorithms across a broad range of ECG signal shapes and patient diagnoses. A case study for the recently proposed wavelet-based algorithm is presented.

Introduction

Recording the electrical activity of the heart or electrocardiography is one of the basic medical diagnostic means employed for assessing cardiac activity, in particular, determining the heart rate and rhythm disturbances. The voltage graphs – electrocardiograms (ECG) manifest repeated activity with the commonly identified structural elements of each heart beat image: QRS complex, P and T waves (Fig. 1). Analysis of their amplitudes, shapes (morphologies) and durations allows for identifying cardiac rhythm disorders and cardiovascular diseases, such as ischemia and myocardial infarction [1]. A rich variety of signal morphology, accompanied by their non-stationary nature, potential defects in recordings and noise, makes an automated search for these waves and complexes, also known as ECG delineation, a challenging task.

This problem has been tackled for quite a while, resulting in a number of algorithms solving it at different levels of detail. The first ones were designed to detect the QRS complex only, based on the amplitude of the ECG signal and its first derivative [2]. Detecting boundaries and peaks of P and T waves demanded more sophisticated methods based on wavelet transform [3,4], Hilbert transform [5], phasor transform [6], hidden Markov models [7], gradient based algorithms [8] and morphological transforms [9].
Validating delineation algorithms requires standardized databases with complexes and waves, manually annotated by specialists. Several collections are currently available in the public domain: MIT-BIH Arrhythmia Database [10], European ST-T Database [11], and QT Database [12]. However, their annotation is not exhaustive. For example, MIT-BIH Arrhythmia Database and European ST-T Database has a markup only for QRS complexes. The QT Database contains annotations for P, QRS and T waves, but it has been pointed out that occasional complexes are left unmarked [13].

Assembling a new ECG database at Lobachevsky University (LUDB), we aimed and avoided these issues. The reported database consists of 200 samples of 10-second 12-lead recordings from different subjects, manifesting a wide spectrum of ECG morphologies. The boundaries of the ECG complexes are manually annotated by cardiologists for all 200 records. Moreover, each subject is assigned with a diagnosis, which altogether makes LUDB unique among the current publicly available sources. This database was used for validating a recently developed wavelet analysis based delineation algorithm [14], that implements multi-lead multi-morphology analysis together with error correction, and thus can take a full advantage of LUDB. The results indeed demonstrate an improvement as compared to its performance on QT database, which has only 2-lead recordings.

The paper is organized as follows. In Section 1, we give an account on LUDB database. Section 2 contains a brief description of the delineation algorithm [14]. A case study of its validation with LUDB and QTDB is reported in Section 3. Section 4 summarizes the results and outlines the perspectives.

1 LUDB Database

A publicly available Lobachevsky University Database contains 200 records from 200 subjects in wdf (PhysioNet) format [15]. ECG recordings were obtained by the Schiller Cardiovit AT-101 cardiograph [16], with conventional 12 leads (i, ii, iii, avr, avl, avf, v1, v2, v3, v4, v5, v6), the duration is 10 seconds. Signals are digitized at 500 samples per second. The boundaries and peaks of QRS, P, and T waves were determined by certified cardiologists (A.V.N. and K.A.K.) by an eye inspection of each ECG signal and independently for each of 12 leads. In total, the database contains 58429 annotated waves, that is almost six times greater than in the widely referred QT database (Table 1), which is the only publicly available database with all the waves annotated.

ECGs were collected from healthy volunteers and patients with various
Table 1. Comparative numbers of annotated waves in QT and LU databases.

|                  | P wave | QRS complex | T wave | Total  |
|------------------|--------|-------------|--------|--------|
| QTDB             | 3194   | 3623        | 3542   | 10359  |
| LUDB             | 16797  | 21966       | 19666  | 58429  |

cardiovascular diseases, some of them had pacemakers. All volunteers provided informed written consent before participating in the experiment. The age of subjects varied from 11 to 90 years, with the average 52 years, the distribution by gender was 85 women and 115 men. Table 2 reports the breakdown by the type of rhythm and Table 3 by the type of heart electrical axis. These parameters are specified for all records in the database.

Table 2. Breakdown in heart rhythm types, represented in the database.

| Rhythm:                  | Number of subjects: |
|--------------------------|----------------------|
| Sinus rhythm             | 143                  |
| Sinus tachycardia        | 4                    |
| Sinus bradycardia        | 25                   |
| Sinus arrhythmia         | 8                    |
| Irregular sinus rhythm   | 2                    |
| Abnormal rhythm          | 19                   |
| Total                    | 200                  |

Table 3. Breakdown in types of electrical axis, represented in the database.

| Electric axis of the heart: | Number of subjects: |
|-----------------------------|----------------------|
| Normal                      | 75                   |
| Left axis deviation         | 66                   |
| Vertical                    | 26                   |
| Horizontal                  | 20                   |
| Right axis deviation        | 3                    |
| Undetermined                | 10                   |
| Total                       | 200                  |

Tables 4 and 5 display content of the database by main cardiovascular disorders and their numbers. Note that some patients would have several issues at the same time.

2 Delineation algorithm

Our delineation algorithm \([14]\) belongs to the family of methods based on discrete wavelet transform (DWT) \([4,13,17,18]\), that stems from the pioneering work by Li \([3]\). Commonly, a single-lead ECG signal \(x[n]\) is decomposed into different frequency components by means of standard filters, Daubechies, Coiflet or biorthogonal wavelets, to name a few, as follows:

\[
A[k] = \sum_n x[n] \times h[2k - n],
\] (1)
Table 4. Breakdown in cardiovascular disorders, represented in the database (conduction abnormalities, extrasystole, hypertrophy, cardiac pacing).

| Conduction abnormalities:          | Number of subjects: |
|------------------------------------|---------------------|
| Sinoatrial blockade, undetermined  | 1                   |
| I degree AV block                  | 10                  |
| III degree AV-block                | 5                   |
| Incomplete right bundle branch block | 29             |
| Incomplete left bundle branch block | 6                |
| Left anterior hemiblock            | 16                  |
| Complete right bundle branch block | 4                   |
| Complete left bundle branch block  | 4                   |
| Non-specific intraventricular conduction delay | 4 |

| Extrasystole:                      | Number of subjects: |
|------------------------------------|---------------------|
| Atrial extrasystole: undetermined  | 2                   |
| Atrial extrasystole: low atrial    | 1                   |
| Atrial extrasystole: left atrial    | 2                   |
| Atrial extrasystole: SA-nodal extrasystole | 3 |
| Atrial extrasystole, type: single PAC | 4 |
| Atrial extrasystole, type: bigemini | 1 |
| Atrial extrasystole, type: quadrigemini | 1 |
| Atrial extrasystole, type: allorhythmic pattern | 1 |
| Ventricular extrasystole, morphology: polymorphic | 2 |
| Ventricular extrasystole, localisation: RVOT, anterior wall | 3 |
| Ventricular extrasystole, localisation: RVOT, antero-septal part | 1 |
| Ventricular extrasystole, localisation: IVS, middle part | 1 |
| Ventricular extrasystole, localisation: LVOT, LVS | 2 |
| Ventricular extrasystole, localisation: LV, undefined | 1 |
| Ventricular extrasystole, type: single PVC | 6 |
| Ventricular extrasystole, type: intercalary PVC | 2 |
| Ventricular extrasystole, type: couplet | 2 |

| Hypertrophy:                       | Number of subjects: |
|------------------------------------|---------------------|
| Right atrial hypertrophy           | 1                   |
| Left atrial hypertrophy            | 102                 |
| Right atrial overload              | 17                  |
| Left atrial overload               | 11                  |
| Left ventricular hypertrophy       | 108                 |
| Right ventricular hypertrophy      | 3                   |
| Left ventricular overload          | 11                  |

| Cardiac pacing:                    | Number of subjects: |
|------------------------------------|---------------------|
| UNIpolar atrial pacing             | 1                   |
| UNIpolar ventricular pacing        | 6                   |
| BIpolar ventricular pacing         | 2                   |
| Biventricular pacing               | 1                   |
| P-synchrony                        | 2                   |
Table 5. Breakdown in cardiovascular disorders, represented in the database (ischemia, repolarisation abnormalities).

| Ischemia:                        | Number of subjects: |
|---------------------------------|---------------------|
| STEMI: anterior wall            | 8                   |
| STEMI: lateral wall             | 7                   |
| STEMI: septal                   | 8                   |
| STEMI: inferior wall            | 1                   |
| STEMI: apical                   | 5                   |
| Ischemia: anterior wall         | 5                   |
| Ischemia: lateral wall          | 8                   |
| Ischemia: septal                | 4                   |
| Ischemia: inferior wall         | 10                  |
| Ischemia: posterior wall        | 2                   |
| Ischemia: apical                | 6                   |
| Scar formation: lateral wall    | 3                   |
| Scar formation: septal          | 9                   |
| Scar formation: inferior wall   | 3                   |
| Scar formation: posterior wall  | 6                   |
| Scar formation: apical          | 5                   |
| Undefined ischemia/scar/supp.NSTEMI: anterior wall | 12 |
| Undefined ischemia/scar/supp.NSTEMI: lateral wall | 16 |
| Undefined ischemia/scar/supp.NSTEMI: septal | 5 |
| Undefined ischemia/scar/supp.NSTEMI: inferior wall | 3 |
| Undefined ischemia/scar/supp.NSTEMI: posterior wall | 4 |
| Undefined ischemia/scar/supp.NSTEMI: apical | 11 |

| Non-specific repolarisation abnormalities: | Number of subjects: |
|--------------------------------------------|---------------------|
| Anterior wall                              | 18                  |
| Lateral wall                               | 13                  |
| Septal                                     | 15                  |
| Inferior wall                              | 19                  |
| Posterior wall                             | 9                   |
| Apical                                     | 11                  |

| Other states:                              | Number of subjects: |
|--------------------------------------------|---------------------|
| Early repolarization syndrome              | 9                   |

\[
D[k] = \sum_n x[n] \times g[2k - n],
\]

where \(h[n]\) is the low-pass filter, \(g[n]\) is the high-pass filter, \(D[k]\) and \(A[k]\) are the resulting approximation coefficients, respectively. A more detailed representation of the frequency content of ECG signals is obtained by repeated DWT, applied to approximation coefficients, calculated at the previous round, according to the general scheme shown in the Fig. 2.

Below we discuss the key features of our algorithm, referring to [14] for a detailed description. We explain the solutions, which allow for a highly accurate delineation of
all waves and complexes of a heart beat in LUDB, which meticulous markup and a rich variety of morphologies presents an exceptional challenge for an algorithm under validation. We also demonstrate a successful error correction and accuracy improvement taking an advantage of multi-lead nature of recordings.

The proposed method of delineation consists of several steps. Delineation of each type of waves is first implemented for all ECG leads independently, and in a particular order. Then, the results are refined by aggregating and comparative processing of signals from all leads. The general scheme of the algorithm is presented in the Fig. 3.

The input of the algorithm is a raw ECG signal, for which, at the first stage, preprocessing is performed. Bandpass filtering removes the baseline drift and the high-frequency noise that can be caused by the muscle tone, interference from electrical appliances, poor contact between electrodes and skin, etc. Next, a discrete wavelet transform is applied to the filtered signal, yielding a set of detailed coefficients at different frequency scales. The following analysis relies on these sets obtained for ECG from each lead.

Identifying waves and complexes of the ECG signal takes place in specific order: QRS complex, T-wave, and then P-wave. QRS complex is detected first, since it typically has the largest amplitude, which simplifies the task. Then, T-wave is located, as its amplitude is usually greater than that of P-wave. Delineation of P-wave is recognized as the most complex task by both the cardiologists and mathematicians [4, 13]. The amplitude of this wave often compares to noise or flutter, so that a quality detection procedure has to rely on restricting the temporal interval of interest from both sides, by QRS complex and T-wave.

Processing each type of wave has a similar pipeline. First, the algorithm explores ECG signal from each lead separately. It selects the best candidates for the corresponding wave, then determines its peak and boundaries. Our algorithm implements yet another feature, classifying the morphology of the detected wave by determining all significant points. Matching it to a certain type offers a much more advanced diagnostic information than duration and amplitude of a complex can offer. The particular morphologies of the QRS complex, recognized by the algorithm, are shown in the Fig. 4. Orientation of the complex, its extremal points, the number of additional peaks or, conversely, the lack of some basic ones are central to the diagnostic process, determining cardiac arrhythmias or the presence of cardiovascular diseases.
After all waves of a certain type are found for the outputs from all leads, the algorithm performs a comparative analysis, aimed at correcting omissions or spurious waves, appearing in recordings for certain leads. As a formal validity threshold for a complex occurrence, we require its presence in at least 8 out of 12 leads. That is, if for some heartbeat the T-wave is detected for ten leads out of twelve, then it is taken that this wave is also present for the other two leads. Conversely, if the complex is found in less than one third of the total number of leads, then it is retracted from delineation. Additionally, averaging the times of the corresponding reference points for the matching complexes across the leads reduces the effect of noise and other disturbances. After this multi-lead correction, delineation steps down to the subsequent wave, taking an advantage of justified locations for preceding waves.

Instructively, some failures in the single-lead signal processing are apparently due to alternating morphologies of a complex in the ECG signal, which the adaptive detection threshold does not follow quick enough after 14. However, when the complexes are missed in less than one third of leads, their delineation is also restored by the multi-lead analysis, as exemplified in Fig. 5 and a corresponding morphological anomaly is recorded.
Fig 4. Examples of QRS complex morphologies. There are many different morphologies of the QRS complex, which can indicate the presence of various cardiovascular diseases. Their classification constitutes a challenge for automatic delineation.

3 Algorithm validation

We validate the described algorithm with two open access databases, the newly introduced LUDB and QTDB [12], both manually annotated by cardiologists, but distinct in the number of leads (12 and 2, respectively), number of subjects (200 and 105) and duration of recordings (10 and 15 seconds). The reference points of complexes found by an automated delineation are validated against the manually marked ones, the tolerance window interval of 150 ms is chosen to comply with ANSI/AAMI-EC57:1998 standard [19].
Fig 5. Multi-lead refinement of delineation. Gray frames show the complexes, which fall short of the single lead analysis, but are recovered by the multi-lead refinement.

When an algorithm determines a point correctly, it is counted as true positive (TP). Likewise, if a point suggested by the algorithm is absent in the specialists markup, the case is counted as false positive (FP). If the algorithm fails to identify the point, which is present in the database, the case is false negative (FN). For TP cases one also calculates a mismatch between the automated and manually assigned locations, referred to as an “error”. The quality of the algorithm is characterized by the following four metrics, implemented in [4, 13, 18, 20]: average error \( m \), its standard deviation \( \sigma \), sensitivity \( Se(\%) = \frac{TP}{TP + FN} \), and positive predictive value \( PPV(\%) = \frac{TP}{TP + FP} \).

Table 6 summarizes the assessment of algorithm [14] against LU an QT databases, with the additionally supplied numbers for validation of the other methods against QTDB [4, 13, 18, 20].

In result, for both LUDB and QTDB, the sensitivity values for the onsets and peaks of the P, QRS and T waves are above 97%, and the standard deviation value is within the limits set by the standard [21] (the exception is the P wave onset, where this value is 3 ms larger). The maximal error is observed for the T-wave offset, which delineation is a well-known hard problem, as from the mathematical perspective, as from the cardiological one [22]. At the same time, the performance of the algorithm by [14] is consistently better for the LUDB due to its 12-lead format, that allows to reduce detection failures and appearance of spurious complexes, and to improve an accuracy of timing the key points by the multi-lead refinement of delineation.
Table 6. Delineation quality of the algorithm [14] assessed by means of the novel LUDB and its performance with QTDB. The quality measures of the other methods as per QTDB are also given.

| Algorithm | P onset | P peak | P offset | QRS onset | QRS offset | T peak | T offset |
|-----------|---------|--------|----------|-----------|-----------|--------|----------|
| Kalyakin et al. [14] (LUDB) | 98.46 ± 0.6 | 96.41 ± 0.4 | 98.41 ± 0.6 | 99.61 ± 1.7 | 99.61 ± 1.7 | 99.61 ± 1.7 | 99.61 ± 1.7 |
|         | 10.2 ± 0.2 | 10.1 ± 0.1 | 5.6 ± 0.5 | 11.6 ± 0.6 | 10.6 ± 0.6 |

4 Conclusions

Despite a keen demand in thoroughly annotated and open databases of human ECGs to serve testbeds for delineation algorithms, the available number is quite limited [10][12]. Moreover, each case is known to come short of meeting the rigorous requirements of having all kinds of waves (P, QRS, and T) marked up by manually by specialists and lacking omissions. Ideally, the recordings would be supplied with diagnosis, that additionally enables training and validating algorithms for an automated identification of pathology. Desirably, a database would contain 12-lead ECG signal recordings, a standard output for modern hospital cardiographs.

The presented Lobachevsky University database is a step to fill the existing gap, meeting the requirements above. Openly accessible at Lobachevsky University website and submitted to PhysioNet [15], it contains 12-lead ECG recordings for 200 subjects (hospital patients and volunteers without a history of complaints) in wfdb (PhysioNet) format, manually annotated and assigned a diagnosis, offering a variety of complex morphologies to challenge delineation algorithms. A case study that employed our recently developed delineation algorithm [14] demonstrates how one can take a full advantage of multi-lead recordings to implement error corrections in signals from separate leads, and improve recognition of complex wave morphologies, as well as precision of timing for delineation points, as compared to the performance on the 2-lead database. The further expansion of LUDB, that would not simply enrich the base, but will make it suitable for exploring machine learning and neural network algorithms for an automated diagnosis, is to follow.

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Author contributions

M.V. Ivanchenko, N.Yu. Zolotykh, K.A. Kosonogov and A.V. Nikolskiy conceived and supervised the study, A.A. Kozlov, V.A. Moskalenko, A.I. Kalyakulina and I.I. Yusipov performed data curation and analysis, M.V. Ivanchenko, N.Yu. Zolotykh, K.A. Kosonogov, A.V. Nikolskiy, A.I. Kalyakulina and I.I. Yusipov wrote the paper.

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