CardioMark User Manual

Version 1.0   *Release Date: September 2025*

Authors:

Samir Abdel-Rahman [a, b, *]**, Pavel Antiperovitch** [c]**, Anthony Tang** [c]**, Vijay Parsa** [a]**, and James C. Lacefield** [a, b, d]

[a] Department of Electrical & Computer Engineering, Western University, London, ON, Canada.

[b] Robarts Research Institute, Western University, London, ON, Canada.

[c] Department of Medicine, Schulich School of Medicine & Dentistry, Western University, London, ON, Canada

[d] Department of Medical Biophysics, Western University, London, ON, Canada.

* Corresponding author:

Name: Samir Abdel-Rahman

E-mail address: sabdel3@uwo.ca (S. Abdel-Rahman).

Phone: 519-661-2111 ext. 84303

Fax: 519-850-2436

About CardioMark

CardioMark is an open-access MATLAB toolbox designed to streamline and enhance ECG annotation via an intuitive graphical interface. It supports multi-observer input, session-based workflows, and straightforward export for machine learning applications. Its modular architecture allows customization for a variety of ECG tasks, making it a valuable tool for research and educational purposes in clinical cardiology.

Disclaimer

CardioMark is intended for research and educational purposes only and is not a diagnostic tool. It is distributed as open-source software under the GPL 3.0 license and has not been certified as a medical device, diagnostic software, or clinical decision support software. Users are responsible for complying with institutional, ethical, and regulatory standards, including the proper de-identification of protected health information (PHI).

Availability

The latest version of CardioMark, along with source code, precompiled binaries, and documentation, is available on GitHub:

https://github.com/CardioMark/CardioMark

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Introduction to CardioMark

CardioMark Overview

CardioMark provides a comprehensive set of tools for ECG analysis, including the ability to display both median beats [1] and raw signals. It enables users to accurately identify and mark key points on the ECG waveform, such as QRS onset, QRS offset, and T-wave offset. To assist with this, it superimposes signals from multiple leads, allowing users to determine the earliest QRS deflection and the latest activation in any lead, in accordance with American Heart Association (AHA) guidelines[2].

The toolbox also allows for the detailed characterization of QRS patterns, such as QS, qR, and Rs types. Users can mark notches, slurs, and R-peaks across all median beats, assign QRS morphology classifications, and add relevant comments. CardioMark also calculates QRS duration and QT interval based on the marked annotations.

System Requirements

CardioMark has been tested on the following systems:

- Operating System: Windows 11
- MATLAB Version: R2024b
- MATLAB Runtime (MCR): v24.2 (required for precompiled binaries on Windows 11)
- Hardware Requirements:
- RAM: Minimum 16 GB
- CPU: Any x86 processor released in the last 10 years (*i.e.*, 2015 or later)

CardioMark Architecture

CardioMark features a GUI structured into three main sections: a File Manager on the left, a Command Bar at the top, and a Central Workspace composed of multiple task-specific tabs. Each tab is designed to focus on a specific aspect of ECG annotation, enhancing both efficiency and accuracy. The first tab, "Superimpose", displays superimposed median beats from the limb and

chest leads side by side, enabling annotation of the QRS onset, QRS offset, and T-wave offset. The second tab, and similarly the third tab, presents individual median beats for the limb and chest leads, respectively, supporting detailed waveform morphology characterization and precise R-peak identification. The fourth tab displays the full lead waveform for further investigation.

CardioMark functionalities are organized into three main areas: the File Manager, the Central Workspace, and the Command Bar. The File Manager contains file-related functions for navigating ECG recordings and annotation files. Its main functionalities include:

- **Username / Observers**: define the username of the current observer performing the ECG annotations. This information is saved in an Excel file named "_username-ECG_Study.xlsx" located in the median beat directory. Additional observers can be added to support seamless review of annotations.
- **File Management**: specify directories for median beat data and, optionally, raw ECG signals. Users can choose from supported file formats (XML, MAT, HEA).
- **File Selection**: loads and selects ECG recordings from the specified directory for annotation. Previously annotated files can be hidden to simplify the processing workflow.
- **Export to MAT**: CardioMark enables the user to export the waveform to a MATLAB data file which can be conveniently imported by MATLAB and python.

The Central Workspace is the core of the annotation process. It is organized into four tabs that reflect the standard flow of ECG annotation. The functionalities of the Central Workspace are as follows:
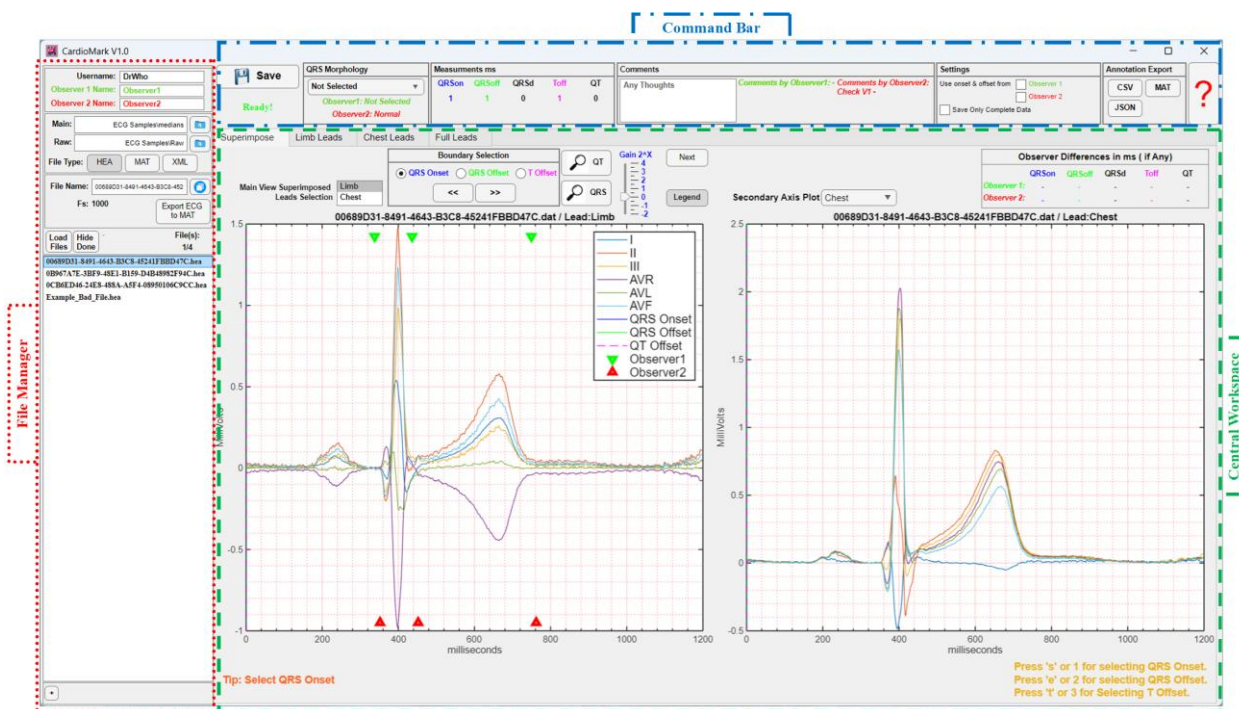

CardioMark GUI

- ***Boundary Selection***: In the first tab (Superimpose), users can select the QRS onset, QRS offset, and T offset using the Superimposed Axis Plots, supported by zoom and gain tools to enhance precision and efficiency. Users can switch between superimposed limb and chest lead views without affecting existing annotations or set the secondary axis plot to specific leads (e.g., lead I, aVL, V1) for more detailed analysis. If available, boundary annotations from other observers are displayed on the main axis plot and visually marked with small triangles.

- ***Median Beat Analysis***: In the second and third tabs of the Central Workspace, users can define the QRS pattern for each median beat and identify the presence and location of notches and slurs, where applicable. Tools such as zooming, smoothing, and gridlines are available to support this analysis and to compare waveforms with the dominant one. The R-peak can also be defined.

- ***Observer Feedback***: If available, annotations from Observers appear as triangular markers indicating notch/slur locations. Users can also compare the QRS complex morphologies defined by the observers and adopt one of them if needed.

- ***Full Lead Review***: The fourth tab (Full Lead) provides access to the full-lead ECG waveform, typically comprising a 10-second recording that includes multiple beats. Users can select one or more leads to display, facilitating further visual inspection and analysis.
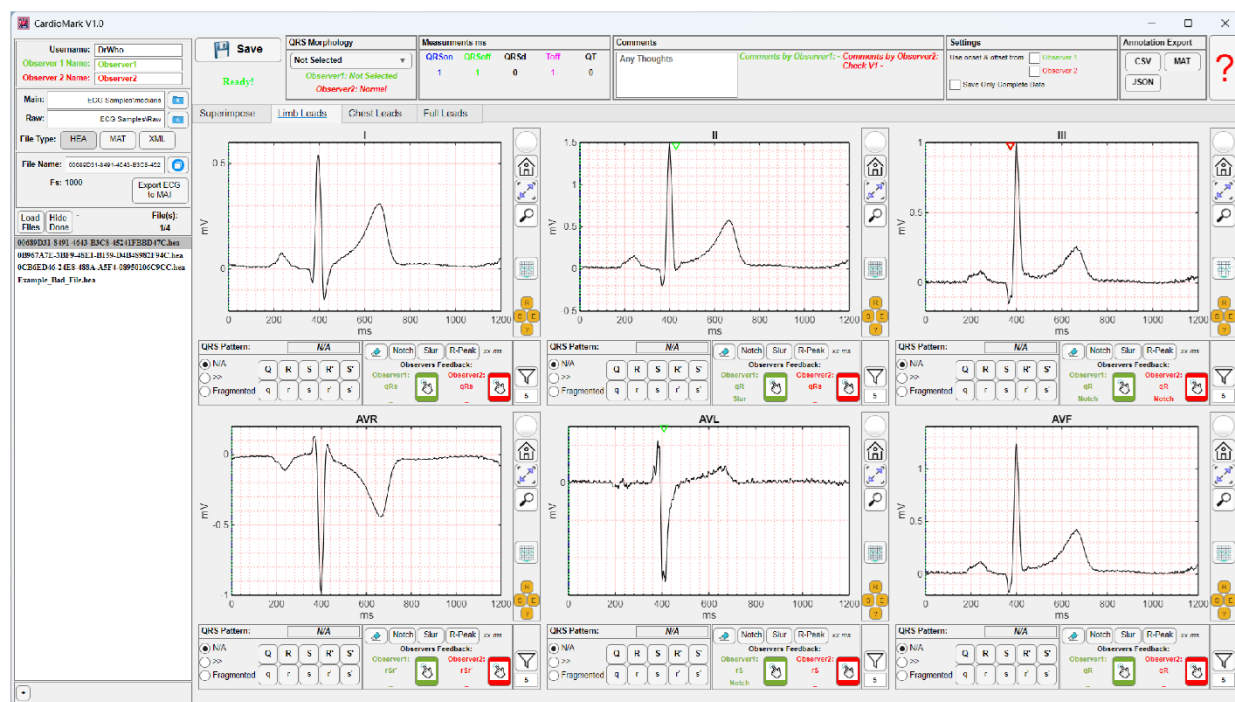
Median Beat Analysis Tab
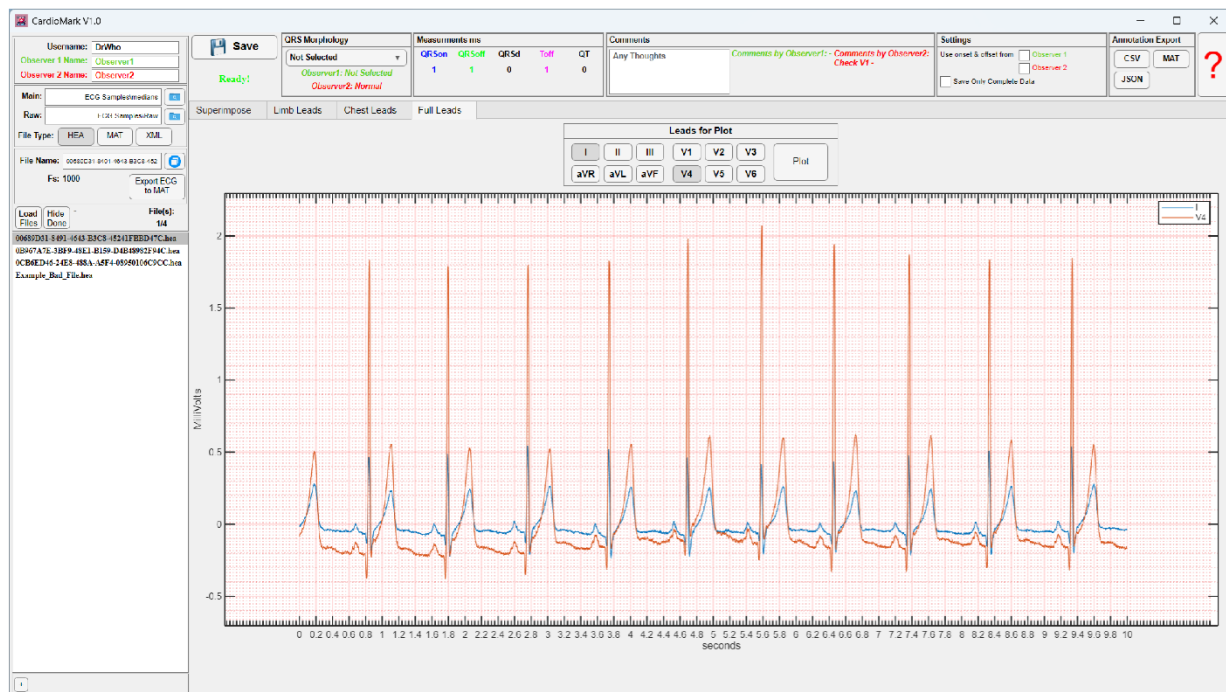
Full Lead Waveform Tab

The Command Bar provides last set of functionalities:

- **QRS Morphology**: Users can assign a QRS morphology from predefined list to speed up the annotation process. If observer-provided QRS morphologies are available, they will be displayed beneath the dropdown menu for comparison.
- **Measurements**: This panel displays key temporal measurements in milliseconds, including QRS onset, QRS offset, T-wave offset, QRS duration (QRSd), and the QT interval
- **Comments**: This section allows users to enter free text comments related to the ECG record. If comments from other observers are available, they will be shown adjacent to the input box.
- **Settings**: Provides access to general configuration options to customize the software's behavior according to user preferences.
- **Save:** This command saves all annotations to the corresponding Excel file.
- **Annotation Export**: Annotations can be exported to CSV, MAT, and JSON formats.

CardioMark Settings and Indicators

CardioMark includes a few settings and indicators that provide additional functionality and support during the annotation process.

Settings:

1. **Use Onset & Offset From:** By selecting the checkbox for Observer 1 or Observer 2, CardioMark will apply QRS onset, QRS offset, and T offset from the chosen observer's annotations if available. If both checkboxes are selected and annotations exist for both, CardioMark prioritizes Observer 2.
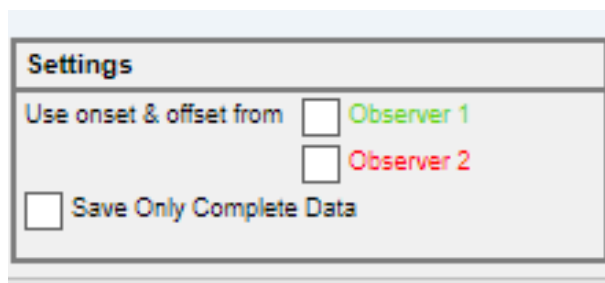

- **Save Only Complete Data**: When selected, CardioMark will reject saving if required fields (e.g., QRS patterns or morphology) are missing. If not selected, the file will still be saved, but a "Saved with missing data!" message will appear. Annotations without R-peaks, notches, or slurs are not restricted, as these features may not be present in all beats. The figure below illustrates the four possible message scenarios.

Indicators:

Median Beat Analysis: Three indicator states help track annotation progress:

1. **White**: Initial state after loading a new ECG recording, indicating that no QRS pattern has been selected yet.
2. **Green**: A valid QRS pattern has been defined. If notches or slurs are annotated, both their start and end points are also defined.
3. **Red**: Either the QRS pattern is missing, or a notch/slur has been marked without both start and end points properly defined.
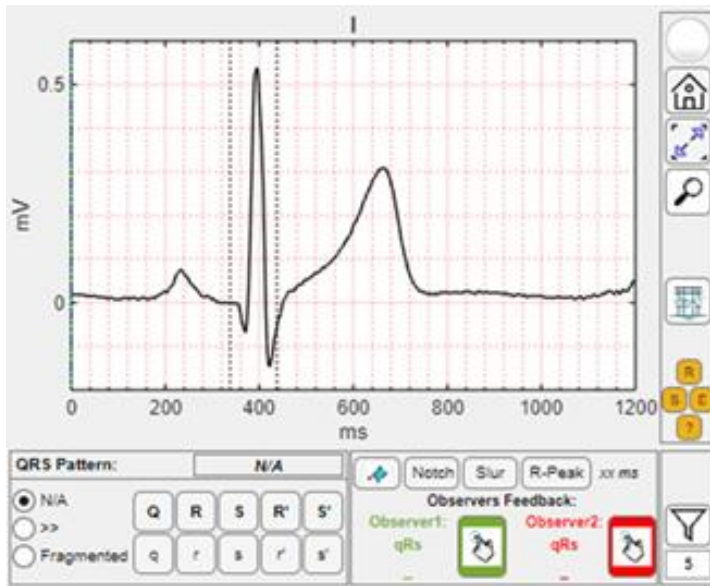
Getting Started

This section guides users through the initial steps of using CardioMark. It covers launching the software, opening ECG files, and familiarizing yourself with the main interface, enabling you to begin annotating recordings efficiently and accurately.

Downloading CardioMark

CardioMark can be obtained from the official GitHub repository:

https://github.com/CardioMark/CardioMark

Download the folder containing the CardioMark files to your local drive.

Recommendation: avoid placing the files directly to the C:\ drive on Windows systems to prevent permission-related issues.

Launching CardioMark

From MATLAB:

1. Add the CardioMark folder to the MATLAB search path, type in MATLAB Command Window:

   >> addpath('Folder path\CardioMark\CardioMark v1.0')

2. Open the application using one of the following methods:
- In the MATLAB Command Window, type:
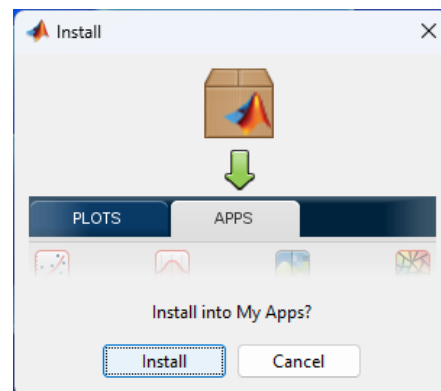
   >> CardioMark

   This will directly launch the software.

- From the MATLAB Home tab: click Open (or use the shortcut Ctrl + O), then select the file CardioMark.mlapp.
   This opens the file in the MATLAB App Designer. To run the software, go to the CANVAS tab and click Run (or press F5).

From Packaged App:

1. Install "CardioMark V1.0.mlappinstall".

2. Once installed, CardioMark will appear in the APPS menu in MATLAB.

3. Click CardioMark from the APPS menu to launch the software.

Using Precompiled Binaries (Windows 11):

1. Locate and run CardioMarkV1Setup.exe in the setup folder.

2. Follow the installation wizard.

3. After installation, launch CardioMark either from the installation directory or by using the desktop shortcut.

Note: Running the precompiled version requires the MATLAB Runtime (MCR) v24.2, which will be installed automatically if not already present.

Step by Step Tutorial

This section provides a practical walk-through of the annotation process in CardioMark. Using a sample 12-lead ECG recording, you will learn how to load a file, navigate the interface, place key annotations (QRS onset, QRS offset, and T-wave offset), and review calculated measurements. The example also demonstrates how to save annotations, compare results between observers, and export the final annotation table for further analysis.

As part of this getting started guide, the following example demonstrates the basic workflow of CardioMark. The steps are numbered in figures on the following pages for clarity and visual guidance. In this example, the files *"00689D31-8491-4643-B3C8-45241FBBD47C.hea"* and *"00689D31-8491-4643-B3C8-45241FBBD47C.DAT"* from the CiPA database [3] are used. These files, along with additional sample files, are provided in the *"ECG Samples"* folder within the *"CardioMark v1.0"* directory. After launching CardioMark, follow the step-by-step tutorial below to explore its basic functions:
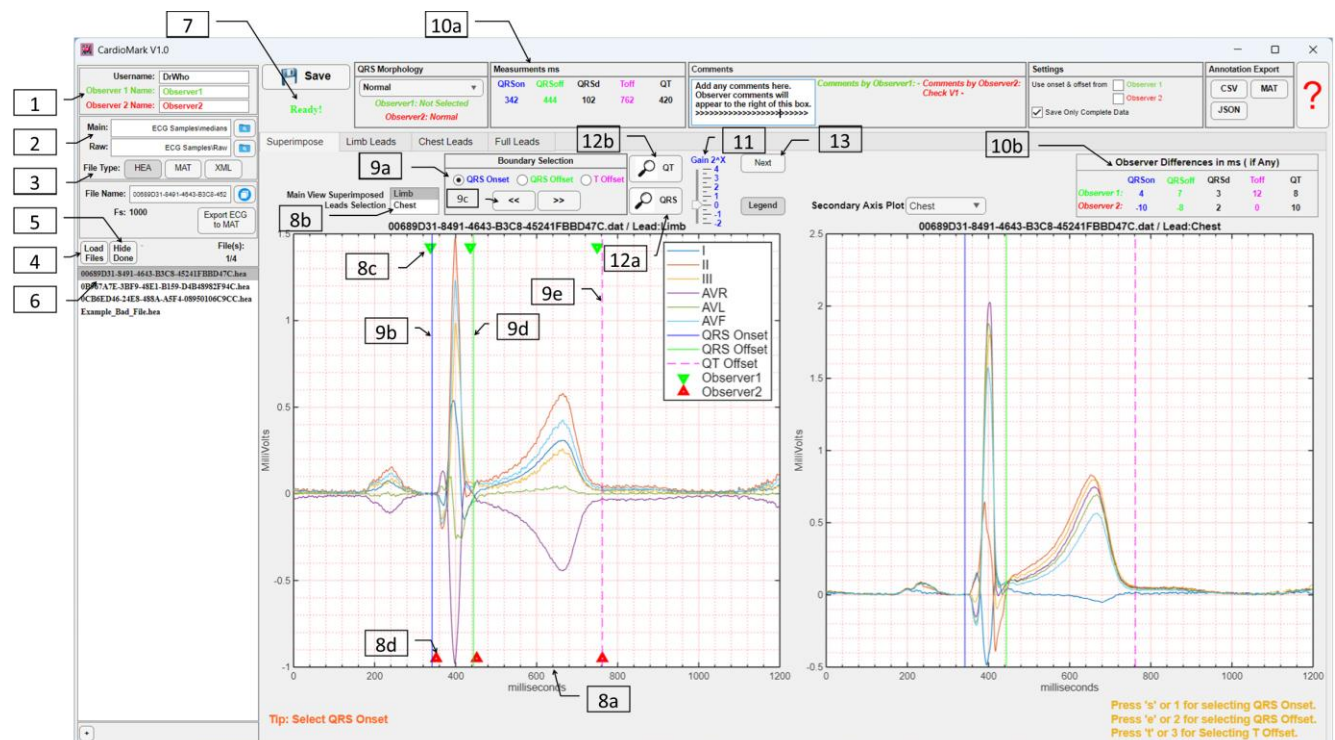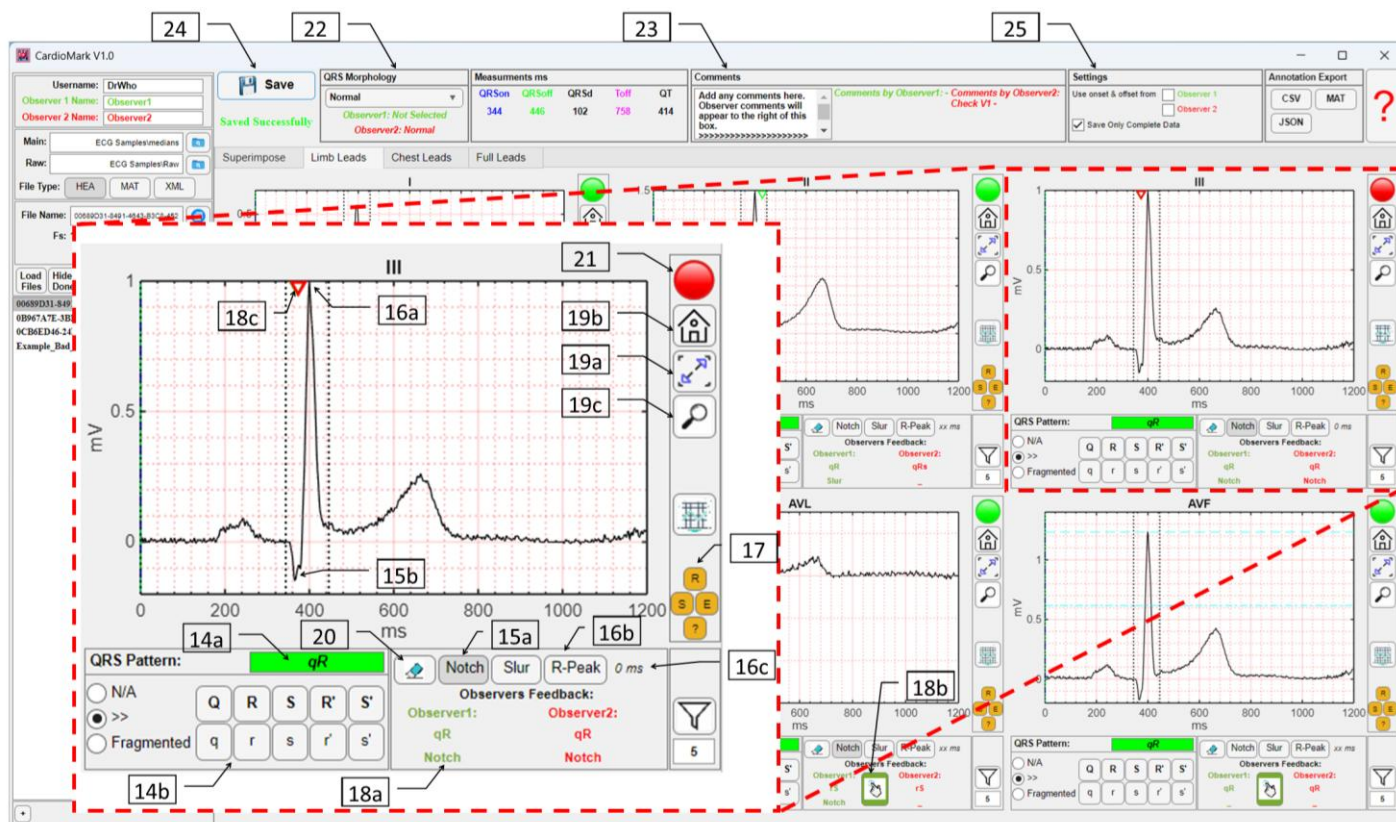
Illustrative example of usage steps 1 to 13 in CardioMark.

1. Enter the username for the current observer. Optionally, type names for Observer 1 and Observer 2. For this example, use your own name as the current observer, and type "Observer1" and "Observer2" in the respective fields (Observer 1 Name and Observer 2 Name, respectively).

2. Specify the directory containing the ECG recording files. You can either type the path directly into the text boxes or use the folder selection button.

   2.1. In the Main folder section, click the blue folder icon and select the "Median" folder inside the "ECG Samples" directory.

   2.2. In the Raw folder section, click the blue folder icon and select the "Raw" folder inside the ECG "Samples directory". This step is not required if you are working with XML or MAT file types.

   2.3. Alternatively, you may type the full folder paths directly into the text boxes without browsing.

3. Choose the appropriate file format for your ECG recordings. In this example, select "**HEA**" format.

4. Click the **"Load Files"** button to display all files with the selected extension in the specified directory.

5. Click the "Hide Done" button to filter out ECG recordings that have already been annotated and saved in the corresponding Excel file. A message next to the button will display the number of files hidden. Since this is the first session, you can ignore this step.

6. After Step 4, the file list box will display all files with the **HEA** extension; click on the first file, *"00689D31-8491-4643-B3C8-45241FBBD47C.hea"*. A rotating hourglass will appear for a few seconds while the file data is loaded.

7. The software will plot the ECG waveforms and display a "Ready!" message, indicating that the system is prepared for annotation and you can begin the process.

8. In the main axis plot (a), superimposed limb leads are shown; this view can be switched to chest leads by selecting **"Chest"** (b). Annotations from Observer 1 (c) and Observer 2 (d) appear as triangular markers indicating **QRS onset, QRS offset,** and **T-wave offset**.

9. To annotate QRS onset, QRS offset, and T-wave offset, select the **"QRS Onset"** radio button (a), click on the main axis plot (b), and fine-tune the position using the left/right adjustment buttons (c). Repeat the same process for **"QRS Offset"** (d) and **"T Offset"** (e).

10. The Measurements panel (a) displays the automatically calculated QRS duration (QRSd) and QT interval based on the selected boundaries, including the positions of QRS Onset, QRS Offset, and T Offset. Observer differences, if any, are shown in milliseconds in this panel (b) for the current delineation.

11. Increasing the gain amplifies each waveform, making it easier to identify the **T-wave offset** by distinguishing differences between overlapping waves.

12. The **QRS Zoom** (a) and **QT Zoom** (b) buttons zoom into the region between QRS onset and QRS offset or T offset, respectively, to aid in precise boundary adjustment. *Do not use these buttons if the initial boundaries have not been selected.*

13. To begin identifying QRS morphologies, move to the next tab by clicking the **Next** button (a) or by selecting the **"Limb Leads"** tab.

14. For each lead, label the QRS complex pattern by selecting the buttons (a) to construct the name, or alternatively, type the pattern directly into the text box (b).

15. If a slur or notch is present, select the appropriate button (a), then on the axis plot (b), press the left mouse button to mark the beginning and the right mouse button to mark the end of the slur/notch.

16. To identify an R-peak, click the middle mouse button at the desired location (a), or use the **"R-Peak"** button (b) to automatically select a location. The position can be adjusted with the middle mouse button, and the R-peak time (c) will be displayed next to the **R-Peak** button.

Illustrative example of usage steps 14 to 25 in CardioMark.

17. For Mac users, the **"S"**, **"E"**, and **"R"** keys can be used as alternatives to the left, middle, and right mouse buttons, respectively, for marking slurs/notches and identifying R-peaks.

18. Observers' annotations (a) for QRS patterns, notches, and slurs are displayed. If an observer's QRS pattern differs from the current user's, a **pointer button** (b) appears. Clicking this button will apply the observer's QRS pattern to the current annotation. Red or green triangles (c) indicate the locations of notches or slurs made by the observers.

19. To zoom into a specific area for more accurate boundary definition, use the **Zoom to Select** button (a) to zoom without stretching the waveform. Press the **Home** button (b) to reset the view. The **QRS Zoom Toggle** button (c) stretches the selected area and zooms between the QRS onset and QRS offset defined in the previous tab. *Do not use the QRS Zoom Toggle if QRS onset and QRS offset have not been selected in the previous tab.*

20. To revert the selection of a notch, slur, or R-peak, press the **Erase** button.

21. The indicator turns **green** if all required data are entered. It turns **red** if data are incomplete, such as marking a notch or slur without labeling its boundary or type, or failing to label the QRS pattern. Use **Step 20** to revert any incorrect selection of a notch or slur.

22. After identifying all QRS features, select a QRS morphology from the dropdown list (a). The QRS morphologies of other observers (b) are displayed below the dropdown list for comparison.

23. To add comments, type text into the comment box. Comments from other observers are displayed next to the current user's comment for comparison.

24. After finalizing all annotations, click the **"Save"** button. A confirmation message will appear below it, or a warning will be displayed if some annotations are missing.

Data Management and Annotation Guidelines

This chapter provides a comprehensive guide to managing and handling ECG annotation data in CardioMark. It describes the structure of the annotation table, outlines supported file formats and explains available export options for integration with analysis tools or machine learning workflows. In addition, it presents information on computational performance and memory usage and offers practical guidelines for safe and consistent annotation workflows, ensuring accurate, reproducible, and efficient use of the software.

Annotation Table Schema

CardioMark organizes all annotation data in a structured Excel table to ensure consistent, reproducible, and easily reviewable records. The table captures all relevant ECG information, QRS morphologies, notches, slurs, R-peak timings, and observer details in clearly labeled columns. This structure allows efficient comparison across multiple observers, facilitates integration with AI applications, and supports detailed analysis of ECG recordings.

All annotation data are stored in an Excel file named "_username-ECG_Study.xlsx" in the main directory of the ECG recordings. This flat-format table contains 68 columns covering all annotations for each record. A filled example of this table is available in the "ECG Samples\Medians\DrWho.xlsx" folder within the "CardioMark V1.0" directory. The table is organized into seven regions:

1. Main ECG information: contains the essential data for each ECG record:

    1.1. File name [FileName] (text)

    1.2. Time stamp [Timestamp] (date-time)

    1.3. QRS morphology [QRSMorph] (text)

    1.4. QRS onset [Onset] (numerical in ms)

    1.5. QRS duration [QRSd] (numerical in ms)

    1.6. QT interval [QTd] (numerical in ms)

1.7. Comments [Comment] (text)

FileName	Timestamp	QRSMorph	Onset	QRSd	QTd	Comment
ECGFile_1.hea	2025-09-07 21:29:13	Normal	344	102	414	V1 ?

2. QRS Pattern: twelve consecutive columns record the QRS morphology for leads I, II, III, aVR, aVL, aVF, and V1–V6 as text (e.g., qRs, QR), with missing patterns indicated as N/A. The column headers are labelled as "LeadName_P".

I_P	II_P	III_P	aVR_P	aVL_P	aVF_P	V1_P	V2_P	V3_P	V4_P	V5_P	V6_P
qRs	qRs	qR	rSr'	rS	qR	rSr'	RS	qRs	qR	qR	qR

3. QRS Notches/Slurs: twelve consecutive columns indicate the presence of notches or slurs within the QRS complex for leads I, II, III, aVR, aVL, aVF, and V1–V6 as text: "N" for notch, "S" for slur, or "-" if none. The column headers are labelled "LeadName_N_S".

I_N_S	II_N_S	III_N_S	aVR_N_S	aVL_N_S	aVF_N_S	V1_N_S	V2_N_S	V3_N_S	V4_N_S	V5_N_S	V6_N_S
_	_	Notch	_	Notch	_	_	_	_	_	_	_

4. QRS Notches/Slurs start : twelve consecutive columns indicate the start of notches or slurs within the QRS complex for leads I, II, III, aVR, aVL, aVF, and V1–V6 as numeric values in milliseconds; a value of zero indicates not defined. The column headers are labeled "LeadName_N_Son".

I_N_Son	II_N_Son	III_N_Son	aVR_N_Son	aVL_N_Son	aVF_N_Son	V1_N_Son	V2_N_Son	V3_N_Son	V4_N_Son	V5_N_Son	V6_N_Son
0	0	0	0	398	0	0	0	0	0	0	0

5. QRS Notches/Slurs end: twelve consecutive columns indicate the end of notches or slurs within the QRS complex for leads I, II, III, aVR, aVL, aVF, and V1–V6 as numeric values in milliseconds; a value of zero indicates not defined. The column headers are labeled "LeadName_N_Soff".

I_N_Soff	II_N_Soff	III_N_Soff	aVR_N_Soff	aVL_N_Soff	aVF_N_Soff	V1_N_Soff	V2_N_Soff	V3_N_Soff	V4_N_Soff	V5_N_Soff	V6_N_Soff
0	0	0	0	412	0	0	0	0	0	0	0

6. R-Peak Timing : twelve consecutive columns record the R-peak times for leads I, II, III, aVR, aVL, aVF, and V1–V6 as numeric values in milliseconds. The column headers are labeled "LeadName_R_Peak".

I_R_Peak	II_R_Peak	III_R_Peak	aVR_R_Peak	aVL_R_Peak	aVF_R_Peak	V1_R_Peak	V2_R_Peak	V3_R_Peak	V4_R_Peak	V5_R_Peak	V6_R_Peak
0	0	0	0	0	0	0	0	0	0	0	0

7. Provenance: the last column contains information about the software version, current username, and observers. Additional details can be included by modifying the source code.

Supported ECG Files

CardioMark supports multiple ECG file formats to ensure compatibility with commonly used databases and recording systems. The software can load:

- **MUSE XML**: standard export format from GE MUSE ECG systems.
- **PhysioNet HEA/DAT**: header and signal files from PhysioNet databases.
- **MATLAB MAT**: user-prepared MAT files containing ECG signals with the required variable structure.

Both median and raw ECG signals (for HEA/DAT files only) can be visualized, allowing flexible inspection and annotation. Users should ensure that files are properly formatted and stored in accessible directories before loading. CardioMark can also export XML and HEA/DAT files to MAT format to facilitate integration with AI models.

For **MAT files**, the structure must include two structure arrays (structs): **MedianBeat** and **Raw**; see the figure below, each containing the following variables:

- **X**: the ECG signal array.
- **Fs**: the sampling rate in Hz.
- **Lead**: the name of each ECG lead.
- **FileName**: the original ECG record file name.
- **Length**: the number of samples in the signal.
- **TS**: an array of time steps in milliseconds.
- **Unit**: the signal unit, typically millivolts (mV).

In some recordings, files may contain more than 12 leads. CardioMark will use only the first 12 leads and ignore any additional channels.

Exporting the Annotation Table

CardioMark provides flexible options to export annotation data for further analysis or integration with other software, including machine learning systems. All annotations are saved in a structured Excel file (**_username-ECG_Study.xlsx**) within the main directory of the ECG recordings. Users can export the data to multiple formats: **CSV**, **MAT**, and **JSON**.

To export, simply click on the desired format in the **Annotation Export** panel on the CardioMark command bar. All exported files will include the complete annotations from the Excel file, retain the same base name, adopt the appropriate file extension, and be saved in the same folder as the Excel file.
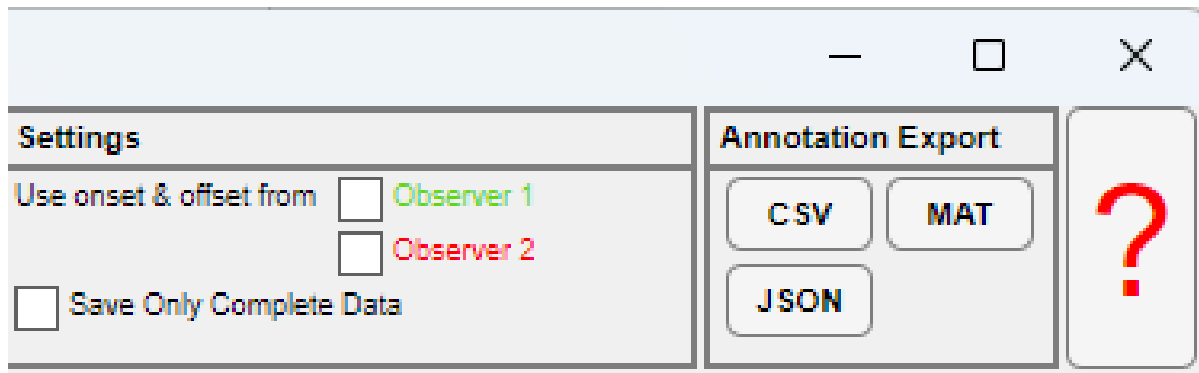
Computational Performance and Memory Footprint

CardioMark is optimized for typical ECG datasets, but performance can be affected by very large cohorts due to Excel file size limitations (≈1 million rows). Most publicly available databases are much smaller; for example, the PTB-XL database [4], one of the largest open-access ECG datasets, contains approximately 21,800 records.

The table below summarizes the computational performance and memory footprint of CardioMark for different cohort sizes, showing typical load, annotation, and save times per ECG, as well as the resulting Excel file size. Performance is constrained mainly by spreadsheet I/O, not computation.

Annotated Records in file	Load (s)	Annotate (s)	Save (s)	Total Annotation Time/ ECG (s)	Excel Size
10,000	2.5	114	6.5	~ 124 s	~3 MB
1,000	2.5	114	0.68	~ 118 s	~233 KB
258	2.5	114	0.18	~ 117 s	~84 KB

Safe and Compliant Use, and Usage Recommended Guidelines

CardioMark is research and educational software only. It is not a medical device and must not be used for clinical diagnosis, patient monitoring, or patient care. All outputs are intended strictly for research, methodological development, and academic studies.

Data Privacy and De-Identification

Before using CardioMark with clinical data, users must ensure that all personally identifiable information (PHI) has been removed in compliance with institutional and regulatory standards. A minimum de-identification checklist includes:

1. Names: patient, physician, or institution names must be stripped.
2. Medical Record Numbers (MRNs): or any equivalent identifiers must not be included.
3. Dates: admission, procedure, or birth dates must be removed or replaced with relative or shifted time indices.
4. Other Identifiers: any information that can directly or indirectly reveal patient identity must be excluded. Such as:
   - Addresses: full home or street address, city, or postal code
   - Contact information: phone numbers, fax numbers, email addresses.
   - Geographic data: GPS coordinates or facility-specific identifiers.
   - Health insurance information,
   - Billing account numbers.
   - Comments within ECG headers or reports that may include personal information.

Recommended Annotation Workflow

To promote accuracy and consistency in annotations, the following workflow is recommended:

1. Two independent annotators begin the annotation process without consulting each other, ensuring unbiased labeling.
2. A third, more experienced annotators review their annotations, acting as the primary observer. In case of disagreement, this annotator breaks the tie.
3. ECGs with significant disagreement among annotators should be flagged and deferred for a second review round, where annotators meet to reach consensus.
4. For quality assurance, periodic inter-rater reliability checks (e.g., Cohen's kappa or percent agreement) should be conducted to measure consistency across annotators.
5. Annotators are encouraged to keep brief comments (e.g., uncertain morphologies, signal quality issues). It is recommended to have list of specific wording for easier filtering.
6. For large datasets, assigning ECGs in balanced batches across annotators helps reduce fatigue and improve annotation quality.

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