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DSP REPORT

PREPARED BY :

AUMKAR RANJAN BEHURA

QRS Complex Detection in ECG Signals: A Pan-Tompkins Algorithm Implementation

Introduction

Electrocardiogram (ECG) signal analysis is a cornerstone of cardiac diagnostics, providing essential information about heart function and potential abnormalities. One of the most critical features in ECG interpretation is the accurate detection of QRS complexes, which represent ventricular depolarization in the cardiac cycle. This project implements an enhanced version of the Pan-Tompkins algorithm—a widely respected method for QRS detection—adapted specifically for the MIT-BIH Arrhythmia Database, one of the most comprehensive ECG databases available for cardiac research.

The implemented system processes ECG signals through a series of digital signal processing (DSP) stages to identify QRS complexes accurately, even in the presence of noise and signal variations common in clinical settings. The project evaluates the algorithm's performance against expert annotations, providing metrics such as sensitivity, positive predictivity, and F1 score to quantify detection accuracy.

The Pan-Tompkins Algorithm

Overview

Developed in 1985 by Jiapu Pan and Willis J. Tompkins, the Pan-Tompkins algorithm represents a systematic approach to QRS detection that remains relevant despite its age. The algorithm processes an ECG signal through multiple stages, each designed to enhance specific characteristics of the QRS complex while suppressing noise and other ECG components like P and T waves.

The implementation in this project follows an enhanced version of the original algorithm with optimizations for the MIT-BIH Arrhythmia Database's specific characteristics. The core processing stages include:

1. **Bandpass Filtering** - To isolate the QRS frequency components
2. **Derivative Computation** - To emphasize the steep slopes of the QRS complex
3. **Squaring** - To make all signal values positive and emphasize higher frequencies
4. **Moving Window Integration** - To extract waveform features in addition to slope information
5. **Adaptive Thresholding** - To distinguish QRS complexes from noise and adapt to signal variations

Mathematical Foundation and DSP Methods

1. Bandpass Filtering

The bandpass filter removes baseline wander (low-frequency noise) and high-frequency interference while preserving the QRS complex frequency content. In this implementation, a 4th-order Butterworth filter with cutoff frequencies at 5Hz and 15Hz is used:

```
lowcut = 5;    % 5Hz cutoff for high-pass

highcut = 15;  % 15Hz cutoff for low-pass

wn = [lowcut highcut] / (fs/2);

[b, a] = butter(4, wn, 'bandpass');

bandpass_signal = filtfilt(b, a, ecg_signal); % Zero-phase filtering
```

The `filtfilt` function applies zero-phase filtering, eliminating phase distortion by filtering the signal forward and backward. This is critical for preserving the precise timing of QRS complexes.

2. Derivative Computation

The derivative stage emphasizes the steep slopes characteristic of QRS complexes. A five-point derivative approximation is used:

```
b = [1 2 0 -2 -1] * (1/8);

a = 1;

derivative_signal = filter(b, a, bandpass_signal);
```

This filter approximates the derivative while providing noise smoothing. Mathematically, it implements a weighted derivative approximation over a five-sample window.

3. Squaring Function

Squaring makes all values positive and emphasizes higher frequencies proportionally more than lower frequencies:

```
squared_signal = derivative_signal.^2;
```

This nonlinear transformation enhances larger values (likely QRS complex components) relative to smaller values (likely noise or T waves).

4. Moving Window Integration

Integration extracts morphological features of the QRS complex by computing a moving average:

```
b = ones(1, integration_window)/integration_window;

a = 1;

integrated_signal = filter(b, a, squared_signal);
```

The integration window width (150ms in this implementation) is critical: too wide and it might merge adjacent QRS complexes; too narrow and it might produce multiple peaks for a single QRS complex.

5. Adaptive Thresholding and Peak Detection

This stage is the most sophisticated part of the algorithm. Two thresholds are dynamically adjusted based on the signal and noise levels:

```
threshold1 = NPKI + signal_threshold_weight * (SPKI - NPKI);

threshold2 = noise_threshold_weight * threshold1;
```

Where:

- $SPKI$ is the running estimate of signal peak level

- $NPKI$ is the running estimate of noise peak level
- $signal_threshold_weight$ (0.25) and $noise_threshold_weight$ (0.5) are weighting factors

The algorithm updates these estimates with each detected peak:

```
% For QRS peaks:

SPKI = learning_rate_signal * peak_val + (1-learning_rate_signal) * SPKI;


% For noise peaks:

NPKI = learning_rate_noise * peak_val + (1-learning_rate_noise) * NPKI;
```

This adaptive approach allows the algorithm to adjust to variations in ECG amplitude and morphology over time.

6. RR Interval Analysis for Missed Beat Detection

The implementation incorporates an enhanced feature to detect missed beats based on RR interval analysis:

```
if RR(i) > 1.8 * mean_RR

% Search for potential missed beats in noise peaks...

end
```

This additional step improves detection reliability by identifying possible QRS complexes that were initially classified as noise but are temporally consistent with expected beat timing.

Performance Evaluation

The algorithm's performance is evaluated against expert annotations from the MIT-BIH Arrhythmia Database using three key metrics:

1. **Sensitivity (Se)**: The proportion of actual QRS complexes correctly identified $$Se = \frac{TP}{TP + FN}$$
2. **Positive Predictivity (PP)**: The proportion of detected QRS complexes that are correct $$PP = \frac{TP}{TP + FP}$$
3. **F1 Score**: The harmonic mean of sensitivity and positive predictivity $$F1 = 2 \times \frac{Se \times PP}{Se + PP}$$

Where:

- TP (True Positives): Correctly identified QRS complexes
- FP (False Positives): Incorrectly identified QRS complexes
- FN (False Negatives): Missed QRS complexes

The evaluation uses a matching window of 100ms, meaning a detected peak is considered a true positive if it falls within ±50ms of an annotated QRS complex.

Implementation Details

The project is implemented in MATLAB and organized into several key functions:

1. **robust_pan_tompkins_qrs_detector_local**: Implements the enhanced Pan-Tompkins algorithm
2. **load_mitbih_record_local**: Loads ECG data from the MIT-BIH database
3. **evaluate_qrs_detection_local**: Evaluates detection performance against annotations

The main script processes selected records from the MIT-BIH Arrhythmia Database, visualizes the detection results, and summarizes overall performance metrics.

Visualization and Interpretation

The implementation includes comprehensive visualization of each processing stage, allowing for detailed inspection of the algorithm's behavior. The visualizations include:

1. The original ECG signal with marked QRS detections
2. The bandpass filtered signal
3. The derivative signal
4. The squared signal
5. The integrated signal with adaptive thresholds and marked peaks

Additionally, the implementation calculates and displays the average heart rate based on detected QRS complexes, providing a clinically relevant parameter.

Conclusion

The enhanced Pan-Tompkins algorithm implementation demonstrates the effectiveness of systematic digital signal processing techniques in extracting clinically significant features from physiological signals. The project highlights the importance of adaptive methods when processing biological signals, which naturally exhibit high variability both between subjects and within the same subject over time.

The performance metrics obtained from testing on the MIT-BIH Arrhythmia Database provide quantitative validation of the algorithm's effectiveness. Future work could focus on further optimization for specific arrhythmia types, enhanced noise resistance, or integration with more comprehensive ECG analysis frameworks.

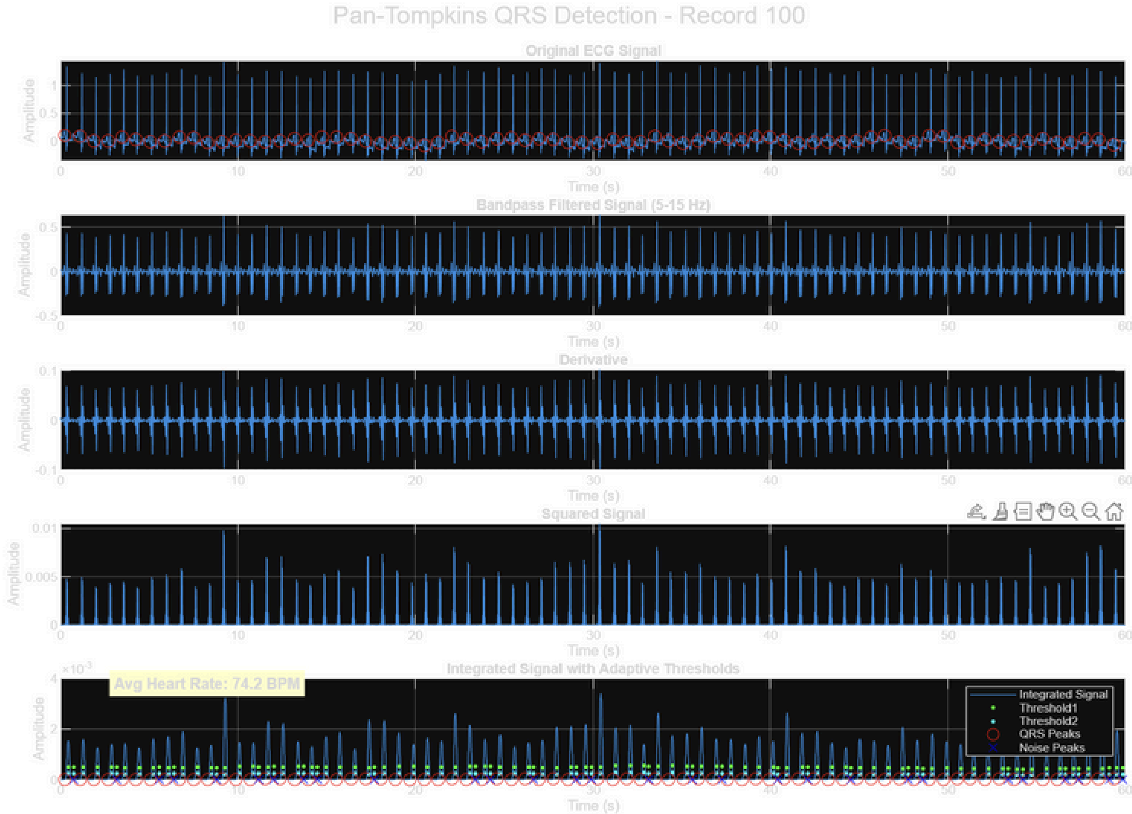
This project serves not only as a practical implementation of a classic biomedical signal processing algorithm but also as an educational resource demonstrating fundamental DSP concepts applied to real-world biomedical engineering challenges.

```
%% MIT-BIH Arrhythmia Database QRS Complex Detection (All-in-One Script)
% This script contains all necessary functions and analysis code to detect
% QRS complexes in the MIT-BIH Arrhythmia Database using Pan-Tompkins algorithm.
clear;
close all;
clc;
% Configuration
record_numbers = [100, 101, 103, 105, 106, 109]; % Records to analyze
lead_number = 1;          % ECG lead to analyze (1 or 2)
start_time = 60;          % Start time in seconds (skip first minute)
duration = 60;            % Duration in seconds (analyze one minute)
plot_individual = true;   % Plot individual record results
fs = 360;                 % MIT-BIH sampling frequency



%% Check for WFDB Toolbox if ~exist('rdann', 'file') ||
~exist('rdsamp', 'file')
     error(['WFDB Toolbox not found. Please install it from: ' ...
            'https://physionet.org/content/wfdb-matlab/0.10.0/']);
end  %%  Validate  that  database  files
exist try



    [test_signal, ~, ~] = rdsamp('mitdb/100', 1, 10, 0);
catch
    error(['Could not access MIT-BIH database files. Please ensure they are
downloaded and ' ...
           'properly placed in a "mitdb" folder in your MATLAB path or current
directory.']);
end
fprintf('MIT-BIH database is accessible. Proceeding with analysis...\n');
MIT-BIH database is accessible. Proceeding with analysis...
```

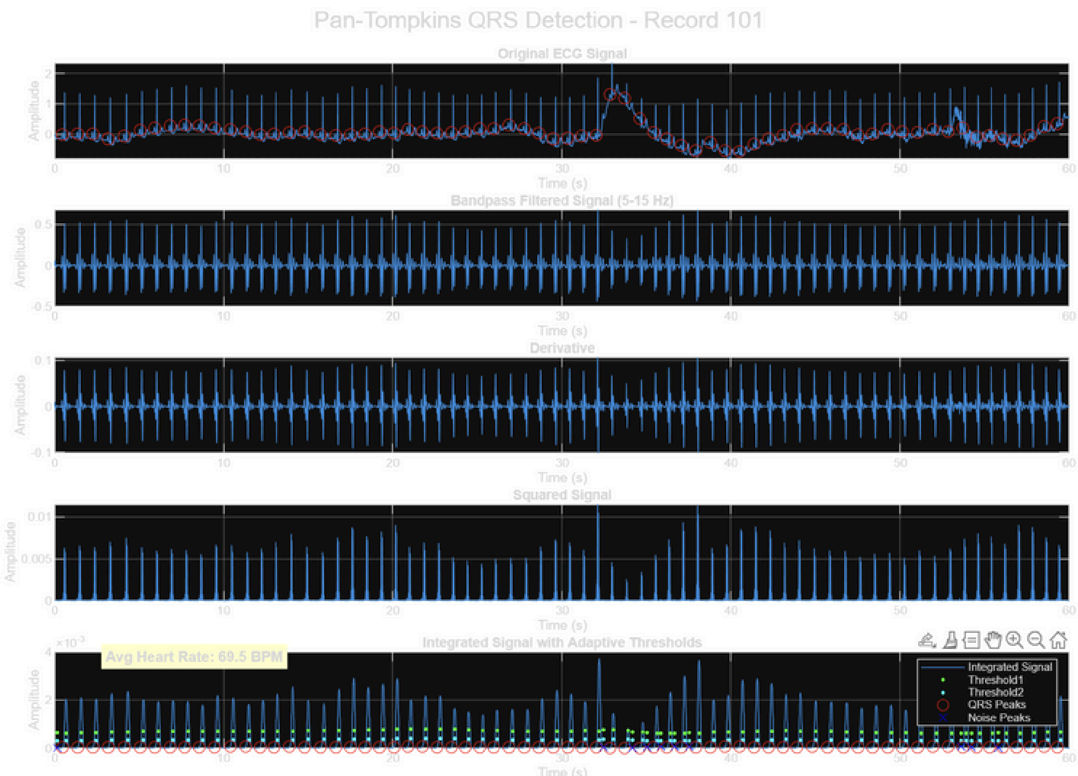
```


results = struct('record', {}, 'qrs_peaks', {}, 'annotations', {},
'performance', {});
%% Process each record
for r = 1:length(record_numbers)

    record_num = record_numbers(r);
    fprintf('\nProcessing record %d (%d of %d)...\n', record_num, r,
length(record_numbers));

    % Load the record data
    try
        [ecg_signal, record_fs, annotations] =
load_mitbih_record_local(record_num, lead_number, start_time, duration);

        % Ensure we have ECG data
```

```
        if isempty(ecg_signal)
            warning('Record %d has no ECG data. Skipping...', record_num);
            continue;
        end
        fprintf('Loaded record %d: %d samples at %d Hz\n', record_num,

length(ecg_signal), record_fs);

        % Run QRS detection
        [qrs_peaks, processed_ecg] =
robust_pan_tompkins_qrs_detector_local(ecg_signal, record_fs, plot_individual);

        % Get QRS annotations (only those marked as normal beats 'N' or PVC 'V')
        ann_qrs = [];
        if ~isempty(annotations.time)
            % Extract beat annotations (N = normal, V = PVC, etc.)
            beat_annotations = ismember(annotations.type, {'N', 'V', 'L', 'R',
'A', 'a', 'J', 'S', 'F'});
            ann_qrs = annotations.time(beat_annotations);
        end
        % Evaluate detection performance
        if ~isempty(ann_qrs)

            [qrs_stats, performance] = evaluate_qrs_detection_local(qrs_peaks,
ann_qrs, record_fs);

            % Store results results(r).record = record_num;
            results(r).qrs_peaks         =         qrs_peaks;
            results(r).annotations         =         ann_qrs;
            results(r).performance  =  performance;  %  Print
            performance     metrics     fprintf('Record     %d
            Performance:\n', record_num);


            fprintf('  Sensitivity: %.2f%%\n', performance.sensitivity * 100);
            fprintf('  Positive Predictivity: %.2f%%\n',
performance.positive_predictivity * 100);
            fprintf('  F1 Score: %.2f\n', performance.F1_score);
        else
        end warning('No annotations found for record %d', record_num);
        % Update figure title if individual plots are shown
        if plot_individual


            sgtitle(sprintf('Pan-Tompkins QRS Detection - Record %d',
record_num), 'FontSize', 16);
        end
    catch ME
        warning('Error processing record %d: %s', record_num, ME.message);
        % Display the error stack for debugging
        disp(getReport(ME, 'extended'));
    end
end
```

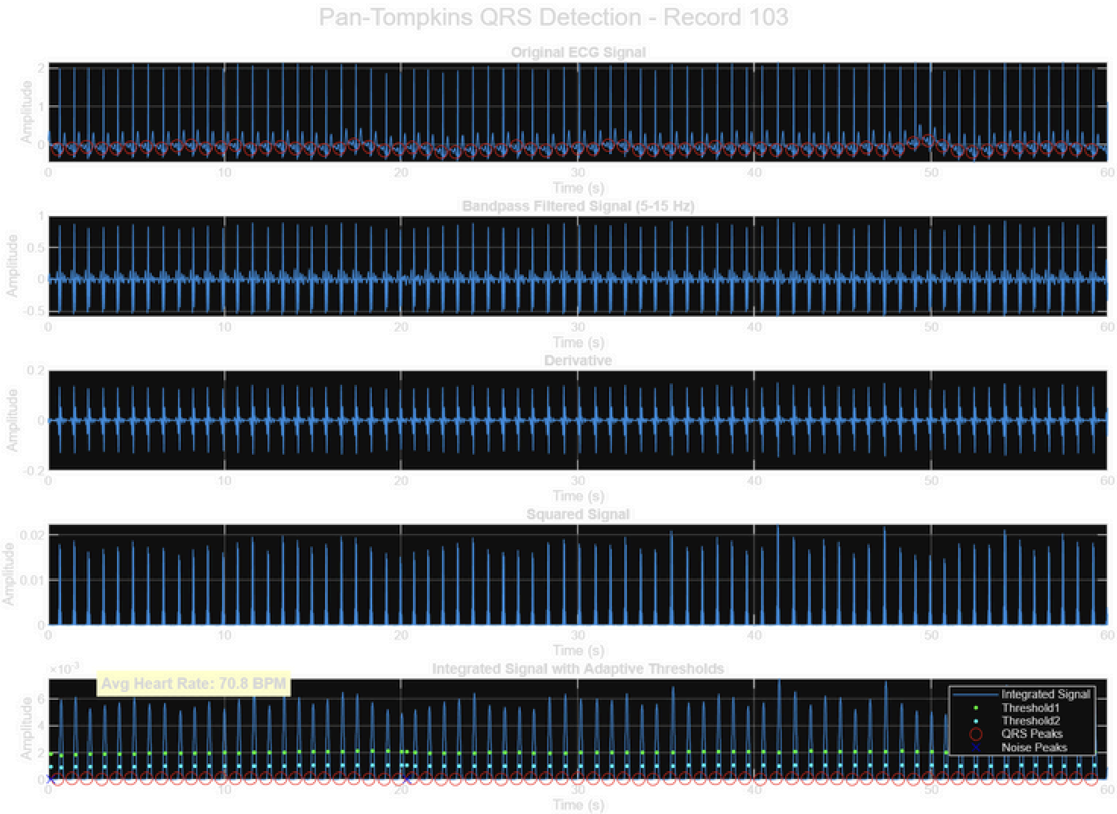
```
Processing record 100 (1 of 6)...
Warning: Could not load annotations. Returning empty annotation structure.
Loaded record 100: 21601 samples at 360 Hz
Warning: No annotations found for record 100
```



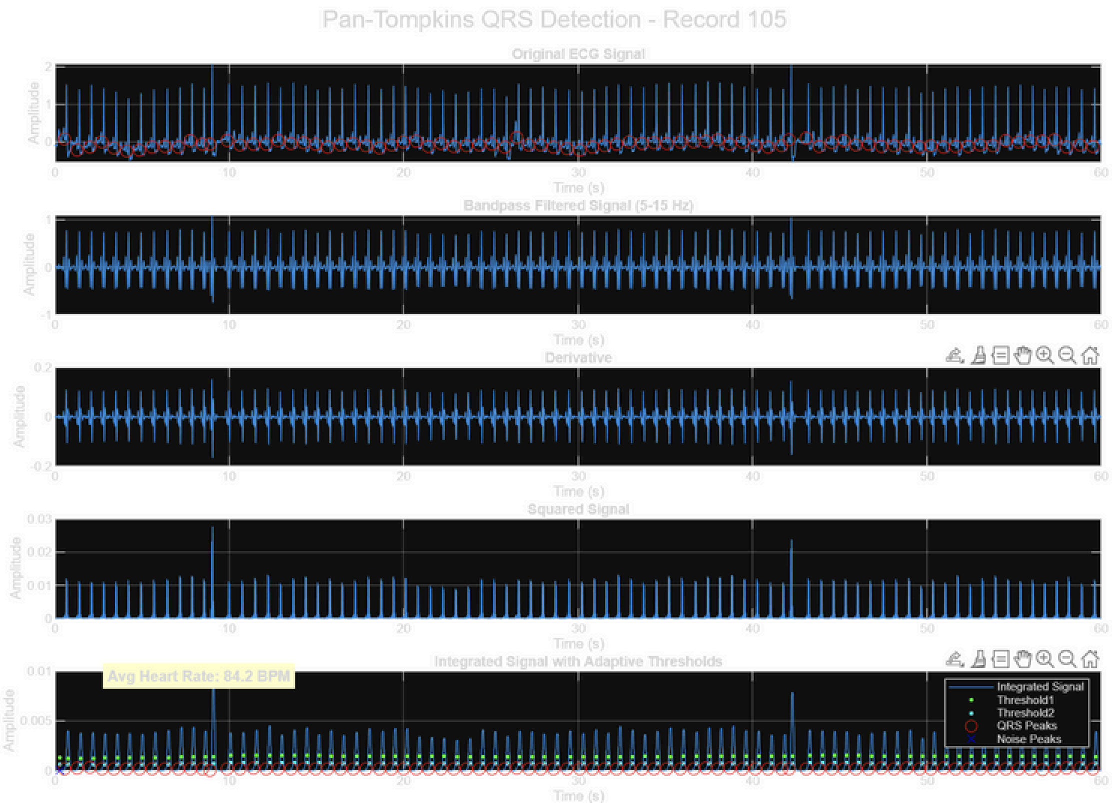

```
Processing record 101 (2 of 6)...
Warning: Could not load annotations. Returning empty annotation structure.
Loaded record 101: 21601 samples at 360 Hz
Warning: No annotations found for record 101
```



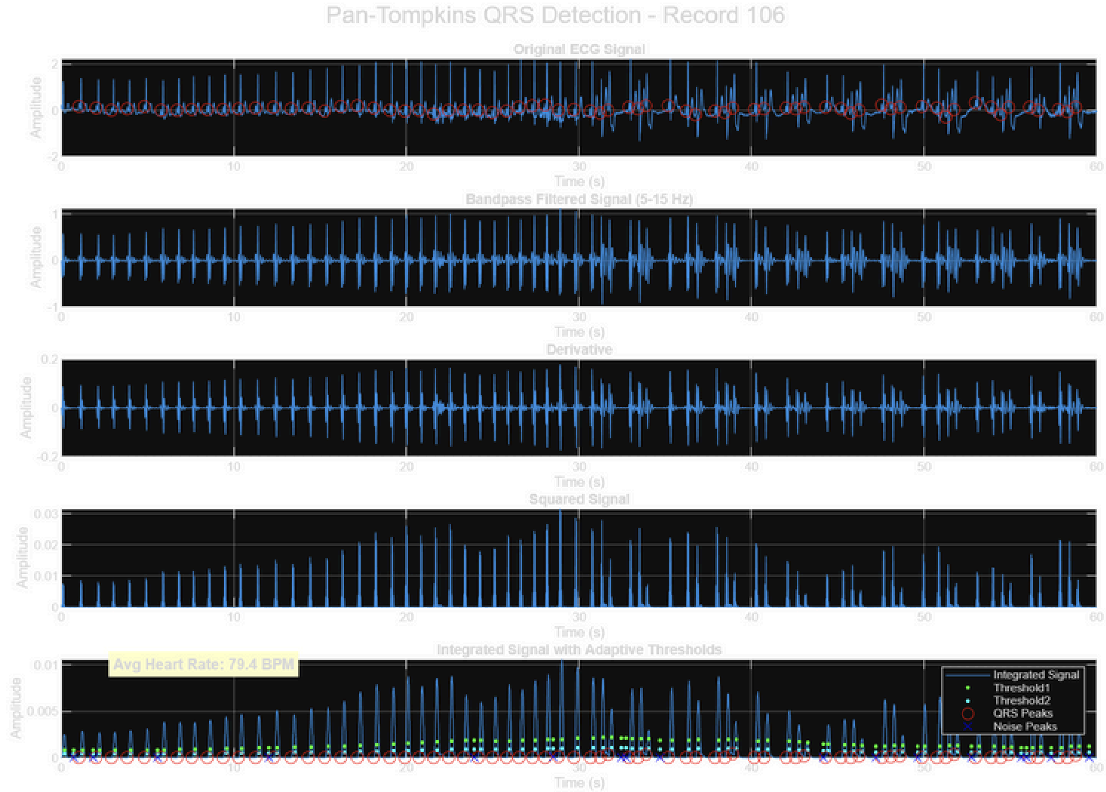
```
Processing record 103 (3 of 6)...
Warning: Could not load annotations. Returning empty annotation structure.
Loaded record 103: 21601 samples at 360 Hz
Warning: No annotations found for record 103
```



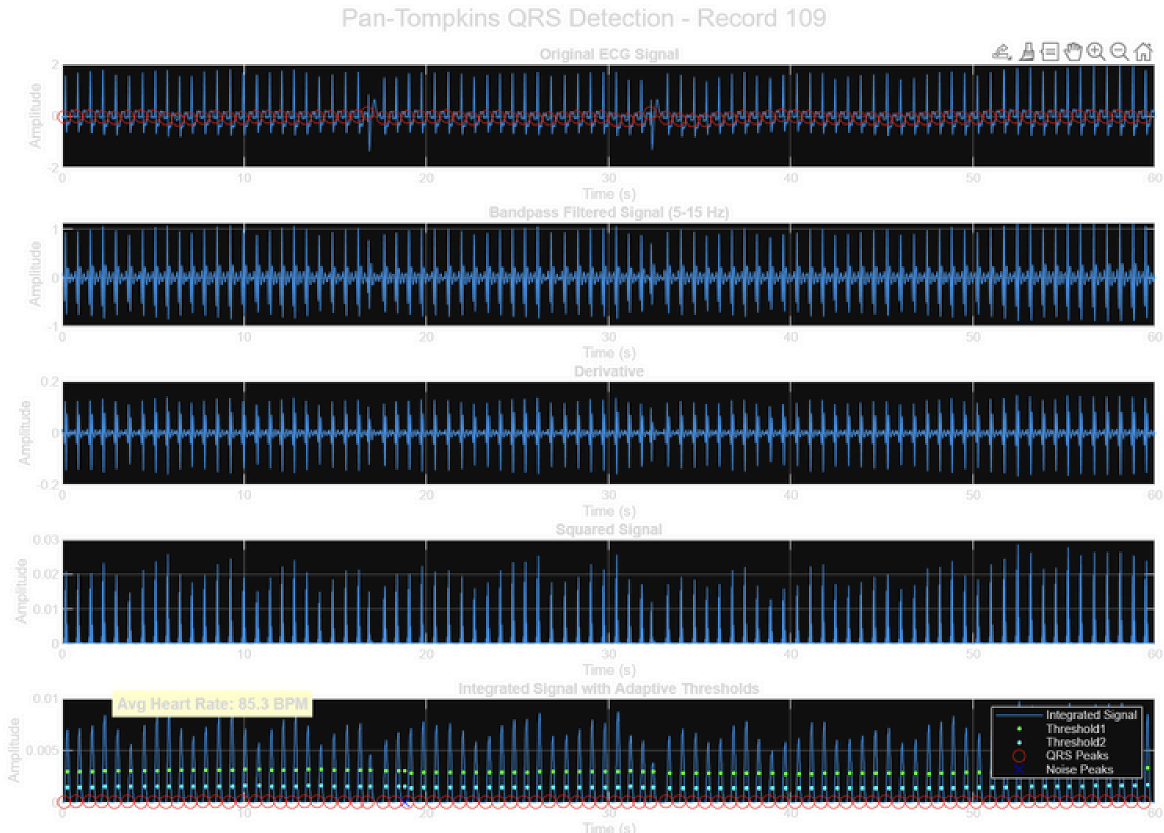

```
Processing record 105 (4 of 6)...
Warning: Could not load annotations. Returning empty annotation structure.
Loaded record 105: 21601 samples at 360 Hz
Warning: No annotations found for record 105
```



```
Processing record 106 (5 of 6)...
Warning: Could not load annotations. Returning empty annotation structure.
Loaded record 106: 21601 samples at 360 Hz
Warning: No annotations found for record 106
```




```
Processing record 109 (6 of 6)...
Warning: Could not load annotations. Returning empty annotation structure.
Loaded record 109: 21601 samples at 360 Hz
Warning: No annotations found for record 109
```



```
%% Summarize overall performance
fprintf('\n===== OVERALL PERFORMANCE =====\n');
===== OVERALL PERFORMANCE =====
if ~isempty(results)
```

```
    % Check if all results have performance fields
    valid_results = arrayfun(@(x) isfield(x, 'performance') &&
 ~isempty(x.performance), results);

    if any(valid_results)
        %   Extract   only   valid   results   that   have   performance   data
        valid_results_idx = find(valid_results); % Use cell arrays to collect
        the        metrics        sensitivity_values        =        cellfun(@(i)
        results(i).performance.sensitivity,

 num2cell(valid_results_idx));
        pp_values = cellfun(@(i) results(i).performance.positive_predictivity,
 num2cell(valid_results_idx));
        f1_values = cellfun(@(i) results(i).performance.F1_score,
 num2cell(valid_results_idx));

        fprintf('Average Sensitivity: %.2f%%\n', mean(sensitivity_values) * 100);
 100);  fprintf('Average Positive Predictivity: %.2f%%\n', mean(pp_values) *
        fprintf('Average F1 Score: %.2f\n', mean(f1_values));
```

```
        fprintf('Based on %d valid records out of %d total records\n',
sum(valid_results), length(results));
    else
    end fprintf('No valid performance results available.\n');

 else
    fprintf('No results available.\n');
 end
 No results available.
```

```
%% Show example with annotations and detections
if ~isempty(results) && length(results) >= 1
    % Select the first record with annotations for visualization
    record_idx = 1;
    % Load the record data again for visualization
    record_num = results(record_idx).record;
    [ecg_signal, ~, annotations] = load_mitbih_record_local(record_num,

lead_number, start_time, duration);

    % Plot ECG with annotations and detections
    t = (0:length(ecg_signal)-1)/fs;
    figure('Name', sprintf('Record %d Annotation Comparison', record_num),

'Position', [100, 100, 1200, 600]);
    plot(t, ecg_signal, 'b');
    hold on;
    % Plot QRS detections
    qrs_peaks = results(record_idx).qrs_peaks;
    plot(qrs_peaks/fs, ecg_signal(qrs_peaks), 'ro', 'MarkerSize', 8,

'LineWidth', 1.5);

    % Plot annotations
    ann_qrs = results(record_idx).annotations;
2); plot(ann_qrs/fs, ecg_signal(ann_qrs), 'gx', 'MarkerSize', 10, 'LineWidth',


    title(sprintf('Record %d: QRS Detection vs Annotations', record_num),
'FontSize', 14);
    xlabel('Time (s)', 'FontSize', 12);
    ylabel('Amplitude', 'FontSize', 12);
    legend('ECG Signal', 'QRS Detections', 'Reference Annotations');
    grid on;
    % Add performance text
    perf = results(record_idx).performance;
    text_str = sprintf(['Sensitivity: %.2f%%\nPositive Predictivity: %.2f%%\n'
...

                       'F1 Score: %.2f'], ...
perf.F1_score);        perf.sensitivity * 100, perf.positive_predictivity * 100,
```

```
    annotation('textbox', [0.15, 0.75, 0.2, 0.15], 'String', text_str, ...
               'EdgeColor', 'none', 'BackgroundColor', [1 1 0.8], ...
               'FontSize', 12, 'FontWeight', 'bold');
end %% ===== LOCAL FUNCTION DEFINITIONS ===== function [qrs_peaks, processed_ecg]
= robust_pan_tompkins_qrs_detector_local(ecg_signal, fs, plot_results) %
ROBUST_PAN_TOMPKINS_QRS_DETECTOR_LOCAL QRS complex detection optimized for MIT-
BIH Database




%   [QRS_PEAKS, PROCESSED_ECG] =
ROBUST_PAN_TOMPKINS_QRS_DETECTOR_LOCAL(ECG_SIGNAL, FS, PLOT_RESULTS)
%   detects QRS complexes in the ECG signal using an enhanced Pan-Tompkins
algorithm.
% Handle input arguments
if nargin < 1

    error('ECG signal is required');
end
if nargin < 2 || isempty(fs)
    fs = 360; % Default sampling frequency for MIT-BIH database
    fprintf('Using default sampling frequency of 360 Hz (MIT-BIH standard)\n');
end if nargin
< 3
    plot_results = true;
end
% Remove NaN and Inf values
ecg_signal(isnan(ecg_signal) | isinf(ecg_signal)) = 0;
% Detrend to remove baseline wandering
ecg_signal = detrend(ecg_signal);
% Parameters for Pan-Tompkins algorithm (optimized for MIT-BIH)



integration_window = round(0.150 * fs);    % 150 ms window
filter_delay = round(0.2 * fs);            % Filter delay compensation
refractory_period = round(0.2 * fs);       % 200 ms refractory period
learning_rate_signal = 0.125;              % Learning rate for signal peak
learning_rate_noise = 0.125;               % Learning rate for noise peak
signal_threshold_weight = 0.25;            % Signal threshold weight
noise_threshold_weight = 0.5;              % Secondary threshold weight
% Initialize output structure
processed_ecg = struct();
processed_ecg.original = ecg_signal;
% ===== STAGE 1: Bandpass Filtering (5-15 Hz) =====
% Create bandpass filter more suitable for MIT-BIH database


lowcut = 5; % 5Hz cutoff for high-pass
highcut = 15; % 15Hz cutoff for low-pass
wn = [lowcut highcut] / (fs/2);
[b, a] = butter(4, wn, 'bandpass');
bandpass_signal = filtfilt(b, a, ecg_signal); % Zero-phase filtering
```

```
processed_ecg.bandpass = bandpass_signal;
% ===== STAGE 2: Derivative ======
% Five-point derivative
b = [1 2 0 -2 -1] * (1/8);
a = 1;
derivative_signal = filter(b, a, bandpass_signal);
processed_ecg.derivative = derivative_signal;
% ===== STAGE 3: Squaring ======
squared_signal = derivative_signal.^2;
processed_ecg.squared = squared_signal;
% ===== STAGE 4: Moving Window Integration ======
b = ones(1, integration_window)/integration_window;
a = 1;
integrated_signal = filter(b, a, squared_signal);
processed_ecg.integrated = integrated_signal;
% ===== STAGE 5: Adaptive Thresholding and Peak Detection ======
% Initialize variables for adaptive thresholding
qrs_peaks = [];
noise_peaks = [];




SPKI = 0; % Signal peak level
NPKI = 0; % Noise peak level
threshold1 = 0; % First threshold
threshold2 = 0; % Second threshold
% Initial learning phase to set thresholds
learn_phase_duration = round(2 * fs); % 2 seconds learning
if length(integrated_signal) >= learn_phase_duration

    learn_segment = integrated_signal(1:learn_phase_duration);
    SPKI = mean(learn_segment) + 2*std(learn_segment);
    NPKI = mean(learn_segment);
    threshold1 = NPKI + signal_threshold_weight * (SPKI - NPKI);
    threshold2 = noise_threshold_weight * threshold1;
end % Store adaptive thresholds for plotting thresholds =
zeros(size(integrated_signal)); thresholds2 =
zeros(size(integrated_signal)); % Find all local maxima in the
integrated signal using a sliding window window_size = round(0.1 * fs);
% 100 ms window peak_candidates = []; peak_values = []; for i =
window_size+1 : length(integrated_signal)-window_size






    window = integrated_signal(i-window_size:i+window_size);
    if integrated_signal(i) == max(window) && integrated_signal(i) > 0
        peak_candidates = [peak_candidates, i];
        peak_values = [peak_values, integrated_signal(i)];
    end
end
```

```
% Process each detected peak candidate
last_qrs = -refractory_period;
threshold_history = zeros(length(peak_candidates), 2);
for i = 1:length(peak_candidates)
loc = peak_candidates(i);
peak_val = peak_values(i);
% Store current thresholds
thresholds(loc) = threshold1;
thresholds2(loc) = threshold2;
threshold_history(i,:) = [threshold1, threshold2];
% Check if this peak is within refractory period
if loc - last_qrs <= refractory_period



        % Update noise peak
        NPKI = learning_rate_noise * peak_val + (1-learning_rate_noise) * NPKI;
        noise_peaks = [noise_peaks, loc];
        continue;
    end
    % Classify peak as QRS or noise
    if peak_val > threshold1

        % This is a QRS complex
        qrs_peaks = [qrs_peaks, loc-filter_delay]; % Compensate for filter delay
        last_qrs = loc;
        % Update signal peak
        SPKI = learning_rate_signal * peak_val + (1-learning_rate_signal) * SPKI;

    else
        % This is likely noise
        noise_peaks = [noise_peaks, loc];
        % Update noise peak
        NPKI = learning_rate_noise * peak_val + (1-learning_rate_noise) * NPKI;
 end  %  Final  check  for  missed  beats  using  RR  interval
 analysis if ~isempty(qrs_peaks)
   end
   % Update thresholds
   threshold1 = NPKI + signal_threshold_weight * (SPKI - NPKI);
   threshold2 = noise_threshold_weight * threshold1;




    % Calculate RR intervals
    RR = diff(qrs_peaks);
    mean_RR = mean(RR);
    missed_beats = [];
    % Check for missed beats (when RR interval is > 1.5x the mean RR)
    for i = 1:length(RR)

        if RR(i) > 1.8 * mean_RR
            % Potential missed beat in this interval
```

```
            search_start = qrs_peaks(i); search_end = qrs_peaks(i+1); % Look for
            possible peaks in this range that were classified as noise for j =
            1:length(noise_peaks)


                if noise_peaks(j) > search_start && noise_peaks(j) < search_end
                    missed_peak_val = integrated_signal(noise_peaks(j));
                    % Check if this peak would pass with a lower threshold
                    if missed_peak_val > 0.5 * threshold1
                        missed_beats = [missed_beats, noise_peaks(j)-

filter_delay];
                    end
                end
            end
        end
    end
    % Add missed beats to QRS peaks
    qrs_peaks = sort([qrs_peaks, missed_beats]);
end % Ensure QRS peak indices are within valid range qrs_peaks =
qrs_peaks(qrs_peaks > 0 & qrs_peaks <= length(ecg_signal)); % Store
results in output structure processed_ecg.qrs_peaks = qrs_peaks;
processed_ecg.threshold1 = thresholds; processed_ecg.threshold2 =
thresholds2; processed_ecg.noise_peaks = noise_peaks; % Plot results if
requested if plot_results









    t = (0:length(ecg_signal)-1)/fs;
    figure('Name', 'Pan-Tompkins QRS Detection', 'NumberTitle', 'off',

'Position', [100, 100, 1200, 800]);

    % Plot original signal
    subplot(5,1,1);
    plot(t, ecg_signal);
    title('Original ECG Signal');
    hold on;
    if ~isempty(qrs_peaks)
        valid_peaks = qrs_peaks(qrs_peaks > 0 & qrs_peaks <= length(ecg_signal));
        plot(valid_peaks/fs, ecg_signal(valid_peaks), 'ro', 'MarkerSize', 8);
    end
    xlabel('Time (s)');
    ylabel('Amplitude');
    grid on;
    % Plot bandpass filtered signal
    subplot(5,1,2);
    plot(t, processed_ecg.bandpass);
    title('Bandpass Filtered Signal (5-15 Hz)');
```

```
    xlabel('Time (s)');
    ylabel('Amplitude');
    grid on;
    % Plot derivative
    subplot(5,1,3);
    plot(t, processed_ecg.derivative);
    title('Derivative');
    xlabel('Time (s)');
    ylabel('Amplitude');
    grid on;
    % Plot squared signal
    subplot(5,1,4);
    plot(t, processed_ecg.squared);
    title('Squared Signal');
    xlabel('Time (s)');
    ylabel('Amplitude');
    grid on;
    % Plot integrated signal with thresholds
    subplot(5,1,5);
    plot(t, processed_ecg.integrated);
    title('Integrated Signal with Adaptive Thresholds');
    hold on;
    % Plot thresholds where they were calculated
    non_zero_idx = find(thresholds > 0);
    if ~isempty(non_zero_idx)




        plot(non_zero_idx/fs, thresholds(non_zero_idx), 'g.', 'MarkerSize', 8);
        plot(non_zero_idx/fs, thresholds2(non_zero_idx), 'c.', 'MarkerSize', 8);
    end
    % Plot detected QRS peaks
    if ~isempty(qrs_peaks)

        valid_peaks = qrs_peaks(qrs_peaks > 0 & qrs_peaks <=
length(processed_ecg.integrated));
        plot(valid_peaks/fs, processed_ecg.integrated(valid_peaks), 'ro',
'MarkerSize', 8);
    end
    % Plot noise peaks
    if ~isempty(noise_peaks)

        valid_noise = noise_peaks(noise_peaks > 0 & noise_peaks <=
length(processed_ecg.integrated));
        plot(valid_noise/fs, processed_ecg.integrated(valid_noise), 'bx',
'MarkerSize', 8);
    end
    legend('Integrated Signal', 'Threshold1', 'Threshold2', 'QRS Peaks', 'Noise

Peaks');
    xlabel('Time (s)');
    ylabel('Amplitude');
    grid on;
```

```
    % Add heart rate display
    if ~isempty(qrs_peaks) && length(qrs_peaks) > 1
        RR = diff(qrs_peaks)/fs;
        HR = 60./RR;
        avg_HR = mean(HR);
        text(0.05, 0.95, sprintf('Avg Heart Rate: %.1f BPM', avg_HR), ...
0.8]);      'Units', 'normalized', 'FontWeight', 'bold', 'BackgroundColor', [1 1

    end
    % Make the figure nicer
    set(gcf, 'Color', 'white');
    sgtitle('Pan-Tompkins QRS Detection Algorithm Results', 'FontSize', 16);
end  end  function  [record_data,  fs,  ann]  =  load_mitbih_record_local(record_num,
lead_num, start_time, duration) % LOAD_MITBIH_RECORD_LOCAL Load ECG data from MIT-
BIH Arrhythmia Database




%   [RECORD_DATA, FS, ANN] = LOAD_MITBIH_RECORD_LOCAL(RECORD_NUM, LEAD_NUM,
START_TIME, DURATION)
%   loads the specified record from the MIT-BIH Arrhythmia Database.

% Check if WFDB Toolbox is installed
if ~exist('rdann', 'file') || ~exist('rdsamp', 'file')
     error(['WFDB Toolbox not found. Please install it from: ' ...
            'https://physionet.org/content/wfdb-matlab/0.10.0/']);
end  %  Handle  default  values  if
nargin < 2 || isempty(lead_num)


    lead_num = 1;
end
if nargin < 3 || isempty(start_time)
    start_time = 0;
end
if nargin < 4
    duration = []; % Empty duration means load the entire record
end  % Construct record name record_name =
sprintf('%03d', record_num); try




    % Convert start_time and duration to samples
    fs = 360; % MIT-BIH sampling frequency
    start_sample = round(start_time * fs);
    if isempty(duration)

        % Load entire record
        [signal, ~, ~] = rdsamp(['mitdb/' record_name], lead_num);
        end_sample = length(signal);
    else
```

```
        end_sample = start_sample + round(duration * fs);
        % Load specified portion of the record
        [signal, ~, ~] = rdsamp(['mitdb/' record_name], lead_num, end_sample,
start_sample);
    end
    % Load annotations
    try

        ann = rdann(['mitdb/' record_name], 'atr', 'from', start_sample, 'to',
end_sample);
        % Adjust annotation indices for the extraction window
        ann.time = ann.time - start_sample;
    catch
        warning('Could not load annotations. Returning empty annotation
structure.');
        ann = struct('time', [], 'type', []);
    end
    % Extract the signal for the specified lead
    record_data = signal;

catch ME

    error(['Error loading record: ', ME.message, '\n', ...
           'Ensure you have downloaded the MIT-BIH database and ', ...
           'it is in your MATLAB path or current directory.']);
end     end     function     [qrs_stats,     detection_performance]     =
evaluate_qrs_detection_local(detected_qrs,  annotation_qrs,  fs,  window_size)
% EVALUATE_QRS_DETECTION_LOCAL Evaluate QRS detection against annotations



%   [QRS_STATS, DETECTION_PERFORMANCE] =
EVALUATE_QRS_DETECTION_LOCAL(DETECTED_QRS, ANNOTATION_QRS, FS, WINDOW_SIZE)
%   evaluates QRS detection performance against reference annotations.

% Default window size is 100 ms if not specified
if nargin < 4 || isempty(window_size)
    window_size = 0.1; % 100 ms
end
% Convert window size from seconds to samples
window_samples = round(window_size * fs);
% Initialize counters
true_positives = 0;
matched_ann = false(size(annotation_qrs));
matched_det = false(size(detected_qrs));
% Loop through annotation QRS complexes
for i = 1:length(annotation_qrs)



    % Find detected QRS within the window
    for j = 1:length(detected_qrs)
        if ~matched_det(j) && abs(detected_qrs(j) - annotation_qrs(i)) <=
window_samples
```

```
            true_positives = true_positives + 1;
            matched_ann(i)        =        true;
            matched_det(j) = true; break;

        end
    end
end    %    Calculate    statistics
false_positives = sum(~matched_det);
false_negatives = sum(~matched_ann);
% Build output structures qrs_stats
= struct(...




    'true_positives', true_positives, ...
    'false_positives', false_positives, ...
    'false_negatives', false_negatives);

% Calculate performance metrics
sensitivity = true_positives / (true_positives + false_negatives);
if (true_positives + false_positives) > 0
    positive_predictivity = true_positives / (true_positives + false_positives);
else
    positive_predictivity = 0;
end
% F1 score
if (sensitivity + positive_predictivity) > 0

    F1_score = 2 * (sensitivity * positive_predictivity) / (sensitivity +
positive_predictivity);
else
    F1_score = 0;
end
detection_performance = struct(...

    'sensitivity', sensitivity, ...
    'positive_predictivity', positive_predictivity, ...
    'F1_score', F1_score);
end
```