BIOE 340 Lab 2

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Introduction:

An electrocardiogram (ECG) is a measurement of the electrical impulses controlling the contractions and relaxations of a cardiac cycle. Abnormalities in the structures and patterns of an ECG can provide insights into abnormal heart function. A healthy heart will display a consistent heart rate and identifiable P, QRS, and T waves (Lab2_ECG Instructions). A specific change in these electrical waves can be used to diagnose a particular disease and identify areas of the heart that are not properly functioning, allowing clinicians to quickly and efficiently treat a patient.

The procedure of an ECG is relatively quick and noninvasive. Sticky electrodes are adhered at certain spots on the chest, arms, and legs, which are then connected to an ECG machine (Electrocardiogram). The machine measures the electrical activity from each lead and prints out a reading of an ECG from each lead. No electricity is actually sent to the body, and the patient is now free to take off the electrodes.

Ventricular Tachycardia (VT) is an abnormal heart rhythm that occurs when the ventricles of the heart beats too fast (defined as 3 or more beats at a rate of 100 beats per minute) and as a result vital tissues cannot receive enough oxygen. VT can include many symptoms including palpitations, chest pain, shortness of breath, and cardiac arrest (Foth 2023). VT is life threatening and is responsible for the majority of sudden cardiac deaths with 300,000 deaths per year in the US (Foth 2023). VT can be diagnosed using the ECG based on the QRS morphology monitored, "VT is divided into monomorphic and polymorphic ventricular tachycardia. Monomorphic VT is characterized by a single, stable QRS morphology with no beat-to-beat variation, while polymorphic VT has beat-to-beat variation in QRS shape and multiple QRS morphologies" (Foth 2023).

Methods:

We first developed MATLAB code based on the sample data provided to construct a graphical representation of the ECG of a healthy patient. We built the model based upon the specifications outlined in the assignment and in the lab lecture to help inform our code. We identified relevant markers in the ECG, such as the QRS complex, heart rate, and MEA that would be used to compare the ECG data between the healthy and diseased patient. After fully constructing our model, we then analyzed the same features in the diseased sample data. We compared the relevant markers in the ECG between healthy and diseased patient, which allowed us to identify physiological differences between the two patients and possible diagnoses related to those differences. These data and visually examining the ECG data allowed us to determine which of the possible diseases could explain those ECG differences.

Results:

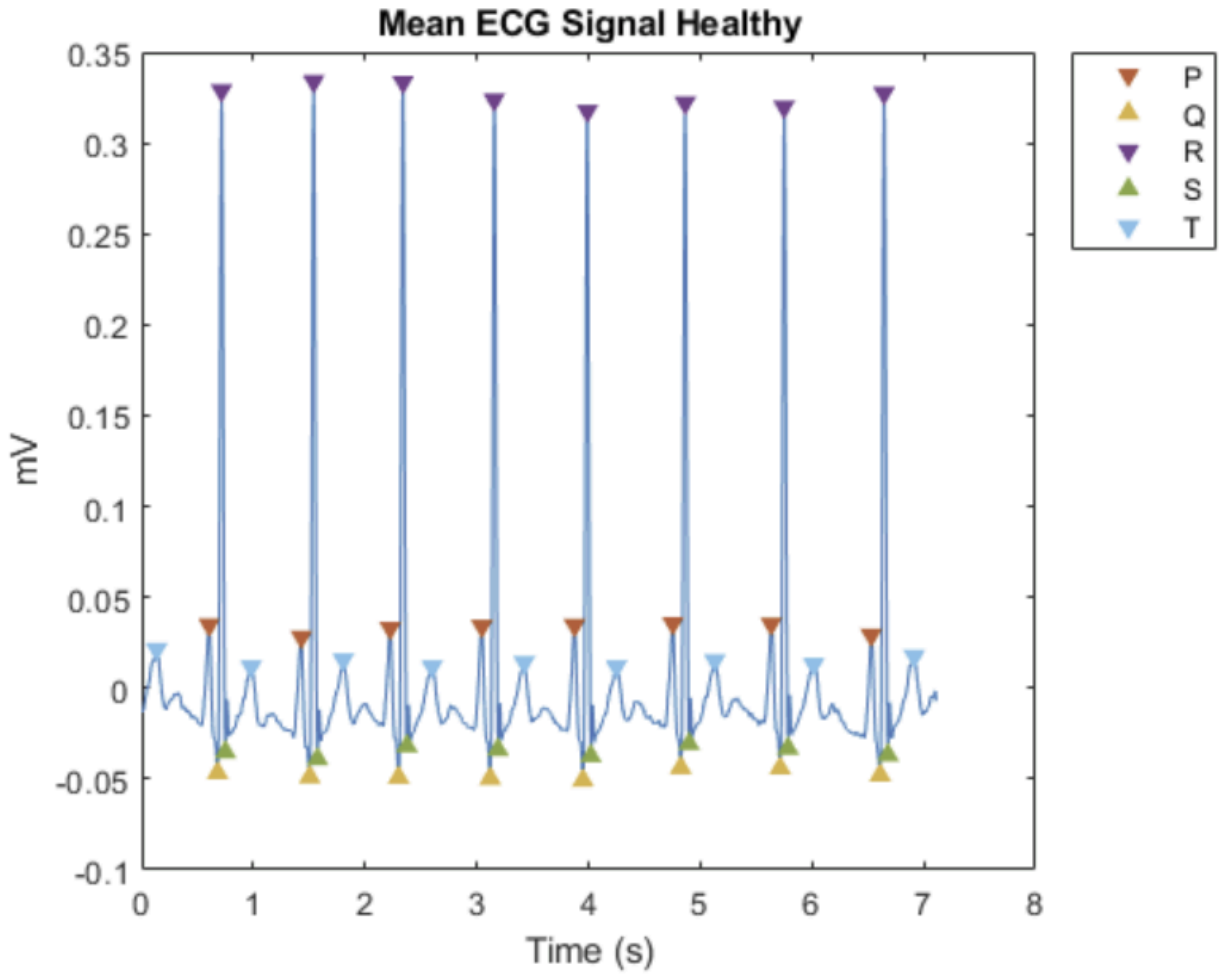

Figure 1. Mean ECG signal over time for a healthy patient.

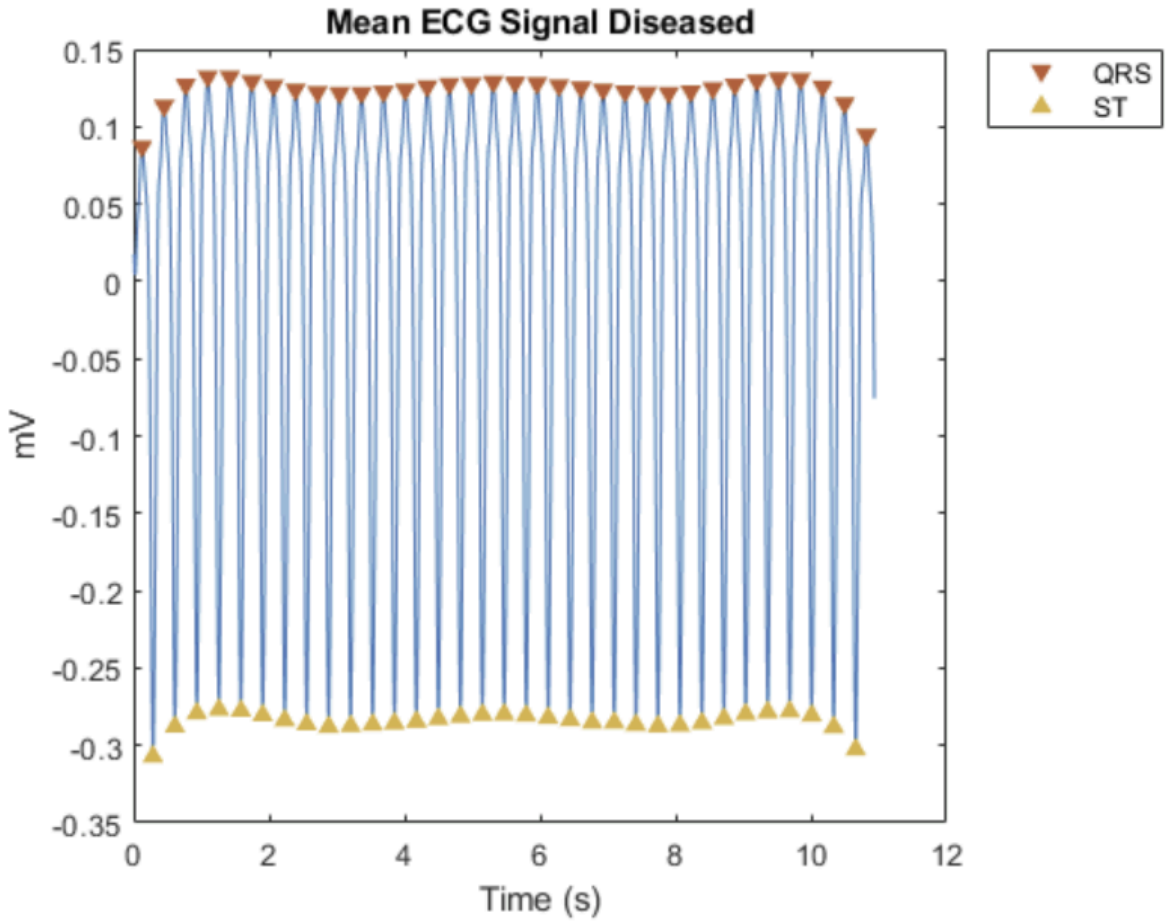

Figure 2. Mean ECG signal over time for a diseased patient with ventricular tachycardia.

Diagnosis	Criteria
High BPM	Measured Heart Rate > 100 bpm
Low BPM	Measured Heart Rate < 60 bpm
Low Voltage	Sum of QRS Voltage < 0.5 mV
High Voltage	Sum of QRS Voltage > 2.0 mV
Prolonged QRS Wave	QRS Interval > 0.08 s
Left Axis Deviation	270 < MEA < 330
Right Axis Deviation	100 < MEA < 180

Extreme Axis Deviation	180 < MEA < 270

Table 1. Criteria and corresponding disease diagnoses.

Type	Healthy State	Diseased State
Measured Heart Rate (bpm)	70.8263	185.2198
Maximum Voltage (mV)	0.3338	0.1323
Minimum Voltage (mV)	-0.0508	-0.3072
Average P-Q Interval (s)	0.0756	N/A
Average P-R Interval (s)	0.1125	N/A
Average Q-T Interval (s)	0.3019	N/A
Mean Electrical Axis (degrees)	80.5383	57.6793

Table 2. Comparison of healthy ECG to diseased (Ventricular Tachycardia) ECG.

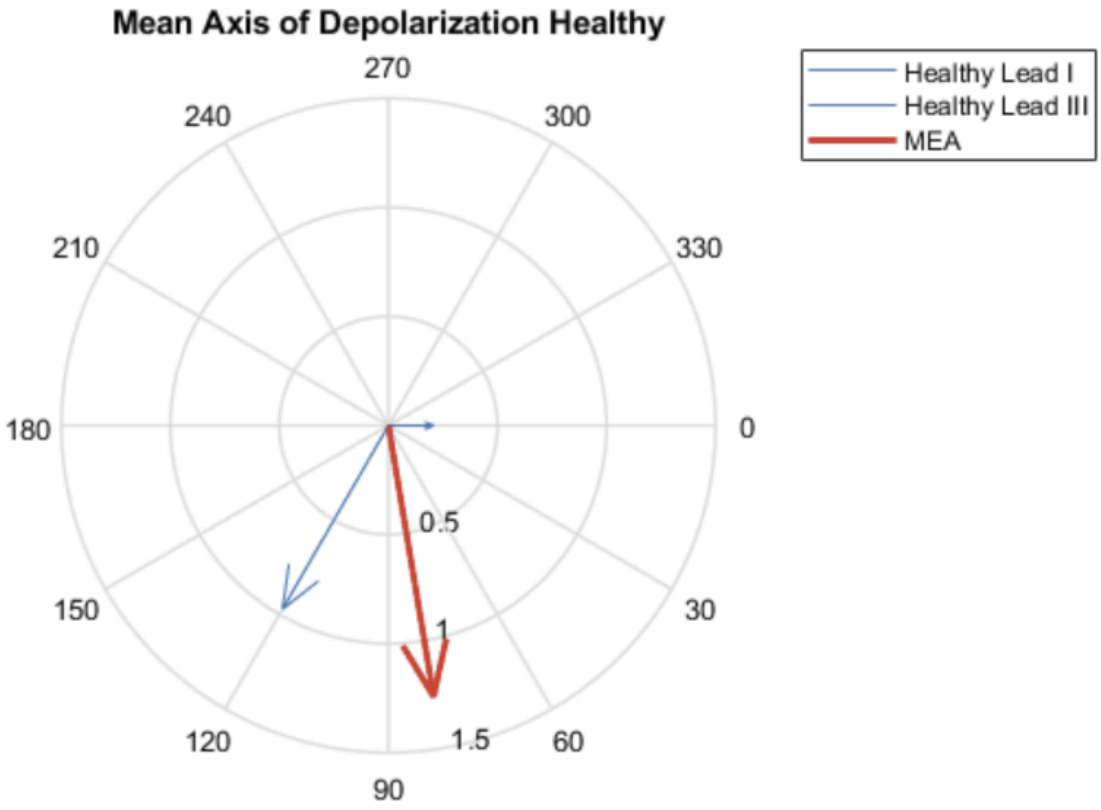

Figure 3. Mean Electrical Axis for a healthy patient.

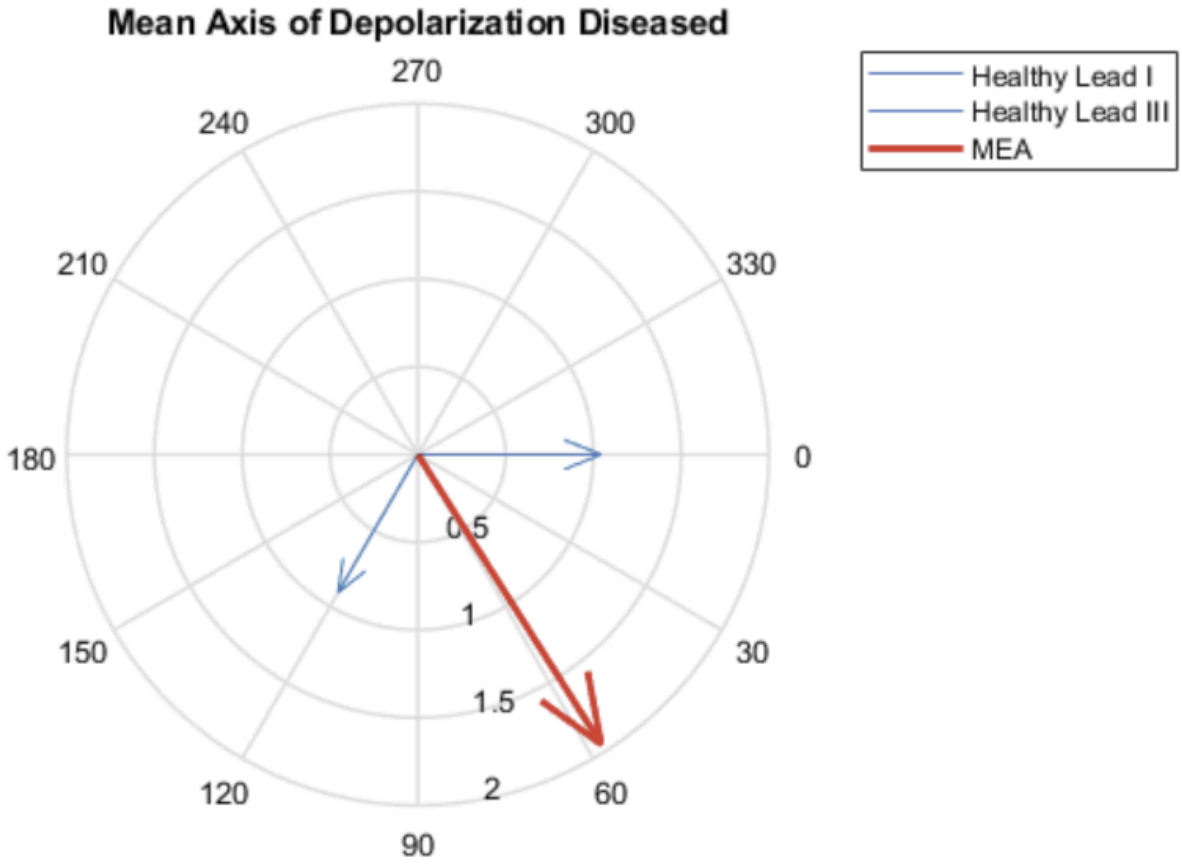

Figure 4. Mean Electrical Axis for a diseased patient with ventricular tachycardia.

Discussion:

An ECG is a graphical representation of the changing electrical activity in the heart. These electrical changes represent contractions of the cardiac muscles to allow blood to circulate throughout the body. The P wave signals the start of atrial contraction, a signal that originates in the sinoatrial (SA) node and spreads to allow the atria to contract and fill the ventricle. The QRS waves occur at the beginning of ventricular contraction, and represent the flow of electrical signal through the atrioventricular (AV) node and bundle. Finally, the T wave signals the end of ventricular contraction and indicates a preparation for the next cardiac cycle (Maisel and Annan).

The sampling frequency used was 200 Hz, representing 200 data points for every second of time that has passed. Sufficiently high frequencies can improve the resolution of the ECG, and specific features of ventricular conduction are only present at specific frequencies (Tereshchenko 2015). Higher frequency sampling is considered more accurate, but ECG machines need to be specially designed to be able to filter out unwanted signals and noise in the readings (N-T 2021).

There are multiple criteria for diagnosing an ECG as healthy or diseased. For a healthy ECG, the heart rate must be in the range of 60 to 100 beats per minute (*2 Easy, Accurate Ways to Measure Your Heart Rate*, n.d.). Also, the sum of the QRS voltages from all of the leads must be inbetween 0.5mV and 2.0mV, and the average QRS interval must be less than 0.08 seconds long (Maisel 2023). For the mean electrical axis, healthy ranges are between -30 and +90 degrees (Kashou 2024).

Anything outside of the ranges specified for the healthy ECG indicate that the ECG is from a diseased patient. Heart rate out of the healthy ranges can be dangerous because they prevent enough blood to be pumped to the rest of the body. This is done by not giving enough time for the ventricles to fill up in the case if ventricular tachycardia or not circulating your blood fast enough in the case of bradycardia. For a heart rate higher than 100 beats per minute, the ECG indicates that the patient has tachycardia, and for heart rates lower than 60 beats per minute, the ECG indicates that the patient has bradycardia (*2 Easy, Accurate Ways to Measure Your Heart Rate*, n.d.). For our data, the heart rate was 185.2, which is indicative of moderate ventricular tachycardia (*Ventricular Tachycardia (VT)*, n.d.).

ECG's with QRS voltages lower than 0.5mV are considered low voltage and indicate diseases such as pericardial fluid buildup, pulmonary emphysema, and previous myocardial infarctions (Maisel 2023). QRS voltage describes the voltage threshold required to depolarize the ventricles and begin ventricular contraction. High voltages greater than 2.0 mV indicate hypertrophy (Maisel 2023). QRS waves longer than 0.08 seconds indicate hypertrophy and dilation if the wave is less than 0.12 seconds long, and if the wave is longer than 0.12 seconds, the ECG indicates that the pation has damage to cardiac muscle or blocks in the Purkinje system (Maisel 2023).

Mean electrical axes that indicate disease are of three types: left axis devating, right axis deviating, or extreme axis deviating. Left axis deviation is between -90 and -30 degrees. This deviation indicates left ventricular hypertrophy, conduction defects in the left bundle branch or left anterior fascicular block, inferior wall myocardial infarction, preexcitation syndromes, ventricular ectopic rhythms, congenital heart disease, hyperkalemia, emphysema, or mechanical shifts (Kashou 2024). Right axis deviation is between 100 and 180 degrees. RAD indicates right ventricular overload, right ventricular hypertrophy, conduction defects in the left posterior fasicuar block or the right bundle branch block, lateral wall myocardial infarction, preexitation syndromes, ventricular ectopic rhythms, congenital heart disease, dextrocardia, left pneumothorax, or mechanical shifts (Kashou 2024). Extreme axis deviation is between 180 and -90 degrees and indicates ventricular ectopic rhythms, hyperkalemia, or emphysema (*Extreme Axis Deviation*, n.d.).

The outputs reported in the results section seem accurate and realistic. The healthy ECG satisfies all of the checkpoints listed above, having a normal heart rate, QRS voltage sum, QRS wave duration, and mean electrical axis. The diseased data on the other hand indicates that there are problems with the patients heart related to a high heart rate, low voltage, and a prolonged QRS wave (longer than 0.12 seconds). The high heart rate specifically indicates that there is

ventricular tachycardia occurring. And low voltages and prolonged QRS waves indicate that there are conduction issues in the patient's heart.

References:

2 easy, accurate ways to measure your heart rate. (n.d.). Mayo Clinic. Retrieved March 13, 2024, from https://www.mayoclinic.org/healthy-lifestyle/fitness/expert-answers/heart-rate/faq-20057979

"Electrocardiogram." *Johns Hopkins Medicine*, 8 Aug. 2021.

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Foth C, Gangwani MK, Ahmed I, et al. Ventricular Tachycardia. [Updated 2023 Jul 30]. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; 2024 Jan-. Available from: https://www.ncbi.nlm.nih.gov/books/NBK532954/

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N-T, Byun G-s. The Comparison Features of ECG Signal with Different Sampling Frequencies and Filter Methods for Real-Time Measurement. Symmetry. 2021; 13(8):1461. https://doi.org/10.3390/sym13081461

Tereshchenko LG, Josephson ME. Frequency content and characteristics of ventricular conduction. J Electrocardiol. 2015;48(6):933-937. doi:10.1016/j.jelectrocard.2015.08.034

Ventricular tachycardia (VT): ECG criteria, causes, classification, treatment. (n.d.). Cardiovascular Education. Retrieved March 13, 2024, from https://ecgwaves.com/topic/ventricular-tachycardia-vt-ecg-treatment-causes-management/

Supplemental Figures:

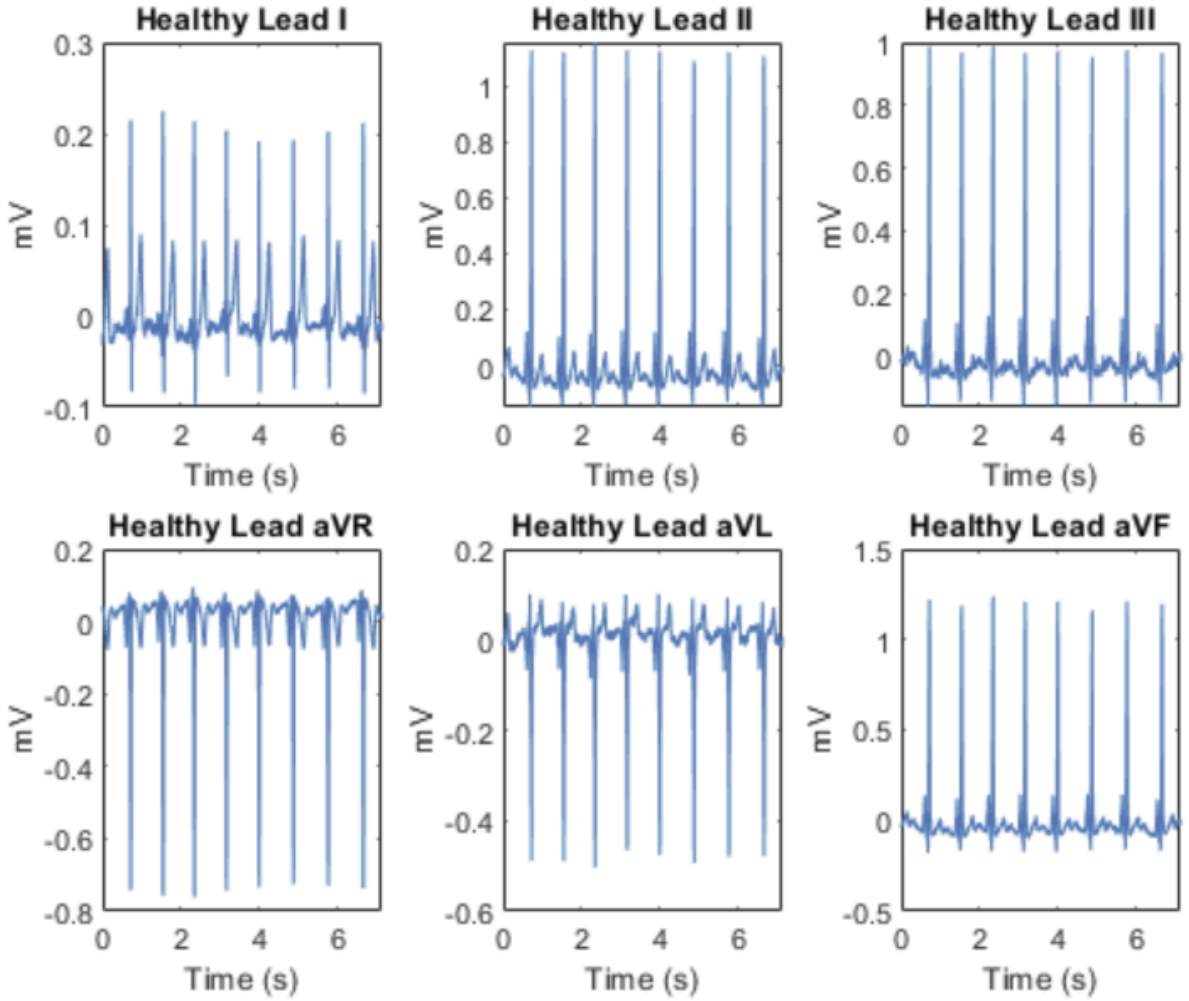

Figure 5. Individual ECG lead signals over time of a healthy patient.

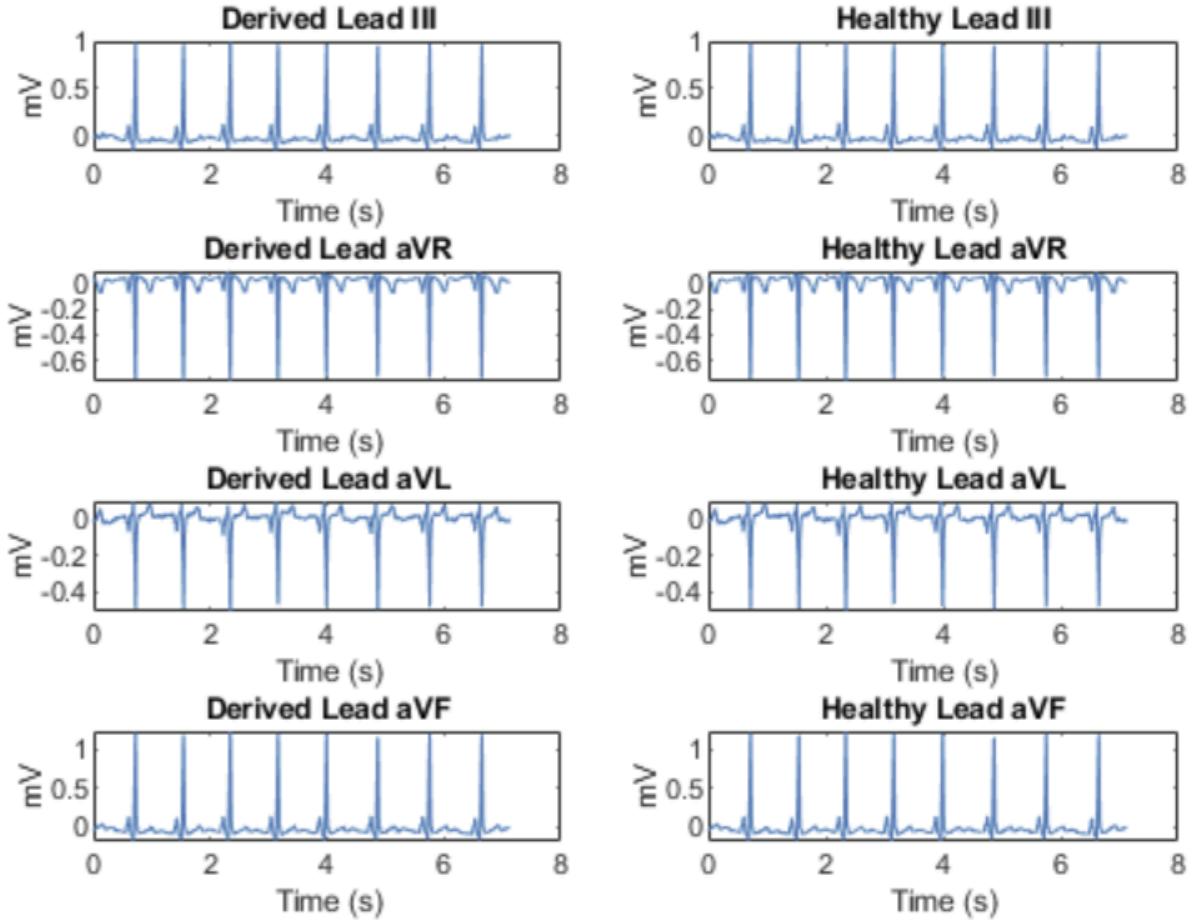

Figure 6. Comparison of the derived Leads III, aVR, aVL, and aVF from Lead I and II to the actual readings.

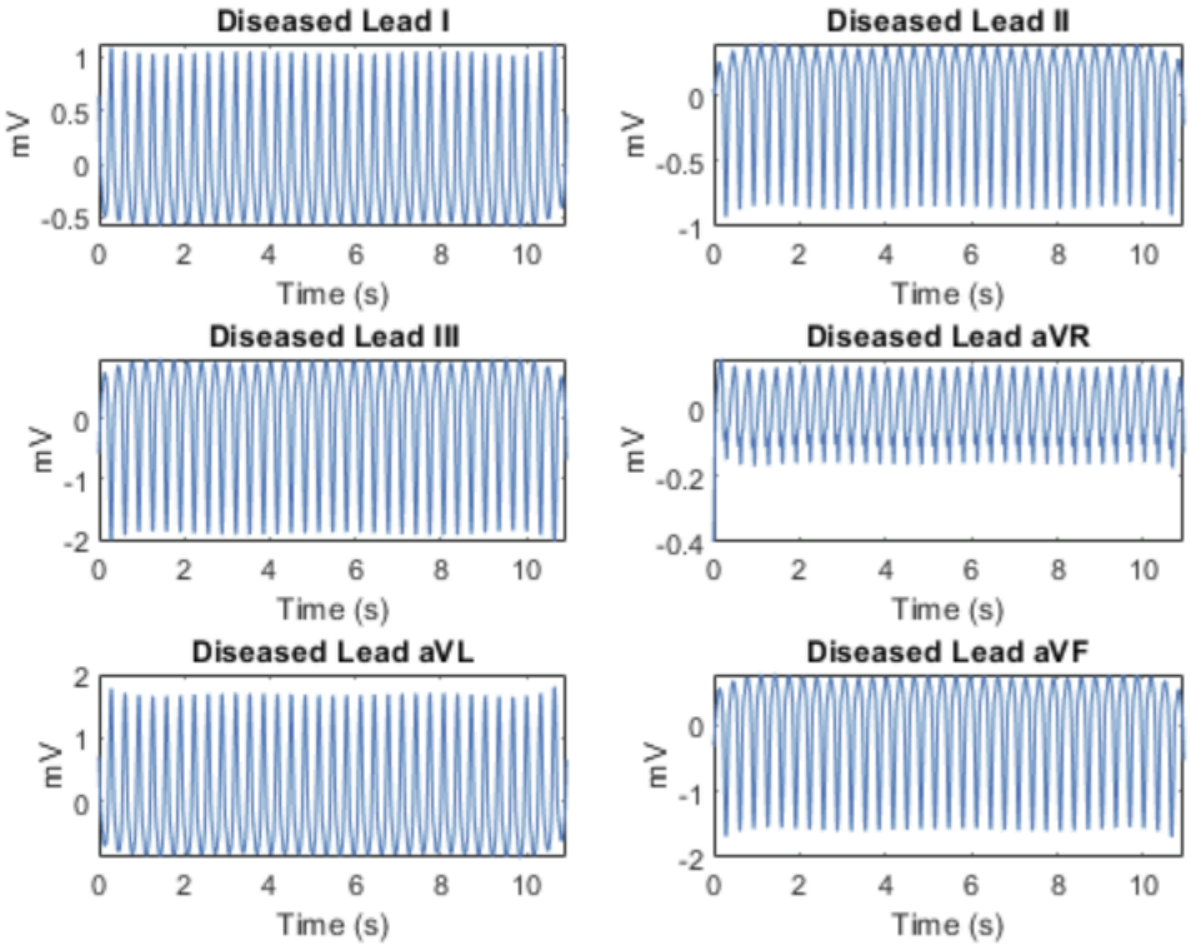

Figure 7. Individual ECG lead signals over time of a diseased patient with ventricular tachycardia.

Appendix:
MATLAB code used to analyze ECG.

```
%% Part 1
clear; clc; close all
% Import healthy data
healthy = readtable("Lab2_Healthy_Data_ECG.xlsx");
healthy_time = healthy.Time;
healthy_leadI = healthy.LeadI./1000;
healthy_leadII = healthy.LeadII./1000;
healthy_leadIII = healthy.LeadIII./1000;
healthy_aVR = healthy.aVR./1000;
healthy_aVL = healthy.aVL./1000;
```

```
healthy_aVF = healthy.aVF./1000;
% Detrend healthy data
healthy_leads =
[healthy_leadI,healthy_leadII,healthy_leadIII,healthy_aVR,healthy_aVL,healthy_aVF];
detrend_healthy_leads = [];
for i = 1:6
  [p1, ~, mu1] = polyfit(healthy_time,healthy_leads(:,i),7);
  detrend_healthy_leads(:,end+1) = healthy_leads(:,i) - polyval(p1, healthy_time, [], mu1);
end
% Plot ECG data
figure(Name = '6-Lead ECG Healthy')
subplot_titles_1 = ["Healthy Lead I","Healthy Lead II","Healthy Lead III","Healthy Lead
aVR","Healthy Lead aVL","Healthy Lead aVF"];
for i = 1:6
  subplot(2,3,i)
  plot(healthy_time,detrend_healthy_leads(:,i))
  title(subplot_titles_1(i))
  xlabel('Time (s)')
  ylabel('mV')
end
% Derive LeadIII, aVF, aVL, aVR
Cal_LeadIII = detrend_healthy_leads(:,2) - detrend_healthy_leads(:,1);
Cal_aVF = ((2.*detrend_healthy_leads(:,2))-detrend_healthy_leads(:,1))./(sqrt(3));
Cal_aVL = ((2.*detrend_healthy_leads(:,1))-detrend_healthy_leads(:,2))./(sqrt(3));
Cal_aVR = -(detrend_healthy_leads(:,2)+detrend_healthy_leads(:,1))./(sqrt(3));
a = isequal(Cal_LeadIII,detrend_healthy_leads(:,3))
% Compare derived leads to actual
figure(Name = 'Derived 6-Lead ECG')
compare_derived =
[Cal_LeadIII,detrend_healthy_leads(:,3),Cal_aVR,detrend_healthy_leads(:,4),Cal_aVL,detrend_
healthy_leads(:,5),Cal_aVF,detrend_healthy_leads(:,6)];
subplot_titles_2 = ["Derived Lead III","Healthy Lead III","Derived Lead aVR","Healthy Lead
aVR","Derived Lead aVL","Healthy Lead aVL","Derived Lead aVF","Healthy Lead aVF"];
for i = 1:8
  subplot(4,2,i)
  plot(healthy_time,compare_derived(:,i))
  title(subplot_titles_2(i))
  xlabel('Time (s)')
  ylabel('mV')
end
```

```
for i = 1:2:8
  b = isequal(compare_derived(:,i),compare_derived(:,i+1))
end
%% Part 2
% Average leads/detrend data
average_healthy_lead = mean(detrend_healthy_leads,2);
[p2, ~, mu2] = polyfit(healthy_time,average_healthy_lead,7);
detrend_avg_healthy = average_healthy_lead - polyval(p2, healthy_time, [], mu2);
smoothECG_healthy = sgolayfilt(detrend_avg_healthy,7,21);
% Initialize PQRST arrays
P_peaks_healthy = [];
P_locs_healthy = [];
Q_peaks_healthy = [];
Q_locs_healthy = [];
T_peaks_healthy = [];
T_locs_healthy = [];
S_peaks_healthy = [];
S_locs_healthy = [];
R_peaks_healthy = [];
R_locs_healthy = [];
% Find P, R, and T
[PRT_peaks_healthy,PRT_locs_healthy] =
findpeaks(smoothECG_healthy,NPeaks=25,MinPeakHeight=0.01,MinPeakDistance=20);
for i = 1:length(PRT_peaks_healthy)
  if mod(i-1,3) == 0
     T_peaks_healthy(end+1) = PRT_peaks_healthy(i);
     T_locs_healthy(end+1) = PRT_locs_healthy(i);
  elseif  mod(i-2,3) == 0
     P_peaks_healthy(end+1) = PRT_peaks_healthy(i);
     P_locs_healthy(end+1) = PRT_locs_healthy(i);
  else
     R_peaks_healthy(end+1) = PRT_peaks_healthy(i);
     R_locs_healthy(end+1) = PRT_locs_healthy(i);
  end
end
% Find Q and S
[QS_peaks_healthy,QS_locs_healthy] =
findpeaks(-smoothECG_healthy,MinPeakHeight=0.020,MinPeakProminence=0.03);
for i = 1:length(QS_peaks_healthy)
  if mod(i-2,3) == 0
```

```
        Q_peaks_healthy(end+1) = -QS_peaks_healthy(i);
        Q_locs_healthy(end+1) = QS_locs_healthy(i);
    elseif mod(i,3) == 0
        S_peaks_healthy(end+1) = -QS_peaks_healthy(i);
        S_locs_healthy(end+1) = QS_locs_healthy(i);
    end
end

% Plot PQRTS
figure(Name = 'PQRST Plot')
plot(healthy_time,smoothECG_healthy,'-');
hold on
scatter(healthy_time(P_locs_healthy),P_peaks_healthy,'v','filled');
scatter(healthy_time(Q_locs_healthy),Q_peaks_healthy,'^','filled');
scatter(healthy_time(R_locs_healthy),R_peaks_healthy,'v','filled');
scatter(healthy_time(S_locs_healthy),S_peaks_healthy,'^','filled');
scatter(healthy_time(T_locs_healthy),T_peaks_healthy,'v','filled');
legend('','P','Q','R','S','T');
xlabel('Time (s)');
ylabel('mV');
title('Mean ECG Signal Healthy')
% Measure Heart Rate
RR_int_healthy = [];
for i = 1:length(S_locs_healthy)-1
    RR_int_healthy(end+1) =
healthy_time(R_locs_healthy(i+1))-healthy_time(R_locs_healthy(i));
end
average_RR_int_healthy = mean(RR_int_healthy);
bpm_healthy = 60/average_RR_int_healthy
% Maximum and Minimum
healthy_max = max(smoothECG_healthy)
healthy_min = min(smoothECG_healthy)
% Average Interval Calculations
average_PQ_int_healthy = mean(healthy_time(Q_locs_healthy)-healthy_time(P_locs_healthy))
average_PR_int_healthy = mean(healthy_time(R_locs_healthy)-healthy_time(P_locs_healthy))
average_QT_int_healthy =
mean(healthy_time(T_locs_healthy(2:end))-healthy_time(Q_locs_healthy))
% MEA
[peaks_healthy_I,~] =
findpeaks(detrend_healthy_leads(:,1),MinPeakHeight=0.15,MinPeakDistance=20);
```

```
[peaks_healthy_III,~] =
findpeaks(detrend_healthy_leads(:,3),MinPeakHeight=0.3,MinPeakDistance=20);
x1_healthy = mean(peaks_healthy_I)*cosd(0);
y1_healthy = mean(peaks_healthy_I)*sind(0);
x2_healthy = mean(peaks_healthy_III)*cosd(120);
y2_healthy = mean(peaks_healthy_III)*sind(120);
slope_healthy = tand(120);
slope_tang_healthy = -1/slope_healthy;
y3_healthy = slope_tang_healthy*(x1_healthy-x2_healthy)+y2_healthy;
magnitude_healthy = sqrt(x1_healthy^2 + y3_healthy^2);
dir_healthy = atan2d(y3_healthy,x1_healthy)
figure(Name = 'Mean Axis of Depolarization')
c_healthy =
compass([x1_healthy,x2_healthy,magnitude_healthy*cosd(dir_healthy)],[y1_healthy,y2_healthy,
magnitude_healthy*sind(dir_healthy)]);
c_healthy(3).LineWidth = 2;
c_healthy(3).Color = 'r';
view(0,-90)
title('Mean Axis of Depolarization Healthy')
legend('Healthy Lead I','Healthy Lead III','MEA')
% Data for report
healthy_data =
{bpm_healthy,healthy_max,healthy_min,average_PQ_int_healthy,average_PR_int_healthy,avera
ge_QT_int_healthy,dir_healthy};
%% Part 3 (Written Specifically for Ventricular Tachycardia)
% Criteria for peaks from:
%
https://ecgwaves.com/topic/ventricular-tachycardia-vt-ecg-treatment-causes-management/#:~:tex
t=ECG%20features%20of%20ventricular%20tachycardia,-%E2%89%A53%20consecutive&text
=Ventricular%20tachycardia%20with%20rate%20100,%E2%89%A50%2C12%20s).
diseased = readtable("Lab2_Disease_Data_ECG.xlsx");
diseased_time = diseased.Time;
diseased_LeadI = diseased.LeadI;
diseased_LeadII = diseased.LeadII;
diseased_LeadIII = diseased.LeadIII;
diseased_aVR = diseased.aVR;
diseased_aVL = diseased.aVL;
diseased_aVF = diseased.aVF;
diseased_leads =
[diseased_LeadI,diseased_LeadII,diseased_LeadIII,diseased_aVR,diseased_aVL,diseased_aVF];
```

```
detrend_diseased_leads = [];
for i = 1:6
  [p3, ~, mu3] = polyfit(diseased_time,diseased_leads(:,i),7);
  detrend_diseased_leads(:,end+1) = diseased_leads(:,i) - polyval(p3, diseased_time, [], mu3);
end
figure
subplot_titles_2 = ["Diseased Lead I","Diseased Lead II","Diseased Lead III","Diseased Lead
aVR","Diseased Lead aVL","Diseased Lead aVF"];
for i = 1:6
  subplot(3,2,i)
  plot(diseased_time,detrend_diseased_leads(:,i))
  title(subplot_titles_2(i))
  xlabel('Time (s)')
  ylabel('mV')
end
% Average leads/detrend data
average_diseased_lead = mean(detrend_diseased_leads,2);
[p4, ~, mu4] = polyfit(diseased_time,average_diseased_lead,7);
detrend_avg_diseased = average_diseased_lead - polyval(p4, diseased_time, [], mu4);
smoothECG_diseased = sgolayfilt(detrend_avg_diseased,7,21);
% Find QRS peaks and ST peaks
[QRS_peaks_diseased,QRS_locs_diseased] =
findpeaks(smoothECG_diseased,MinPeakHeight=0.01,MinPeakDistance=20);
[ST_peaks_diseased,ST_locs_diseased] =
findpeaks(-smoothECG_diseased,MinPeakHeight=0.020,MinPeakProminence=0.03);

figure(Name = 'PQRST Plot')
plot(diseased_time,smoothECG_diseased,'-');
hold on
scatter(diseased_time(QRS_locs_diseased),QRS_peaks_diseased,'v','filled');
scatter(diseased_time(ST_locs_diseased),-ST_peaks_diseased,'^','filled');
legend('','QRS','ST');
xlabel('Time (s)');
ylabel('mV');
xlabel('Time (s)');
ylabel('mV');
title('Mean ECG Signal Diseased')
% Measured Heart Rate
RR_int_diseased = [];
for i = 1:length(QRS_locs_diseased)-1
```

```
  RR_int_diseased(end+1) =
diseased_time(QRS_locs_diseased(i+1))-diseased_time(QRS_locs_diseased(i));
end
average_RR_int_diseased = mean(RR_int_diseased);
bpm_diseased = 60/average_RR_int_diseased
% Maximum and Minimum
diseased_max = max(smoothECG_diseased)
diseased_min = min(smoothECG_diseased)
% Average Interval Calculations (NO Specific P, Q, R, S, T peaks)
% % average_PQ_int_diseased =
mean(diseased_time(Q_locs_diseased)-diseased_time(P_locs_diseased))
% % average_PR_int_diseased =
mean(diseased_time(R_locs_diseased)-diseased_time(P_locs_diseased))
% % average_QT_int_diseased =
mean(diseased_time(T_locs_diseased(2:end))-diseased_time(Q_locs_diseased))
% MEA
[peaks_diseased_I,~] =
findpeaks(detrend_diseased_leads(:,1),MinPeakHeight=0.15,MinPeakDistance=20);
[peaks_diseased_III,~] =
findpeaks(detrend_diseased_leads(:,3),MinPeakHeight=0.3,MinPeakDistance=20);
x1_diseased = mean(peaks_diseased_I)*cosd(0);
y1_diseased = mean(peaks_diseased_I)*sind(0);
x2_diseased = mean(peaks_diseased_III)*cosd(120);
y2_diseased = mean(peaks_diseased_III)*sind(120);
slope_diseased = tand(120);
slope_tang_diseased = -1/slope_diseased;
y3_diseased = slope_tang_diseased*(x1_diseased-x2_diseased)+y2_diseased;
magnitude_diseased = sqrt(x1_diseased^2 + y3_diseased^2);
dir_diseased = atan2d(y3_diseased,x1_diseased)
figure(Name = 'Mean Axis of Depolarization Diseased')
c_diseased =
compass([x1_diseased,x2_diseased,magnitude_diseased*cosd(dir_diseased)],[y1_diseased,y2_di
seased,magnitude_diseased*sind(dir_diseased)]);
c_diseased(3).LineWidth = 2;
c_diseased(3).Color = 'r';
view(0,-90)
title('Mean Axis of Depolarization Diseased')
legend('Healthy Lead I','Healthy Lead III','MEA')
% Data for report
diseased_data = {bpm_diseased,diseased_max,diseased_min,"N/A","N/A","N/A",dir_diseased};
```

```
%% Diagnosis
% Find Voltages
[peaks1,locs1] =
findpeaks(detrend_diseased_leads(:,1),MinPeakHeight=0.15,MinPeakDistance=20);
[peaks2,locs2] =
findpeaks(detrend_diseased_leads(:,2),MinPeakHeight=0.15,MinPeakDistance=20);
[peaks3,locs3] =
findpeaks(detrend_diseased_leads(:,3),MinPeakHeight=0.15,MinPeakDistance=20);
[npeaks1,nlocs1] =
findpeaks(-detrend_diseased_leads(:,1),MinPeakHeight=0.15,MinPeakDistance=20);
[npeaks2,nlocs2] =
findpeaks(-detrend_diseased_leads(:,2),MinPeakHeight=0.15,MinPeakDistance=20);
[npeaks3,nlocs3] =
findpeaks(-detrend_diseased_leads(:,3),MinPeakHeight=0.15,MinPeakDistance=20);
v1 = [];
v2 = [];
v3 = [];
for i = 1:length(peaks1)
  if mod(i,3) == 0
      v1(end+1) = peaks1(i) - npeaks1(i);
      v2(end+1) = peaks2(i) - npeaks2(i);
      v3(end+1) = peaks3(i) - npeaks3(i);
  end
end
sum_QRS_voltage = mean(v1) + mean(v2) + mean(v3)
QRS_int_diseased = [];
for i = 1:length(ST_locs_diseased)-1
  QRS_int_diseased(end+1) =
diseased_time(ST_locs_diseased(i+1))-diseased_time(ST_locs_diseased(i));
end
average_QRS_int_diseased = mean(QRS_int_diseased)
issues = string();
possible_diseases = string();
% Heart Rate Check
if bpm_diseased > 100
  issues(end+1) = "High BPM";
  possible_diseases(end+1) = "Tachycardia";
elseif bpm_diseased < 60
  issues(end+1) = "Low BPM";
  possible_diseases(end+1) = "Bradycardia";
```

```
end
% Voltage Check
if sum_QRS_voltage < 0.5
   issues(end+1) = "Low Voltage";
   possible_diseases(end+1) = "Pericardial fluid buildup";
   possible_diseases(end+1) = "Pulmonary emphysema";
   possible_diseases(end+1) = "Previous myocardial infarctions/diminished cardiac muscle
mass";
elseif sum_QRS_voltage >2.0
   issues(end+1) = "High Voltage";
   possible_diseases(end+1) = "Hypertrophy (High Voltage)";
end
% QRS Wave Check
if average_QRS_int_diseased > 0.08
   issues(end+1) = "Prolonged QRS Wave";
   if average_QRS_int_diseased <= 0.12
      possible_diseases(end+1) = "Hypertrophy (Prolonged QRS Wave)";
      possible_diseases(end+1) = "Dilation";
   elseif average_QRS_int_diseased > 0.12
      possible_diseases(end+1) = "Damage to cardiac muscle";
      possible_diseases(end+1) = "Blocks in the Purkinje system";
   end
end
% MEA Check
if dir_diseased >= 270 && dir_diseased <= 330
   issues(end+1) = "Left Axis Deviation (LAD)";
   possible_diseases(end+1) = "Left ventricular hypertrophy";
   possible_diseases(end+1) = "Conduction defects: left bundle branch block, left anterior
fascicular block";
   possible_diseases(end+1) = "Inferior wall myocardial infarction";
   possible_diseases(end+1) = "Preexcitation syndromes (LAD)";
   possible_diseases(end+1) = "Ventricular ectopic rhythms (LAD)";
   possible_diseases(end+1) = "Congenital heart disease (eg, primum atrial septal defect,
endocardial cushion defect)";
   possible_diseases(end+1) = "Hyperkalemia (LAD)";
   possible_diseases(end+1) = "Emphysema (LAD)";
   possible_diseases(end+1) = "Mechanical shift, such as with expiration or raised diaphragm";
elseif dir_diseased >= 110 && dir_diseased <= 180
   issues(end+1) = "Right Axis Deviation (RAD)";
   possible_diseases(end+1) = "Right ventricular overload syndromes";
```

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    possible_diseases(end+1) = "Right ventricular hypertrophy";
    possible_diseases(end+1) = "Conduction defects: left posterior fascicular block, right bundle
branch block";
    possible_diseases(end+1) = "Lateral wall myocardial infarction";
    possible_diseases(end+1) = "Preexcitation syndromes (RAD)";
    possible_diseases(end+1) = "Ventricular ectopic rhythms (RAD)";
    possible_diseases(end+1) = "Congenital heart disease (eg, secundum atrial septal defect)";
    possible_diseases(end+1) = "Dextrocardia";
    possible_diseases(end+1) = "Left pneumothorax";
    possible_diseases(end+1) = "Mechanical shift, such as with inspiration or emphysema";
elseif dir_diseased > 180 && dir_diseased < 270
    issues(end+1) = "Extreme Axis Deviation (EAD)";
    possible_diseases(end+1) = "Ventricular ectopic rhythms (EAD)";
    possible_diseases(end+1) = "Hyperkalemia (EAD)";
    possible_diseases(end+1) = "Emphysema (EAD)";
end
if isempty(issues) == true
    fprintf('Patient is healthy.\n')
else
    fprintf('Issues:\n')
    fprintf('%s\n',issues(2:end))
    fprintf('\nPossible Diseases:\n')
    fprintf('%s\n',possible_diseases(2:end))
end
%% Tables for report
filename = 'Lab2_report_table.xlsx';
rownames = ["Measured Heart Rate (bpm)","Maximum Voltage (mV)","Minimum Voltage
(mV)"...
    ,"Average P-Q Interval (s)","Average P-R Interval (s)","Average Q-T Interval (s)","Mean
Electrical Axis (degrees)"];
T = table(rownames',healthy_data.',diseased_data');
T.Properties.Description = 'Table for report';
T.Properties.VariableNames = ["Type","Healthy State","Diseased State"];
T.Properties.RowNames = rownames;
writetable(T,filename,'Sheet','Data');
filename2 = 'Lab2_diagnostic_criteria.xlsx';
diagnosis = ["High BPM","Low BPM","Low Voltage","High Voltage","Prolonged QRS
Wave",...
    "Left Axis Deviation","Right Axis Deviation","Extreme Axis Deviation"]
criteria = ["Measured Heart Rate > 100 bpm","Measured Heart Rate < 60 bpm",...
```

```
    "Sum of QRS Voltage < 0.5 mV","Sum of QRS Voltage > 2.0 mV",...
    "QRS Interval > 0.08 s","270 < MEA < 330","100 < MEA < 180","180 < MEA < 270"]
T2 = table(diagnosis',criteria')
T2.Properties.Description = 'Criteria Table';
T2.Properties.VariableNames = ["Diagnosis","Criteria"]
writetable(T2,filename2,'Sheet','Data');
```