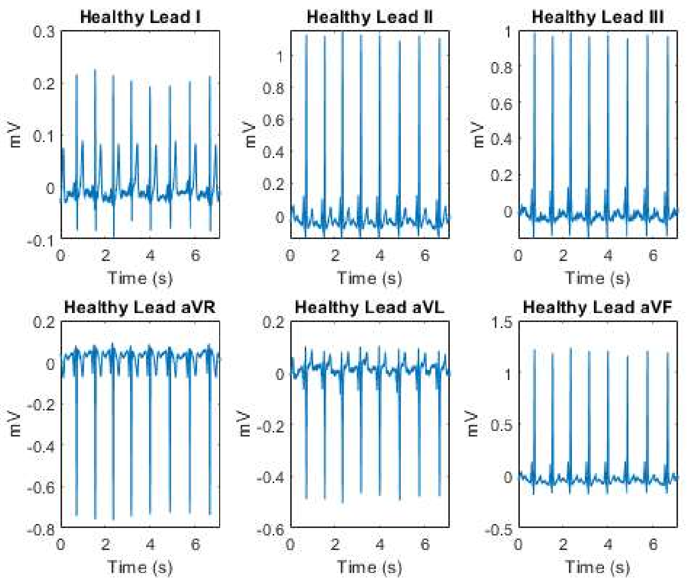
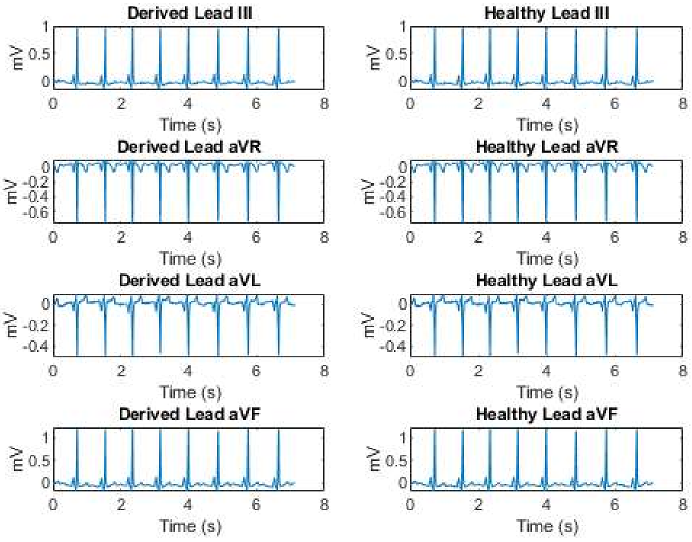
Contents

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
```

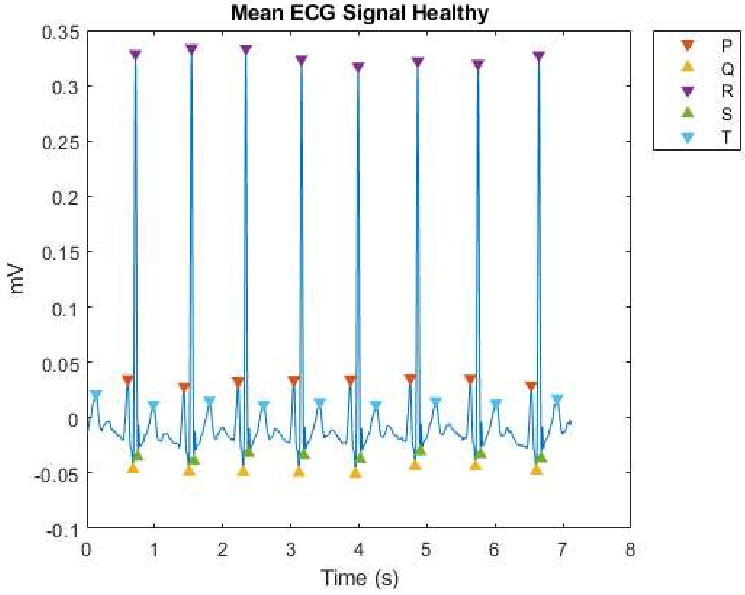
```
Warning: Column headers from the file were modified to make them valid MATLAB
identifiers before creating variable names for the table. The original column
headers are saved in the VariableDescriptions property.
Set 'VariableNamingRule' to 'preserve' to use the original column headers as
table variable names.
```

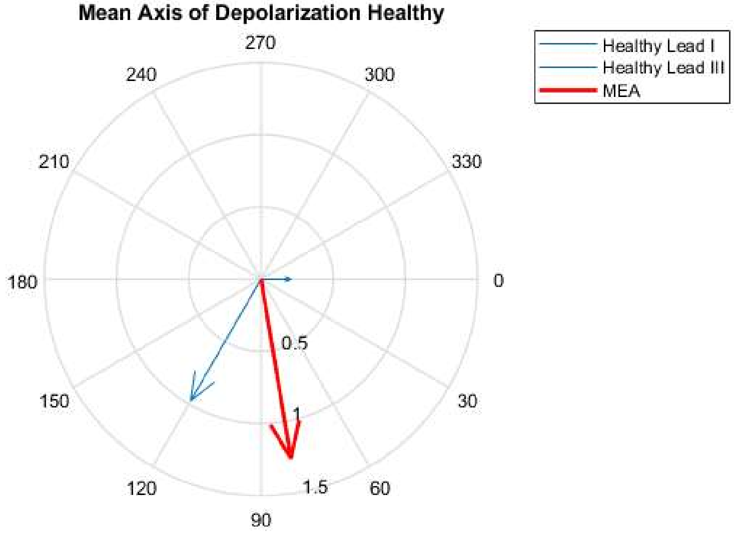




Part 2

```
% 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','Location','northeastoutside');
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,average_QT_int_healthy,dir_healthy};
```



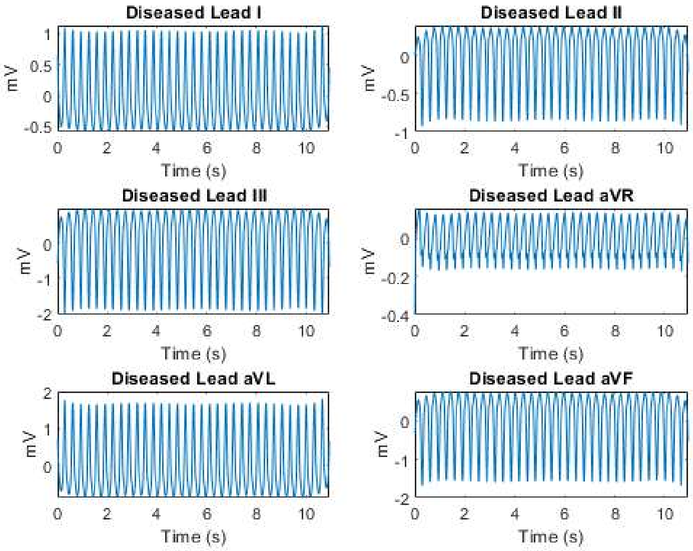


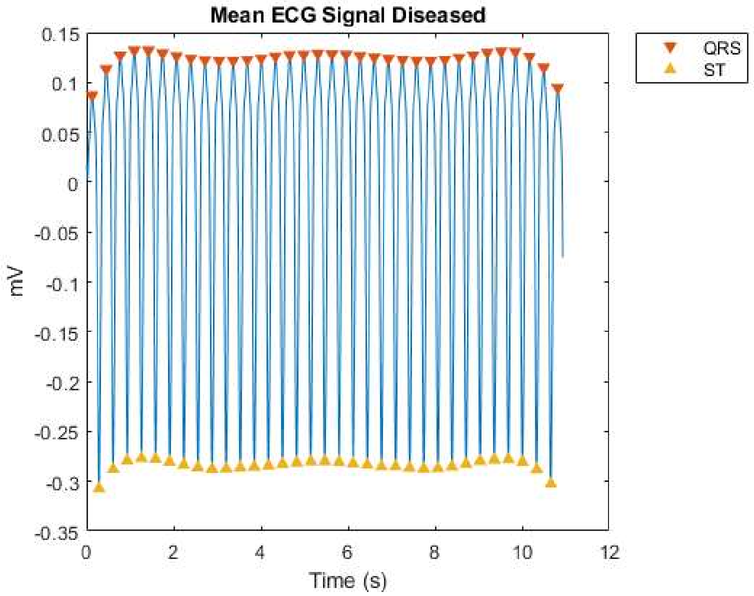
Part 3 (Written Specifically for Ventricular Tachycardia)

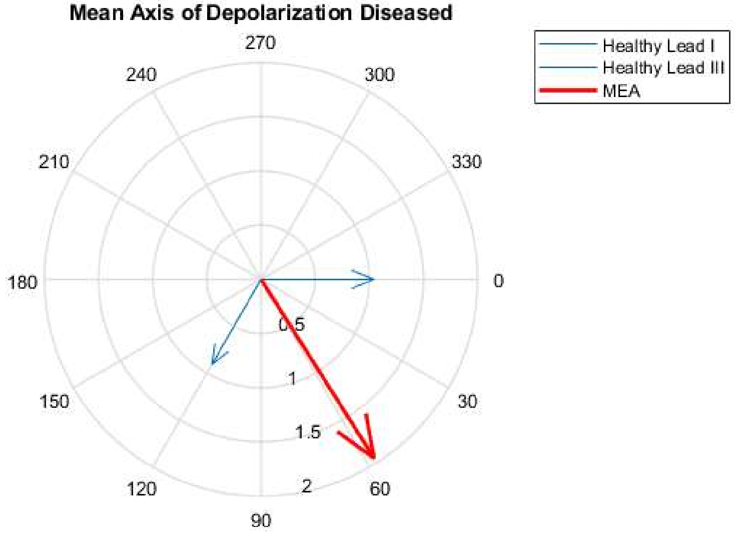
Criteria for peaks from: https://ecgwaves.com/topic/ventricular-tachycardia-vt-ecg-treatment-causes-management/#:~:text=ECG%20features%20of%20ventricular%20tachycardia,-%E2%89%A53%20consecutive&text=Ventricular%20tachycardia%20with%20rate%20100,%E2%89%A50%2C12%20s).

```
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','Location','northeastoutside');
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_diseased,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};
```

```
Warning: Column headers from the file were modified to make them valid MATLAB
identifiers before creating variable names for the table. The original column
headers are saved in the VariableDescriptions property.
Set 'VariableNamingRule' to 'preserve' to use the original column headers as
table variable names.
```


Diseased Lead I
mV
1
0.5
0
-0.5
0
2
4
6
8
10
Time (s)
Diseased Lead II
mV
0
-0.5
-1
0
2
4
6
8
10
Time (s)
Diseased Lead III
mV
0
-1
-2
0
2
4
6
8
10
Time (s)
Diseased Lead aVR
mV
0
-0.2
-0.4
0
2
4
6
8
10
Time (s)
Diseased Lead aVL
mV
2
1
0
0
2
4
6
8
10
Time (s)
Diseased Lead aVF
mV
0
-1
-2
0
2
4
6
8
10
Time (s)


Mean ECG Signal Diseased
mV
0.15
0.1
0.05
0
-0.05
-0.1
-0.15
-0.2
-0.25
-0.3
-0.35
0
2
4
6
8
10
12
Time (s)
▼ QRS
▲ ST


Mean Axis of Depolarization Diseased
270
300
330
0
30
60
90
120
150
180
210
240
0.5
1
1.5
2
Healthy Lead I
Healthy Lead III
MEA

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";
    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
```

```
Issues:
High BPM
Low Voltage
Prolonged QRS Wave

Possible Diseases:
Tachycardia
Pericardial fluid buildup
Pulmonary emphysema
Previous myocardial infarctions/diminished cardiac muscle mass
Damage to cardiac muscle
Blocks in the Purkinje system
```

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"];
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');

disp(T)
disp(T2)
```

```
                  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]}

           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"
```

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