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```

```
T = input_data();
```

```
%Part A)
ans = var_prob(T, 'npreg', 2);
disp(ans);
```

```
%Part B)
compareFigure(T);
```

```
%Part C)
```

```
D = table2array(rmmissing(T(:,[1:6])));
D = squareform(pdist(D));
```

```
%Classical MDS
MDS = cmdscale(D, 2);
```

```
figure
```

```
newTable = readtable("diabetes-pima.csv");
```

```
newTable.npreg = str2double(newTable.npreg);
newTable.bp = str2double(newTable.bp);
newTable.glu = str2double(newTable.glu);
newTable.skin = str2double(newTable.skin);
newTable.bmi = str2double(newTable.bmi);
newTable.age = str2double(newTable.age);
```

```
%Changing the NA to be defaulted to 0
for idx = 1:length(newTable.diabetic)

    if newTable.diabetic{idx} == "NA"
        newTable.diabetic{idx} = 'No';
    end
end
```

```
newTable=newTable(~any(ismissing(newTable),2),:);
gscatter(MDS(:,1), MDS(:,2),newTable.diabetic);
title("MDS by Diabetic Status");
```

```
%The MDS figure is not homogenous between the diabetic and non
diabetic
% individuals. There is a clear split, the non diabetic are closer
to
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```

    % the left, while the diabetic individuals tend to be on the
    right.
    %The fact that they are split shows there is hetrogenity and there
    are
    %other factors, the other variables, that somehow impact the
    occurance
    %of diabetes amogst indivuals.

%A) Funciton that calcualtes the probaility for any five biological
%variables
function prob = var_prob(T, varType, value)
X = table2array( T(:, {varType}) );

    % Isolate the response variable:
    Y = T.diabetic;

    % Fit the bivariate logistic regression:
    model = glmfit(X, Y, 'binomial');

    % The variable `b` stores the regression coefficients

    % the probability given the values
    prob = logistic_fct(value, model);

end

function y = logistic_fct(x1,b)

    %Function used for logisitc regression
    y = 1 / (1 + exp(-(b(1) + b(2) * x1)));
end

%Funciton for part B)
function compareFigure(T)

    XnPreg = linspace(0,20,21);
    YxnPreg = [];

    XbP = linspace(50,100,101);
    YbP = [];

    XGlu = linspace(70,200,131);
    YGlu = [];

    XSkin = linspace(10,100,91);
    YSkin = [];

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Xbmi = linspace(15,50,100);
Ybmi = [];

Xage = linspace(20,80,61);
Yage = [];

%All the forloops are used to create corresponding y values for
each
%variable type
for idx = 1:length(XnPreg)
    YxnPreg(idx) = var_prob(T, 'npreg', idx);
end

for idx = 1:length(XbP)
    YbP(idx) = var_prob(T, 'bp', idx);
end

for idx = 1:length(XGlu)
    YGlu(idx) = var_prob(T, 'glu', idx);
end

for idx = 1:length(XSkin)
    YSkin(idx) = var_prob(T, 'skin', idx);
end

for idx = 1:length(Xbmi)
    Ybmi(idx) = var_prob(T, 'bmi', idx);
end

for idx = 1:length(Xage)
    Yage(idx) = var_prob(T, 'age', idx);
end

%The following section is used to plot the 6 charts

figure
subplot(2, 3, 1);
plot(XnPreg ,YxnPreg);
title("Probability of Diabetes Vs. Number of Pregnancies");
ylabel("Probability");
xlabel("Number of Pregnancies");


    subplot(2, 3, 2);
plot(XGlu ,YGlu);
title("Probability of Diabetes Vs. Plasma Glucose Concentration
(mg/dL) ");
ylabel("Probability");
xlabel("plasma glucose concentration (mg/dL)");

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        subplot(2, 3, 3);
        plot(XbP ,YbP);
        title("Probability of Diabetes Vs. Blood Pressure");
        ylabel("Probability");
        xlabel("Blood Pressure (mm Hg)");

        subplot(2, 3, 4);
        plot(XSkin ,YSkin);
        title("Probability of Diabetes Vs. Tricep Skin Fold Thickness
(mm)");
        ylabel("Probability");
        xlabel("Tricep Skin Fold Thickness (mm)");

        subplot(2, 3, 5);
        plot(Xbmi ,Ybmi);
        title("Probability of Diabetes Vs. BMI (kg m-2)");
        ylabel("Probability");
        xlabel("BMI (kg m-2)");

        subplot(2, 3, 6);
        plot(Xage ,Yage);
        title("Probability of Diabetes Vs. Age (years) ");
        ylabel("Probability");
        xlabel("Age (years)");

    end

function T = input_data()

%Function to read in values and cast them accordingly
T = readtable("diabetes-pima.csv");
T.npreg = str2double(T.npreg);
T.bp = str2double(T.bp);
T.glu = str2double(T.glu);
T.skin = str2double(T.skin);
T.bmi = str2double(T.bmi);
T.age = str2double(T.age);

%Going over the length of T.diabetic and casting and making it
    boolean
    %based
    for idx = 1:length(T.diabetic)

        if T.diabetic{idx} == "NA"
            T.diabetic{idx} = '0';
        end

        if T.diabetic{idx} == "Yes"
            T.diabetic{idx} = '1';
        end
    end

```

```

end

if T.diabetic{idx} == "No"
    T.diabetic{idx} = '0';
end

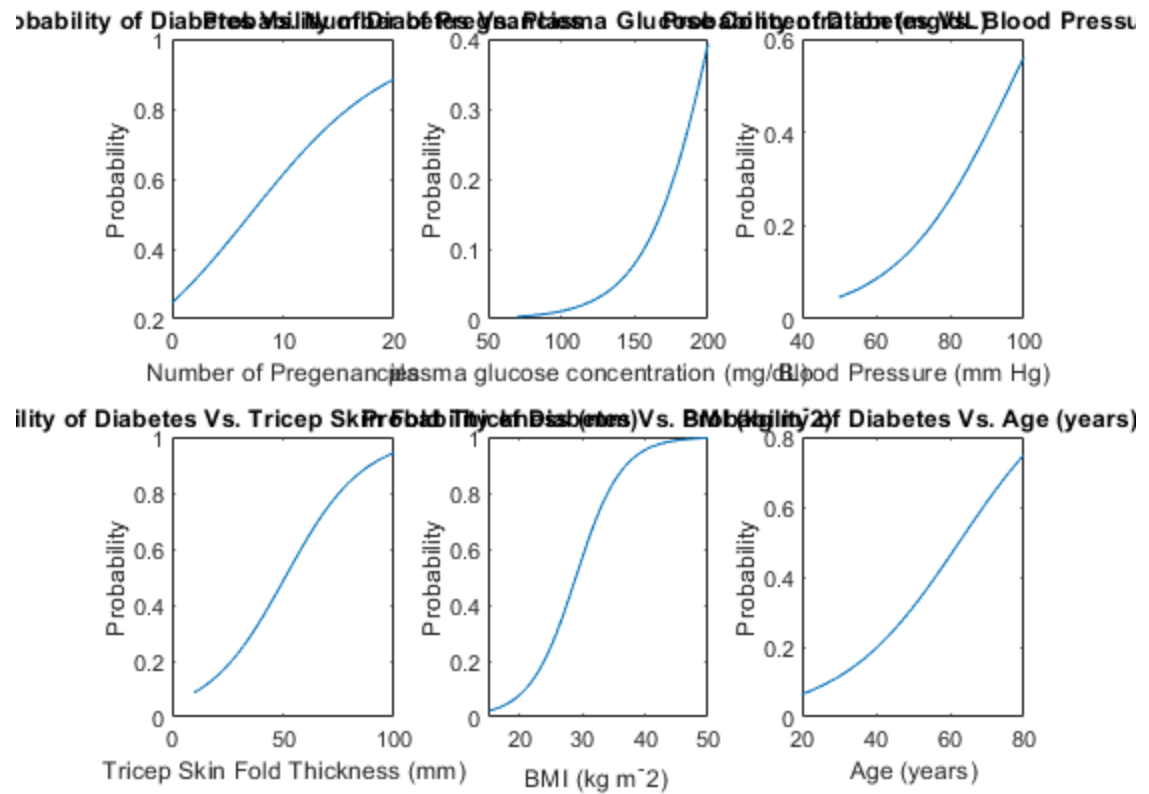
end

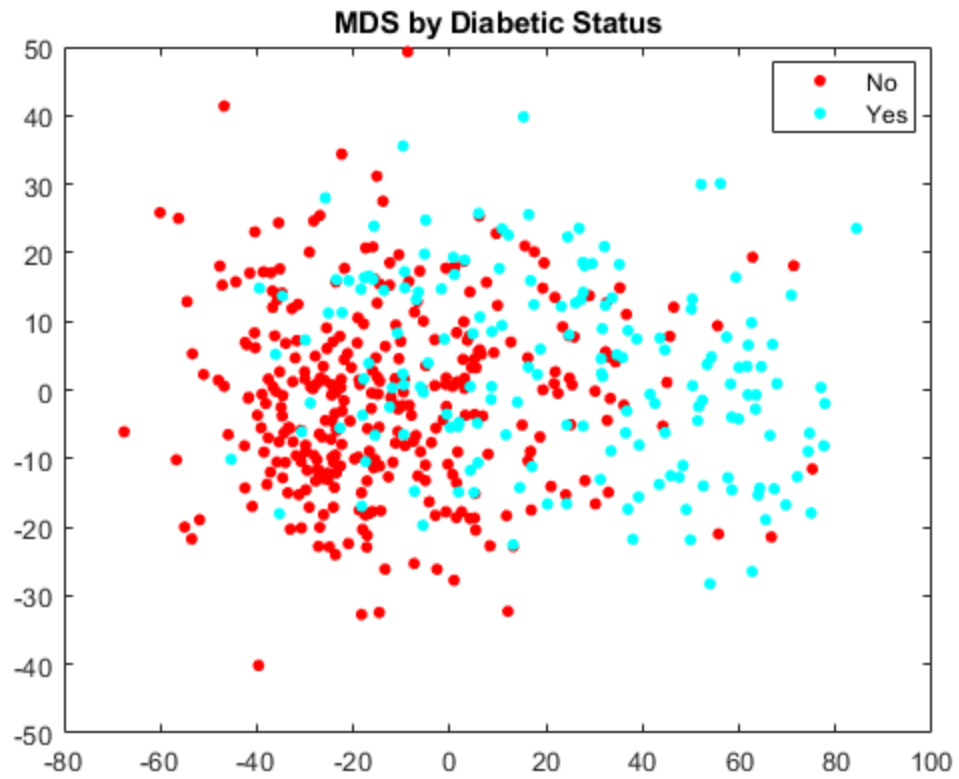
T.diabetic = str2double(T.diabetic);

```

```
end
```

0.276386489000900





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