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## Example 1 - Setup

```
load( "DaphneIsland.txt" );
```

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## Example 2 - Are the Father Beak Sizes averaging 10 mm?

```
ChildBeakSize = DaphneIsland(:,1);
MotherBeakSize = DaphneIsland(:,2);
FatherBeakSize = DaphneIsland(:,3);
[h1, p1, c1] = ttest(FatherBeakSize, 10);
fprintf(['Do the Father Beak Sizes average 10 mm?\n\t' ...
'h = %g, p = %g, ci = [%g, %g] \n'], h1, p1, c1);
```

```
Do the Father Beak Sizes average 10 mm?
h = 1, p = 3.17679e-05, ci = [9.02567, 9.57705]
```

## Exercise 1 - Do Mother Finches have an average beak size of 10mm?

```
[h1, p1, c1] = ttest(MotherBeakSize, 10);
fprintf(['Do Mother Finches have an average beak size of 10mm?\n\t' ...
'h = %g, p = %g, ci = [%g, %g] \n'], h1, p1, c1);
% Null Hypothesis: Mother beak sizes average 10mm
% Alternative hypothesis: Mother beak sizes do not average 10mm
% Significance level: alpha 0.05
% Result: The p- level is more than 0.05 so the h-value is 0 indicating
% that we accept the null hypothesis that the Mother beak sizes average
% 10mm.
```

```
Do Mother Finches have an average beak size of 10mm?
h = 0, p = 0.0942843, ci = [9.28933, 10.0607]
```

## Example 3 - Do the mother and father have similar beak size?

```
[h3, p3, c3] = ttest2(MotherBeakSize, FatherBeakSize);
fprintf(['Do the Mother and Father have similar Beak Sizes?\n\t' ...
'h = %g, p = %g, ci = [%g, %g] \n'], h3, p3, c3);
```

```
Do the Mother and Father have similar Beak Sizes?
h = 0, p = 0.108679, ci = [-0.0864116, 0.833684]
```

## Exercise 2 - Do Children and Mother Finches have similar average beak sizes?

```
[h4, p4, c4] = ttest2(ChildBeakSize, MotherBeakSize);
fprintf(['Do Children and Mother Finches have similar average beak sizes?
\n\t' ...
'h = %g, p = %g, ci = [%g, %g] \n'], h4, p4, c4);
% Null Hyp: Children and Mother Finches have similar average beak sizes
```

---

```
% Alt Hyp: Children and Mother Finches do not have similar average beak
% sizes
% Significance Level: alpha 0.05
% Result: The p-level is less than 0.05 so the h-value is 1 indicating that
% we accept the alternate hypothesis that the Children and Mother Finch
% average beak sizes are not similar.
```

```
Do Children and Mother Finches have similar average beak sizes?
    h = 1, p = 0.0125611, ci = [-1.13767, -0.145055]
```

## Example 4 - Calculate and output the Average Parent to Child beak size correlations

```
parent = mean(DaphneIsland(:, 2:3), 2); % Average the parent beak sizes
pCorr = corr(parent, ChildBeakSize);
fprintf('Parent-child beak correlation: %g\n', pCorr)
```

```
Parent-child beak correlation: 0.72319
```

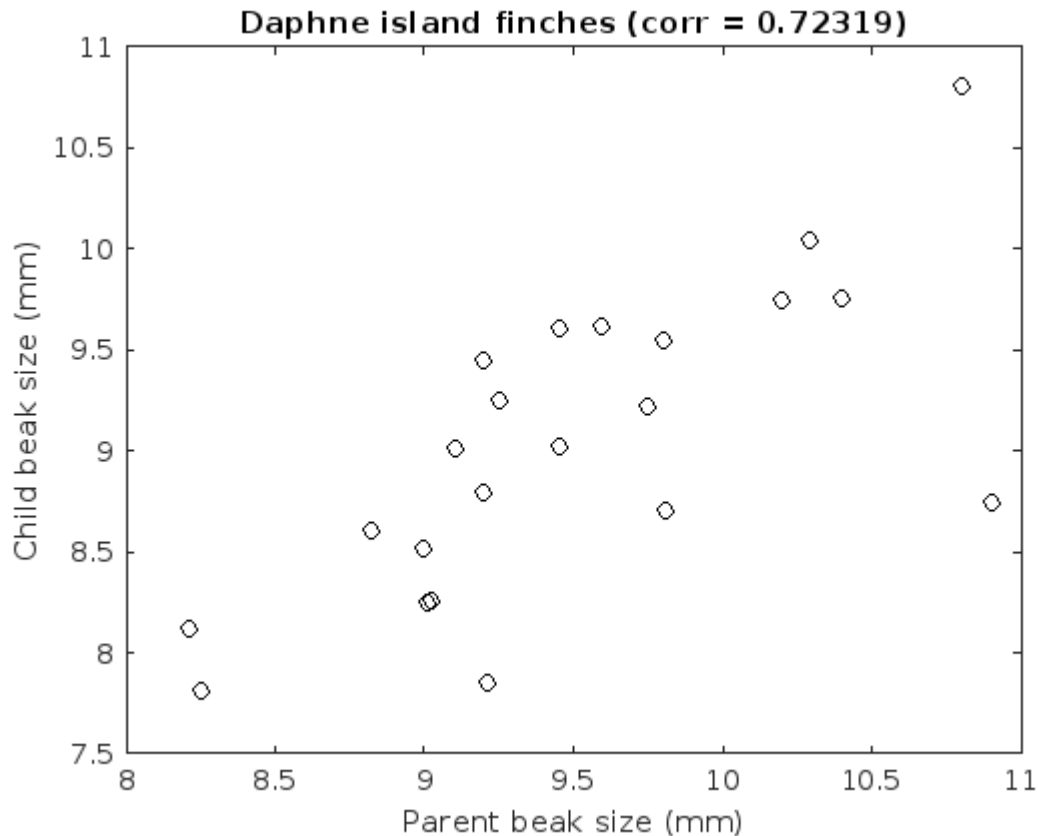
## Exercise 3

```
mCorr = corr(ChildBeakSize, MotherBeakSize);
fprintf('Child beak-Mother beak correlation: %g\n', mCorr)
fCorr = corr(ChildBeakSize, FatherBeakSize);
fprintf('Child beak-Father beak correlation: %g\n', fCorr)
% The correlation is higher than 0.5 indicating there is positive
% correlation between child beak size and Mother beak size. The correlation
% is higher than 0.7 indicating there is a positive correlation between
% child beak size and Father beak size. Of the two correlations, the
% positive correlation between the child and Father beak size is higher
% than the correlation between the child and Mother beak sizes. This
% indicates that the sizes of the child and Father beaks are more similar.
```

```
Child beak-Mother beak correlation: 0.75621
Child beak-Father beak correlation: 0.605284
```

## Example 5 - Plot the average parent beak size against the child beak size

```
tString = ['Daphne island finches (corr = ', num2str(pCorr) ' )'];
figure('Name', tString) % Put title on the window
plot(parent, ChildBeakSize, 'ko') % Plot a scatter plot
xlabel('Parent beak size (mm)'); % Label the x-axis
ylabel('Child beak size (mm)'); % Label the y-axis
title(tString); % Put title on the graph
```



## Example 7 - Calculate and output the best fit lines for beak par entage

```
pPoly = polyfit(parent, ChildBeakSize, 1); % Linear fit of parent vs child  
fprintf('Model: child = %g*parent + %g\n', pPoly(1), pPoly(2))
```

```
Model: child = 0.766283*parent + 1.763
```

## Exercise 4

```
mPoly = polyfit(MotherBeakSize, ChildBeakSize, 1);  
fprintf('model: child = %g*parent + %g\n', mPoly(1), mPoly(2))
```

```
model: child = 0.658622*parent + 2.66147
```

## Example 8 Predict the child beak sizes from its parent beak sizes (Linear Model)

```
pPred = polyval(pPoly, parent); % Find parent-child relationship
```

---

## Example 9 - Calculate the error between child beak sizes and the model

```
pError = ChildBeakSize - pPred; % Actual - predicted by parent's size
```

## Example 10 - Find mean square error (MSE)

```
pMSE = mean(pError.*pError);  
fprintf('Mean squared prediction error: %g\n', pMSE);
```

```
Mean squared prediction error: 0.261331
```

## Example 11 - Find root mean squared error (RMS)

```
pRMS = sqrt(pMSE);  
fprintf('RMS prediction error: %g mm\n', pRMS);
```

```
RMS prediction error: 0.511205 mm
```

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