ANOVA Example

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GEEN 3853

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INTRODUCTION

Selenium (Se) is a trace metal that is an essential component of a balanced diet, and the amount of selenium in meats can vary based on region based on the selenium levels in that regions soil and plants [1]. A 2002 study looked at the Se content of different meats in a low-Se region of the US, namely Ohio [2]. While certain regions can have low Se content, this often does not result in Se deficiencies in developed countries because of how much food is distributed across regional boundaries [1].

The abstract of the 2002 study is included below. Utilize a simplified version of this study's dataset and verify this study's results. I.e., conduct a comparison of the Se content of non- region-raised beef, region-raised beef, squirrel, and venison (deer) using the appropriate statistical procedures. Submit complete 7-step procedures for each phase of the hypothesis testing. Also, include a final section that discusses the implications/conclusions of your analysis—what does your analysis tell you with regard to your overall research question? Be sure to include an effect size, post-hoc-analysis table, group subsets, and point and interval estimates, if applicable.

Abstract:

The selenium (Se) content (AOAC fluorometric method) of: 1) raw and cooked venison, squirrel, and beef from a low selenium region of the United States and 2) nonregion- raised beef was assessed and compared by region, species, and gender. For both raw and cooked meats, the Se content of venison was not different from region-raised beef ($p > .05$), and their contents were generally less than squirrel, which was less than nonregion-raised beef ($p < .05$). Gender and age did not influence Se content of the meats. Field-dressed weight did not affect Se content of deer, and antler size did not impact Se content of meat from male deer. [2]

PREP WORKSPACE

```
clear all
close all
clc
```

LOAD THE DATA

We first load the dataset titled "NoDifference"

```
opts = delimitedTextImportOptions("NumVariables", 2);

% Specify range and delimiter
opts.DataLines = [2, Inf];
opts.Delimiter = ",";

% Specify column names and types
opts.VariableNames = ["type", "selenium"];
opts.VariableTypes = ["categorical", "double"];

% Specify file level properties
opts.ExtraColumnsRule = "ignore";
opts.EmptyLineRule = "read";

% Specify variable properties
opts = setvaropts(opts, "type", "EmptyFieldRule", "auto");

% Import the data
raw = readtable("C:\Users\andre\OneDrive\Documents\MATLAB\GEEN 3583\Se_meats_OH.csv", opts)
raw = 144×2 table
```

	type	selenium
1	NRB	44.3300
2	NRB	76.8600
3	NRB	4.4500
4	NRB	55.0100
5	NRB	58.2100
6	NRB	74.7200
7	NRB	11.8400
8	NRB	139.0900
9	NRB	69.0100
10	NRB	94.6100
11	NRB	48.3500
12	NRB	37.6500
13	NRB	66.3600
14	NRB	72.4800
15	NRB	87.0900
16	NRB	26.3400
17	NRB	71.2400
18	NRB	90.3800
19	NRB	50.8600
20	RRB	11.2300
21	RRB	29.6300
22	RRB	20.4200
23	RRB	10.1200
24	RRB	39.9100
25	RRB	32.6600
26	RRB	38.3800
27	RRB	36.2100
28	RRB	16.3900
29	RRB	27.4400
30	RRB	17.2900
31	RRB	56.2000
32	RRB	28.9400
33	RRB	20.1100
34	RRB	25.3500
35	RRB	21.7700
36	RRB	31.6200
37	RRB	32.6300
38	RRB	30.3100
39	RRB	46.1600
40	RRB	56.6100
41	RRB	24.4700
42	RRB	29.3900
43	RRB	40.7100
44	RRB	15.8200
45	RRB	27.7400
46	RRB	22.3500
47	RRB	34.7800
48	RRB	35.0900
49	RRB	32.6000
50	RRB	37.0300

	type	selenium
51	RRB	27.0000
52	RRB	44.2000
53	RRB	13.0900
54	RRB	33.0300
55	RRB	9.6900
56	RRB	32.4500
57	RRB	37.3800
58	RRB	34.9100
59	RRB	27.9900
60	RRB	22.3600
61	RRB	22.6800
62	RRB	26.5200
63	RRB	46.0100
64	RRB	38.0400
65	RRB	30.8800
66	RRB	30.0400
67	RRB	25.9100
68	RRB	18.5400
69	RRB	18.5200
70	RRB	25.5100
71	RRB	27.8000
72	RRB	19.4900
73	SQU	37.4200
74	SQU	56.4600
75	SQU	51.9100
76	SQU	62.7300
77	SQU	4.5500
78	SQU	39.1700
79	SQU	38.4400
80	SQU	40.9200
81	SQU	58.9300
82	SQU	61.8800
83	SQU	49.5400
84	SQU	64.3500
85	SQU	82.4900
86	SQU	38.5400
87	SQU	39.5300
88	SQU	68.9900
89	SQU	27.9700
90	SQU	37.5700
91	SQU	25.7100
92	SQU	23.9700
93	SQU	13.8200
94	SQU	42.2100
95	SQU	35.8800
96	SQU	10.5400
97	SQU	41.8900
98	SQU	23.9400
99	SQU	49.8100
100	SQU	30.7100

CLEAN AND SUBSET THE DATA

View the dataset and perform necessary cleanup.

```
%View the first five rows of all columns
raw(:,:)
```

```
ans = 144×2 table
```

	type	selenium
1	NRB	44.3300
2	NRB	76.8600
3	NRB	4.4500
4	NRB	55.0100
5	NRB	58.2100
6	NRB	74.7200
7	NRB	11.8400
8	NRB	139.0900
9	NRB	69.0100
10	NRB	94.6100
11	NRB	48.3500
12	NRB	37.6500
13	NRB	66.3600
14	NRB	72.4800
15	NRB	87.0900
16	NRB	26.3400
17	NRB	71.2400
18	NRB	90.3800
19	NRB	50.8600
20	RRB	11.2300
21	RRB	29.6300
22	RRB	20.4200
23	RRB	10.1200
24	RRB	39.9100
25	RRB	32.6600
26	RRB	38.3800
27	RRB	36.2100
28	RRB	16.3900
29	RRB	27.4400
30	RRB	17.2900
31	RRB	56.2000
32	RRB	28.9400
33	RRB	20.1100
34	RRB	25.3500
35	RRB	21.7700
36	RRB	31.6200
37	RRB	32.6300
38	RRB	30.3100
39	RRB	46.1600
40	RRB	56.6100
41	RRB	24.4700
42	RRB	29.3900
43	RRB	40.7100
44	RRB	15.8200

	type	selenium
45	RRB	27.7400
46	RRB	22.3500
47	RRB	34.7800
48	RRB	35.0900
49	RRB	32.6000
50	RRB	37.0300
51	RRB	27.0000
52	RRB	44.2000
53	RRB	13.0900
54	RRB	33.0300
55	RRB	9.6900
56	RRB	32.4500
57	RRB	37.3800
58	RRB	34.9100
59	RRB	27.9900
60	RRB	22.3600
61	RRB	22.6800
62	RRB	26.5200
63	RRB	46.0100
64	RRB	38.0400
65	RRB	30.8800
66	RRB	30.0400
67	RRB	25.9100
68	RRB	18.5400
69	RRB	18.5200
70	RRB	25.5100
71	RRB	27.8000
72	RRB	19.4900
73	SQU	37.4200
74	SQU	56.4600
75	SQU	51.9100
76	SQU	62.7300
77	SQU	4.5500
78	SQU	39.1700
79	SQU	38.4400
80	SQU	40.9200
81	SQU	58.9300
82	SQU	61.8800
83	SQU	49.5400
84	SQU	64.3500
85	SQU	82.4900
86	SQU	38.5400
87	SQU	39.5300
88	SQU	68.9900
89	SQU	27.9700
90	SQU	37.5700
91	SQU	25.7100
92	SQU	23.9700
93	SQU	13.8200
94	SQU	42.2100
95	SQU	35.8800

	type	selenium
96	SQU	10.5400
97	SQU	41.8900
98	SQU	23.9400
99	SQU	49.8100
100	SQU	30.7100
⋮		

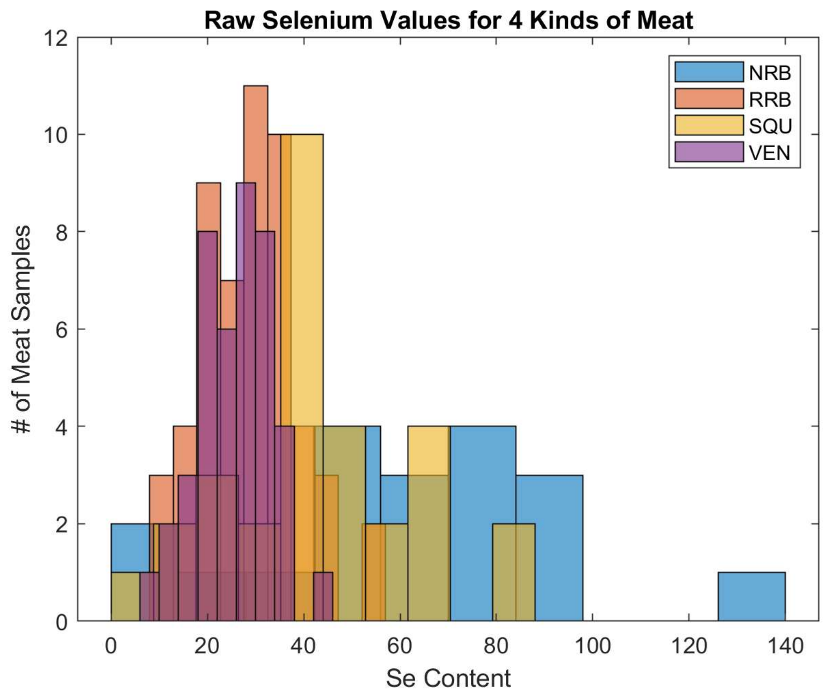
```
%We want all rows and columns.
NRB = table2array(raw(1:19,2));    % Non-region Raised beef
RRB = table2array(raw(20:72,2));   % Region Raised beef
SQU = table2array(raw(73:102,2));  % Squirrel
VEN = table2array(raw(103:144,2)); % Venison
data = [NRB;RRB;SQU;VEN];          % All data
zdata = [zeros(length(NRB), 1); ones(length(RRB), 1); 2*ones(length(SQU), 1); 3*ones(length(VEN), 1)];
meatType = {'NRB','RRB','SQU','VEN'};
extremes_NRB = [min(NRB), max(NRB)];
extremes_RRB = [min(RRB), max(RRB)];
extremes_SQU = [min(SQU), max(SQU)];
extremes_VEN = [min(VEN), max(VEN)];
```

DESCRIPTIVE STATISTICS

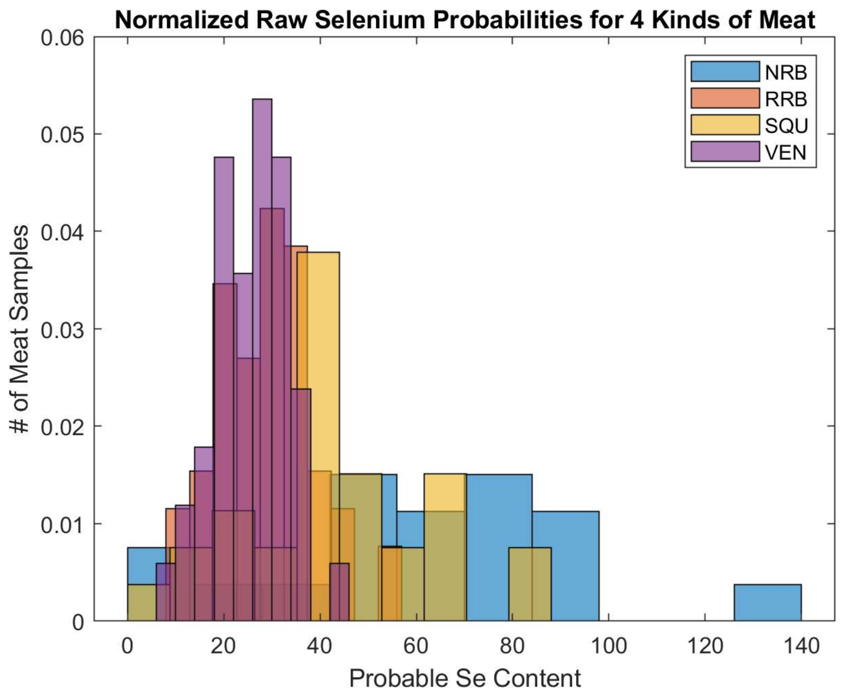
DESCRIPTIVE STATISTICS - VISUAL

Histograms

```
%Obtain the histogram plot of the dataset
figure
histogram(NRB,'NumBins',10)
hold on
histogram(RRB,'NumBins',10)
histogram(SQU,'NumBins',10)
histogram(VEN,'NumBins',10)
hold off

xlabel('Se Content')
ylabel('# of Meat Samples')
legend('NRB','RRB','SQU','VEN')
title('Raw Selenium Values for 4 Kinds of Meat')
```

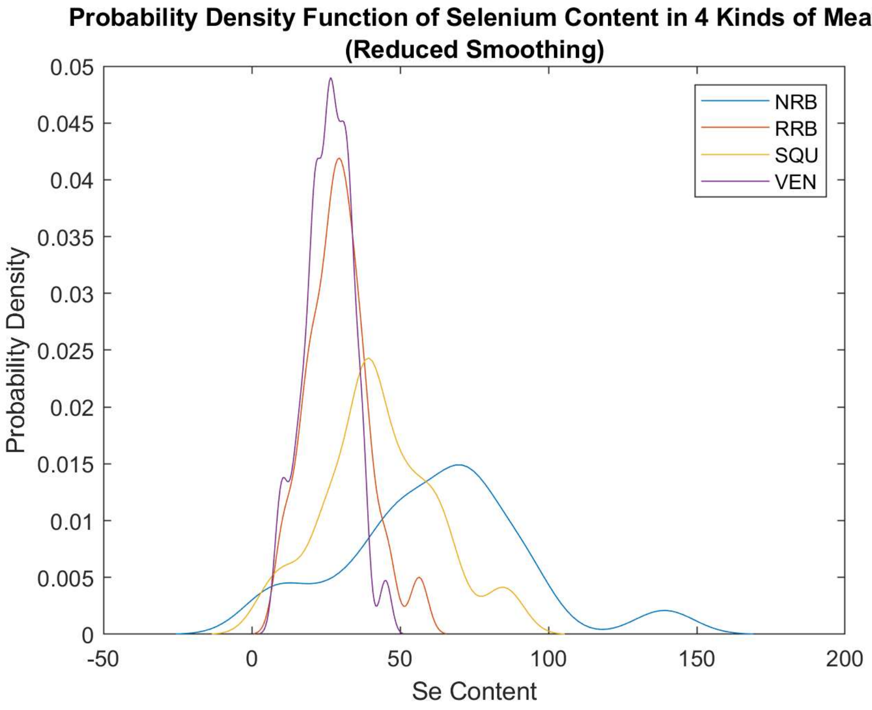


```
figure
%Obtain the histogram plot of the dataset
figure
histogram(NRB,'NumBins',10,'Normalization','pdf')
hold on
histogram(RRB,'NumBins',10,'Normalization','pdf')
histogram(SQU,'NumBins',10,'Normalization','pdf')
histogram(VEN,'NumBins',10,'Normalization','pdf')
hold off

xlabel('Probable Se Content')
ylabel('# of Meat Samples')
legend('NRB','RRB','SQU','VEN')
title('Normalized Raw Selenium Probabilities for 4 Kinds of Meat')
```



Probability Density Functions

```
%'Bandwidth' adjusts how much filtering is applied: larger # = more
%filtering
figure
ksdensity(NRB,'Bandwidth',10) % Default Bandwidth = 15.6953
hold on
ksdensity(RRB,'Bandwidth',3) % Default Bandwidth = 4.6706
ksdensity(SQU,'Bandwidth',6) % Default Bandwidth = 9.5208
ksdensity(VEN,'Bandwidth',2) % Default Bandwidth = 3.7814
hold off


xlabel('Se Content')
ylabel('Probability Density')
legend('NRB','RRB','SQU','VEN')
title("Probability Density Function of Selenium Content in 4 Kinds of Meat"+newline+"(Reduced Smoothing)")
```



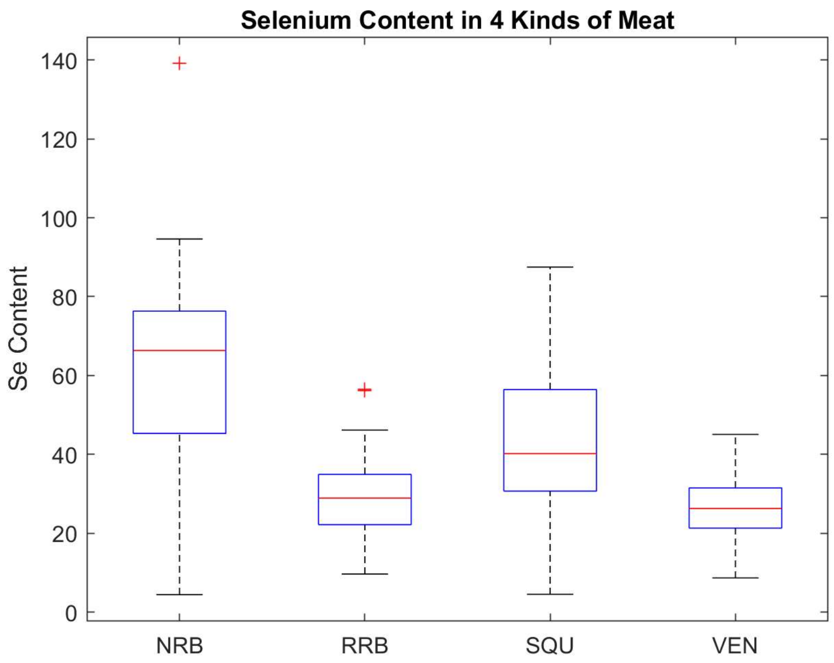
Take Aways

From the histograms/pdfs, it looks like with regards to Selenium content, Venison and Regional Raised Beef have similar concentrations and variance, while the Non-Regional Raised Beef and the Squirrel Meat follow this same pattern. However the latter seem to have larger means and variances.

Boxplots

Boxplots are a great way to compare median, IQR (1st to 3rd), and outliers. In Matlab, the whiskers extend to the farthest data points that are not considered outliers. The default setting for Matlab is that an outliers is any value more extreme than 1.5*(Q3-Q1) away from the Q1 or Q3 value.

```
figure
boxplot(data,zdata,"Labels",{'NRB','RRB','SQU','VEN'})
ylabel ('Se Content')
title('Selenium Content in 4 Kinds of Meat')
hold off
```



Take Aways

These box plots also suggest that with regards to Selenium content, Venison and Regional Raised Beef have similar concentrations and variance, while the Non-Regional Raised Beef and the Squirrel Meat follow this same pattern. However the latter seem to have larger means and variances. It becomes more obvious, though, with this diagram, that the Non-Regional Raised Beef seems to have the highest mean Selenium concentration.

DESCRIPTIVE STATISTICS - NUMERIC

Univariate

```
%Set up a results table
tNRB = table();

tNRB.Mean = mean(NRB)';
tNRB.SD = std(NRB)';
tNRB.Med = median(NRB)';
tNRB.Max = max(NRB)';
tNRB.Min = min(NRB)';
tNRB.IQR = iqr(NRB)';

tRRB = table();

tRRB.Mean = mean(RRB)';
tRRB.SD = std(RRB)';
tRRB.Med = median(RRB)';
tRRB.Max = max(RRB)';
tRRB.Min = min(RRB)';
tRRB.IQR = iqr(RRB)';

tSQU = table();

tSQU.Mean = mean(SQU)';
tSQU.SD = std(SQU)';
tSQU.Med = median(SQU)';
tSQU.Max = max(SQU)';
tSQU.Min = min(SQU)';
tSQU.IQR = iqr(SQU)';
```

```
tVEN = table();

tVEN.Mean = mean(VEN)';
tVEN.SD = std(VEN)';
tVEN.Med = median(VEN)';
tVEN.Max = max(VEN)';
tVEN.Min = min(VEN)';
tVEN.IQR = iqr(VEN)';

ds = vertcat(tNRB,tRRB,tSQU,tVEN);
ds.Properties.RowNames = {'NRB','RRB','SQU','VEN'};
ds
```

```
ds = 4×6 table
```

	Mean	SD	Med	Max	Min	IQR
1 NRB	62.0463	31.1498	66.3600	139.0900	4.4500	30.9900
2 RRB	29.0830	10.3767	28.9400	56.6100	9.6900	12.7500
3 SQU	43.2457	19.5087	40.2250	87.5000	4.5500	25.7500
4 VEN	25.8755	8.0324	26.3000	45.0800	8.7000	10.1700

Take Aways

The numeric, univariate statistics also suggest that with regards to average time spent on hold, Classical > Advertisement > Muzak. The other variables also generally follow this pattern.

Bivariate

The most common bivariate statistic that we will utilize is the correlation coefficient.

This doesn't make sense to compute for this data/problem.

INFERENTIAL STATISTICS

Our ultimate goal is to test the difference in means. However, to do that, we need to first test the normality of the groups. We also need to know if the groups have equal or unequal variance so that we know what t-test to use in our test of location.

TEST OF NORMALITY

For a two-sample, independent test, we need to test the normality of each group.

Underlying Assumptions of the Test :

1. The data are continuous.
2. The data are from a sample that was randomly drawn from a process/population.

Method: Anderson-Darling and Normality Plot

Step 1 : (Note that a non-directional test is assumed.)

H0 :γ_3 = 0 and γ_4 = 0 for all groups

H1 : γ_3 $\neq$ 0 and γ_4 $\neq$ 0 for some/all groups

Step 2: Alpha level; i.e., significance level, or how much Type I error you are willing to make

```
alpha1 = 0.05
```

```
alpha1 = 0.0500
```

Step 3 : We will use the AD test statistic.

Step 4 : We will use the AD RSD

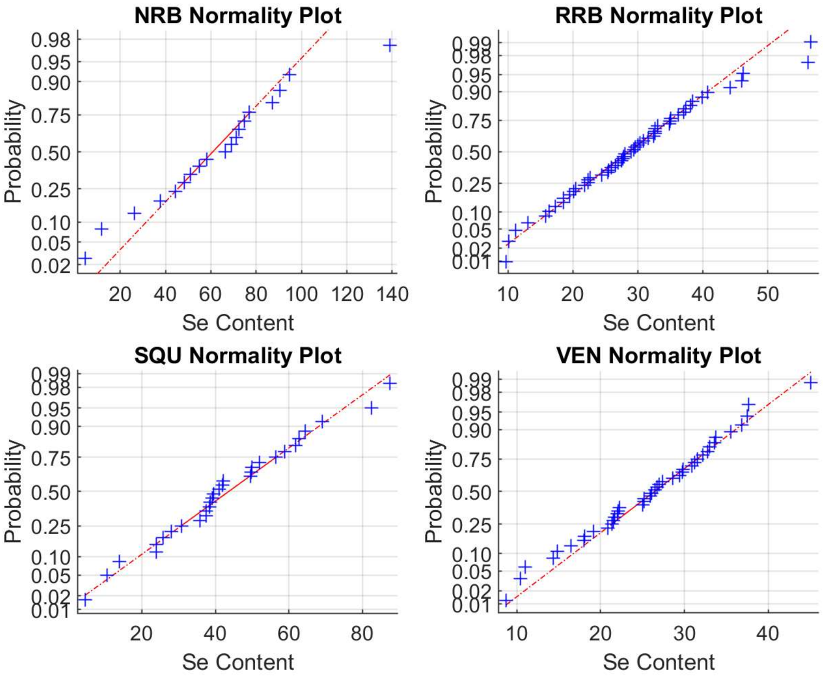
Step 5 : State the Critical Value for Rejecting the Null Hypothesis

Quantitative: Reject H0 if any p-value < α

Step 6 : Calculations

Normality Plot & Anderson-Darling Statistic

```
figure
subplot(2,2,1)
normplot(NRB) %quanlitative check
title('NRB Normality Plot')
xlabel('Se Content')

subplot(2,2,2)
normplot(RRB) %quanlitative check
title('RRB Normality Plot')
xlabel('Se Content')

subplot(2,2,3)
normplot(SQU) %quanlitative check
title('SQU Normality Plot')
xlabel('Se Content')

subplot(2,2,4)
normplot(VEN) %quanlitative check
title('VEN Normality Plot')
xlabel('Se Content')
```



Take Aways

This normality plot shows that all 4 populations roughly follow their respective linear regression lines, showing normality and a probable null hyopthesis for their respctive Anderson-Darling Tests.

```

%anderson-darling test for normality
% Ho: sample is normal, H1: sample is non-normal
[h1_norm(1),p1_norm(1), AD_stat(1), cv_norm(1)] = adtest(NRB);
[h1_norm(2),p1_norm(2), AD_stat(2), cv_norm(2)] = adtest(RRB);
[h1_norm(3),p1_norm(3), AD_stat(3), cv_norm(3)] = adtest(SQU);
[h1_norm(4),p1_norm(4), AD_stat(4), cv_norm(4)] = adtest(VEN);

h1_norm
```

```
h1_norm = 1×4 logical array
   0   0   0   0
```

```
p1_norm
```

```
p1_norm = 1×4
    0.7214    0.7539    0.6894    0.9083
```

Decision

Step 7a) Decision : **Fail to Reject H0** (for all 4 groups)

7b) p = see above

7c) We have sufficient statistical evidence to infer that the populations from which these data were randomly sampled are symmetrical and mesokurtic, and, therefore, may be approximated by the Normal distribution.

Based on n = (see below), the A-D tests are appropriate for this analysis.

```
n = [size(NRB,1) size(RRB,1) size(SQU,1) size(VEN,1)]
```

```
n = 1×4
    19    53    30    42
```

Multiple sample size variables are appropriate for this problem because all groups have different sample sizes.

TEST OF VARIANCE

The test of variance will tell us what t-test to use in the test of location.

Underlying Assumptions of the Test :

1. The data are continuous.
2. The data are from a sample that was randomly drawn from a process/population.
3. The data are normally distributed (all groups).

Method: For a three-sample, independent test: Levene Test

Step 1 : (Note that a non-directional test is assumed.)

H0 : variance is equal for all groups

H1: variance is not equal across one or more groups

Step 2: Alpha level; i.e., significance level, or how much Type I error you are willing to make

We will use the same alpha as that for the normality test

```
alpha1
```

```
alpha1 = 0.0500
```

Step 3 : We will use the Levene's Test Statistic (F Statistic)

Step 4 : We will use the RSD for F with (n1-1, n2-1) degrees of freedom

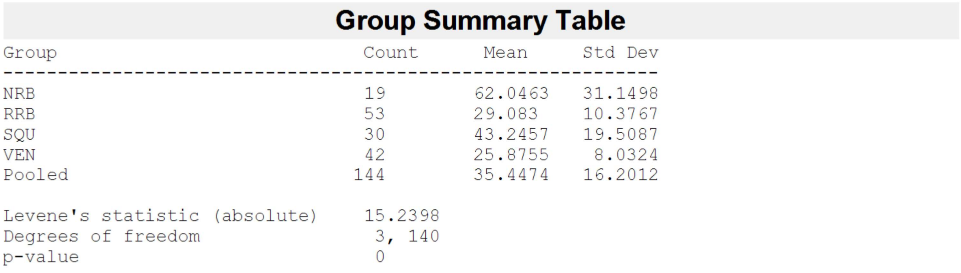
Step 5 : State the Critical Value for Rejecting the Null Hypothesis

We will reject the null if p < 0.05

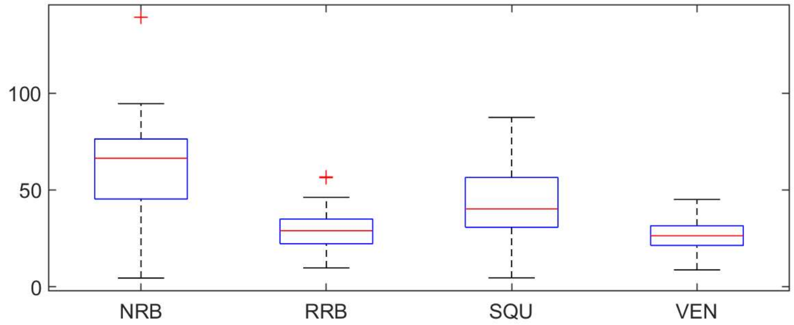
Step 6: Calculations

Levene test for Variance

```
[p_var,STATS_var] = vartestn(raw.selenium,raw.type,'TestType','LeveneAbsolute');
```



```
                    Group Summary Table
Group                                  Count      Mean      Std Dev
---------------------------------------------------------------
NRB                                     19       62.0463    31.1498
RRB                                     53       29.083     10.3767
SQU                                     30       43.2457    19.5087
VEN                                     42       25.8755     8.0324
Pooled                                 144       35.4474    16.2012

Levene's statistic (absolute)           15.2398
Degrees of freedom                        3, 140
p-value                                   0
```



Notice that the p-value is 0 .

Decision

Step 7a) Decision : **Reject H0**

7b) p = 0; Less than alpha

7c) We have sufficient statistical evidence to infer that one or more of the variances of the populations from which these samples were drawn are not equal.

TEST OF LOCATION

Underlying Assumptions of the Test :

1. The data are continuous.
2. The data are from a randomly-drawn sample from a process/population (independent specimens).
3. Independent, Unequal Variance may be known or assumed.

Method: Welche's ANNOVA

Step 1 : (Note that a non-directional test is assumed.)

H0 : All means are equal

H1: All means are not equal (at least two means are statistically different)

Step 2: Alpha level; i.e., significance level, or how much Type I error you are willing to make

We will use the same alpha as that for the normality test

```
alpha1
```

```
alpha1 = 0.0500
```

Step 3 : We will use the F statistic.

Step 4 : We will use the RSD for F with 3 and 140 degrees of freedom.

Step 5 : State the Critical Value for Rejecting the Null Hypothesis

We will reject the null if p < alpha

Step 6: Calculations

```
[p_WANOVA,f_WANOVA,df1_WANOVA,df2_WANOVA] = wanova(data,zdata)
```

```
p_WANOVA = 9.6034e-05
f_WANOVA = 10.7539
df1_WANOVA = 2
df2_WANOVA = 62.9488
```

The p-value is less than alpha.

Decision

Step 7a) Decision : **Reject H0**

7b) p < .001 (p less than alpha)

7c) We have sufficient statistical evidence to infer that the means of one or more of the populations from which these samples were drawn are unequal. (If equal: The difference between mu_1 and mu_2 is due to sampling error, and sampling error alone.)

7d) Appropriate Point Estimates (Selenium Concentrations)

M_NRB = 62.05 | *M_RRB = 29.08* | *M_SQU = 43.25* | *M_VEN = 25.88*

7e) Appropriate Interval Estimate(s)

```
%CI_NRB = paramci(extremes_NRB)
%CI_RRB = paramci(extremes_RRB)
%CI_SQU = paramci(extremes_SQU)
%CI_VEN = paramci(extremes_VEN)
```

7f) Effect Size

FOR ANOVA: We will need to find which groups are different, if we reject the null. We do that through post-hoc analysis.

Post-Hoc Analysis

Games-Howell b/c unequal variances (take into account that they are unbalanced)

```
[h_GH,p_GH,stats_GH]=games_howell(data,zdata,alpha1)
```

```
h_GH = 4×4
   NaN     1     0     1
     1   NaN     1     0
     0     1   NaN     1
     1     0     1   NaN
p_GH = 4×4
       NaN    0.0027    0.1117    0.0020
    0.0027       NaN    0.0046    0.3308
    0.1117    0.0046       NaN    0.0014
    0.0020    0.3308    0.0014       NaN
stats_GH = struct with fields:
    gnames: [4×1 double]
        md: [4×4 double]
         q: [4×4 double]
        df: [4×4 double]
```

```
stats_GH.md
```

```
ans = 4×4
       NaN   32.9633   18.8006   36.1708
  -32.9633       NaN  -14.1626    3.2075
  -18.8006   14.1626       NaN   17.3702
  -36.1708   -3.2075  -17.3702       NaN
```

```
stats_GH.q
```

```
ans = 4×4
```

```
       NaN    6.3973    3.3299    7.0528
   -6.3973       NaN   -5.2208    2.4015
   -3.3299    5.2208       NaN    6.5137
   -7.0528   -2.4015   -6.5137       NaN
```

```
stats_GH.df
```

```
ans = 4×4
       NaN   19.4500   27.0189   19.0916
   19.4500       NaN   38.4816   92.9600
   27.0189   38.4816       NaN   36.0743
   19.0916   92.9600   36.0743       NaN
```

Take Aways:

From the Games-Howell Test, we learn that the pairs of meat that do not reject H0 that there is no statistical difference in the populaiton means are [NRB, SQU] and [RRB,VEN]. The rest of the meats have statistically different means of Selenium content: [NRB > RRB], [NRB > VEN], [SQU > RRB] and [SQU > VEN].

Effect Size

```
[STATS_MES, varargout_mes] = mes1way(data,{'eta2','partialeta2','omega2','partialomega2'},'group',zdata);
```

```
summaryTable = 4×18 cell
```

	1	2	3	4	5	6	7	8	9	
1	'source'	'SS'	'df'	'MS'	'F'	'p'	'eta2'	'ci_lo'	'ci_up'	'pa
2	'between-gr…	2.1262e+04	3	7.0873e+03	27.0012	7.6827e-14	0.3665	0.2338	0.4618	
3	'within-grou…	3.6747e+04	140	262.4802	[ ]	[ ]	[ ]	[ ]	[ ]	
4	'total'	5.8009e+04	143	405.6577	[ ]	[ ]	[ ]	[ ]	[ ]	

CONCLUSION

Ultimately, we learned quite a few different things about our samples. First, from the Anderson-Darling Test we learned that all 4 populations can be assumed to be normally distributed. Second, we learned from the Levene test, that one or more of the variances of the groups was statistically different from the rest. Third, we learned from the Welche's ANOVA that one or more of our populations have a mean that is statistically different. Fourth, we learned from our Games-Howell Test in our Post-Hoc Analysis there is no statistical difference of the means for the following pairs of meat types: [NRB, SQU] and [RRB,VEN]. The rest of the meats have statistically different means of Selenium content: [NRB > RRB], [NRB > VEN], [SQU > RRB] and [SQU > VEN]. Finally, we learned from our omega squared values that 35% of the overall variance comes from the difference in the means between the groups.