**Proc** **format**;

value fmtins **0** = "Memorial Sloan-Kettering"

**1** = "Mayo Clinic"

**2** = "John Hopkins" ;

value fmtgp **1** = "Study"

**0** = "Control";

value fmtmd **0** = "Routine Cytology"

**1** = "Routine X-ray"

**2** = "Both X-ray and Cytology"

**3** = "Interval" ;

value fmtsc **0** = "Alive"

**1** = "Dead of lung cancer"

**2** = "Dead of other causes";

value fmtct **0** = 'Epidermoid'

**1** = 'Adenocarcinoma'

**2** = 'Large Cell'

**3** = 'Oat Cell'

**4** = 'Other';

value fmtyn **1** = 'yes'

**0** = 'no';

**run**;

\*1 and 2 ,Label and Format SAS variables and read permanent SAS data set;

libname IN 'E:\Fall 2021\HandsOn\handson2';

**data** tumor;

set IN.tumor;

Label ptid = "Patient ID"

detectiontype = "Means of Detection"

celltype = "Cell Type"

survivalcat = "Survival Category";

format institution fmtins. group fmtgp. detectiontype fmtmd. survivalcat fmtsc. celltype fmtct.

Operated fmtyn.;

**proc** **print** data=tumor label;

**run**;

\* 3;

**proc** **contents** data=tumor varnum short;

**run**;

\*4;

**proc** **freq** data=tumor;

tables group survivalcat group\*survivalcat/ nocol norow;\* nopercent; \*out=IN.temp ;\* table and tables are same;

**run**;

\*5;

**proc** **means** data=tumor n mean std median;\* noprint;

class group;

var survival;

output out=outmean mean=ave\_surv max=max\_surv min = min\_surv;

**run**;

**proc** **sort** data=tumor;

by group;

**proc** **means** data=tumor n mean std median;

var survival;

by group;

\*output out=outmean mean=ave\_surv max=max\_surv min = min\_surv;

**run**;

\*6;

**proc** **univariate** data=tumor plot normal;

class group;

var survival;

title 'Descriptive Statistics on Survival';

title2 'By Treatment Group';

**run**;

**proc** **sort** data=tumor;

by group;

**run**;

**proc** **plot** data=tumor;

plot survival\*stagea="o";

by group;

**run**;

\*7;

**proc** **ttest** data=tumor;

class group;

var survival;

title ' T-test to compare the mean difference between treatment group';

footnote 'Hands on section 2';

**run**;

\*8 and 9;

**proc** **ttest** data=tumor;

where stagea = **2**;

class group;

var survival;

title ' T-test to compare the mean difference between treatment group in Stage = 2';

footnote 'Hands on section 2';

**run**;

\*\* Question2;

**data** OB;

input gender infection count;

datalines;

1 19 90

1 20 12

1 23 9

1 25 4

2 21 3

2 23 10

2 25 4

2 29 30

;

**proc** **print**;

**run**;

\*1;

**proc** **sort**;

by gender;

;

**proc** **means** data=ob;

by gender;

freq count;

**run**;

**proc** **ttest** data=ob;

class gender;

var infection;

freq count;

title "T-test using 'freq' option";

**run**;

\*2;

**proc** **freq** data=ob;

table gender;

weight count;

title "Frequence table using 'weight' option";

**run**;