**SPSS 25 Syntax used for Muscle mass analysis:**

\*\*\*create diagnostic scatterplots for assumptions\*\*\*

GGRAPH

/GRAPHDATASET NAME="graphdataset" VARIABLES=control treated Treatment MISSING=LISTWISE

REPORTMISSING=NO

/GRAPHSPEC SOURCE=INLINE

/FITLINE TOTAL=NO SUBGROUP=NO.

BEGIN GPL

SOURCE: s=userSource(id("graphdataset"))

DATA: control=col(source(s), name("control"))

DATA: treated=col(source(s), name("treated"))

DATA: Treatment=col(source(s), name("Treatment"), unit.category())

GUIDE: axis(dim(1), label("control"))

GUIDE: axis(dim(2), label("treated"))

GUIDE: legend(aesthetic(aesthetic.color.exterior), label("Treatment"))

GUIDE: text.title(label("Grouped Scatter of treated by control by Treatment"))

SCALE: linear(dim(1), min(100), max(450))

SCALE: linear(dim(2), min(100), max(450))

SCALE: cat(aesthetic(aesthetic.color.exterior), include("1", "2"))

ELEMENT: point(position(control\*treated), color.exterior(Treatment))

END GPL.

\*\*\*Homogenity of regression slopes\*\*\*

UNIANOVA treated BY Treatment WITH control

/METHOD=SSTYPE(3)

/INTERCEPT=INCLUDE

/CRITERIA=ALPHA(0.05)

/DESIGN=Treatment control Treatment\*control.

\*\*\*Univariate ANCOVA\*\*\*

UNIANOVA treated BY Treatment WITH control

/METHOD=SSTYPE(3)

/INTERCEPT=INCLUDE

/SAVE=RESID ZRESID

/EMMEANS=TABLES(Treatment) WITH(control=MEAN) COMPARE ADJ(BONFERRONI)

/PRINT ETASQ DESCRIPTIVE HOMOGENEITY

/CRITERIA=ALPHA(.05)

/DESIGN=control Treatment.

\*\*\*Testing for Normality\*\*\*

EXAMINE VARIABLES=ZRE\_1 BY Treatment

/PLOT BOXPLOT NPPLOT

/COMPARE GROUPS

/STATISTICS DESCRIPTIVES

/CINTERVAL 95

/MISSING LISTWISE

/NOTOTAL.

\*\*\*Testing for homoscedasticity \*\*

GGRAPH

/GRAPHDATASET NAME="graphdataset" VARIABLES=PRE\_1 ZRE\_1 Treatment MISSING=LISTWISE

REPORTMISSING=NO

/GRAPHSPEC SOURCE=INLINE

/FITLINE TOTAL=NO.

BEGIN GPL

SOURCE: s=userSource(id("graphdataset"))

DATA: PRE\_1=col(source(s), name("PRE\_1"))

DATA: ZRE\_1=col(source(s), name("ZRE\_1"))

DATA: Treatment=col(source(s), name("Treatment"), unit.category())

GUIDE: axis(dim(1), label("Predicted Value for treated"))

GUIDE: axis(dim(2), label("Standardized Residual for treated"))

GUIDE: axis(dim(3), label("Treatment"), opposite())

GUIDE: text.title(label("Simple Scatter of Standardized Residual for treated by Predicted ",

"Value for treated by Treatment"))

SCALE: cat(dim(3), include("1", "2"))

ELEMENT: point(position(PRE\_1\*ZRE\_1\*Treatment))

END GPL.

**SPSS 25 Syntax used for retrograde labeling analysis:**

\*Nonparametric Tests: Independent Samples.

NPTESTS

/INDEPENDENT TEST (labeled\_neurons) GROUP (Treatment)

/MISSING SCOPE=ANALYSIS USERMISSING=EXCLUDE

/CRITERIA ALPHA=0.05 CILEVEL=95.

\*\*\*medians\*\*\*

MEANS TABLES=labeled\_neurons BY Treatment

/CELLS=COUNT MEDIAN.

\*\*\*mean ranks\*\*\*

NPAR TESTS

/K-W=labeled\_neurons BY Treatment(0 2)

/MISSING ANALYSIS.

\*\*\*boxplot\*\*\*

EXAMINE VARIABLES=labeled\_neurons BY Treatment

/PLOT BOXPLOT NPPLOT

/COMPARE GROUPS

/STATISTICS NONE

/CINTERVAL 95

/MISSING LISTWISE

/NOTOTAL.