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| **Block** | **R Code** | **Process Code** |
| 1 | #upper anterior measurement | comment |
| 1 | anterior <- lm(ProximateAnalysisData$PSUA~ProximateAnalysisData$Lipid) | lm, create object |
| 1 | summary(anterior) | summary of lm object |
| 1 | with(ProximateAnalysisData, plot(PSUA ~ Lipid, las = 1)) | scatterplot of variables in lm, using with() |
| 1 | abline(anterior) | adding lm line to plot |
| 1 | plot(anterior) | diagnostic plot |
| 2 | posterior <- lm(ProximateAnalysisData$PSUP ~ ProximateAnalysisData$Lipid) | lm, create object |
| 2 | summary(posterior) | summary of lm object |
| 2 | posterior | inspect lm object |
| 2 | with(ProximateAnalysisData, plot(PSUP ~ Lipid, las = 1)) | scatterplot of variables in lm, using with() |
| 2 | abline(posterior) | add lm line to plot |
| 2 | plot(posterior) | diagnostic plot |
| 3 | #OUTLIER REMOVED | comment |
| 3 | anterior2 <- lm(ProximateAnalysisDataOutlier$PSUA ~ ProximateAnalysisDataOutlier$Lipid) | lm, create object |
| 3 | summary(anterior2) | summary of lm object |
| 3 | with(ProximateAnalysisDataOutlier, plot(PSUA ~ Lipid, las = 1, xlab = "Whole-body Lipid Content (%)", ylab = "UA Fatmeter Reading")) | scatterplot of variables in lm, using with(), changing axis labels |
| 3 | abline(anterior2) | adding lm line to plot |
| 3 | plot(anterior2) | diagnostic plot |
| 3 | anterior2 | inspecting lm object |
| 4 | posterior2 <- lm(ProximateAnalysisDataOutlier$PSUP ~ ProximateAnalysisDataOutlier$Lipid) | lm, create object |
| 4 | summary(posterior2) | summary of lm object |
| 4 | with(ProximateAnalysisDataOutlier, plot(PSUP ~ Lipid, las = 1, xlab = "Whole-body Lipid Content (%)", ylab = "UP Fatmeter Reading")) | scatterplot of variables in lm, using with(), changing axis labels |
| 4 | abline(posterior2) | add lm line to plot |
| 4 | plot(posterior2) | diagnostic plot |
| 4 | posterior2 | inspect lm object |
| 5 | qt(.975,9) | function calculation |
| 6 | #upper Middle measurements only | comment |
| 6 | middle <- lm(ProximateAnalysisData$PSUM ~ ProximateAnalysisData$Lipid) | lm, create object |
| 6 | summary(middle) | summary of lm object |
| 6 | with(ProximateAnalysisData, plot(PSUM ~ Lipid, las = 1, xlab = "Whole-body Lipid Content (%)", ylab = "UM Fatmeter Reading")) | scatterplot of variables in lm, using with(), changing axis labels |
| 6 | abline(middle) | adding lm line to plot |
| 6 | plot(middle) | diagnostic plot |
| 6 | middle | inspect lm object |
| 7 | middleLog <- lm(ProximateAnalysisData$logPSUM ~ ProximateAnalysisData$Lipid) | lm, create object |
| 7 | summary(middleLog) | summary of lm object |
| 7 | with(ProximateAnalysisData, plot(logPSUM ~ Lipid, las = 1)) | scatterplot of variables in lm, using with() |
| 7 | abline(middleLog) | add lm line to plot |
| 7 | plot(middle) | diagnostic plot |
| 7 | with(ProximateAnalysisData, plot(Lipid ~ logPSUM, las = 1)) | scatterplot of variables in lm, using with() |
| 8 | #Means and sd of data | comment |
| 8 | mean(ProximateAnalysisData$Lipid) | data summary (mean) |
| 8 | sd(ProximateAnalysisData$Lipid) | data summary (sd) |