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| > # loading the library  > library(faraway)  > # specifying the dataset  > data("prostate")  > head(prostate)  lcavol lweight age lbph svi lcp gleason pgg45 lpsa  1 -0.5798185 2.7695 50 -1.386294 0 -1.38629 6 0 -0.43078  2 -0.9942523 3.3196 58 -1.386294 0 -1.38629 6 0 -0.16252  3 -0.5108256 2.6912 74 -1.386294 0 -1.38629 7 20 -0.16252  4 -1.2039728 3.2828 58 -1.386294 0 -1.38629 6 0 -0.16252  5 0.7514161 3.4324 62 -1.386294 0 -1.38629 6 0 0.37156  6 -1.0498221 3.2288 50 -1.386294 0 -1.38629 6 0 0.76547  > lmod = lm(lpsa~lcavol,data=prostate)  >  > # generating output  > summary(lmod)  Call:  lm(formula = lpsa ~ lcavol, data = prostate)  Residuals:  Min 1Q Median 3Q Max  -1.67625 -0.41648 0.09859 0.50709 1.89673  Coefficients:  Estimate Std. Error t value Pr(>|t|)  (Intercept) 1.50730 0.12194 12.36 <2e-16 \*\*\*  lcavol 0.71932 0.06819 10.55 <2e-16 \*\*\*  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1  Residual standard error: 0.7875 on 95 degrees of freedom  Multiple R-squared: 0.5394, Adjusted R-squared: 0.5346  F-statistic: 111.3 on 1 and 95 DF, p-value: < 2.2e-16  >  > # saving the output in a pdf file  > pdf(file="C:/Users/buchh/OneDrive/Desktop/cmp and graph in stat/hw5/output.pdf")  > # drawing histogram  > hist(residuals(lmod),main="Histogram of the Residuals")  > anova(lmod)  Analysis of Variance Table  Response: lpsa  Df Sum Sq Mean Sq F value Pr(>F)  lcavol 1 69.003 69.003 111.27 < 2.2e-16 \*\*\*  Residuals 95 58.915 0.620  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1  > dev.off()  null device  1 |
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