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| **Evaluating Conditions of Residuals for Regression** |
| **Distribution of residuals (to evaluate normality condition)**  broom::augment(my\_model) %>%  ggplot(mapping = aes(x = .resid)) +  geom\_histogram() +  labs(x = "Residual")  ***Note:*** In the above code my\_model represents the linear model that was fit, this can be either a simple **or** multiple linear regression! |
| **Residuals versus fitted values (to evaluate equal variance condition)**  broom::augment(my\_model) %>%  ggplot(mapping = aes(y = .resid, x = `<NAME OF EXPLANATORY VARIABLE>`)) +  geom\_point() +  geom\_hline(yintercept = 0, color = "red", linewidth = 3) +  labs(x = "<NAME OF EXPLANATORY VARIABLE>",  y = "Residuals")  ***Note:*** In the above code my\_model represents the linear model that was fit, this can be either a simple **or** multiple linear regression! |