

## Results

Table 1 shows descriptive statistics of the study variables. There were no missing values in the data and all participants were included for our final analysis. In the first analysis step, we regressed height on weight and age. The assumptions of normality of residuals and homogeneity of variance were violated (figure 1). The diagnostic plots suggest that a curvilinear model should be more suitable. Following the guidelines of de Weerth (2017) we fitted a quadratic model in the next step, which led to a more appropriate model (figure 2). The final model was as follows:

$$y_i \sim N(\mu, \sigma)$$
$$\mu_i = \beta_0 + \beta_1 \times \text{weight} + \beta_2 \times \text{weight}^2 + \beta_3 \times \text{weight}^3 + \beta_4 \times \text{gender}$$

We found that weight is positively associated with height (table 2) and that the relation can best be described using a polynomial regression model. However, the assumptions of constant variance remains violated as the error variation increases with age indicating that we miss important predictors that explain height development in humans. Furthermore we found that males are 0.122 taller than females on average ( $p < .001$ ). Figure 3 shows the regression lines for each gender that are most compatible with the real observations (black dots).

## References

de Weerth, Carolina. 2017. “Do Bacteria Shape Our Development? Crosstalk Between Intestinal Microbiota and HPA Axis.” *Neuroscience & Biobehavioral Reviews* 83 (December): 458–71. <https://doi.org/10.1016/j.neubiorev.2017.09.016>.

Table 1: Descriptive Statistics

variable	mean	sd	min	max
height	138.26	27.60	53.98	179.07
weight	35.61	14.72	4.25	62.99
age	29.34	20.75	0.00	88.00

*Note:* Some table note

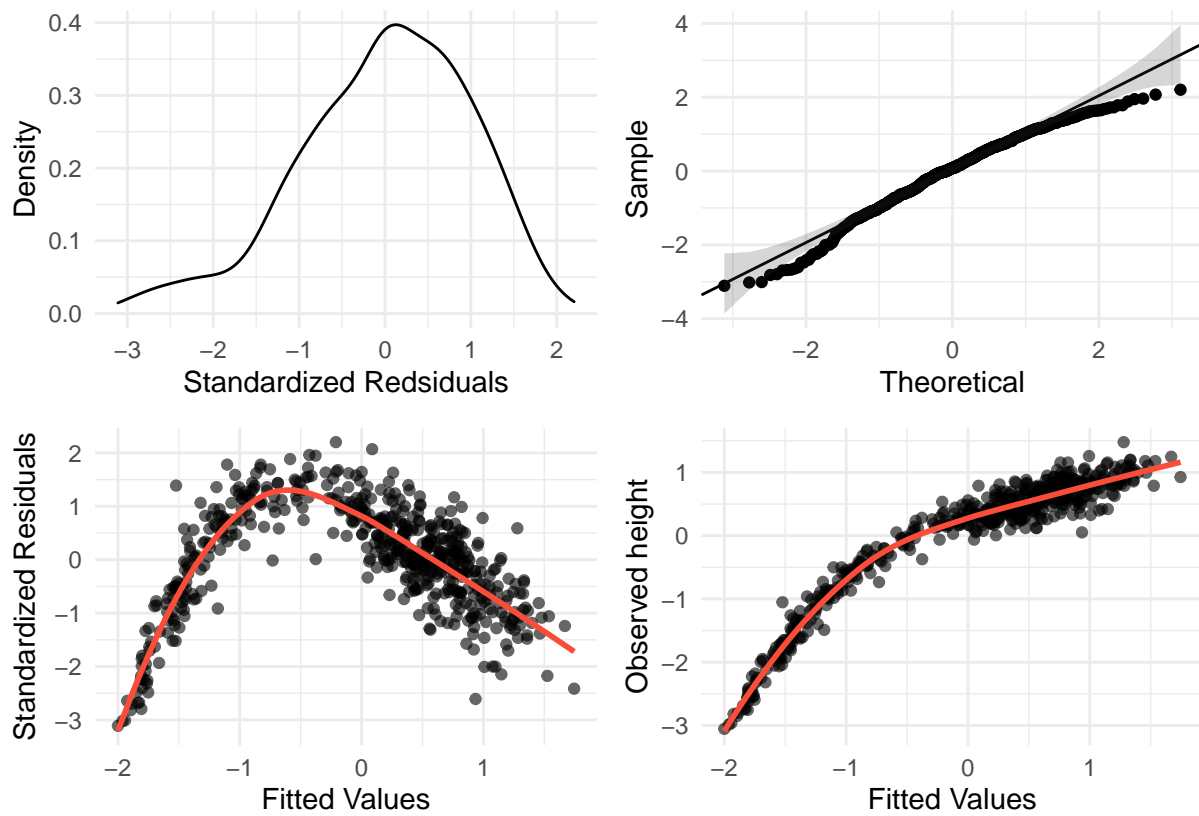


Figure 1: Diagnostic Plots Standard Regression Model

Table 2: Regression Coefficients

Parameter	Estimate	Standard Error	t-value	p-value
intercept	0.269	0.012	22.812	< .001
weight_s	0.544	0.017	32.581	< .001
weight_s2	-0.262	0.010	-27.032	< .001
weight_s3	0.119	0.008	14.500	< .001
male	0.122	0.015	7.977	< .001

*Note:* Some table note

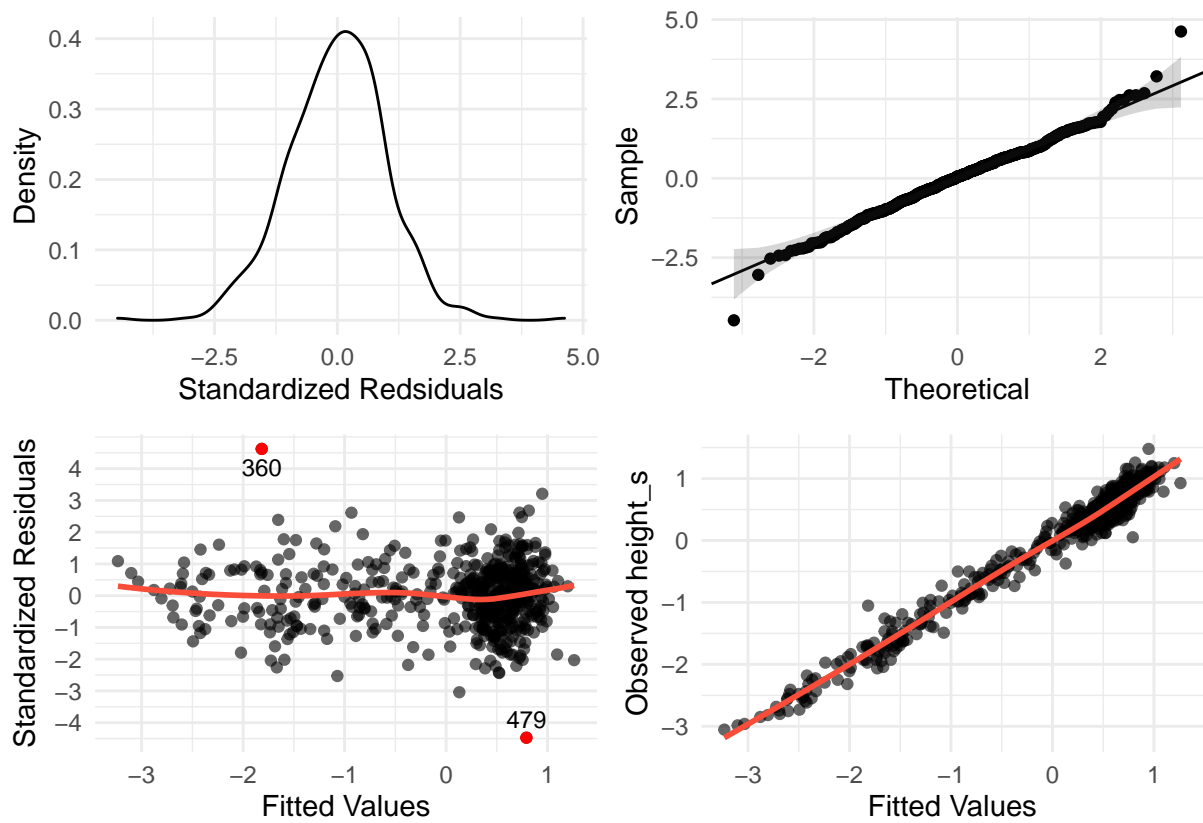


Figure 2: Diagnostic Plots Polynomial Regression

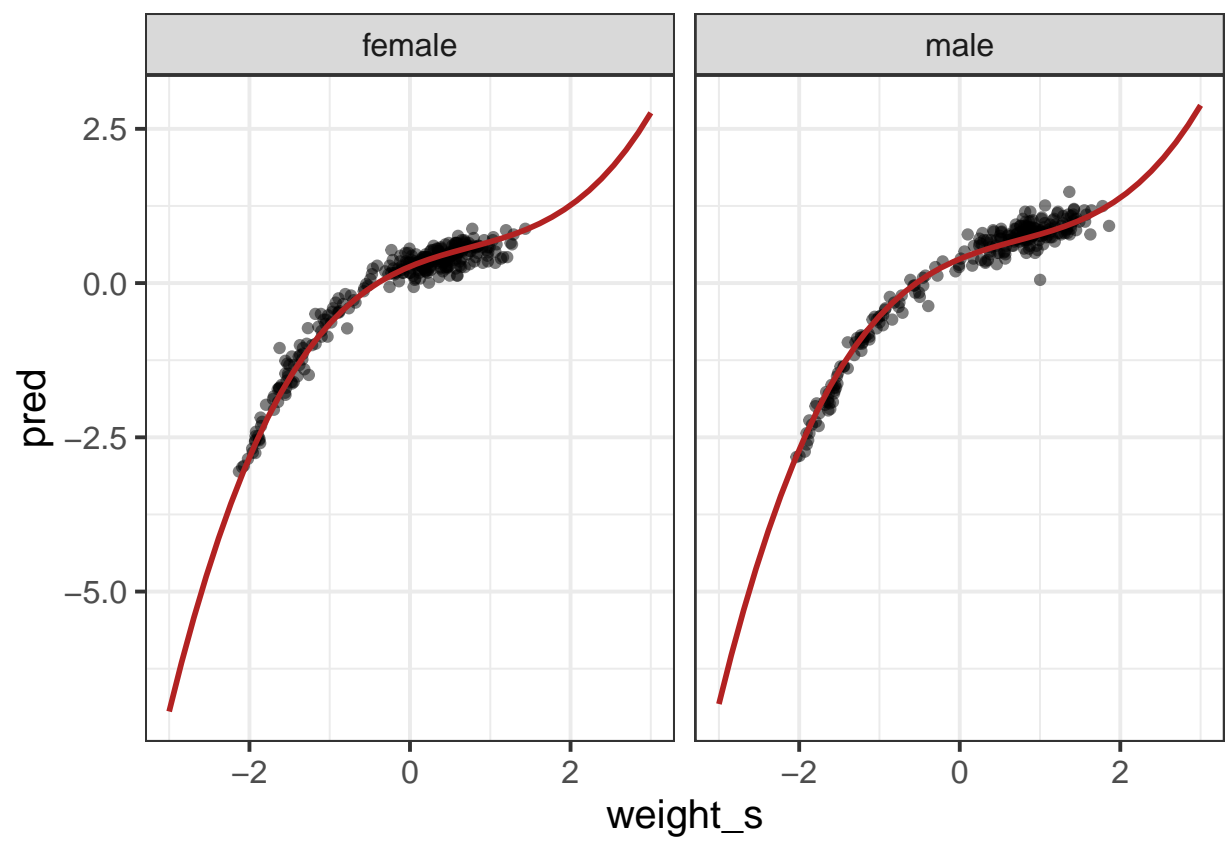


Figure 3: Regression lines of the final model