

Sta 440 Case 4

Christina Lee, Steph Reinke

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1. Background

Root growth in the rice plant is characterized by a distinct rotational motion called circumnutiation. Researchers want to better understand this process. Experimental data was collected on the developing roots of two strains of rice plants, one a wild type (WT) variety and the other a mutant (MU) variety that lacks circumnutiation. In particular, cell length and position measurements were collected on cells on the inner and outer curves of a sample of roots representing the two genetic strains. The protocol utilized in this study is as follows:

1. The mid-line on the central slice of a root and its point of maximum curvature are identified
2. The lengths of the cells on the inner and outer curves of the root slice are measured and recorded for those cells falling in a window around the point of maximum curvature.

This process was repeated on nine WT and eleven MU genotype roots. By understanding the differences in growth based on side and genotype, researchers can gain a better understanding of circumnutiation and rice plants.

Research Questions

Can the physical mechanism behind root circumnutiation in the wild type plants be explained by differential patterns of cell growth on opposing sides of the root? Is there evidence that these patterns are diminished in the mutant genotype?

2. Data and Frequentist Model

To answer these questions we examined the resulting dataset of the process described above. The dataset contains: length, midline (distance from root tip along midline), root ID ((WT)1-9 \$ (MU)1-11), side (inner or outer), and genotype (wild type (WT) & mutant (MU)) for each observation. We conducted exploratory data analysis to see how length varied by root, side, and genotype. For WT roots, there is a visible difference between inner and outer cell lengths, and this difference varies by root id (Fig 1). For MU roots, the inner and outer cell lengths tend to be similar (Fig 2). A combined analysis showed that inner and outer cell lengths are distributed the same for MU roots, while outer tends to be longer than inner cells for WT roots (Fig 3).

We began with a frequentist nonlinear model to explore if Length varied by side and genotype. Our initial approach used was a seven parameter logistic curve with side and genotype effects. However, after discussion we determined that this model inappropriately assumed a constant midline across roots, which limited its biological realism. To address this issue, we refit the data using a four parameter logistic growth model with root specific random effects. The model estimates cell length (Length) as a function of scaled midline position (M):

$$\log(\text{Length}) = L + \frac{U - L}{1 + \exp\left(-\frac{M_{\text{scaled}} - x_{\text{mid}}}{s}\right)}$$

Where: L: lower asymptote (minimum log Length), U: upper asymptote (maximum log Length), xmid: midpoint (inflection point) of sigmoid curve, s: scale parameter

We included fixed effects for side (inner vs outer) and genotype (WT vs MU), as well as their interaction on U and xmid to test whether growth patterns differ across genotypes and sides of the root. Random effects for xmid and s were included at the root level to allow for root specific inflection points and slopes, accounting for biological variability in growth. Because residual plots from earlier indicated heteroskedasticity we log transformed our response variable (Length) to improve model fit.

The model was fit using the nlme package in R. Convergence was achieved by extending the max iterations to 200. Residuals versus fitted values by genotype, side, and root do not show any systematic structure (Fig 4-7). The QQ plot of the residuals followed the diagonal line suggesting that normality was met (Fig 8). The predicted curves by side (outer vs inner) were plotted against the data, which showed goodness of fit. No visible difference could be seen between the two MU curves, but the outer curve had consistently larger lengths for the WT (FIG 9 & 10). The key parameters are the side and genotype interaction terms for U and xmid. The estimated coefficient for the interaction between side, genotype and U was negative, but not statistically significant (p-value of 0.5603) (TABLE 1). The estimated coefficient for the interaction between side, genotype, and xmid was negative and statistically significant (p-value of <0.001) (TABLE 1). This suggests that for WT roots the inflection point occurs closer to the root base on the outer side compared to the inner side and compared to MU roots. Thus supporting differential patterns of cell growth by side and genotype.

3. Bayesian Model

4. Shortcomings and Assumptions

5. Conclusion

#6. Appendix

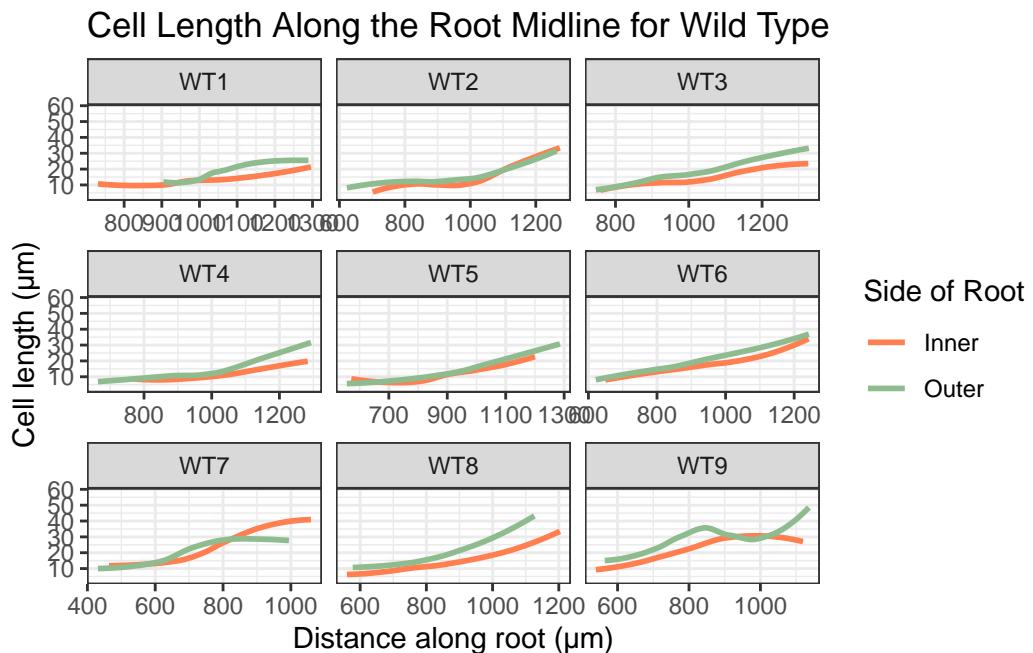


Figure 1: The difference between inner and outer cell lengths changes root by root

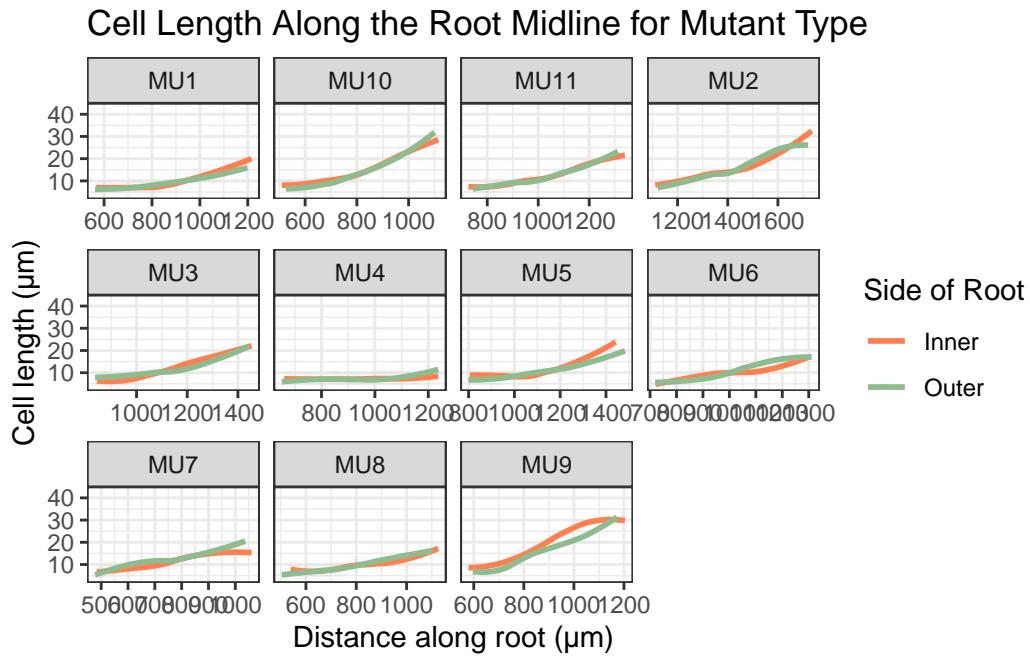


Figure 2: There is only slight differences between inner and outer cell lengths

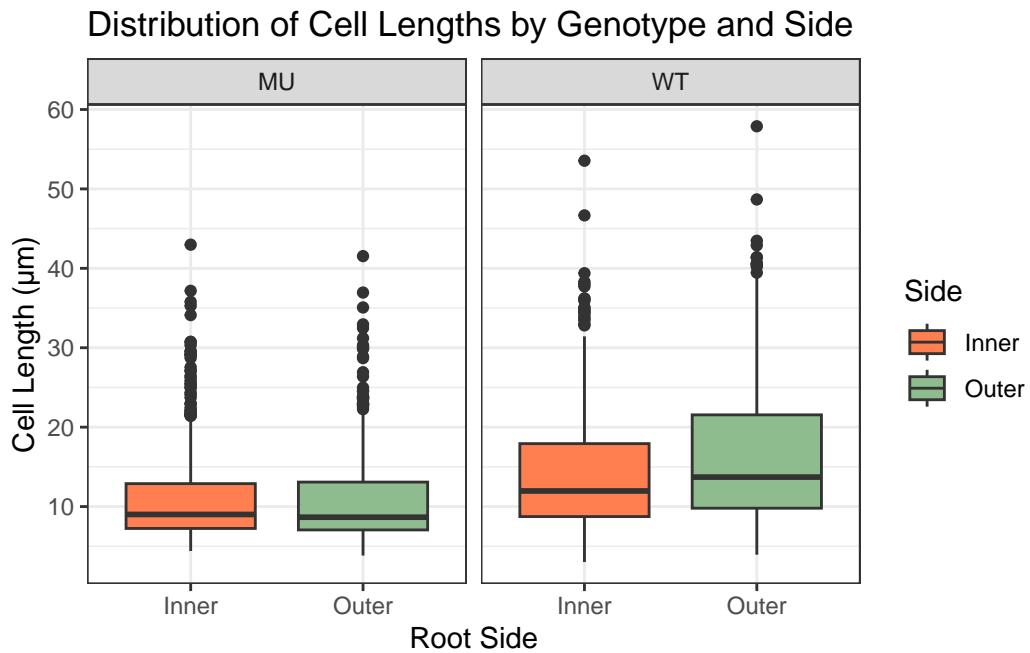


Figure 3: MU cells have similar inner vs outer lengths; WT outer has longer lengths than inner

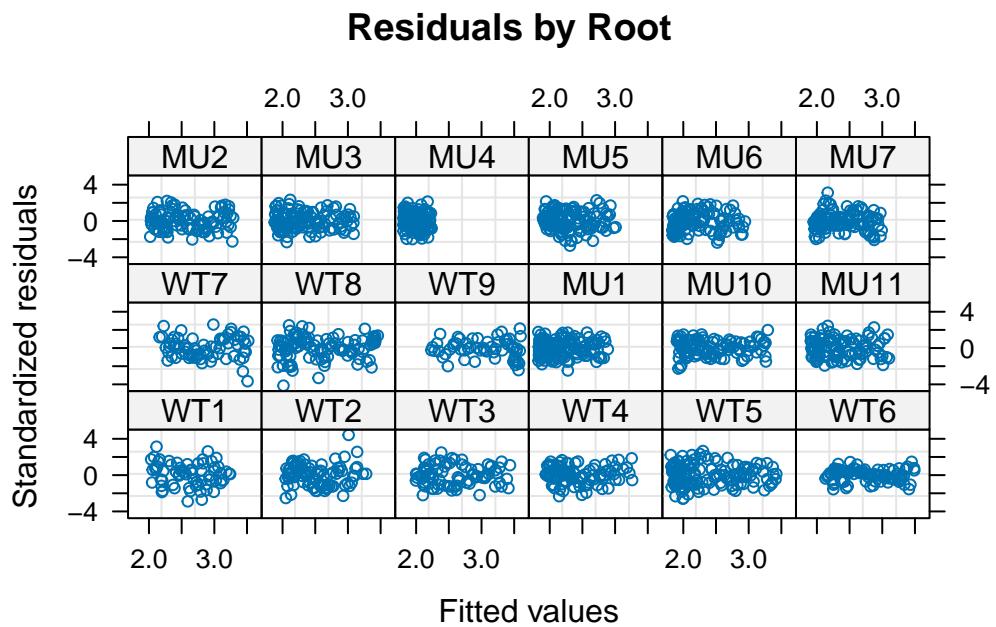


Figure 4: Residual plot

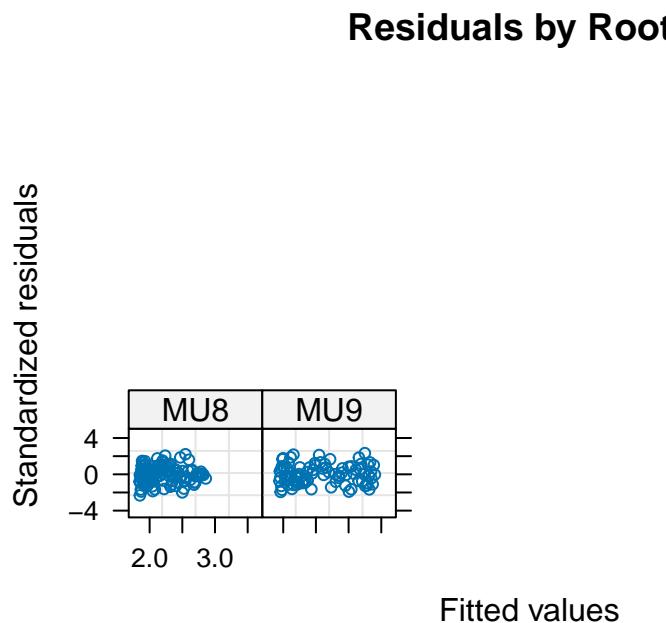


Figure 5: Residual plot

Residuals by Genotype

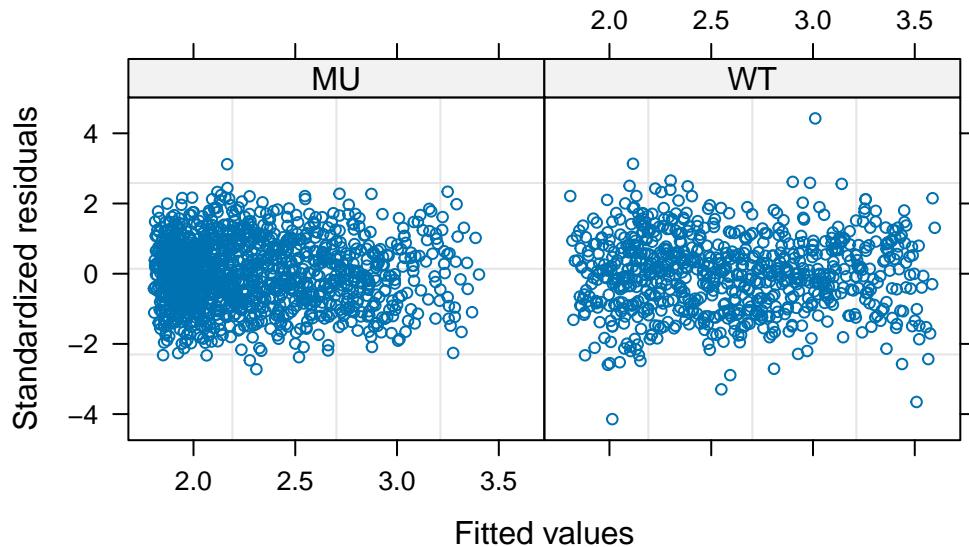


Figure 6: Residual plot

Residuals by Side

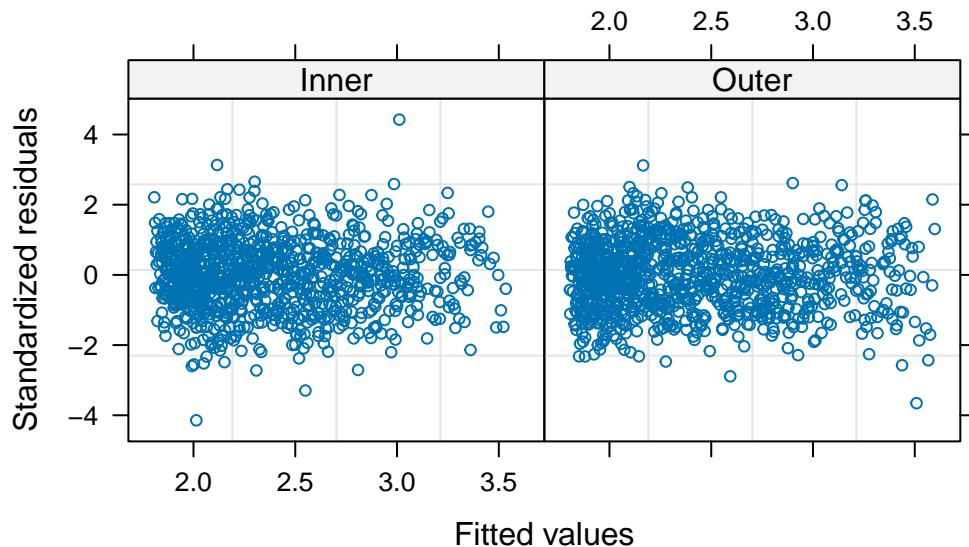


Figure 7: Residual plot

Residuals vs Fitted

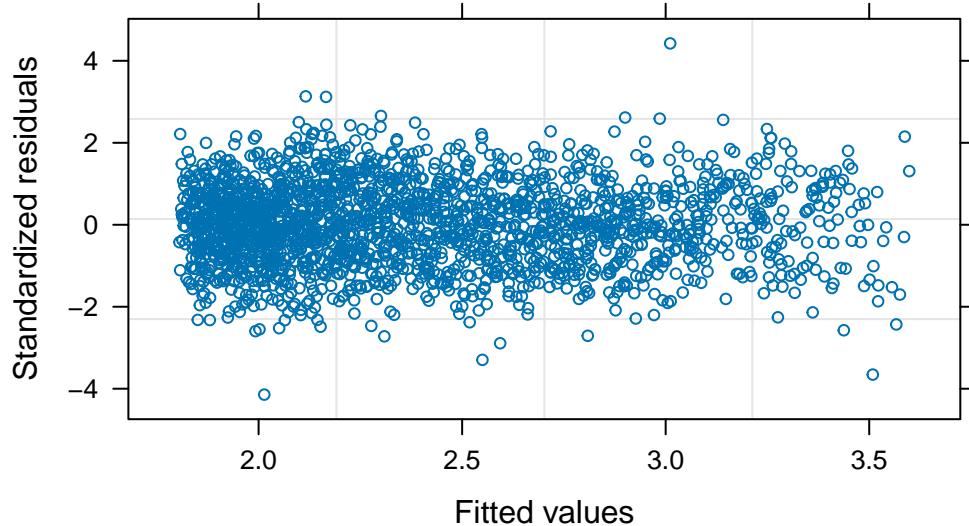


Figure 8: Residual plot

Normal Q–Q Plot

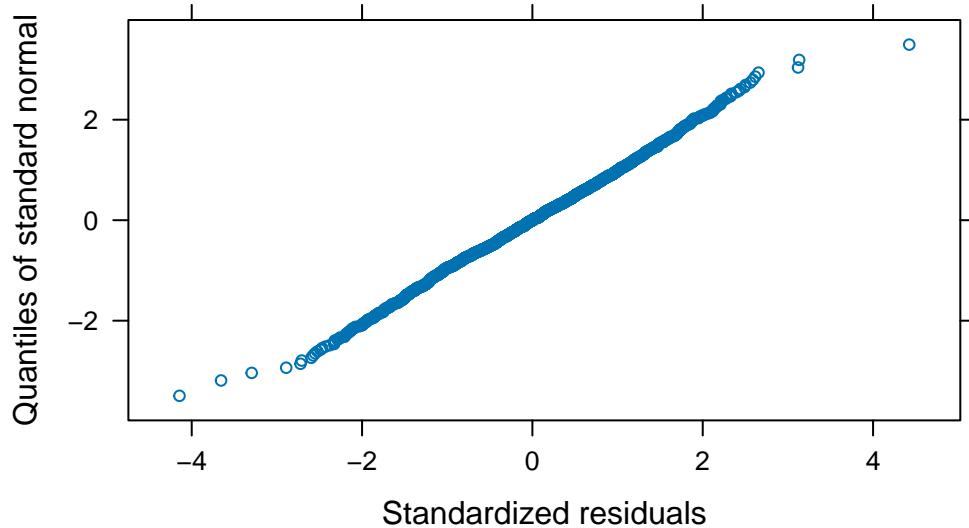


Figure 9: Residual plot

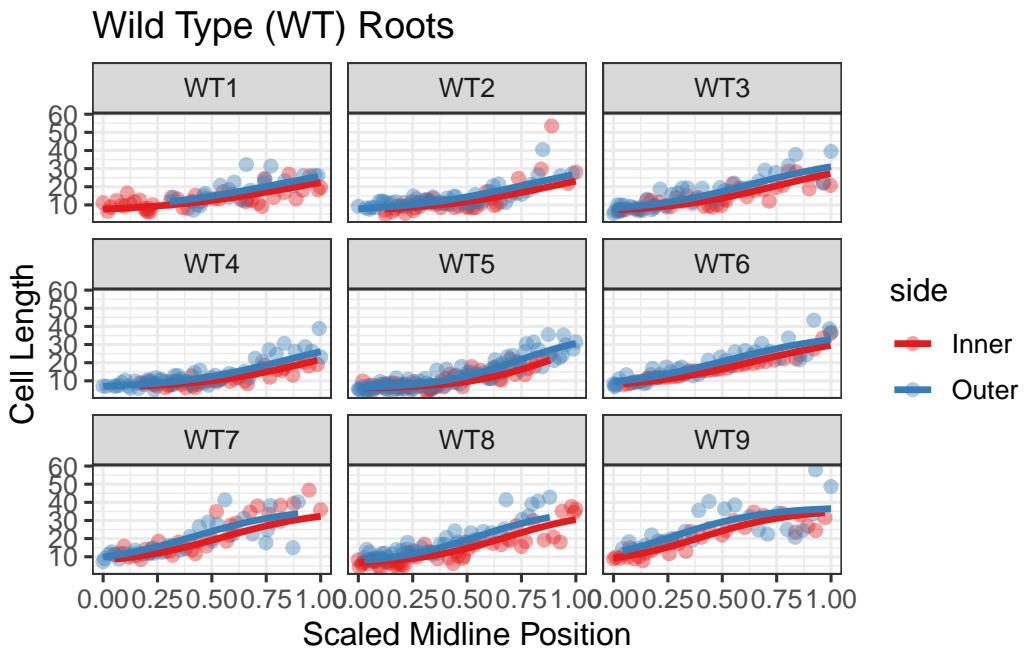


Figure 10: Residual plot

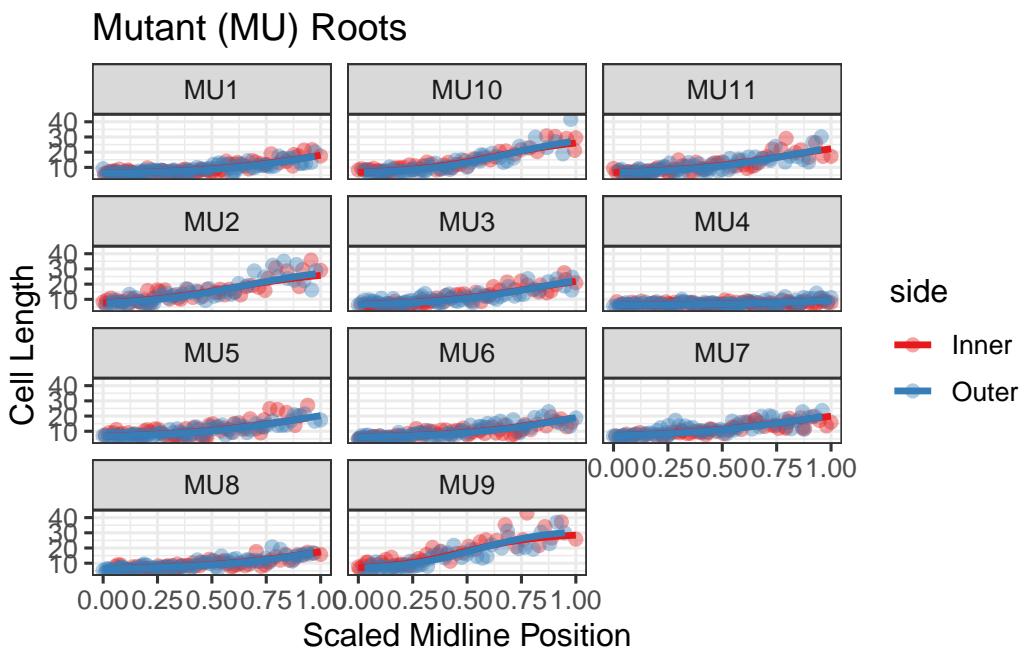


Figure 11: Residual plot

	Value	Std.Error	DF	t-value	p-value
L	1.7376245	0.0318986	2077	54.4734396	0.0000000
U.(Intercept)	3.3913224	0.0716386	2077	47.3393166	0.0000000
U.sideOuter	0.0886904	0.0690895	2077	1.2837020	0.1993894
U.GenotypeWT	0.2004287	0.0899438	2077	2.2283765	0.0259621
U.sideOuter:GenotypeWT	-0.0531306	0.0912027	2077	-0.5825553	0.5602559

	Value	Std.Error	DF	t-value	p-value
xmid.(Intercept)	0.6468256	0.0641757	2077	10.0789831	0.0000000
xmid.sideOuter	0.0455478	0.0233569	2077	1.9500751	0.0513015
xmid.GenotypeWT	-0.1064539	0.0764380	2077	-1.3926832	0.1638647
xmid.sideOuter:GenotypeWT	-0.1750729	0.0317632	2077	-5.5118061	0.0000000
s	0.2777700	0.0213874	2077	12.9875252	0.0000000

Residual plot