Sta 440 Case 4

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1. Background

Root growth in the rice plant is characterized by a distinct rotational motion called circumnutation. 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 circumnutation. 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 circumnutation and rice plants.

Research Questions

Can the physical mechanism behind root circumnutation 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):

$$\log(\text{Length}) = L + \frac{U - L}{1 + \exp\left(-\frac{\text{M}_{\text{scaled}} - \text{xmid}}{s}\right)}$$

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). 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.f

3. Bayesian Model

Main model equation

$$\log(\text{Length}_{ij}) \sim \mathcal{N}(\mu_{ij}, \tau_{\text{within}})$$

$$\mu_{ij} = L + \frac{U_{ij} - L}{1 + \exp\left(-\frac{M_{ij} - \text{xmid}_{ij}}{s_{ij}}\right)}$$

Fixed Effects (same as frequentist)

Upper asymptote (U)**:**

$$U_{ij} = \beta_{U,0} + \beta_{U,\text{side}} \cdot \text{Side}_{ij} + \beta_{U,\text{geno}} \cdot \text{Genotype}_{ij} + \beta_{U,\text{side}\times\text{geno}} \cdot \text{Side}_{ij} \times \text{Genotype}_{ij}$$

Midpoint (xmid):

$$\text{xmid}_{ij} = \beta_{\text{xmid},0} + \beta_{\text{xmid,side}} \cdot \text{Side}_{ij} + \beta_{\text{xmid,geno}} \cdot \text{Genotype}_{ij} + \beta_{\text{xmid,side}\times\text{geno}} \cdot \text{Side}_{ij} \times \text{Genotype}_{ij} + b_{\text{xmid},j}$$

Scale parameter (on log scale for positivity):

$$s_{ij} = \exp(b_{s,0} + b_{s,j})$$

Random Effects Priors

$$b_{\text{xmid},j} \sim \mathcal{N}(0, \tau_{\text{xmid}})$$

$$b_{s,j} \sim \mathcal{N}(0, \tau_s)$$

Fixed Effects Priors

$$
\begin{aligned}
L &\sim \text{Uniform}(1, 3) \\
\beta_{U,0} &\sim \text{Uniform}(2, 4) \\
\beta_{U,\text{side}}, \beta_{U,\text{geno}}, \beta_{U,\text{side}\times\text{geno}} &\sim \mathcal{N}(0, 10) \\
\beta_{\text{xmid},0} &\sim \text{Uniform}(0.3, 0.7) \\
\beta_{\text{xmid,side}}, \beta_{\text{xmid,geno}}, \beta_{\text{xmid,side}\times\text{geno}} &\sim \mathcal{N}(0, 10) \\
b_{s,0} &\sim \mathcal{N}(\log(0.2), 1)
\end{aligned}
$$

Variance Parameter Priors

$$
\begin{aligned}
\sigma &\sim \text{Uniform}(0, 2) \\
\sigma_{\text{xmid}} &\sim \text{Uniform}(0, 1) \\
\sigma_s &\sim \text{Uniform}(0, 1)
\end{aligned}
$$

Next, we fit a Bayesian version of our frequentist model using JAGS and MCMC sampling. Because our nonlinear growth model was complex, the dataset was relatively small (20 roots), and the data had a hierarchical structure, a Bayesian approach was beneficial to use. It allowed us to use prior knowledge about biologically reasonable parameter ranges and to obtain stable estimates through partial pooling across roots. We used the four-parameter logistic growth model to describe how cell length (after applying a log transformation) changes along the middle of the root. The model parameters represent key features of growth including the lower asymptote (L) which reflects baseline cell size near the root tip, the upper asymptote (U) which represents maximum cell length in the differentiation zone, the midpoint (xmid) which indicates where elongation is most rapid, and the scale parameter (s) which controls how steeply the transition between zones occurs. To test our main hypothesis that uneven growth between the inner and outer sides of the root causes circumnutation and that it is not present in the mutant, we included fixed effects for side, genotype, and their interaction on both the U and xmid parameters. The interaction terms directly test whether the inner-outer growth difference changes between wild-type and mutant plants. We included random effects for xmid and s (modeled on the log scale to maintain positivity) to account for variation among individual roots and within-root correlation. We also made sure to specify weakly informative priors in order to best reflect reasonable expectations in terms of biology and plants. For example, L had a Uniform(1, 3) prior, U had a Uniform(2, 4) prior to make sure mature cells are larger than the young growing cells, xmid had a Uniform(0.3, 0.7) prior to keep the midpoint within the main root region, and the log-scale parameter for s had a Normal(log(0.2), 1) prior. All side and genotype effects were given Normal(0, 10) priors, which limited extreme values but allowed effects in either direction (positive or negative). Standard deviation parameters had Uniform(0, 2) priors for observation level error and Uniform(0, 1) priors for random effect variability. In total, we ran four MCMC chains for 50,000 iterations, discarded the first 10,000 as burn-in, and retained every 10th sample, which resulted in 16,000 posterior samples.

The Bayesian hierarchical model showed good convergence and fit to the data. For example, the MCMC trace plots showed good mixing across all four chains, and the Gelman-Rubin statistics were near 1.0 for all parameters (Table 2). Effective sample sizes for all key parameters exceeded 1,300, and most of the random effects achieved ESS values between 3,000 and 8,000 (Table 3). This shows that there was sufficient posterior sampling. Furthermore, the fitted curves of the Wild Type Roots (Fig 14) show that the model accurately captured the sigmoidal growth pattern in all nine wild-type roots. They also show a clear separation between inner (red) and outer (blue) curves, which adds to supporting the differential growth based on our research question. The residual tests (Fig 15) show that the model assumptions were met. This includes how the

residuals were approximately normally distributed according to the Normal Q-Q plot, no systematic patterns being present across the fitted values or scaled midline position, and consistent variance being present across the genotypes and sides (Fig 16). Additionally, the posterior density plots (Fig 17) provided strong evidence supporting the gravitropism hypothesis. The density for the side_effect_WT_U parameter was positive and clearly separated from zero, which indicates that the wild-type roots showed a big enough differential growth, where the outer cells reached greater maximum lengths than inner cells. In contrast, the density for side_effect_MU_U was centered near zero with greater overlap, which shows that there was minimal differential growth in the mutant roots. The density for interaction_xmid showed a negative peak, which indicates that the midpoint of elongation occurred earlier on the outer side in wild-type roots compared to mutants, which is consistent with the asymmetric developmental timing mentioned in the background. The trace plots (Fig 10 & 11) for these parameters indicated stable chains with no signs of non-convergence or autocorrelation, which supports the posterior estimates. Overall, these results provide strong Bayesian evidence that differential cell elongation between the inner and outer sides of the root is emphasized in wild-type plants and reduced in the mutant genotype. This supports the conclusion that differential growth driven by gravitropism is a key feature underlying root circumnutation in rice plants.

4. Shortcomings and Assumptions

There were several important limitations and assumptions regarding our insights. The first is that the sample size was relatively small with only 20 root types. This limits statistical power and increases uncertainty around parameter estimates. This is particularly an issue with MU roots, where between root variability was higher. Another limitation is that the frequentist model we chose may have oversimplified the data. A four parameter logistic curve may oversimplify the true biological process of root growth because it assumes smooth, systematic growth along the midline. We assumed that U and L did not vary significantly across roots, which may not reflect reality. Lastly the priors that we chose for our Bayesian model were not chosen through a formal sensitivity analysis. Even though we chose weakly informative priors, they could still have constrained parameters beyond bounds seen in reality.

Both modeling frameworks assume that the residuals are approximately normal with constant variance. Normality was met in both models, with QQ plots that followed the diagonal line (Fig 8). Residuals for our frequentist model were randomly scattered when examined all together and by side, root, and genotype (Fig 4-7). There were slight variances in range for differing roots, but all individual roots roughly followed a random scatter with roughly constant variance. Overall the residuals tended to be more concentrated at lower fitted values. This effect was more prominent in the MU roots than the WT roots.

5. Conclusion

Across both frequentist and Bayesian frameworks, we found consistent evidence that wild-type (WT) roots exhibit significant asymmetry in cell elongation, while mutant (MU) roots do not. The frequentist nonlinear mixed-effects model revealed that the inflection point (xmid) occurred significantly closer to the root base on the outer side for WT roots, suggesting earlier elongation onset relative to the inner side. In contrast, MU roots showed no such difference. The Bayesian hierarchical model corroborated these findings, providing strong posterior support that outer-side cells in WT roots achieved larger maximum lengths (U) and earlier elongation midpoints (xmid) than inner-side cells, consistent with asymmetric growth driving circumnutation.

Together, these findings suggest that differential elongation across root sides is a defining feature of wild-type root development and likely represents the physical mechanism underlying circumnutation. The absence of such asymmetry in mutant roots reinforces the hypothesis that the genetic mutation disrupts the gravitropic signaling or growth response necessary for this motion.

6. Appendix

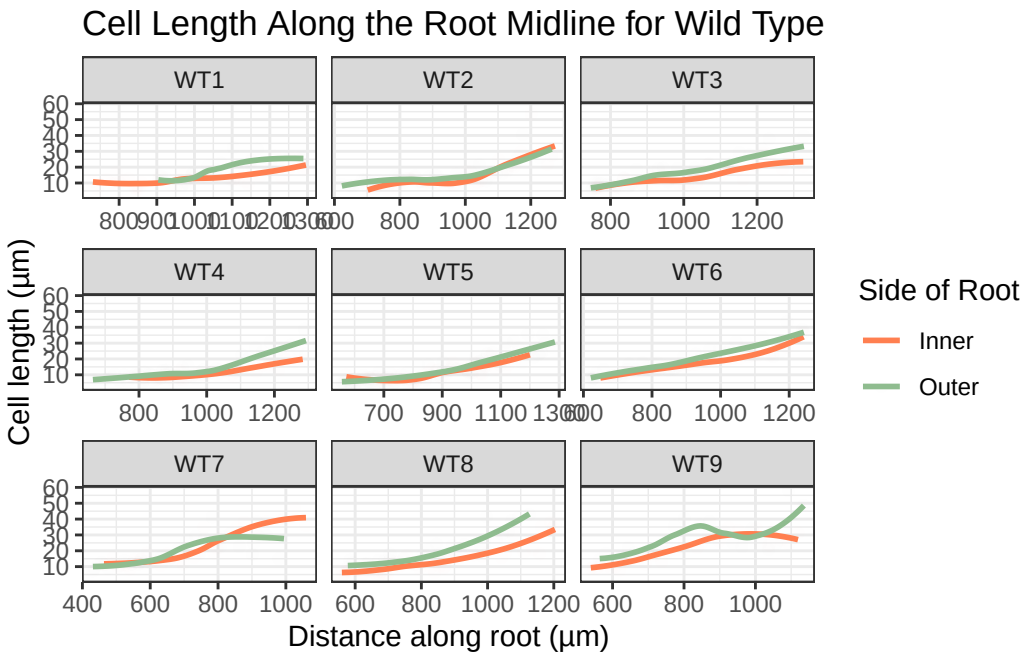

Figure 1: The difference between inner and outer cell lengths changes root by root

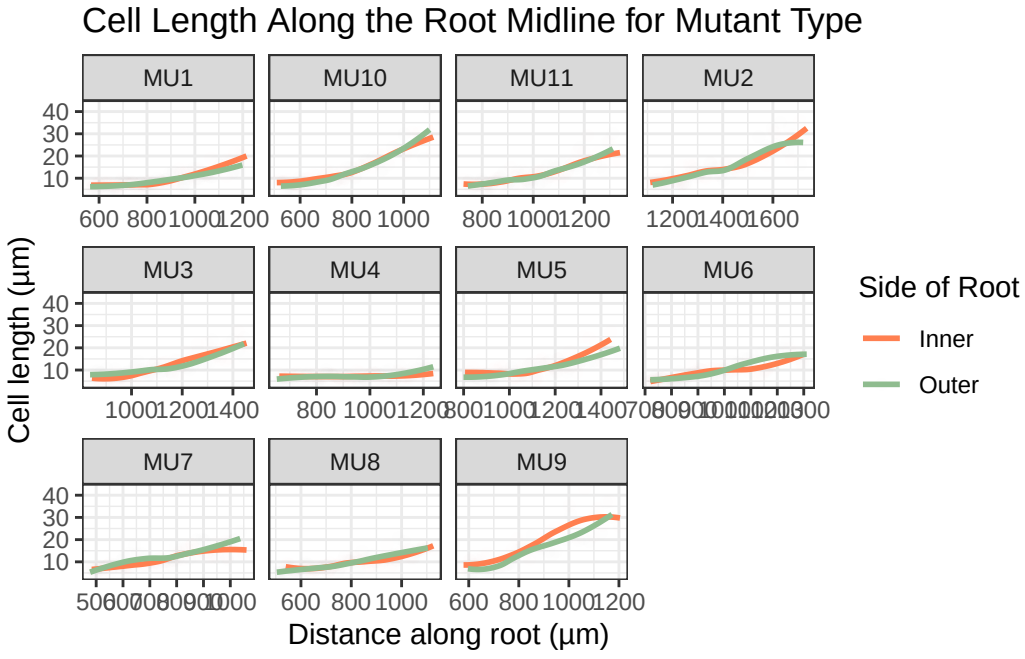

Figure 2: There is only slight differences between inner and outer cell lengths

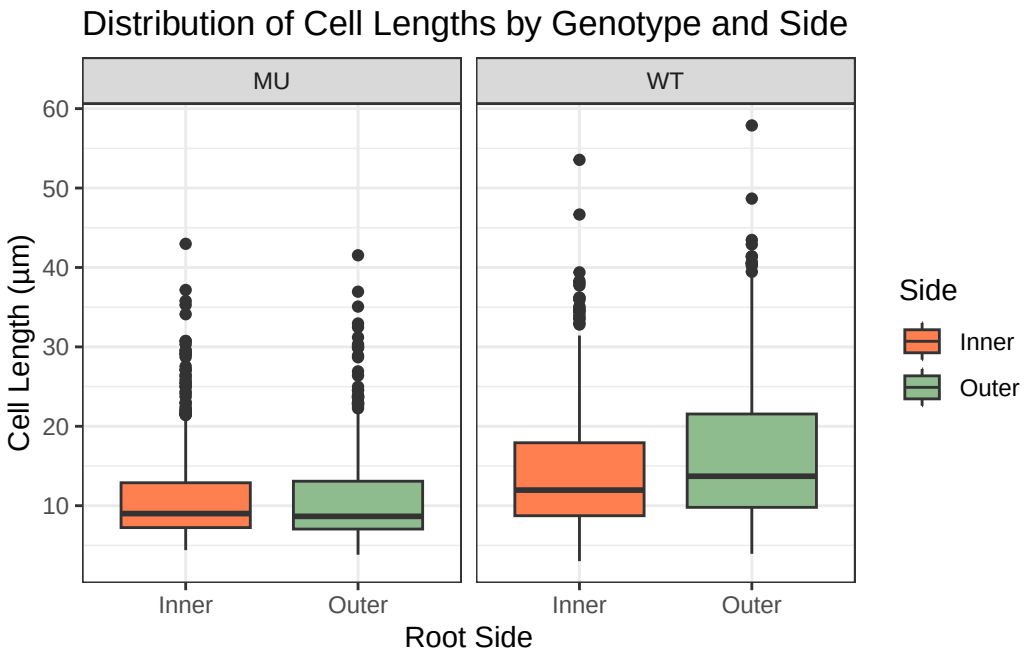

Figure 3: MU cells have similar inner vs outer lengths; WT outer has longer lengths than inner

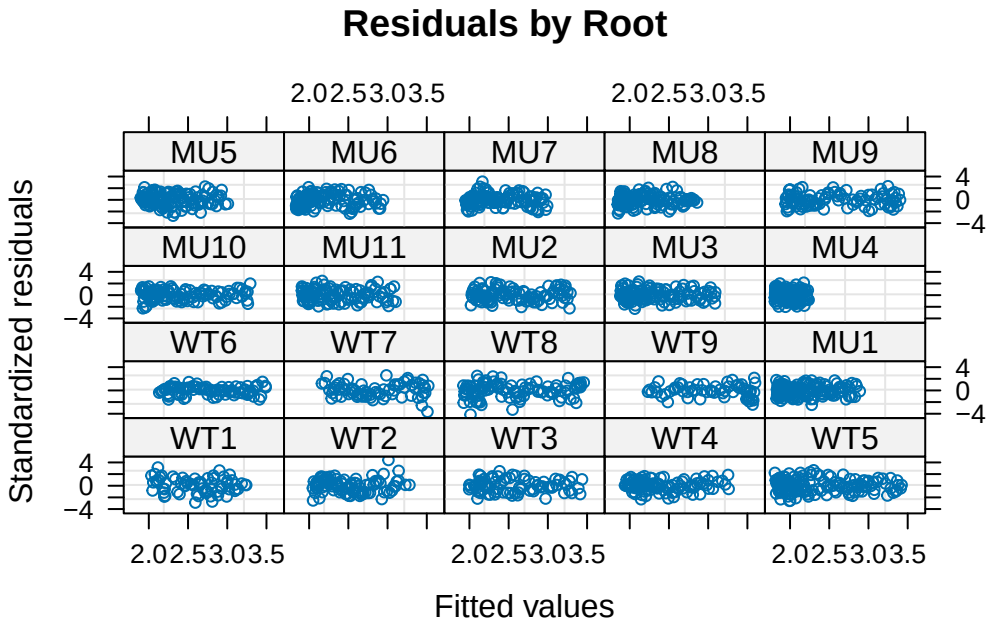

Figure 4: Residual plot by root id shows variation by root with better scatters for WT

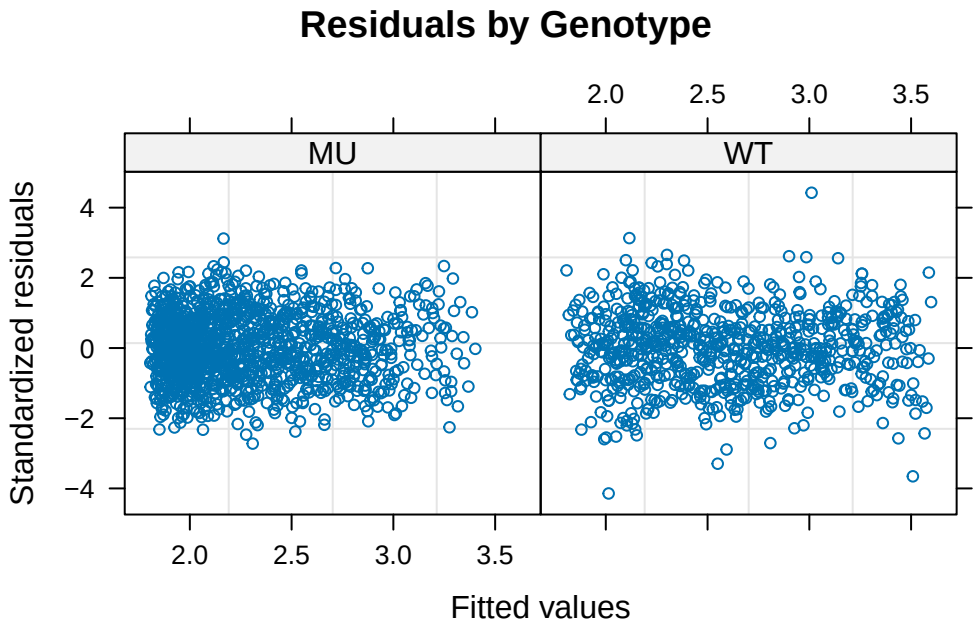

Figure 5: Residuals by Genotype show random scatter and constant variance, MU more dense at lower values

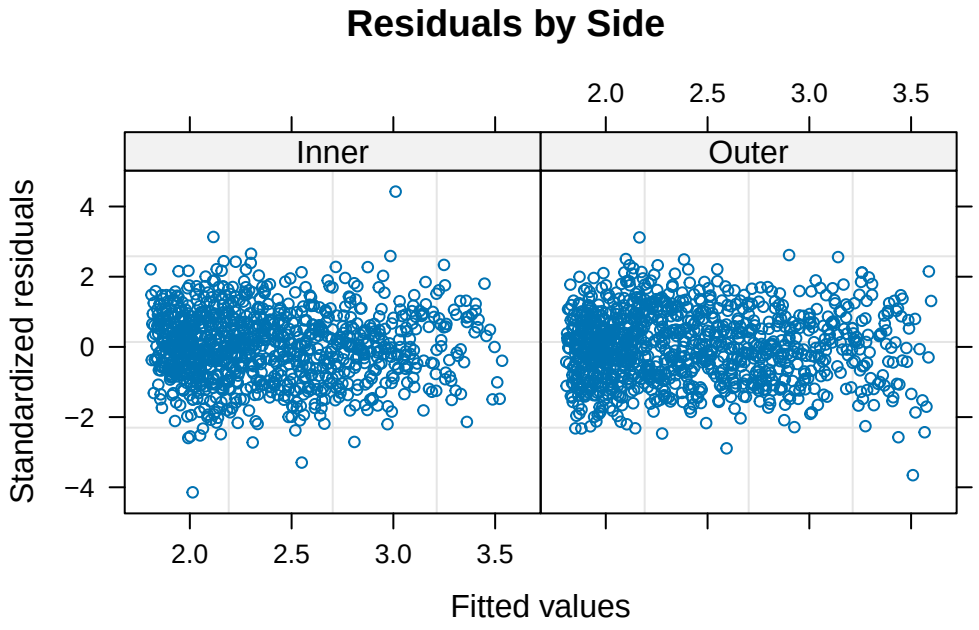

Figure 6: Residuals by Side show random scatter and constant variance more dense at lower values

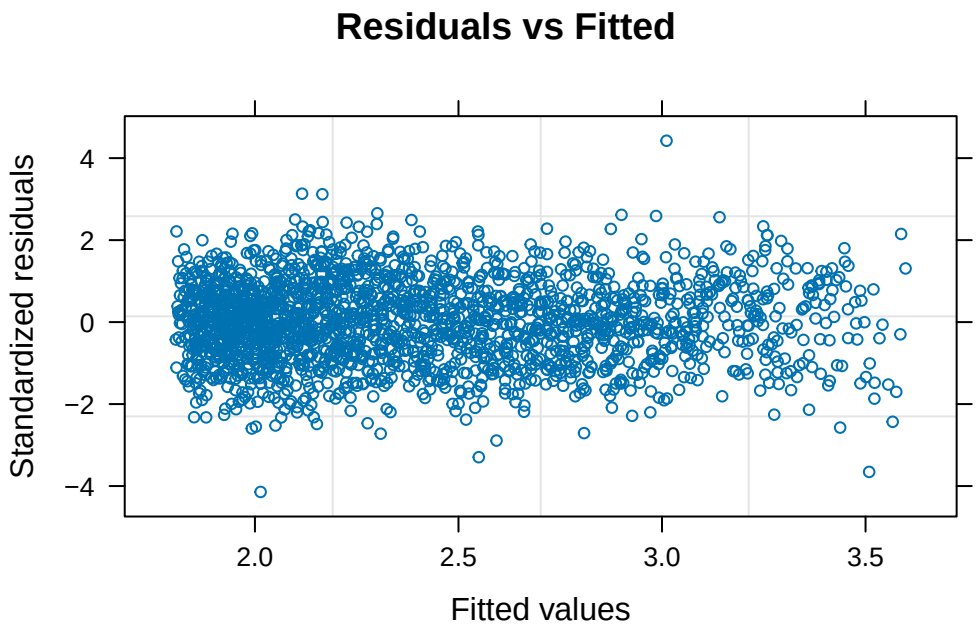

Figure 7: Residual plot for all data shows random scatter and constant variance, more dense at lower values

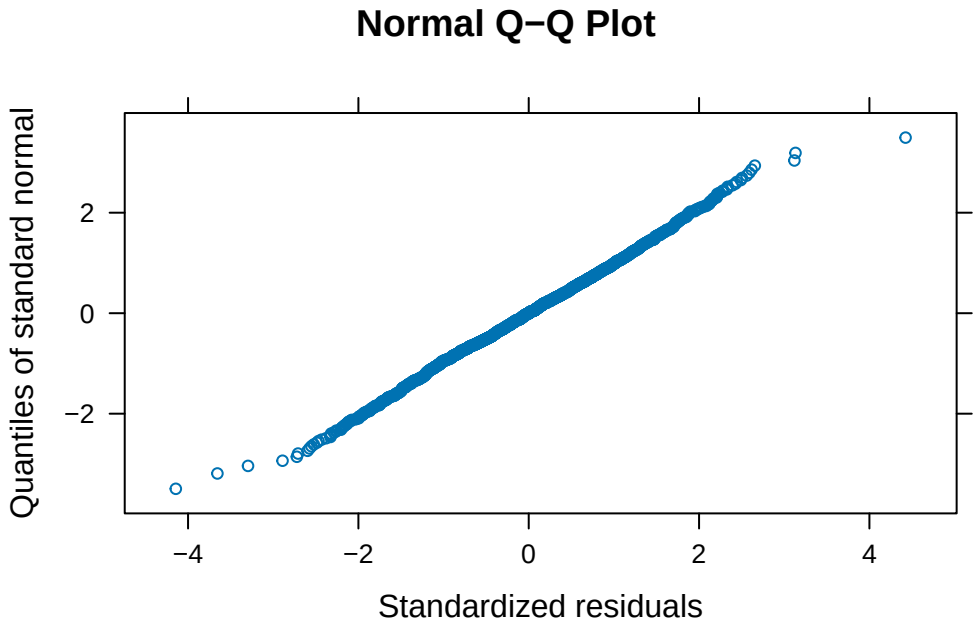

Figure 8: QQ plot shows residuals follow diagnol line, shows normality

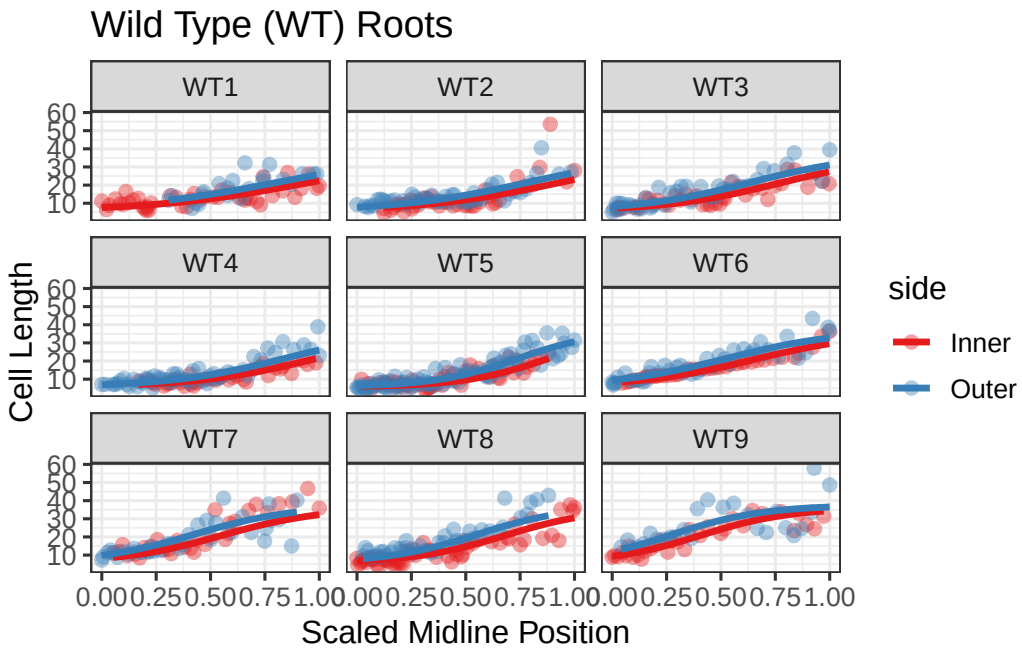

Figure 9: Data vs fitted curves shows goodness of fit for WT

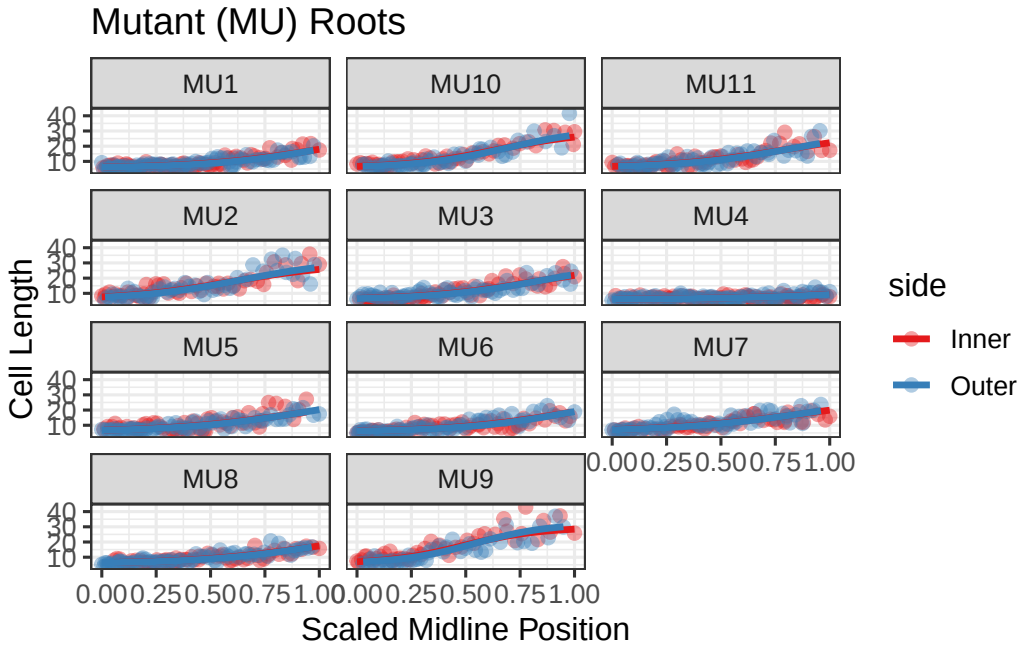

Figure 10: Data vs fitted curves shows goodness of fit for MU

Table 1: Model output for frequentist model

	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
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

```
Running JAGS with 4 chains...

Compiling model graph
   Resolving undeclared variables
   Allocating nodes
Graph information:
   Observed stochastic nodes: 2106
   Unobserved stochastic nodes: 53
   Total graph size: 25441

Initializing model

Inference for Bugs model at "rootModel.jags", fit using jags,
 4 chains, each with 50000 iterations (first 10000 discarded), n.thin = 10
 n.sims = 16000 iterations saved. Running time = 1583.942 secs
                     mu.vect sd.vect     2.5%      25%      50%      75%
L                     1.727   0.045    1.626    1.700    1.732    1.759
b_s[1]                0.369   0.108    0.163    0.296    0.366    0.440
b_s[2]                0.156   0.095   -0.029    0.093    0.155    0.219
b_s[3]                0.013   0.092   -0.169   -0.047    0.013    0.075
b_s[4]               -0.009   0.089   -0.186   -0.068   -0.009    0.049
b_s[5]               -0.297   0.080   -0.458   -0.349   -0.297   -0.244
b_s[6]                0.059   0.097   -0.132   -0.005    0.059    0.123
b_s[7]               -0.080   0.106   -0.292   -0.150   -0.080   -0.010
b_s[8]               -0.208   0.086   -0.378   -0.264   -0.207   -0.150
b_s[9]               -0.118   0.134   -0.384   -0.206   -0.116   -0.028
b_s[10]              -0.011   0.092   -0.192   -0.073   -0.011    0.049
b_s[11]              -0.224   0.091   -0.406   -0.284   -0.223   -0.162
b_s[12]              -0.016   0.091   -0.192   -0.075   -0.016    0.046
b_s[13]              -0.033   0.093   -0.217   -0.095   -0.033    0.030
b_s[14]              -0.025   0.088   -0.202   -0.083   -0.024    0.035
b_s[15]               0.397   0.177    0.052    0.279    0.398    0.515
b_s[16]               0.107   0.093   -0.074    0.045    0.107    0.170
b_s[17]              -0.018   0.088   -0.191   -0.077   -0.018    0.040
b_s[18]               0.234   0.093    0.051    0.171    0.234    0.295
b_s[19]               0.081   0.090   -0.094    0.021    0.080    0.141
b_s[20]              -0.376   0.102   -0.582   -0.443   -0.373   -0.305
b_s0                 -1.251   0.095   -1.428   -1.315   -1.254   -1.191
b_xmid[1]             0.091   0.082   -0.073    0.037    0.093    0.145
b_xmid[2]             0.115   0.080   -0.044    0.063    0.115    0.167
```

b_xmid[3]	0.004	0.080	-0.155	-0.048	0.005	0.056
b_xmid[4]	0.203	0.080	0.046	0.152	0.204	0.255
b_xmid[5]	0.168	0.079	0.012	0.117	0.169	0.220
b_xmid[6]	-0.111	0.080	-0.270	-0.162	-0.110	-0.058
b_xmid[7]	-0.181	0.080	-0.339	-0.232	-0.180	-0.128
b_xmid[8]	-0.033	0.079	-0.188	-0.084	-0.032	0.019
b_xmid[9]	-0.310	0.081	-0.472	-0.363	-0.309	-0.258
b_xmid[10]	0.156	0.058	0.058	0.115	0.150	0.193
b_xmid[11]	-0.142	0.056	-0.236	-0.182	-0.148	-0.107
b_xmid[12]	-0.030	0.058	-0.129	-0.070	-0.035	0.007
b_xmid[13]	-0.219	0.058	-0.318	-0.260	-0.224	-0.182
b_xmid[14]	-0.007	0.058	-0.105	-0.048	-0.013	0.029
b_xmid[15]	0.736	0.115	0.539	0.654	0.726	0.807
b_xmid[16]	0.043	0.059	-0.059	0.001	0.037	0.080
b_xmid[17]	0.121	0.059	0.020	0.078	0.115	0.157
b_xmid[18]	0.010	0.061	-0.099	-0.033	0.005	0.049
b_xmid[19]	0.162	0.060	0.059	0.121	0.157	0.200
b_xmid[20]	-0.265	0.055	-0.357	-0.305	-0.271	-0.230
beta_U_geno	0.217	0.101	0.021	0.150	0.214	0.282
beta_U_int	3.434	0.077	3.295	3.380	3.430	3.483
beta_U_int_sg	-0.081	0.102	-0.292	-0.147	-0.079	-0.013
beta_U_side	0.102	0.080	-0.047	0.048	0.100	0.153
beta_xmid_geno	-0.084	0.098	-0.264	-0.152	-0.089	-0.021
beta_xmid_int	0.625	0.054	0.497	0.592	0.635	0.667
beta_xmid_int_sg	-0.186	0.035	-0.257	-0.209	-0.185	-0.162
beta_xmid_side	0.050	0.027	-0.001	0.032	0.049	0.067
interaction_U	-0.081	0.102	-0.292	-0.147	-0.079	-0.013
interaction_xmid	-0.186	0.035	-0.257	-0.209	-0.185	-0.162
s0	0.287	0.028	0.240	0.268	0.285	0.304
side_effect_MU_U	0.102	0.080	-0.047	0.048	0.100	0.153
side_effect_MU_xmid	0.050	0.027	-0.001	0.032	0.049	0.067
side_effect_WT_U	0.021	0.064	-0.106	-0.022	0.022	0.064
side_effect_WT_xmid	-0.136	0.023	-0.181	-0.152	-0.136	-0.121
sigma	0.220	0.003	0.213	0.217	0.220	0.222
sigma_s	0.230	0.050	0.150	0.195	0.224	0.259
sigma_xmid	0.248	0.049	0.172	0.213	0.242	0.275
deviance	-408.653	11.099	-428.568	-416.496	-409.271	-401.786

	97.5%	Rhat	n.eff
L	1.804	1.001	5400
b_s[1]	0.586	1.001	4600
b_s[2]	0.345	1.001	6600
b_s[3]	0.196	1.002	2800
b_s[4]	0.168	1.001	6900
b_s[5]	-0.144	1.001	16000
b_s[6]	0.249	1.001	4900
b_s[7]	0.127	1.001	6100
b_s[8]	-0.042	1.001	4800
b_s[9]	0.142	1.001	15000
b_s[10]	0.170	1.001	12000
b_s[11]	-0.048	1.002	3100
b_s[12]	0.163	1.001	16000
b_s[13]	0.146	1.002	3300
b_s[14]	0.147	1.001	4700
b_s[15]	0.744	1.001	6500

```
b_s[16]               0.292 1.001  5400
b_s[17]               0.153 1.001 16000
b_s[18]               0.418 1.001  9200
b_s[19]               0.261 1.002  3000
b_s[20]              -0.184 1.002  2000
b_s0                 -1.058 1.002  2400
b_xmid[1]             0.251 1.014   230
b_xmid[2]             0.270 1.016   210
b_xmid[3]             0.157 1.016   200
b_xmid[4]             0.358 1.016   210
b_xmid[5]             0.321 1.016   210
b_xmid[6]             0.044 1.016   210
b_xmid[7]            -0.028 1.016   200
b_xmid[8]             0.120 1.017   200
b_xmid[9]            -0.156 1.015   230
b_xmid[10]            0.283 1.013   240
b_xmid[11]           -0.017 1.012   270
b_xmid[12]            0.095 1.012   250
b_xmid[13]           -0.093 1.011   270
b_xmid[14]            0.117 1.012   250
b_xmid[15]            0.988 1.007   430
b_xmid[16]            0.171 1.012   250
b_xmid[17]            0.248 1.013   240
b_xmid[18]            0.139 1.010   290
b_xmid[19]            0.291 1.010   310
b_xmid[20]           -0.143 1.014   230
beta_U_geno           0.418 1.002  3600
beta_U_int            3.596 1.001  5400
beta_U_int_sg         0.112 1.001  4100
beta_U_side           0.267 1.002  2900
beta_xmid_geno        0.122 1.030   130
beta_xmid_int         0.696 1.020   190
beta_xmid_int_sg     -0.120 1.002  4000
beta_xmid_side        0.104 1.002  2800
interaction_U         0.112 1.001  4100
interaction_xmid     -0.120 1.002  4000
s0                    0.347 1.002  2400
side_effect_MU_U      0.267 1.002  2900
side_effect_MU_xmid   0.104 1.002  2800
side_effect_WT_U      0.144 1.001 16000
side_effect_WT_xmid  -0.092 1.001 16000
sigma                 0.227 1.001 16000
sigma_s               0.344 1.001  7200
sigma_xmid            0.361 1.005   650
deviance           -384.653 1.001 10000

For each parameter, n.eff is a crude measure of effective sample size,
and Rhat is the potential scale reduction factor (at convergence, Rhat=1).

DIC info (using the rule: pV = var(deviance)/2)
pV = 61.6 and DIC = -347.1
DIC is an estimate of expected predictive error (lower deviance is better).
```

```
=== GELMAN-RUBIN ===

Potential scale reduction factors:

                    Point est. Upper C.I.
b_s[1]                    1.00       1.00
b_s[10]                   1.00       1.00
b_s[11]                   1.00       1.00
b_s[12]                   1.00       1.00
b_s[13]                   1.00       1.00
b_s[14]                   1.00       1.00
b_s[15]                   1.00       1.00
b_s[16]                   1.00       1.00
b_s[17]                   1.00       1.00
b_s[18]                   1.00       1.00
b_s[19]                   1.00       1.00
b_s[2]                    1.00       1.00
b_s[20]                   1.00       1.00
b_s[3]                    1.00       1.00
b_s[4]                    1.00       1.00
b_s[5]                    1.00       1.00
b_s[6]                    1.00       1.00
b_s[7]                    1.00       1.00
b_s[8]                    1.00       1.00
b_s[9]                    1.00       1.00
b_s0                      1.00       1.00
b_xmid[1]                 1.01       1.04
b_xmid[10]                1.01       1.02
b_xmid[11]                1.01       1.02
b_xmid[12]                1.01       1.02
b_xmid[13]                1.01       1.02
b_xmid[14]                1.01       1.02
b_xmid[15]                1.00       1.01
b_xmid[16]                1.01       1.02
b_xmid[17]                1.01       1.03
b_xmid[18]                1.01       1.02
b_xmid[19]                1.01       1.02
b_xmid[2]                 1.02       1.04
b_xmid[20]                1.01       1.02
b_xmid[3]                 1.02       1.05
b_xmid[4]                 1.02       1.05
b_xmid[5]                 1.02       1.05
b_xmid[6]                 1.02       1.05
b_xmid[7]                 1.02       1.05
b_xmid[8]                 1.02       1.05
b_xmid[9]                 1.02       1.04
beta_U_geno               1.00       1.01
beta_U_int                1.00       1.01
beta_U_int_sg             1.00       1.00
beta_U_side               1.00       1.01
beta_xmid_geno            1.02       1.05
beta_xmid_int             1.01       1.02
beta_xmid_int_sg          1.00       1.01
beta_xmid_side            1.00       1.01
```

```
deviance                 1.00       1.00
interaction_U            1.00       1.00
interaction_xmid         1.00       1.01
L                        1.00       1.00
s0                       1.00       1.00
side_effect_MU_U         1.00       1.01
side_effect_MU_xmid      1.00       1.01
side_effect_WT_U         1.00       1.00
side_effect_WT_xmid      1.00       1.00
sigma                    1.00       1.00
sigma_s                  1.00       1.00
sigma_xmid               1.00       1.01


=== EFFECTIVE SAMPLE SIZE (first 30) ===

    b_s[1]    b_s[10]    b_s[11]    b_s[12]    b_s[13]    b_s[14]    b_s[15]
 7755.8965  8053.4711  5401.1199  6789.9085  5112.0797  7026.5848  2948.4994
   b_s[16]    b_s[17]    b_s[18]    b_s[19]     b_s[2]    b_s[20]     b_s[3]
 7899.6421  6593.8152  6751.1752  7509.6303  5484.4812  4264.7233  5175.4729
    b_s[4]     b_s[5]     b_s[6]     b_s[7]     b_s[8]     b_s[9]       b_s0
 5795.6551  5613.2695  5172.1939  7008.5261  3893.3092  8189.7457  1209.7052
 b_xmid[1] b_xmid[10] b_xmid[11] b_xmid[12] b_xmid[13] b_xmid[14] b_xmid[15]
  359.9957   383.6747   346.4388   370.3932   369.1389   373.0121  1245.2999
b_xmid[16] b_xmid[17]
  372.3421   365.4099


--- Residual summary (log scale) ---

    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
-1.24860 -0.28258 -0.05362 -0.04518  0.17311  1.59934


=== POSTERIOR SUMMARY ===


Iterations = 10010:50000
Thinning interval = 10
Number of chains = 4
Sample size per chain = 4000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

                         Mean        SD  Naive SE Time-series SE
b_s[1]               3.688e-01  0.108493 0.0008577      1.240e-03
b_s[10]             -1.097e-02  0.092065 0.0007278      1.029e-03
b_s[11]             -2.240e-01  0.091218 0.0007211      1.248e-03
b_s[12]             -1.555e-02  0.090681 0.0007169      1.106e-03
b_s[13]             -3.311e-02  0.093429 0.0007386      1.317e-03
b_s[14]             -2.480e-02  0.088447 0.0006992      1.059e-03
b_s[15]              3.972e-01  0.176576 0.0013960      3.275e-03
b_s[16]              1.075e-01  0.093391 0.0007383      1.056e-03
b_s[17]             -1.841e-02  0.087541 0.0006921      1.091e-03
b_s[18]              2.340e-01  0.093274 0.0007374      1.144e-03
b_s[19]              8.138e-02  0.090351 0.0007143      1.044e-03
```

```
b_s[2]               1.561e-01  0.094797 0.0007494      1.293e-03
b_s[20]             -3.755e-01  0.101627 0.0008034      1.560e-03
b_s[3]               1.314e-02  0.092280 0.0007295      1.301e-03
b_s[4]              -9.113e-03  0.089107 0.0007044      1.178e-03
b_s[5]              -2.972e-01  0.079727 0.0006303      1.074e-03
b_s[6]               5.904e-02  0.096799 0.0007653      1.347e-03
b_s[7]              -8.038e-02  0.105796 0.0008364      1.293e-03
b_s[8]              -2.077e-01  0.085833 0.0006786      1.383e-03
b_s[9]              -1.179e-01  0.133795 0.0010577      1.489e-03
b_s0                -1.251e+00  0.094937 0.0007505      2.737e-03
b_xmid[1]            9.114e-02  0.082045 0.0006486      4.401e-03
b_xmid[10]           1.560e-01  0.058244 0.0004605      3.073e-03
b_xmid[11]          -1.415e-01  0.056369 0.0004456      3.175e-03
b_xmid[12]          -2.961e-02  0.057887 0.0004576      3.169e-03
b_xmid[13]          -2.187e-01  0.057843 0.0004573      3.174e-03
b_xmid[14]          -7.248e-03  0.057877 0.0004576      3.127e-03
b_xmid[15]           7.362e-01  0.114980 0.0009090      3.322e-03
b_xmid[16]           4.276e-02  0.058989 0.0004664      3.188e-03
b_xmid[17]           1.205e-01  0.058834 0.0004651      3.247e-03
b_xmid[18]           9.974e-03  0.061020 0.0004824      3.022e-03
b_xmid[19]           1.625e-01  0.059654 0.0004716      3.210e-03
b_xmid[2]            1.150e-01  0.079950 0.0006321      4.525e-03
b_xmid[20]          -2.646e-01  0.055466 0.0004385      3.248e-03
b_xmid[3]            3.656e-03  0.079980 0.0006323      4.537e-03
b_xmid[4]            2.032e-01  0.079797 0.0006309      4.554e-03
b_xmid[5]            1.681e-01  0.079209 0.0006262      4.670e-03
b_xmid[6]           -1.107e-01  0.079973 0.0006322      4.563e-03
b_xmid[7]           -1.808e-01  0.079501 0.0006285      4.603e-03
b_xmid[8]           -3.267e-02  0.079245 0.0006265      4.603e-03
b_xmid[9]           -3.103e-01  0.080629 0.0006374      4.645e-03
beta_U_geno          2.166e-01  0.100735 0.0007964      2.301e-03
beta_U_int           3.434e+00  0.076758 0.0006068      2.215e-03
beta_U_int_sg       -8.123e-02  0.102295 0.0008087      2.226e-03
beta_U_side          1.021e-01  0.079574 0.0006291      1.808e-03
beta_xmid_geno      -8.392e-02  0.097933 0.0007742      7.182e-03
beta_xmid_int        6.245e-01  0.054043 0.0004273      3.267e-03
beta_xmid_int_sg    -1.858e-01  0.035004 0.0002767      8.242e-04
beta_xmid_side       4.952e-02  0.026655 0.0002107      6.556e-04
deviance            -4.087e+02 11.098768 0.0877435      1.260e-01
interaction_U       -8.123e-02  0.102295 0.0008087      2.226e-03
interaction_xmid    -1.858e-01  0.035004 0.0002767      8.242e-04
L                    1.727e+00  0.045489 0.0003596      1.282e-03
s0                   2.874e-01  0.027812 0.0002199      8.118e-04
side_effect_MU_U     1.021e-01  0.079574 0.0006291      1.808e-03
side_effect_MU_xmid  4.952e-02  0.026655 0.0002107      6.556e-04
side_effect_WT_U     2.084e-02  0.064102 0.0005068      7.632e-04
side_effect_WT_xmid -1.363e-01  0.022766 0.0001800      2.859e-04
sigma                2.197e-01  0.003478 0.0000275      2.727e-05
sigma_s              2.303e-01  0.050273 0.0003974      6.189e-04
sigma_xmid           2.480e-01  0.048808 0.0003859      8.146e-04

2. Quantiles for each variable:

                         2.5%        25%        50%        75%      97.5%
```

b_s[1]	1.629e-01	2.958e-01	3.656e-01	0.44032	0.58569
b_s[10]	-1.919e-01	-7.308e-02	-1.081e-02	0.04944	0.16987
b_s[11]	-4.062e-01	-2.836e-01	-2.232e-01	-0.16209	-0.04835
b_s[12]	-1.917e-01	-7.544e-02	-1.647e-02	0.04616	0.16337
b_s[13]	-2.174e-01	-9.537e-02	-3.320e-02	0.02995	0.14626
b_s[14]	-2.021e-01	-8.336e-02	-2.436e-02	0.03504	0.14727
b_s[15]	5.249e-02	2.792e-01	3.975e-01	0.51465	0.74414
b_s[16]	-7.405e-02	4.463e-02	1.066e-01	0.17009	0.29202
b_s[17]	-1.907e-01	-7.670e-02	-1.849e-02	0.03972	0.15299
b_s[18]	5.100e-02	1.705e-01	2.339e-01	0.29532	0.41770
b_s[19]	-9.380e-02	2.083e-02	8.042e-02	0.14113	0.26087
b_s[2]	-2.945e-02	9.264e-02	1.554e-01	0.21851	0.34500
b_s[20]	-5.824e-01	-4.425e-01	-3.730e-01	-0.30535	-0.18360
b_s[3]	-1.689e-01	-4.739e-02	1.294e-02	0.07511	0.19634
b_s[4]	-1.865e-01	-6.777e-02	-8.756e-03	0.04898	0.16791
b_s[5]	-4.580e-01	-3.494e-01	-2.967e-01	-0.24421	-0.14398
b_s[6]	-1.316e-01	-4.616e-03	5.946e-02	0.12330	0.24946
b_s[7]	-2.916e-01	-1.500e-01	-7.971e-02	-0.01049	0.12692
b_s[8]	-3.785e-01	-2.644e-01	-2.065e-01	-0.15000	-0.04188
b_s[9]	-3.837e-01	-2.057e-01	-1.160e-01	-0.02777	0.14249
b_s0	-1.428e+00	-1.315e+00	-1.254e+00	-1.19145	-1.05820
b_xmid[1]	-7.302e-02	3.742e-02	9.281e-02	0.14461	0.25090
b_xmid[10]	5.776e-02	1.146e-01	1.499e-01	0.19290	0.28289
b_xmid[11]	-2.363e-01	-1.821e-01	-1.475e-01	-0.10669	-0.01713
b_xmid[12]	-1.293e-01	-7.043e-02	-3.481e-02	0.00685	0.09515
b_xmid[13]	-3.175e-01	-2.604e-01	-2.238e-01	-0.18235	-0.09328
b_xmid[14]	-1.055e-01	-4.849e-02	-1.263e-02	0.02854	0.11716
b_xmid[15]	5.391e-01	6.542e-01	7.261e-01	0.80716	0.98833
b_xmid[16]	-5.929e-02	1.166e-03	3.718e-02	0.07975	0.17146
b_xmid[17]	2.015e-02	7.817e-02	1.148e-01	0.15722	0.24754
b_xmid[18]	-9.855e-02	-3.267e-02	5.407e-03	0.04929	0.13940
b_xmid[19]	5.871e-02	1.208e-01	1.565e-01	0.19971	0.29135
b_xmid[2]	-4.367e-02	6.349e-02	1.152e-01	0.16728	0.26986
b_xmid[20]	-3.565e-01	-3.046e-01	-2.710e-01	-0.23045	-0.14343
b_xmid[3]	-1.547e-01	-4.793e-02	4.849e-03	0.05627	0.15735
b_xmid[4]	4.557e-02	1.515e-01	2.044e-01	0.25527	0.35797
b_xmid[5]	1.181e-02	1.166e-01	1.691e-01	0.22029	0.32052
b_xmid[6]	-2.699e-01	-1.621e-01	-1.098e-01	-0.05805	0.04429
b_xmid[7]	-3.395e-01	-2.323e-01	-1.795e-01	-0.12832	-0.02795
b_xmid[8]	-1.885e-01	-8.377e-02	-3.163e-02	0.01927	0.12000
b_xmid[9]	-4.721e-01	-3.629e-01	-3.087e-01	-0.25818	-0.15562
beta_U_geno	2.123e-02	1.501e-01	2.139e-01	0.28230	0.41841
beta_U_int	3.295e+00	3.380e+00	3.430e+00	3.48311	3.59612
beta_U_int_sg	-2.919e-01	-1.466e-01	-7.902e-02	-0.01260	0.11247
beta_U_side	-4.703e-02	4.837e-02	1.002e-01	0.15295	0.26655
beta_xmid_geno	-2.636e-01	-1.515e-01	-8.899e-02	-0.02143	0.12249
beta_xmid_int	4.973e-01	5.921e-01	6.351e-01	0.66670	0.69645
beta_xmid_int_sg	-2.570e-01	-2.085e-01	-1.848e-01	-0.16234	-0.12036
beta_xmid_side	-7.117e-04	3.171e-02	4.892e-02	0.06675	0.10378
deviance	-4.286e+02	-4.165e+02	-4.093e+02	-401.78595	-384.65338
interaction_U	-2.919e-01	-1.466e-01	-7.902e-02	-0.01260	0.11247
interaction_xmid	-2.570e-01	-2.085e-01	-1.848e-01	-0.16234	-0.12036
L	1.626e+00	1.700e+00	1.732e+00	1.75946	1.80439
s0	2.399e-01	2.684e-01	2.853e-01	0.30378	0.34708

```
side_effect_MU_U    -4.703e-02  4.837e-02  1.002e-01    0.15295    0.26655
side_effect_MU_xmid -7.117e-04  3.171e-02  4.892e-02    0.06675    0.10378
side_effect_WT_U    -1.065e-01 -2.241e-02  2.169e-02    0.06433    0.14407
side_effect_WT_xmid -1.811e-01 -1.515e-01 -1.363e-01   -0.12079   -0.09227
sigma                2.130e-01  2.173e-01  2.196e-01    0.22203    0.22654
sigma_s              1.500e-01  1.948e-01  2.242e-01    0.25897    0.34425
sigma_xmid           1.716e-01  2.135e-01  2.417e-01    0.27514    0.36077

=== 95% HPD INTERVALS (first 40 rows if available) ===

                 lower       upper
b_s[1]      0.165403732  0.57926998
b_s[10]    -0.194895748  0.16417600
b_s[11]    -0.397907963 -0.05379498
b_s[12]    -0.191854297  0.16028926
b_s[13]    -0.209850291  0.15227441
b_s[14]    -0.199309846  0.14727031
b_s[15]     0.067230684  0.75030916
b_s[16]    -0.070108572  0.28651132
b_s[17]    -0.191796173  0.14246380
b_s[18]     0.065567828  0.42145482
b_s[19]    -0.093210538  0.25242487
b_s[2]     -0.022332644  0.34221021
b_s[20]    -0.569932050 -0.18073366
b_s[3]     -0.151888379  0.19353132
b_s[4]     -0.182813006  0.16350054
b_s[5]     -0.438748261 -0.14660101
b_s[6]     -0.124748205  0.24388721
b_s[7]     -0.285790827  0.11101231
b_s[8]     -0.368124708 -0.04382043
b_s[9]     -0.379407112  0.14014446
b_s0       -1.415922317 -1.07267208
b_xmid[1]  -0.037460183  0.24212435
b_xmid[10]  0.052180218  0.25065204
b_xmid[11] -0.241034355 -0.04931000
b_xmid[12] -0.137651584  0.06322259
b_xmid[13] -0.322215177 -0.11971070
b_xmid[14] -0.104776193  0.09791511
b_xmid[15]  0.513884274  0.93283492
b_xmid[16] -0.063899379  0.14101718
b_xmid[17]  0.014090018  0.21641753
b_xmid[18] -0.105547840  0.11143713
b_xmid[19]  0.060614393  0.27062621
b_xmid[2]  -0.006784385  0.26007599
b_xmid[20] -0.363391738 -0.17159912
b_xmid[3]  -0.126417818  0.14470567
b_xmid[4]   0.070431377  0.34067144
b_xmid[5]   0.045768465  0.31112804
b_xmid[6]  -0.227919671  0.04368215
b_xmid[7]  -0.304887503 -0.03595631
b_xmid[8]  -0.152772143  0.11350021
```

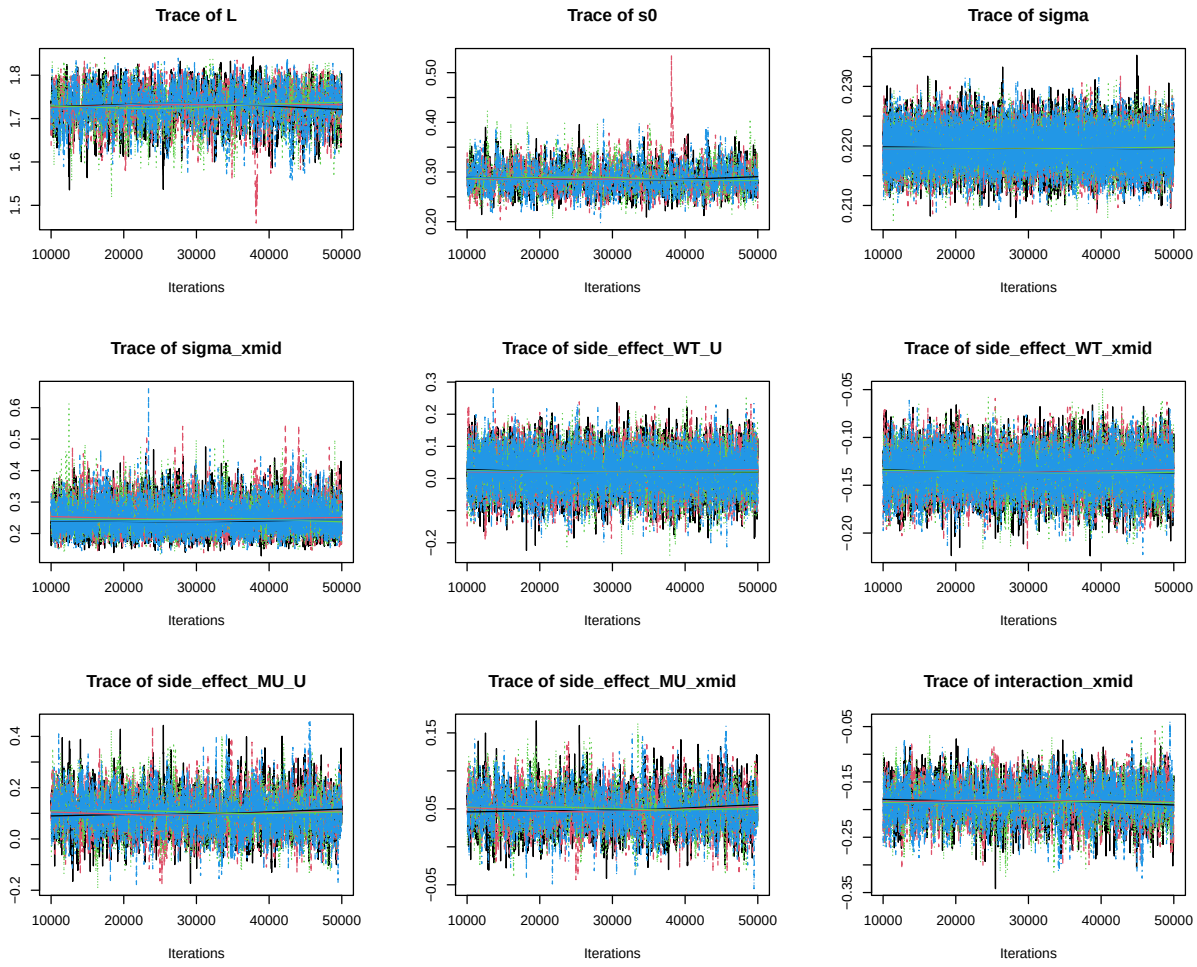

Figure 11: Trace plots for main parameters

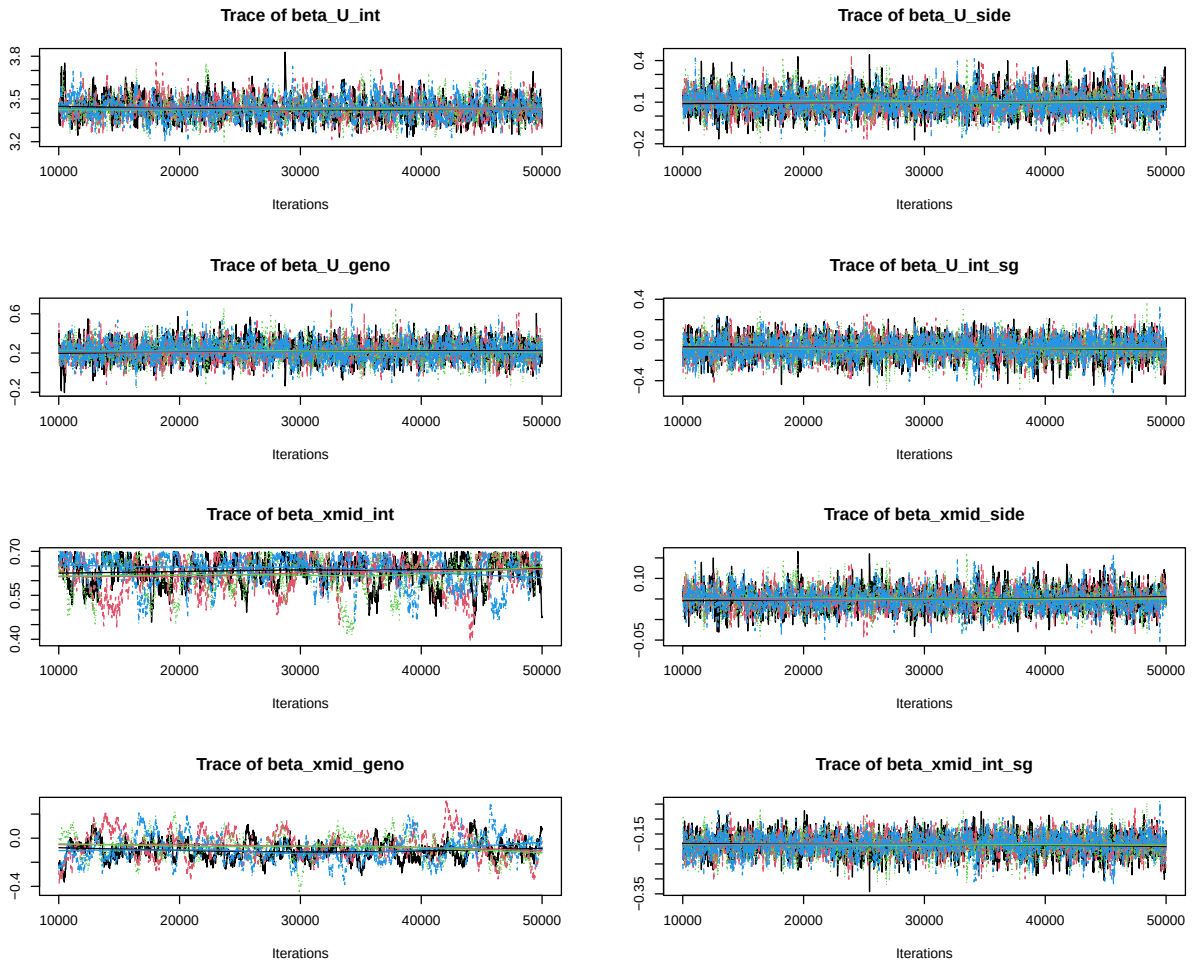

Figure 12: Trace plots for beta parameters

Table 2: Gelman-Rubin convergence diagnostics for main parameters

	Point est.	Upper C.I.
b_s[1]	1.001	1.002
b_s[10]	1.000	1.000
b_s[11]	1.002	1.004
b_s[12]	1.001	1.002
b_s[13]	1.001	1.002
b_s[14]	1.001	1.002
b_s[15]	1.000	1.001
b_s[16]	1.000	1.002
b_s[17]	1.000	1.001
b_s[18]	1.000	1.001
b_s[19]	1.001	1.002
b_s[2]	1.000	1.000
b_s[20]	1.001	1.004
b_s[3]	1.002	1.004
b_s[4]	1.000	1.000

	Point est.	Upper C.I.
b_s[5]	1.001	1.002
b_s[6]	1.001	1.003
b_s[7]	1.001	1.002
b_s[8]	1.001	1.001
b_s[9]	1.000	1.000
b_s0	1.002	1.004
b_xmid[1]	1.014	1.040
b_xmid[10]	1.009	1.023
b_xmid[11]	1.008	1.022
b_xmid[12]	1.009	1.024
b_xmid[13]	1.008	1.021
b_xmid[14]	1.008	1.021
b_xmid[15]	1.002	1.008
b_xmid[16]	1.008	1.021
b_xmid[17]	1.010	1.026
b_xmid[18]	1.009	1.024
b_xmid[19]	1.007	1.019
b_xmid[2]	1.016	1.043
b_xmid[20]	1.009	1.022
b_xmid[3]	1.017	1.047
b_xmid[4]	1.016	1.046
b_xmid[5]	1.016	1.045
b_xmid[6]	1.016	1.045
b_xmid[7]	1.017	1.048
b_xmid[8]	1.017	1.048
b_xmid[9]	1.015	1.042
beta_U_geno	1.003	1.007
beta_U_int	1.003	1.009
beta_U_int_sg	1.002	1.005
beta_U_side	1.002	1.005
beta_xmid_geno	1.021	1.046
beta_xmid_int	1.008	1.020
beta_xmid_int_sg	1.002	1.006
beta_xmid_side	1.003	1.007
deviance	1.000	1.001
interaction_U	1.002	1.005
interaction_xmid	1.002	1.006
L	1.001	1.002
s0	1.003	1.004
side_effect_MU_U	1.002	1.005
side_effect_MU_xmid	1.003	1.007
side_effect_WT_U	1.001	1.002
side_effect_WT_xmid	1.001	1.002
sigma	1.000	1.000
sigma_s	1.000	1.000
sigma_xmid	1.002	1.007

Table 3: Effective sample sizes

Parameter	Effective Sample Size
b_s[1]	7755.9

b_s[10]	8053.5
b_s[11]	5401.1
b_s[12]	6789.9
b_s[13]	5112.1
b_s[14]	7026.6
b_s[15]	2948.5
b_s[16]	7899.6
b_s[17]	6593.8
b_s[18]	6751.2
b_s[19]	7509.6
b_s[2]	5484.5
b_s[20]	4264.7
b_s[3]	5175.5
b_s[4]	5795.7
b_s[5]	5613.3
b_s[6]	5172.2
b_s[7]	7008.5
b_s[8]	3893.3
b_s[9]	8189.7
b_s0	1209.7
b_xmid[1]	360.0
b_xmid[10]	383.7
b_xmid[11]	346.4
b_xmid[12]	370.4
b_xmid[13]	369.1
b_xmid[14]	373.0
b_xmid[15]	1245.3
b_xmid[16]	372.3
b_xmid[17]	365.4

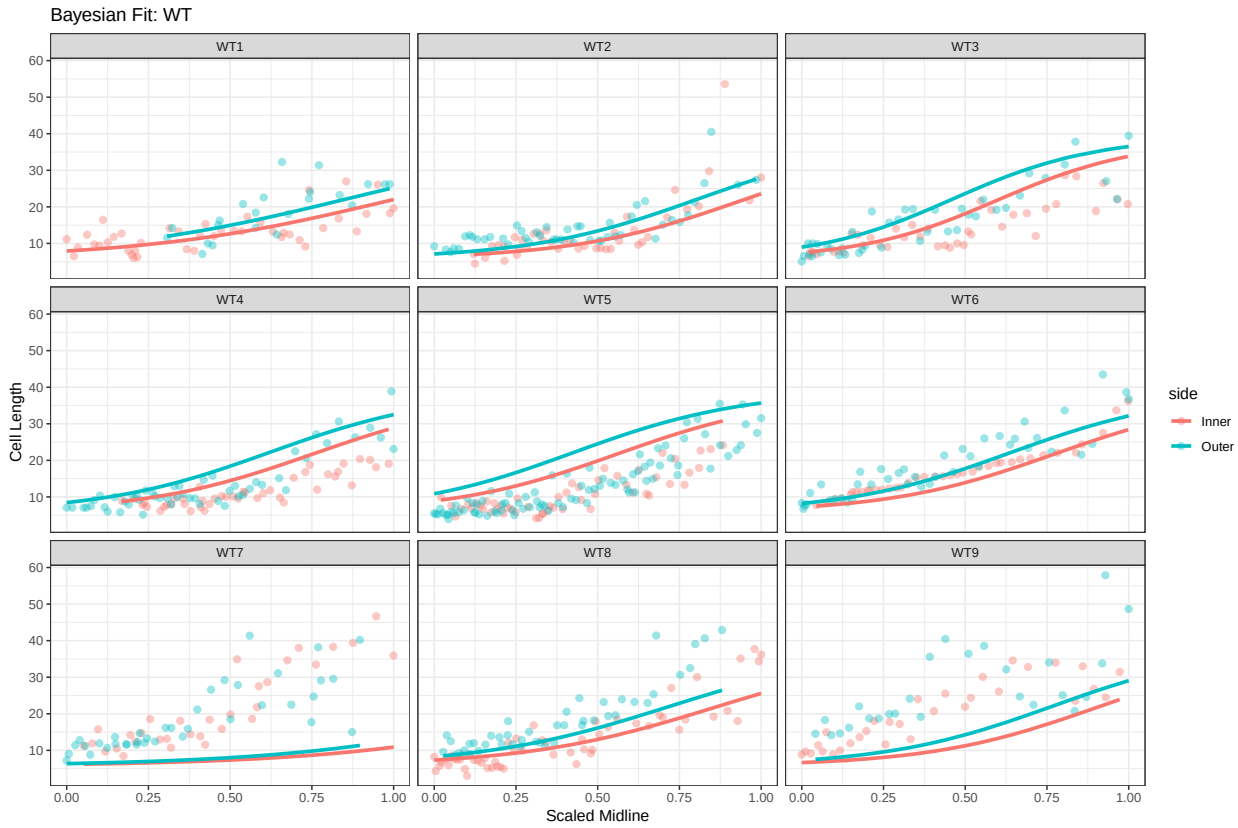

Figure 13: Bayesian fitted curves for WT genotype

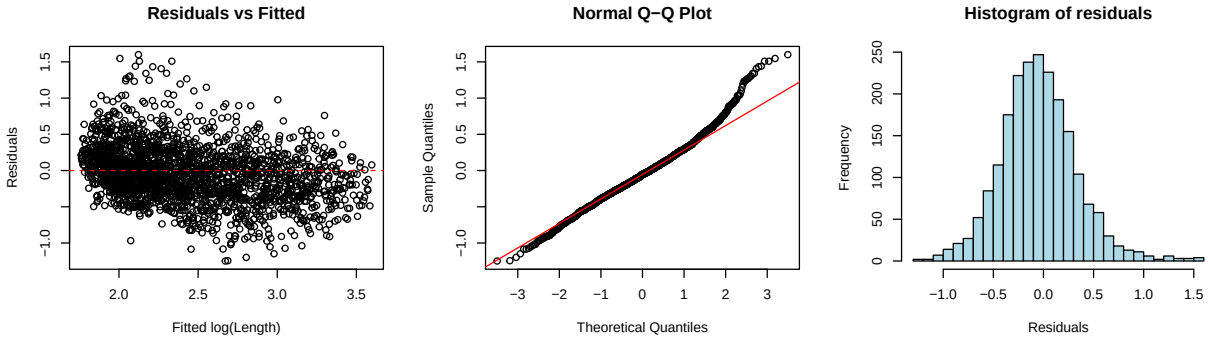

Figure 14: Residuals vs Fitted

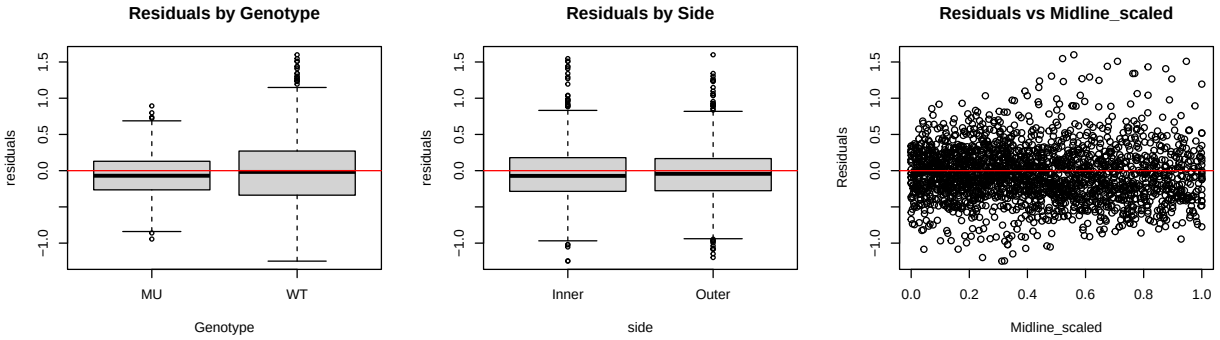

Figure 15: Residuals by grouping variables

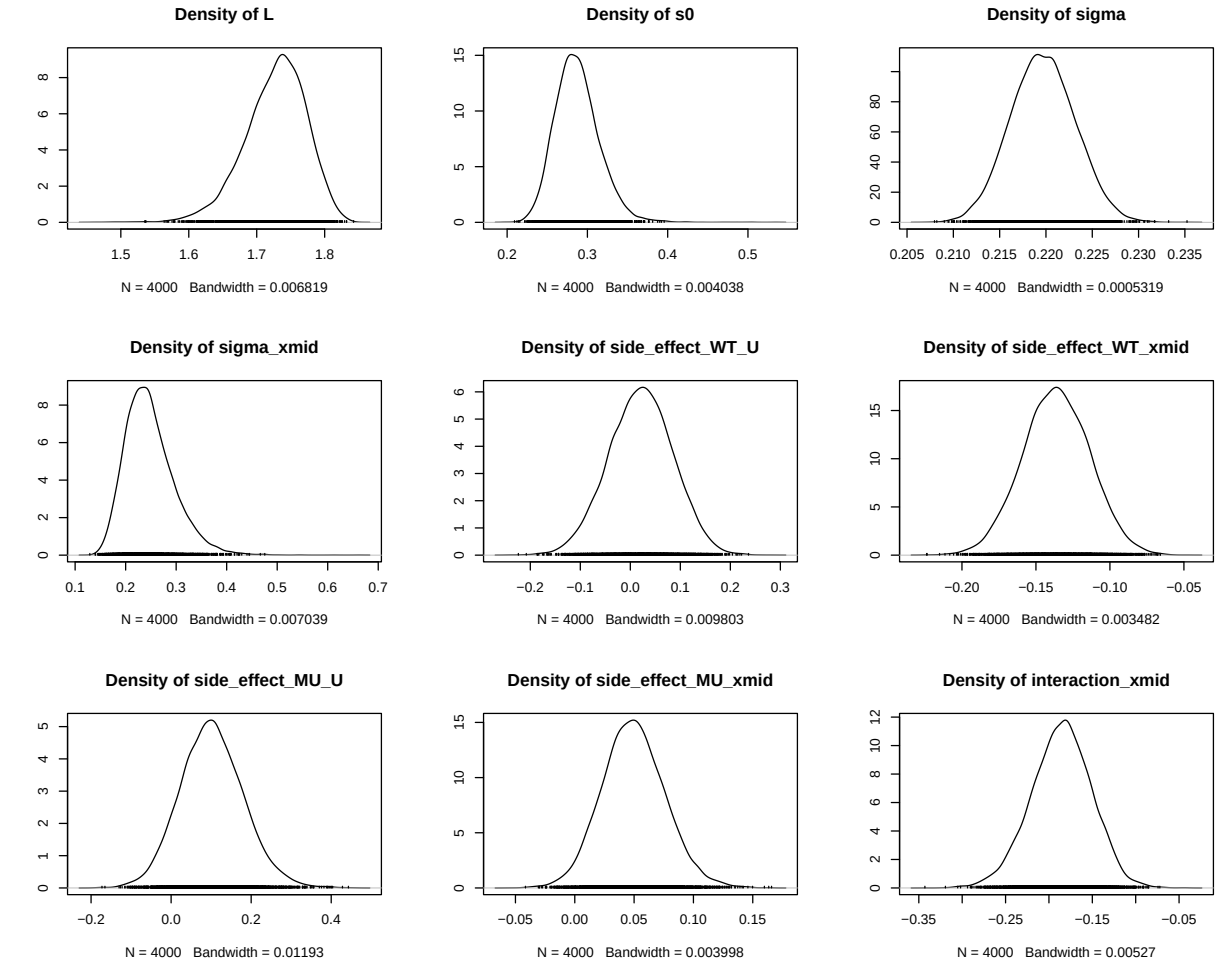

Figure 16: Posterior density plots