

# Sta 440 Case 4

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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). 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):

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

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

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

## 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 (Fig 15). 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 (Fig 16). This shows that there was sufficient posterior sampling. Furthermore, the fitted curves of the Wild Type Roots (Fig 17) 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 18) 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 19). Additionally, the posterior density plots (Fig 20) 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 13 & 14) 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 circumnavigation 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). Residuals for our frequentist model were randomly scattered when examined all together and by side, root, and genotype (FIG). 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 ( $x_{mid}$ ) 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 ( $x_{mid}$ ) than inner-side cells, consistent with asymmetric growth driving circumnavigation.

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 circumnavigation. 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

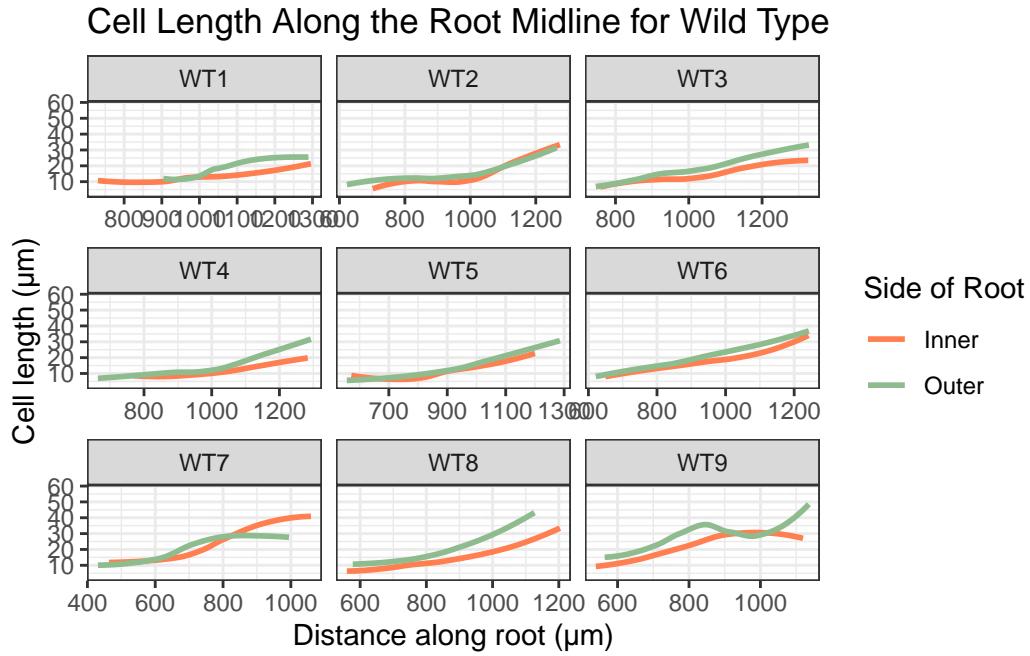


Figure 1: The difference between inner and outer cell lengths changes root by root

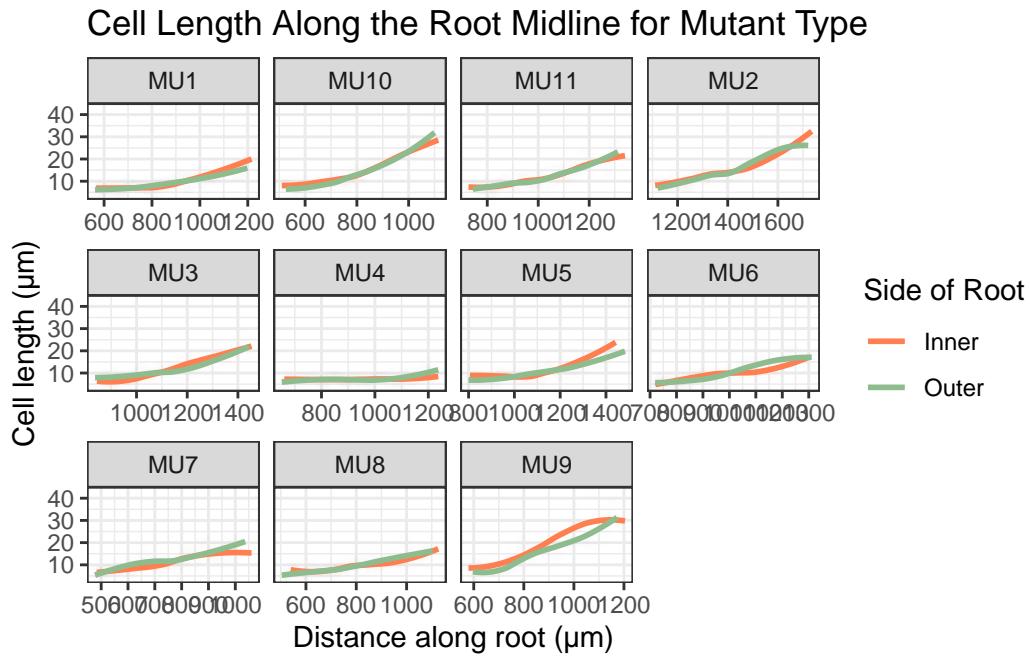


Figure 2: There is only slight differences between inner and outer cell lengths

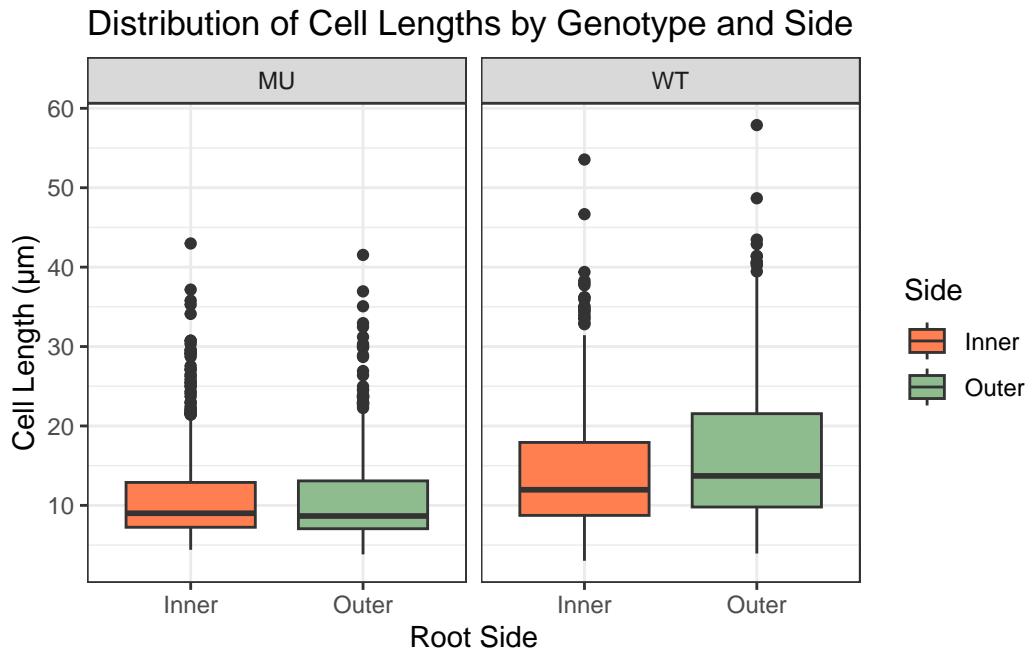


Figure 3: MU cells have similar inner vs outer lengths; WT outer has longer lengths than inner

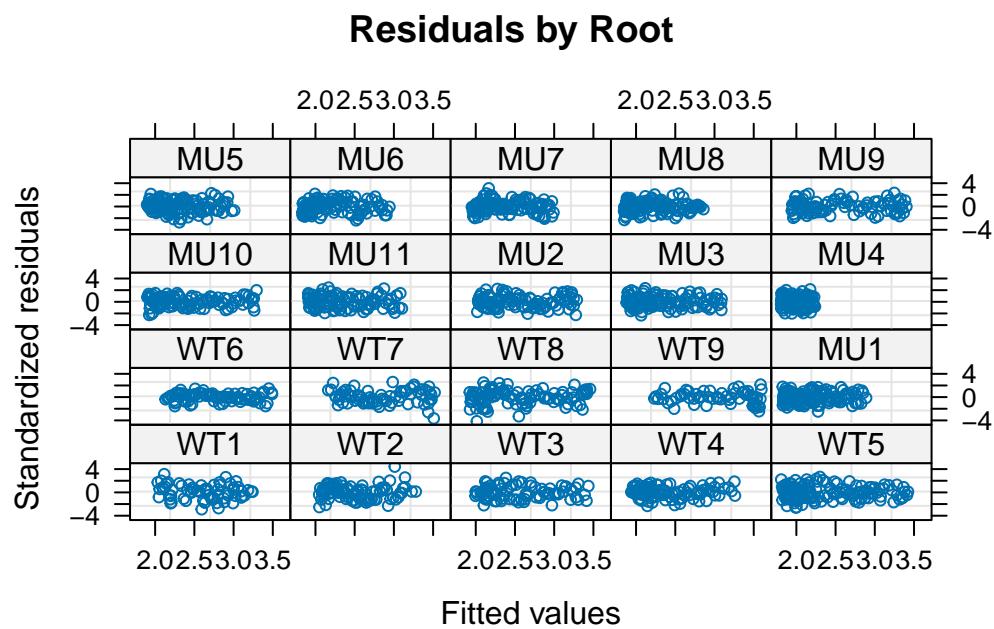


Figure 4: Residual plot by root id shows variation by root with better scatters for WT

### Residuals by Genotype

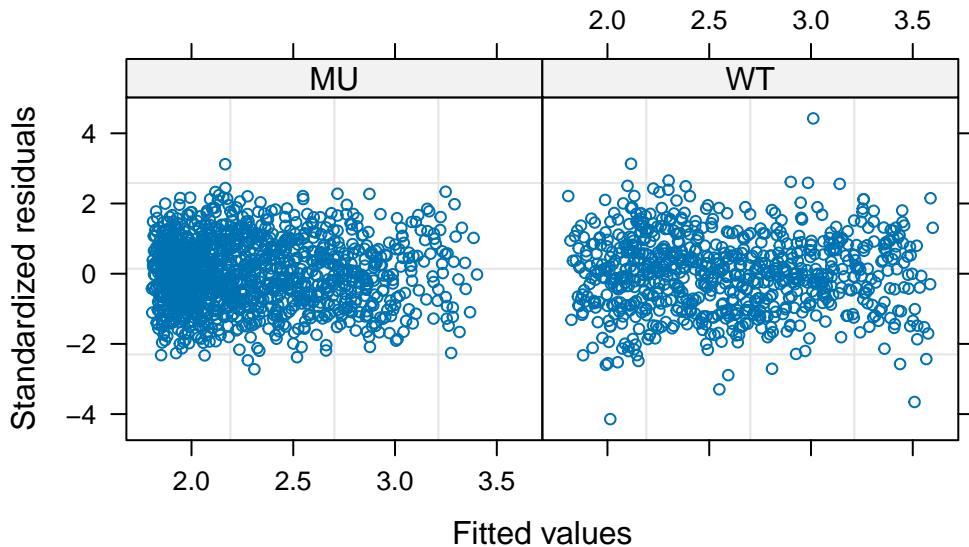


Figure 5: Residuals by Genotype show random scatter and constant variance, MU more dense at lower values

### Residuals by Side

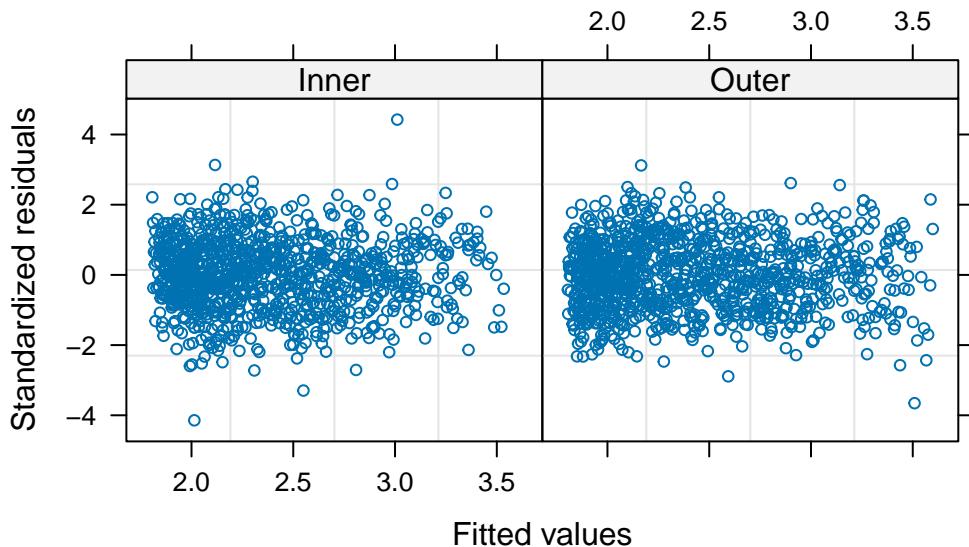


Figure 6: Residuals by Side show random scatter and constant variance more dense at lower values

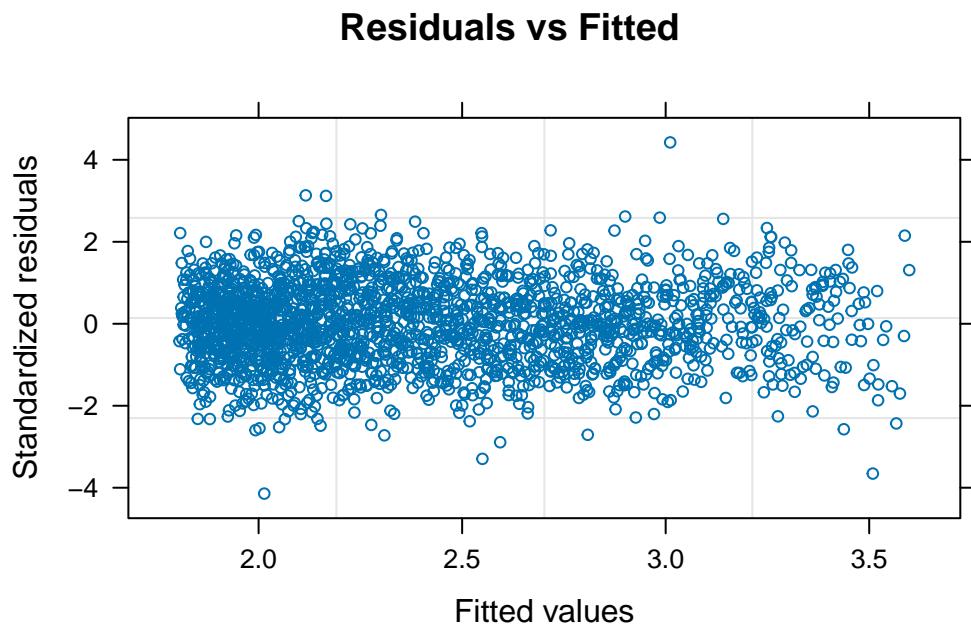


Figure 7: Residual plot for all data shows random scatter and constant variance, more dense at lower values

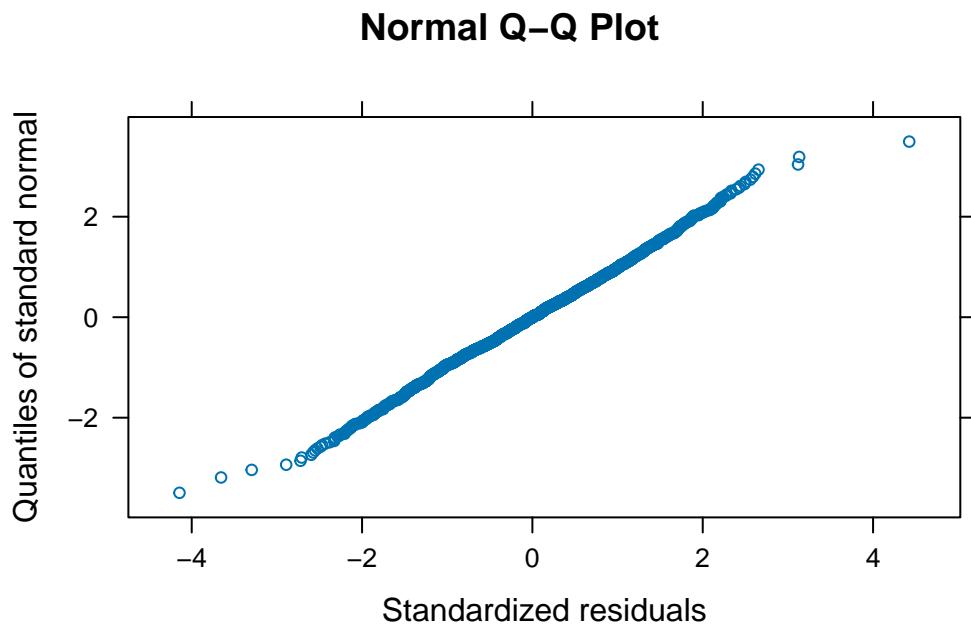


Figure 8: QQ plot shows residuals follow diagonal line, shows normality

## Wild Type (WT) Roots

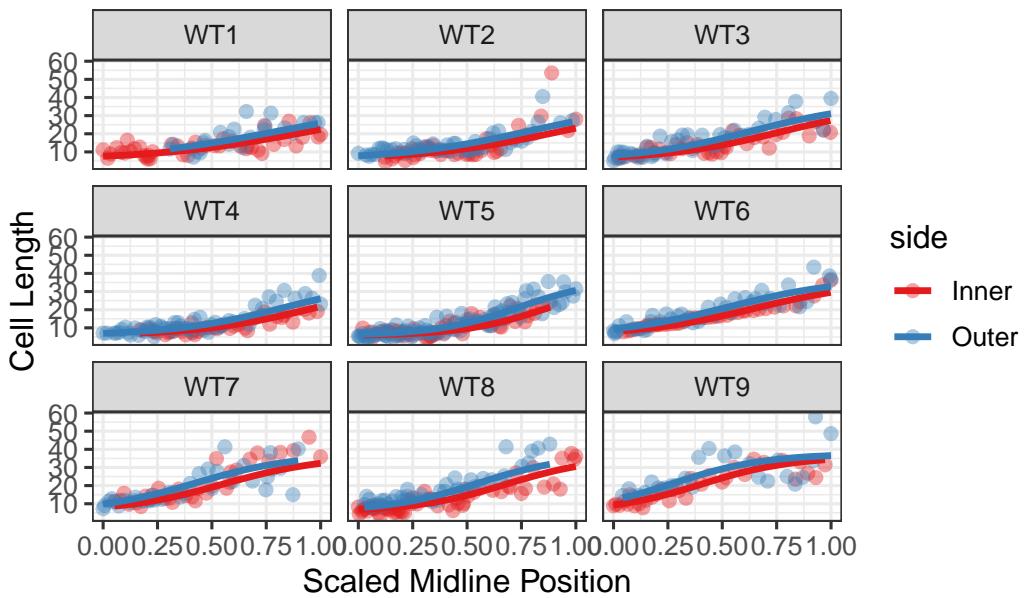


Figure 9: Data vs fitted curves shows goodness of fit for WT

## Mutant (MU) Roots

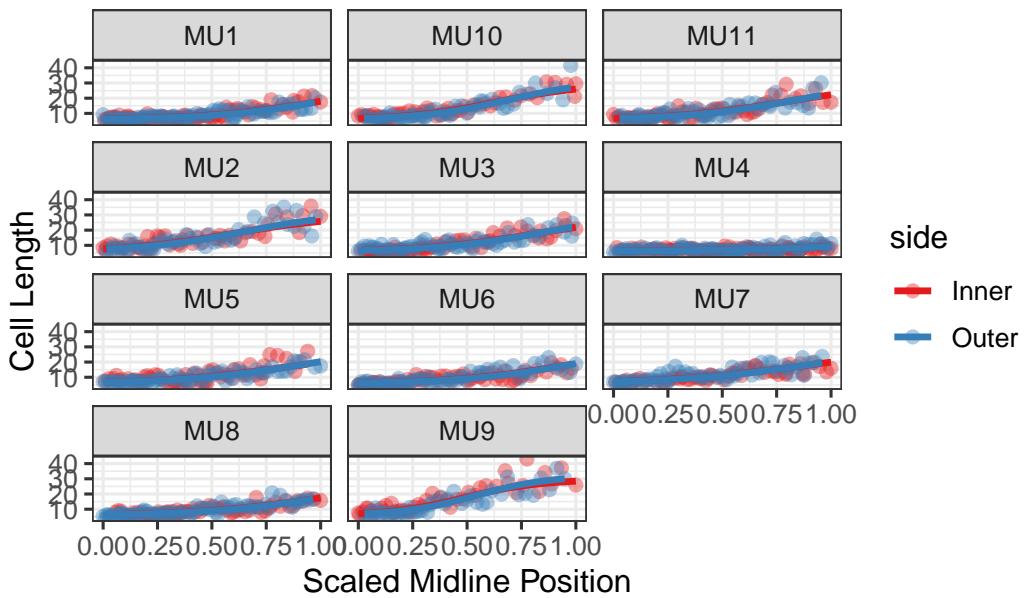


Figure 10: Data vs fitted curves shows goodness of fit for MU

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

	Value	Std.Error	DF	t-value	p-value
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 = 1451.454 secs

	mu.vect	sd.vect	2.5%	25%	50%	75%
L	1.727	0.045	1.628	1.700	1.731	1.759
b_s[1]	0.366	0.108	0.163	0.292	0.364	0.437
b_s[2]	0.153	0.094	-0.028	0.089	0.152	0.215
b_s[3]	0.012	0.093	-0.170	-0.049	0.013	0.073
b_s[4]	-0.009	0.090	-0.185	-0.069	-0.009	0.051
b_s[5]	-0.299	0.080	-0.459	-0.352	-0.298	-0.246
b_s[6]	0.057	0.096	-0.130	-0.007	0.058	0.121
b_s[7]	-0.081	0.105	-0.287	-0.151	-0.081	-0.011
b_s[8]	-0.209	0.085	-0.379	-0.266	-0.208	-0.152
b_s[9]	-0.119	0.132	-0.385	-0.208	-0.118	-0.029
b_s[10]	-0.010	0.093	-0.193	-0.072	-0.009	0.053
b_s[11]	-0.221	0.091	-0.403	-0.282	-0.220	-0.160
b_s[12]	-0.014	0.091	-0.193	-0.075	-0.015	0.046
b_s[13]	-0.029	0.094	-0.217	-0.091	-0.028	0.035
b_s[14]	-0.022	0.089	-0.198	-0.081	-0.021	0.038
b_s[15]	0.398	0.176	0.057	0.278	0.399	0.517
b_s[16]	0.109	0.094	-0.074	0.046	0.108	0.171
b_s[17]	-0.018	0.088	-0.189	-0.076	-0.018	0.041
b_s[18]	0.236	0.093	0.056	0.173	0.235	0.298
b_s[19]	0.083	0.091	-0.094	0.023	0.082	0.143
b_s[20]	-0.371	0.103	-0.579	-0.437	-0.369	-0.300
b_s0	-1.250	0.095	-1.426	-1.315	-1.254	-1.188
b_xmid[1]	0.092	0.084	-0.065	0.034	0.092	0.149
b_xmid[2]	0.116	0.081	-0.036	0.058	0.115	0.171
b_xmid[3]	0.004	0.081	-0.149	-0.052	0.003	0.059
b_xmid[4]	0.204	0.081	0.051	0.147	0.203	0.259
b_xmid[5]	0.169	0.080	0.018	0.112	0.168	0.224
b_xmid[6]	-0.110	0.081	-0.263	-0.167	-0.111	-0.054
b_xmid[7]	-0.180	0.081	-0.333	-0.238	-0.180	-0.124

b_xmid[8]	-0.031	0.080	-0.182	-0.088	-0.033	0.023
b_xmid[9]	-0.309	0.082	-0.462	-0.367	-0.310	-0.254
b_xmid[10]	0.151	0.055	0.057	0.112	0.146	0.185
b_xmid[11]	-0.146	0.053	-0.235	-0.184	-0.152	-0.112
b_xmid[12]	-0.034	0.055	-0.129	-0.073	-0.039	0.000
b_xmid[13]	-0.223	0.055	-0.317	-0.261	-0.228	-0.189
b_xmid[14]	-0.011	0.055	-0.106	-0.050	-0.016	0.023
b_xmid[15]	0.732	0.113	0.541	0.652	0.722	0.800
b_xmid[16]	0.038	0.056	-0.058	-0.001	0.033	0.074
b_xmid[17]	0.116	0.056	0.019	0.076	0.111	0.150
b_xmid[18]	0.007	0.058	-0.098	-0.034	0.002	0.044
b_xmid[19]	0.158	0.056	0.060	0.118	0.153	0.194
b_xmid[20]	-0.269	0.052	-0.356	-0.307	-0.275	-0.237
beta_U_genotype	0.210	0.104	0.007	0.140	0.209	0.278
beta_U_intercept	3.441	0.081	3.298	3.384	3.435	3.491
beta_U_int_sg	-0.082	0.103	-0.292	-0.149	-0.079	-0.012
beta_U_side	0.103	0.082	-0.051	0.047	0.101	0.156
beta_xmid_genotype	-0.092	0.096	-0.269	-0.159	-0.092	-0.028
beta_xmid_intercept	0.631	0.050	0.511	0.601	0.641	0.671
beta_xmid_int_sg	-0.186	0.035	-0.257	-0.209	-0.185	-0.162
beta_xmid_side	0.050	0.027	-0.002	0.031	0.049	0.068
interaction_U	-0.082	0.103	-0.292	-0.149	-0.079	-0.012
interaction_xmid	-0.186	0.035	-0.257	-0.209	-0.185	-0.162
s0	0.288	0.028	0.240	0.268	0.285	0.305
side_effect_MU_U	0.103	0.082	-0.051	0.047	0.101	0.156
side_effect_MU_xmid	0.050	0.027	-0.002	0.031	0.049	0.068
side_effect_WT_U	0.021	0.063	-0.108	-0.020	0.023	0.064
side_effect_WT_xmid	-0.136	0.023	-0.181	-0.151	-0.136	-0.121
sigma	0.220	0.003	0.213	0.217	0.220	0.222
sigma_s	0.231	0.052	0.149	0.195	0.224	0.260
sigma_xmid	0.248	0.049	0.172	0.213	0.242	0.275
deviance	-408.806	11.088	-428.512	-416.633	-409.447	-401.771
	97.5%	Rhat	n.eff			
L	1.803	1.006	460			
b_s[1]	0.586	1.001	4300			
b_s[2]	0.341	1.002	1700			
b_s[3]	0.197	1.003	1300			
b_s[4]	0.168	1.002	2200			
b_s[5]	-0.144	1.002	1600			
b_s[6]	0.244	1.002	1700			
b_s[7]	0.124	1.002	2000			
b_s[8]	-0.046	1.004	710			
b_s[9]	0.136	1.001	5700			
b_s[10]	0.173	1.001	13000			
b_s[11]	-0.045	1.002	3400			
b_s[12]	0.165	1.001	5800			
b_s[13]	0.157	1.002	3100			
b_s[14]	0.150	1.001	5000			
b_s[15]	0.743	1.003	1200			
b_s[16]	0.297	1.001	4200			
b_s[17]	0.156	1.001	5300			
b_s[18]	0.420	1.001	4600			
b_s[19]	0.265	1.001	15000			
b_s[20]	-0.176	1.002	3700			

	Point est.	Upper C.I.
b_s0	-1.053	1.008
b_xmid[1]	0.259	1.006
b_xmid[2]	0.279	1.007
b_xmid[3]	0.166	1.006
b_xmid[4]	0.365	1.007
b_xmid[5]	0.327	1.008
b_xmid[6]	0.052	1.007
b_xmid[7]	-0.019	1.007
b_xmid[8]	0.126	1.007
b_xmid[9]	-0.149	1.007
b_xmid[10]	0.273	1.014
b_xmid[11]	-0.030	1.015
b_xmid[12]	0.084	1.012
b_xmid[13]	-0.104	1.013
b_xmid[14]	0.109	1.013
b_xmid[15]	0.983	1.003
b_xmid[16]	0.160	1.012
b_xmid[17]	0.236	1.014
b_xmid[18]	0.132	1.010
b_xmid[19]	0.282	1.012
b_xmid[20]	-0.153	1.016
beta_U_genotype	0.420	1.004
beta_U_intercept	3.615	1.004
beta_U_intercept_sg	0.113	1.005
beta_U_side	0.271	1.006
beta_xmid_genotype	0.100	1.020
beta_xmid_intercept	0.697	1.026
beta_xmid_intercept_sg	-0.118	1.006
beta_xmid_side	0.105	1.006
interaction_U	0.113	1.005
interaction_xmid	-0.118	1.006
s0	0.349	1.008
side_effect_MU_U	0.271	1.006
side_effect_MU_xmid	0.105	1.006
side_effect_WT_U	0.143	1.001
side_effect_WT_xmid	-0.092	1.002
sigma	0.226	1.001
sigma_s	0.349	1.002
sigma_xmid	0.362	1.003
deviance	-385.010	1.002

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 = 61.4 and DIC = -347.4  
 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	1.01
b_s[12]	1.00	1.00
b_s[13]	1.00	1.01
b_s[14]	1.00	1.01
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	1.01
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	1.01
b_s[9]	1.00	1.00
b_s0	1.01	1.02
b_xmid[1]	1.01	1.02
b_xmid[10]	1.00	1.00
b_xmid[11]	1.00	1.00
b_xmid[12]	1.00	1.00
b_xmid[13]	1.00	1.00
b_xmid[14]	1.00	1.00
b_xmid[15]	1.00	1.01
b_xmid[16]	1.00	1.00
b_xmid[17]	1.00	1.00
b_xmid[18]	1.00	1.00
b_xmid[19]	1.00	1.00
b_xmid[2]	1.01	1.02
b_xmid[20]	1.00	1.00
b_xmid[3]	1.01	1.02
b_xmid[4]	1.01	1.02
b_xmid[5]	1.01	1.02
b_xmid[6]	1.01	1.02
b_xmid[7]	1.01	1.02
b_xmid[8]	1.01	1.02
b_xmid[9]	1.01	1.02
beta_U_genotype	1.00	1.01
beta_U_intercept	1.00	1.01
beta_U_intercept_sg	1.01	1.02
beta_U_side	1.01	1.02
beta_xmid_genotype	1.01	1.02
beta_xmid_intercept	1.00	1.01
beta_xmid_intercept_sg	1.01	1.03
beta_xmid_side	1.01	1.02
deviance	1.00	1.00
interaction_U	1.01	1.02
interaction_xmid	1.01	1.03
L	1.01	1.02
s0	1.01	1.02
side_effect_MU_U	1.01	1.02

side_effect_MU_xmid	1.01	1.02
side_effect_WT_U	1.00	1.00
side_effect_WT_xmid	1.00	1.01
sigma	1.00	1.00
sigma_s	1.00	1.00
sigma_xmid	1.00	1.00

==== 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]
7726.3716	6532.6871	4993.2889	6594.3269	5001.3048	6358.0075	2538.0657
b_s[16]	b_s[17]	b_s[18]	b_s[19]	b_s[2]	b_s[20]	b_s[3]
7680.0654	6285.2789	6194.1674	6996.2503	5263.5810	4193.6048	5742.3402
b_s[4]	b_s[5]	b_s[6]	b_s[7]	b_s[8]	b_s[9]	b_s0
5940.1142	5068.6522	5521.8057	6808.4841	4564.6391	8109.9298	1256.0056
b_xmid[1]	b_xmid[10]	b_xmid[11]	b_xmid[12]	b_xmid[13]	b_xmid[14]	b_xmid[15]
303.8707	457.7671	461.2682	495.3943	489.6663	491.7329	1200.8171
b_xmid[16]	b_xmid[17]					
531.0550	488.5737					

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

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-1.25771	-0.28074	-0.05131	-0.04447	0.17159	1.59482

==== 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]	3.663e-01	0.107995	8.538e-04	1.239e-03
b_s[10]	-9.606e-03	0.093331	7.378e-04	1.161e-03
b_s[11]	-2.214e-01	0.090901	7.186e-04	1.292e-03
b_s[12]	-1.444e-02	0.090595	7.162e-04	1.123e-03
b_s[13]	-2.886e-02	0.094225	7.449e-04	1.343e-03
b_s[14]	-2.170e-02	0.088716	7.014e-04	1.116e-03
b_s[15]	3.980e-01	0.175649	1.389e-03	3.504e-03
b_s[16]	1.090e-01	0.094071	7.437e-04	1.075e-03
b_s[17]	-1.776e-02	0.088040	6.960e-04	1.111e-03
b_s[18]	2.361e-01	0.093069	7.358e-04	1.183e-03
b_s[19]	8.328e-02	0.091116	7.203e-04	1.090e-03
b_s[2]	1.528e-01	0.094305	7.455e-04	1.345e-03
b_s[20]	-3.705e-01	0.102880	8.133e-04	1.596e-03
b_s[3]	1.237e-02	0.092717	7.330e-04	1.244e-03
b_s[4]	-8.987e-03	0.089798	7.099e-04	1.170e-03
b_s[5]	-2.990e-01	0.080024	6.326e-04	1.128e-03
b_s[6]	5.700e-02	0.095842	7.577e-04	1.296e-03

b_s[7]	-8.145e-02	0.105281	8.323e-04	1.307e-03
b_s[8]	-2.092e-01	0.084646	6.692e-04	1.256e-03
b_s[9]	-1.192e-01	0.132459	1.047e-03	1.473e-03
b_s0	-1.250e+00	0.094531	7.473e-04	2.693e-03
b_xmid[1]	9.232e-02	0.083622	6.611e-04	4.938e-03
b_xmid[10]	1.514e-01	0.055208	4.365e-04	2.717e-03
b_xmid[11]	-1.462e-01	0.053040	4.193e-04	2.603e-03
b_xmid[12]	-3.422e-02	0.054825	4.334e-04	2.569e-03
b_xmid[13]	-2.228e-01	0.054738	4.327e-04	2.655e-03
b_xmid[14]	-1.137e-02	0.054740	4.328e-04	2.612e-03
b_xmid[15]	7.323e-01	0.113221	8.951e-04	3.425e-03
b_xmid[16]	3.838e-02	0.056066	4.432e-04	2.540e-03
b_xmid[17]	1.156e-01	0.055894	4.419e-04	2.644e-03
b_xmid[18]	6.571e-03	0.058483	4.624e-04	2.548e-03
b_xmid[19]	1.585e-01	0.056285	4.450e-04	2.556e-03
b_xmid[2]	1.157e-01	0.081364	6.432e-04	4.789e-03
b_xmid[20]	-2.695e-01	0.052358	4.139e-04	2.590e-03
b_xmid[3]	4.491e-03	0.081167	6.417e-04	4.787e-03
b_xmid[4]	2.041e-01	0.081031	6.406e-04	4.807e-03
b_xmid[5]	1.692e-01	0.080299	6.348e-04	4.918e-03
b_xmid[6]	-1.098e-01	0.081148	6.415e-04	4.934e-03
b_xmid[7]	-1.799e-01	0.081234	6.422e-04	4.893e-03
b_xmid[8]	-3.149e-02	0.080245	6.344e-04	4.804e-03
b_xmid[9]	-3.091e-01	0.081569	6.449e-04	4.920e-03
beta_U_gen0	2.099e-01	0.104408	8.254e-04	2.757e-03
beta_U_int	3.441e+00	0.080833	6.390e-04	2.517e-03
beta_U_int_sg	-8.155e-02	0.103133	8.153e-04	2.303e-03
beta_U_side	1.029e-01	0.081949	6.479e-04	1.944e-03
beta_xmid_gen0	-9.191e-02	0.095761	7.571e-04	6.918e-03
beta_xmid_int	6.313e-01	0.050472	3.990e-04	2.984e-03
beta_xmid_int_sg	-1.858e-01	0.035350	2.795e-04	8.280e-04
beta_xmid_side	4.978e-02	0.027316	2.160e-04	7.021e-04
deviance	-4.088e+02	11.088163	8.766e-02	1.313e-01
interaction_U	-8.155e-02	0.103133	8.153e-04	2.303e-03
interaction_xmid	-1.858e-01	0.035350	2.795e-04	8.280e-04
L	1.727e+00	0.045118	3.567e-04	1.291e-03
s0	2.878e-01	0.027581	2.180e-04	7.957e-04
side_effect_MU_U	1.029e-01	0.081949	6.479e-04	1.944e-03
side_effect_MU_xmid	4.978e-02	0.027316	2.160e-04	7.021e-04
side_effect_WT_U	2.132e-02	0.063253	5.001e-04	7.448e-04
side_effect_WT_xmid	-1.360e-01	0.022502	1.779e-04	2.821e-04
sigma	2.197e-01	0.003429	2.711e-05	2.658e-05
sigma_s	2.308e-01	0.051565	4.077e-04	5.995e-04
sigma_xmid	2.480e-01	0.048890	3.865e-04	7.806e-04

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%
b_s[1]	1.631e-01	2.924e-01	3.639e-01	4.374e-01	0.58606
b_s[10]	-1.935e-01	-7.202e-02	-9.132e-03	5.297e-02	0.17341
b_s[11]	-4.027e-01	-2.816e-01	-2.198e-01	-1.604e-01	-0.04463
b_s[12]	-1.926e-01	-7.473e-02	-1.487e-02	4.554e-02	0.16526
b_s[13]	-2.175e-01	-9.086e-02	-2.760e-02	3.481e-02	0.15674
b_s[14]	-1.977e-01	-8.123e-02	-2.109e-02	3.787e-02	0.14993

b_s[15]	5.659e-02	2.782e-01	3.989e-01	5.171e-01	0.74293
b_s[16]	-7.370e-02	4.592e-02	1.085e-01	1.710e-01	0.29737
b_s[17]	-1.892e-01	-7.605e-02	-1.793e-02	4.130e-02	0.15572
b_s[18]	5.621e-02	1.732e-01	2.354e-01	2.978e-01	0.41974
b_s[19]	-9.417e-02	2.253e-02	8.213e-02	1.431e-01	0.26484
b_s[2]	-2.786e-02	8.935e-02	1.520e-01	2.153e-01	0.34073
b_s[20]	-5.789e-01	-4.370e-01	-3.688e-01	-3.004e-01	-0.17576
b_s[3]	-1.705e-01	-4.904e-02	1.279e-02	7.329e-02	0.19726
b_s[4]	-1.854e-01	-6.862e-02	-8.855e-03	5.098e-02	0.16810
b_s[5]	-4.593e-01	-3.518e-01	-2.978e-01	-2.460e-01	-0.14388
b_s[6]	-1.301e-01	-7.130e-03	5.805e-02	1.208e-01	0.24437
b_s[7]	-2.875e-01	-1.512e-01	-8.087e-02	-1.120e-02	0.12370
b_s[8]	-3.790e-01	-2.657e-01	-2.081e-01	-1.518e-01	-0.04620
b_s[9]	-3.849e-01	-2.082e-01	-1.177e-01	-2.883e-02	0.13597
b_s0	-1.426e+00	-1.315e+00	-1.254e+00	-1.188e+00	-1.05303
b_xmid[1]	-6.529e-02	3.360e-02	9.211e-02	1.486e-01	0.25906
b_xmid[10]	5.655e-02	1.121e-01	1.459e-01	1.854e-01	0.27340
b_xmid[11]	-2.353e-01	-1.843e-01	-1.519e-01	-1.125e-01	-0.02959
b_xmid[12]	-1.291e-01	-7.294e-02	-3.916e-02	4.711e-05	0.08422
b_xmid[13]	-3.173e-01	-2.613e-01	-2.280e-01	-1.887e-01	-0.10424
b_xmid[14]	-1.059e-01	-4.986e-02	-1.610e-02	2.318e-02	0.10898
b_xmid[15]	5.411e-01	6.517e-01	7.221e-01	8.001e-01	0.98308
b_xmid[16]	-5.839e-02	-1.124e-03	3.338e-02	7.410e-02	0.15978
b_xmid[17]	1.910e-02	7.585e-02	1.106e-01	1.504e-01	0.23626
b_xmid[18]	-9.755e-02	-3.402e-02	1.854e-03	4.379e-02	0.13162
b_xmid[19]	6.037e-02	1.184e-01	1.532e-01	1.940e-01	0.28150
b_xmid[2]	-3.608e-02	5.769e-02	1.149e-01	1.711e-01	0.27885
b_xmid[20]	-3.564e-01	-3.069e-01	-2.754e-01	-2.368e-01	-0.15319
b_xmid[3]	-1.490e-01	-5.232e-02	2.952e-03	5.933e-02	0.16646
b_xmid[4]	5.143e-02	1.466e-01	2.030e-01	2.594e-01	0.36450
b_xmid[5]	1.820e-02	1.121e-01	1.683e-01	2.237e-01	0.32709
b_xmid[6]	-2.633e-01	-1.666e-01	-1.108e-01	-5.407e-02	0.05206
b_xmid[7]	-3.326e-01	-2.377e-01	-1.801e-01	-1.240e-01	-0.01912
b_xmid[8]	-1.816e-01	-8.827e-02	-3.259e-02	2.323e-02	0.12616
b_xmid[9]	-4.618e-01	-3.671e-01	-3.095e-01	-2.536e-01	-0.14879
beta_U_gen0	7.130e-03	1.401e-01	2.086e-01	2.778e-01	0.41951
beta_U_int	3.298e+00	3.384e+00	3.435e+00	3.491e+00	3.61508
beta_U_int_sg	-2.920e-01	-1.486e-01	-7.940e-02	-1.231e-02	0.11256
beta_U_side	-5.087e-02	4.697e-02	1.009e-01	1.559e-01	0.27105
beta_xmid_gen0	-2.687e-01	-1.589e-01	-9.249e-02	-2.806e-02	0.09964
beta_xmid_int	5.111e-01	6.012e-01	6.413e-01	6.710e-01	0.69709
beta_xmid_int_sg	-2.571e-01	-2.090e-01	-1.852e-01	-1.619e-01	-0.11843
beta_xmid_side	-1.737e-03	3.127e-02	4.901e-02	6.755e-02	0.10460
deviance	-4.285e+02	-4.166e+02	-4.094e+02	-4.018e+02	-385.01029
interaction_U	-2.920e-01	-1.486e-01	-7.940e-02	-1.231e-02	0.11256
interaction_xmid	-2.571e-01	-2.090e-01	-1.852e-01	-1.619e-01	-0.11843
L	1.628e+00	1.700e+00	1.731e+00	1.759e+00	1.80334
s0	2.403e-01	2.684e-01	2.854e-01	3.048e-01	0.34888
side_effect_MU_U	-5.087e-02	4.697e-02	1.009e-01	1.559e-01	0.27105
side_effect_MU_xmid	-1.737e-03	3.127e-02	4.901e-02	6.755e-02	0.10460
side_effect_WT_U	-1.079e-01	-1.994e-02	2.287e-02	6.407e-02	0.14273
side_effect_WT_xmid	-1.811e-01	-1.509e-01	-1.359e-01	-1.209e-01	-0.09224
sigma	2.132e-01	2.173e-01	2.197e-01	2.220e-01	0.22643
sigma_s	1.487e-01	1.949e-01	2.245e-01	2.600e-01	0.34914

```
sigma_xmid      1.716e-01  2.132e-01  2.416e-01  2.755e-01  0.36235
```

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

	lower	upper
b_s[1]	0.17585363	0.58823732
b_s[10]	-0.18848737	0.18024629
b_s[11]	-0.39679264	-0.04129269
b_s[12]	-0.18264416	0.16557940
b_s[13]	-0.21078715	0.16467309
b_s[14]	-0.20257054	0.15051854
b_s[15]	0.03955090	0.73346248
b_s[16]	-0.06227989	0.29756692
b_s[17]	-0.18208417	0.15500882
b_s[18]	0.05429489	0.41863501
b_s[19]	-0.08302512	0.26375952
b_s[2]	-0.02759913	0.34220501
b_s[20]	-0.58085163	-0.17241928
b_s[3]	-0.16528427	0.20216479
b_s[4]	-0.17069815	0.17651744
b_s[5]	-0.44831999	-0.13920484
b_s[6]	-0.11907399	0.25025556
b_s[7]	-0.27931946	0.11856236
b_s[8]	-0.37145863	-0.04528378
b_s[9]	-0.35590491	0.14220435
b_s0	-1.45206772	-1.07609548
b_xmid[1]	-0.06198772	0.25074548
b_xmid[10]	0.05444728	0.28001318
b_xmid[11]	-0.23636833	-0.01912458
b_xmid[12]	-0.13702875	0.09026278
b_xmid[13]	-0.31892223	-0.09620458
b_xmid[14]	-0.10727440	0.11779660
b_xmid[15]	0.52266984	0.96377860
b_xmid[16]	-0.06178701	0.16850447
b_xmid[17]	0.01663878	0.24115142
b_xmid[18]	-0.09722830	0.13648812
b_xmid[19]	0.05705575	0.28967445
b_xmid[2]	-0.03221532	0.27028559
b_xmid[20]	-0.35650324	-0.14651575
b_xmid[3]	-0.14811317	0.15803055
b_xmid[4]	0.05990420	0.36781428
b_xmid[5]	0.01625926	0.31954364
b_xmid[6]	-0.26337056	0.04352020
b_xmid[7]	-0.33395331	-0.02292855
b_xmid[8]	-0.17472694	0.12531182

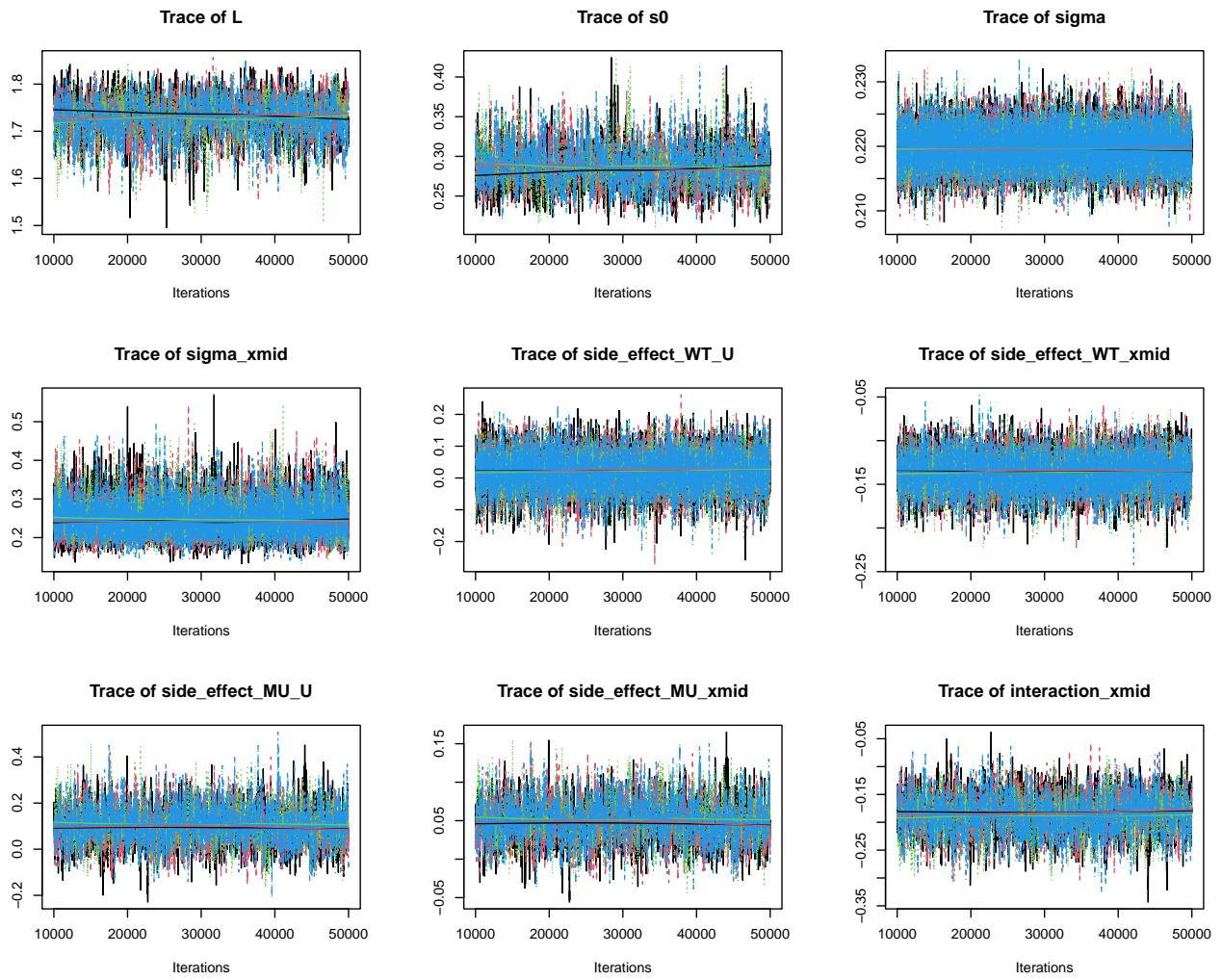


Figure 11: CAP

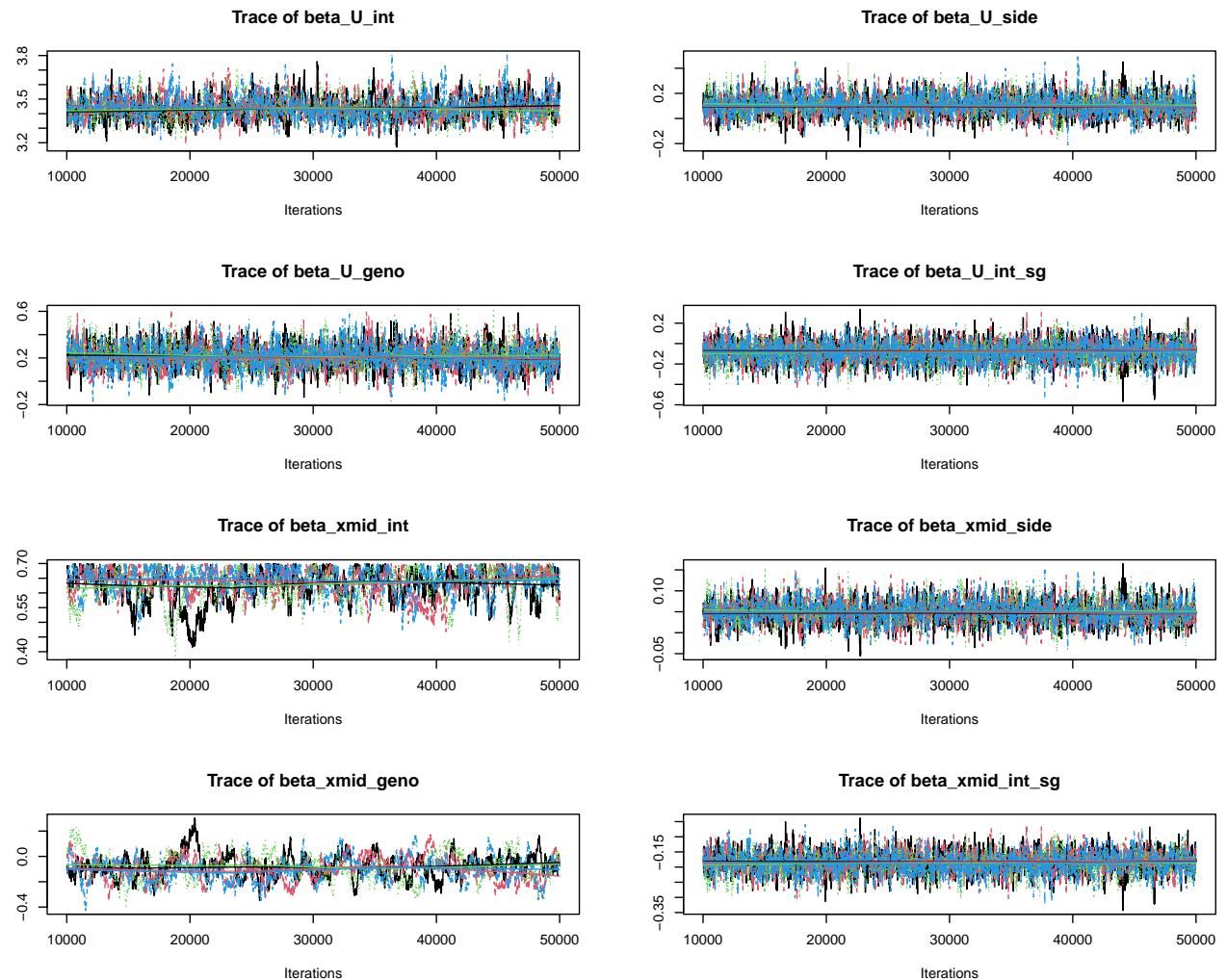


Figure 12: CAP

	Point est.	Upper C.I.
$b_s[1]$	1.001	1.003
$b_s[10]$	1.001	1.002
$b_s[11]$	1.002	1.007
$b_s[12]$	1.001	1.002
$b_s[13]$	1.002	1.006
$b_s[14]$	1.002	1.005
$b_s[15]$	1.001	1.005
$b_s[16]$	1.001	1.004
$b_s[17]$	1.001	1.004
$b_s[18]$	1.001	1.004
$b_s[19]$	1.001	1.002
$b_s[2]$	1.001	1.003
$b_s[20]$	1.001	1.004
$b_s[3]$	1.001	1.004
$b_s[4]$	1.002	1.006
$b_s[5]$	1.002	1.005
$b_s[6]$	1.001	1.004

	Point est.	Upper C.I.
b_s[7]	1.001	1.004
b_s[8]	1.003	1.008
b_s[9]	1.001	1.003
b_s0	1.008	1.023
b_xmid[1]	1.006	1.017
b_xmid[10]	1.002	1.003
b_xmid[11]	1.002	1.003
b_xmid[12]	1.001	1.001
b_xmid[13]	1.001	1.002
b_xmid[14]	1.002	1.003
b_xmid[15]	1.002	1.005
b_xmid[16]	1.001	1.002
b_xmid[17]	1.002	1.003
b_xmid[18]	1.001	1.002
b_xmid[19]	1.001	1.002
b_xmid[2]	1.007	1.019
b_xmid[20]	1.002	1.004
b_xmid[3]	1.006	1.016
b_xmid[4]	1.007	1.020
b_xmid[5]	1.008	1.021
b_xmid[6]	1.007	1.019
b_xmid[7]	1.007	1.018
b_xmid[8]	1.007	1.020
b_xmid[9]	1.007	1.019
beta_U_gen	1.004	1.013
beta_U_int	1.005	1.009
beta_U_int_sg	1.006	1.019
beta_U_side	1.006	1.018
beta_xmid_gen	1.008	1.023
beta_xmid_int	1.005	1.010
beta_xmid_int_sg	1.008	1.026
beta_xmid_side	1.008	1.023
deviance	1.000	1.002
interaction_U	1.006	1.019
interaction_xmid	1.008	1.026
L	1.007	1.020
s0	1.009	1.024
side_effect_MU_U	1.006	1.018
side_effect_MU_xmid	1.008	1.023
side_effect_WT_U	1.001	1.005
side_effect_WT_xmid	1.002	1.007
sigma	1.000	1.000
sigma_s	1.001	1.003
sigma_xmid	1.001	1.005

Gelman-Rubin convergence diagnostics for main parameters

## Appendix

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Parameter	Effective Sample Size
b_s[1]	7726.4
b_s[10]	6532.7
b_s[11]	4993.3
b_s[12]	6594.3
b_s[13]	5001.3
b_s[14]	6358.0
b_s[15]	2538.1
b_s[16]	7680.1
b_s[17]	6285.3
b_s[18]	6194.2
b_s[19]	6996.3
b_s[2]	5263.6
b_s[20]	4193.6
b_s[3]	5742.3
b_s[4]	5940.1
b_s[5]	5068.7
b_s[6]	5521.8
b_s[7]	6808.5
b_s[8]	4564.6
b_s[9]	8109.9
b_s0	1256.0
b_xmid[1]	303.9
b_xmid[10]	457.8
b_xmid[11]	461.3
b_xmid[12]	495.4
b_xmid[13]	489.7
b_xmid[14]	491.7
b_xmid[15]	1200.8
b_xmid[16]	531.1
b_xmid[17]	488.6

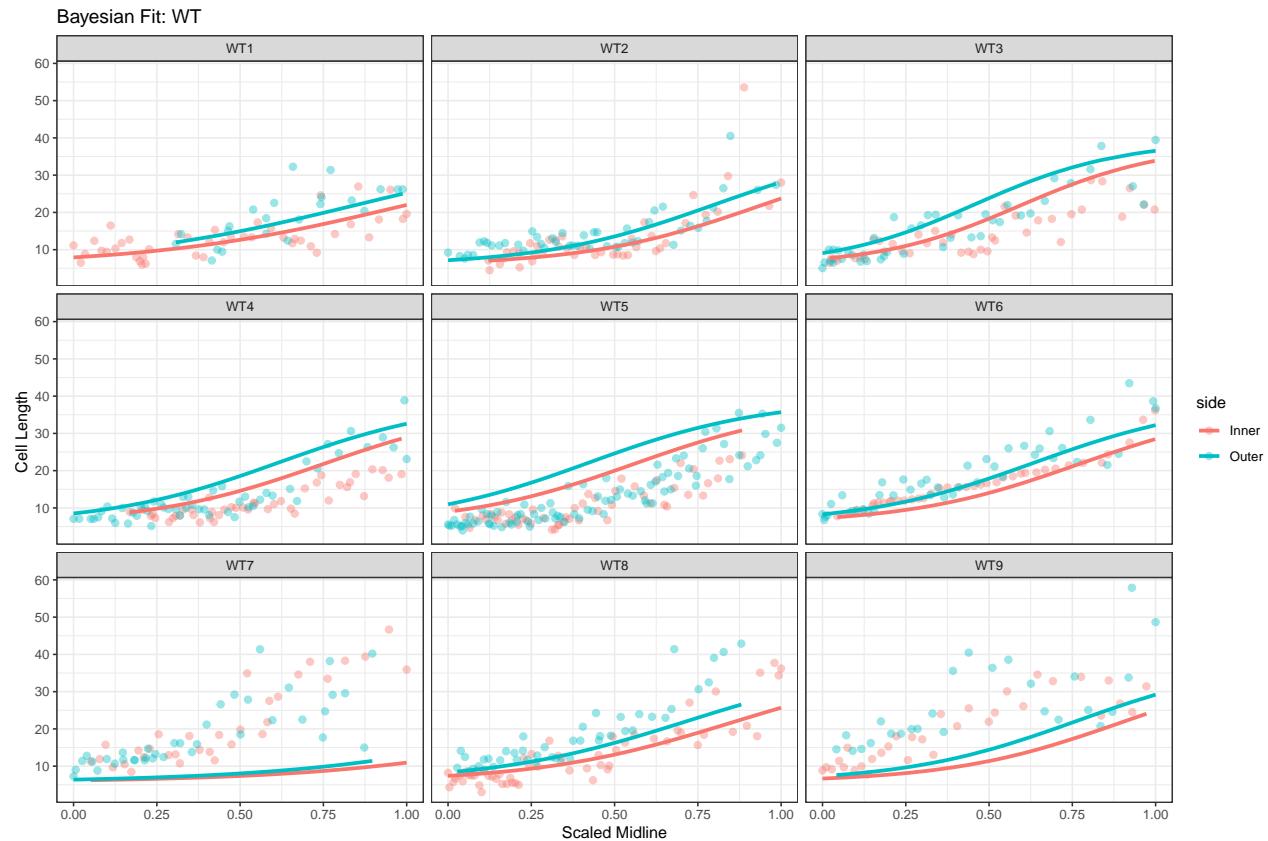


Figure 13: Bayesian fitted curves for WT genotype

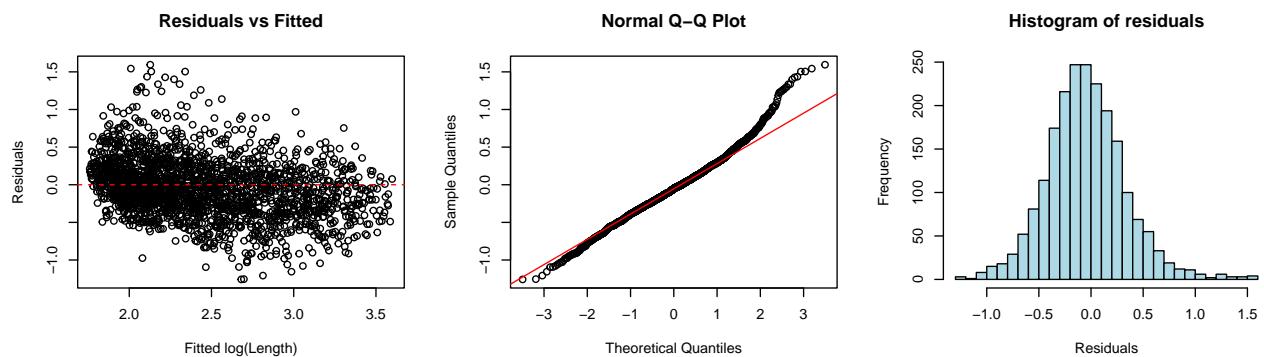


Figure 14: Residuals vs Fitted

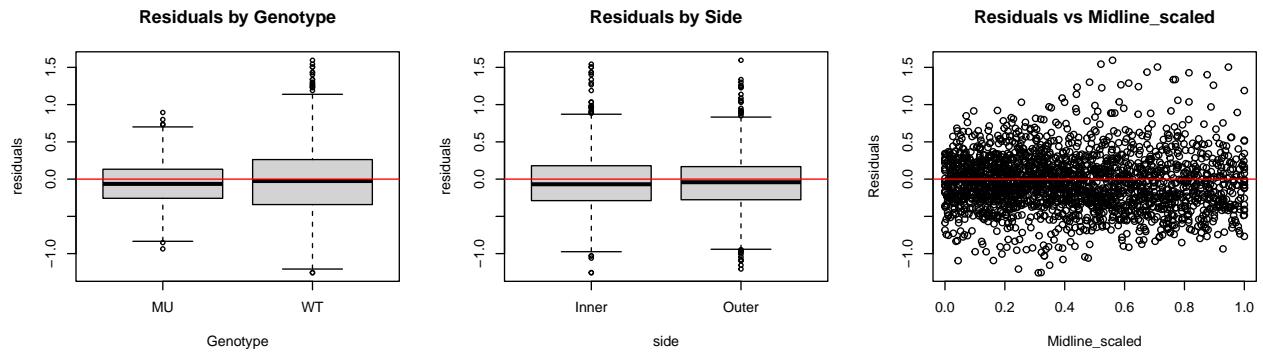


Figure 15: Residuals by grouping variables

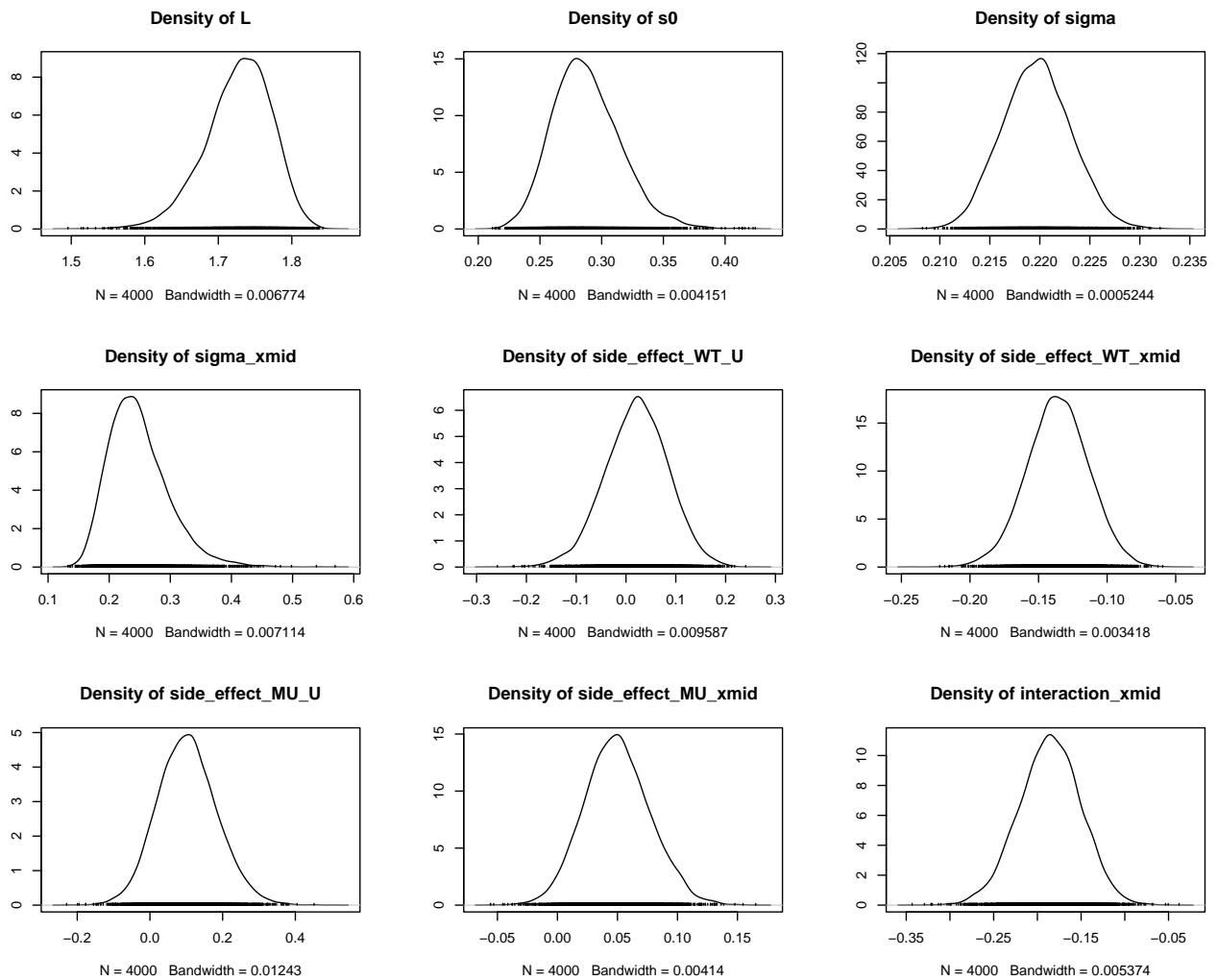


Figure 16: Posterior density plots