

Supplementary Material 2

The spatial distribution of tree-tree interaction effects on soil microbial biomass and respiration

Henriette Christel, Helge Bruelheide, Simone Cesarz, Nico Eisenhauer,
Georg J. A. Hähn, and Remy Beugnon

Contents

Figure S1: Correlation matrix	2
Section S2: Microbial respiration (H1)	3
Section S3: Microbial biomass (H1)	4
Section S4: Overyielding microbial respiration (H2)	5
Section S5: Overyielding microbial biomass (H2)	7
Section S6: Spatial distribution of microbial respiration overyielding (H3)	9
Section S7: Spatial distribution of microbial biomass overyielding (H3)	10
Figure S2: Abiotic and biotic drivers of soil microbial biomass and respiration	11

Figure S1: Correlation matrix

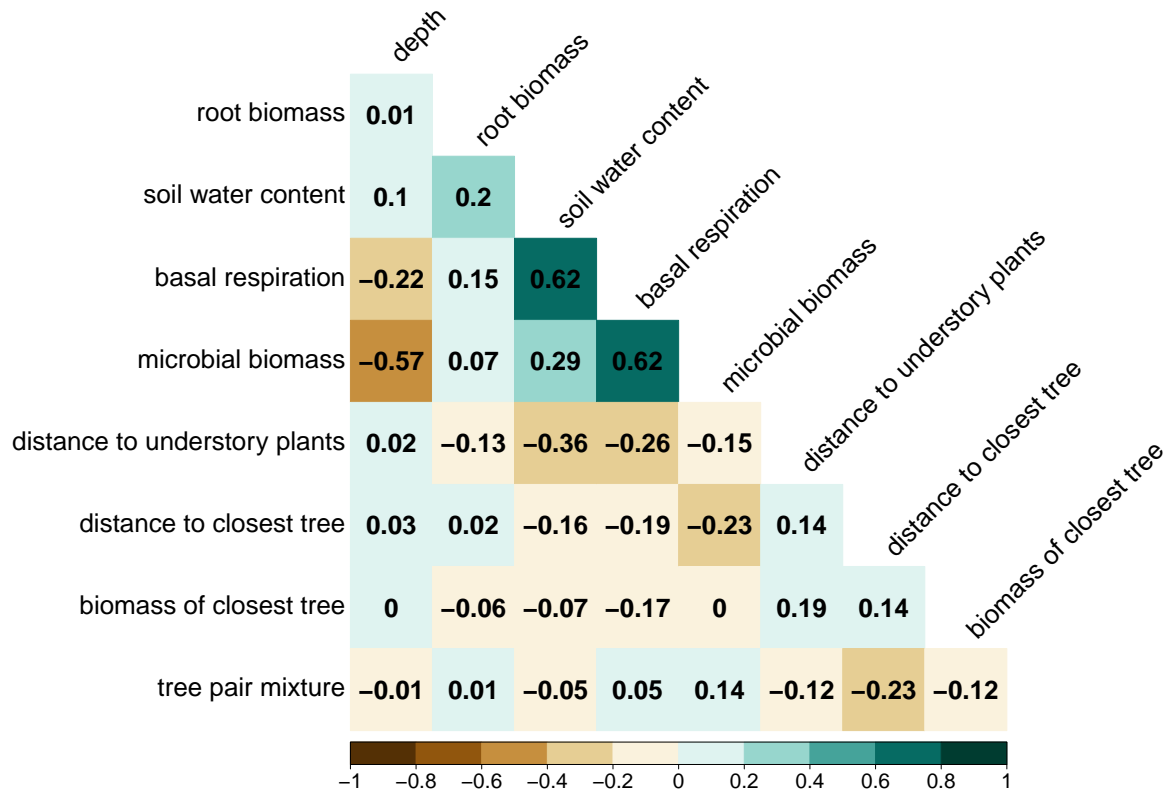


Figure S1: A correlation matrix of the variables used. Brown colour indicates negative correlation, green colour indicates positive correlation.

Section S2: Microbial respiration (H1)

Model summary

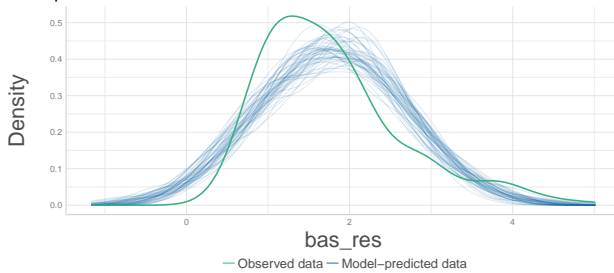
```
lmer(formula = bas_res ~ close_distance * depth + (1|plot), data = df)
```

	Estimate	Std. Error	t-value	p-value
(Intercept)	2.3262195	0.4764510	4.882389	0.0767479
close_distance	-0.0068739	0.0039270	-1.750412	0.0817317
depth	-0.1427127	0.0563661	-2.531891	0.0121907
close_distance:depth	0.0011358	0.0011281	1.006858	0.3153398

Model fit

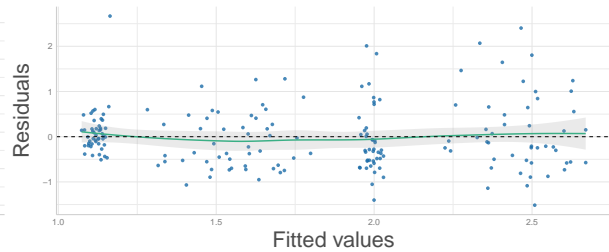
Posterior Predictive Check

Model-predicted lines should resemble observed data line



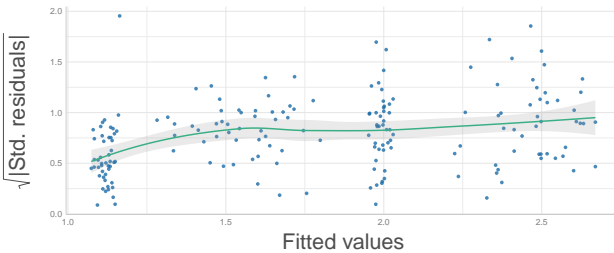
Linearity

Reference line should be flat and horizontal



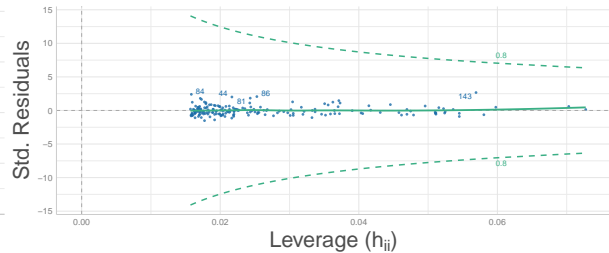
Homogeneity of Variance

Reference line should be flat and horizontal



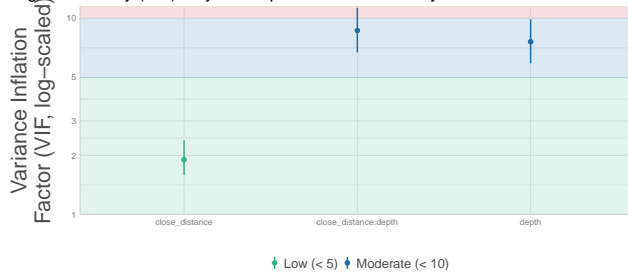
Influential Observations

Points should be inside the contour lines



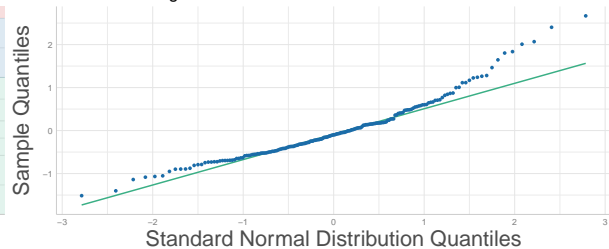
Collinearity

High collinearity (VIF) may inflate parameter uncertainty



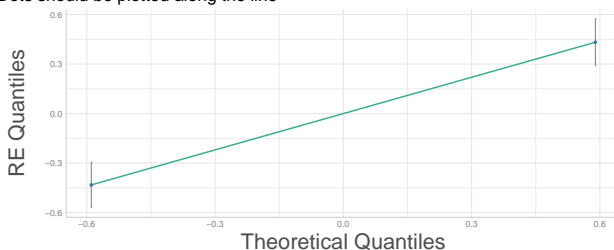
Normality of Residuals

Dots should fall along the line



Normality of Random Effects (plot)

Dots should be plotted along the line



Section S3: Microbial biomass (H1)

Model summary

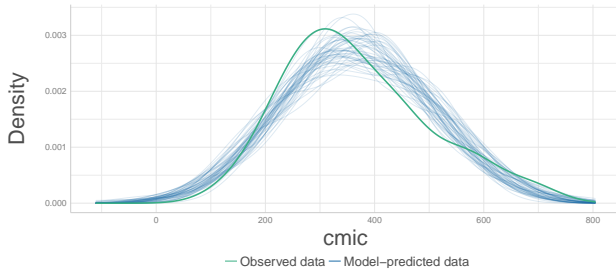
```
lmer(formula = cmic ~ close_distance * depth + (1|plot), data = df)
```

	Estimate	Std. Error	t-value	p-value
(Intercept)	515.8788176	36.9323184	13.968222	0.0000562
close_distance	-1.5954273	0.5709665	-2.794257	0.0057580
depth	-44.9601154	8.1995370	-5.483250	0.0000001
close_distance:depth	0.3061849	0.1640985	1.865861	0.0636699

Model fit

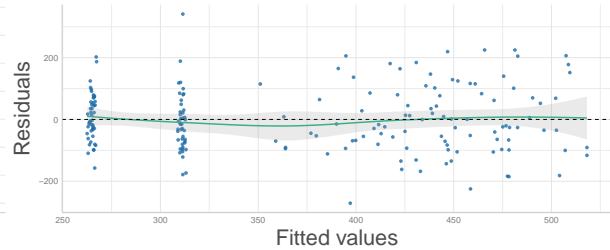
Posterior Predictive Check

Model-predicted lines should resemble observed data line



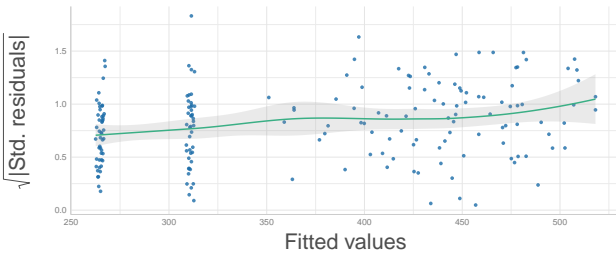
Linearity

Reference line should be flat and horizontal



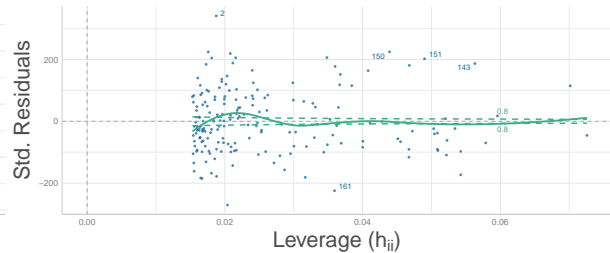
Homogeneity of Variance

Reference line should be flat and horizontal



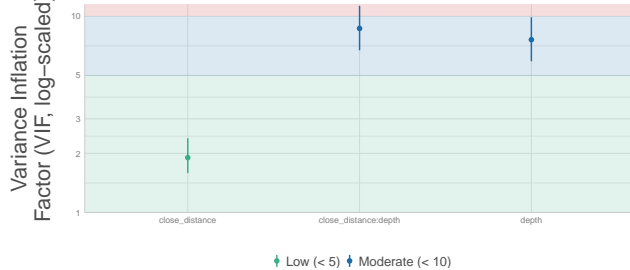
Influential Observations

Points should be inside the contour lines



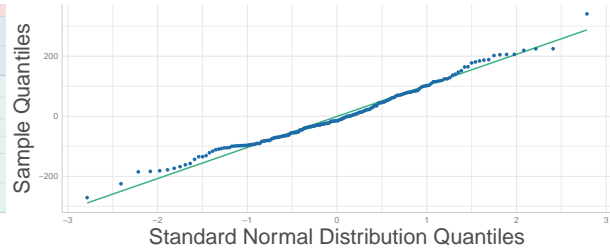
Collinearity

High collinearity (VIF) may inflate parameter uncertainty



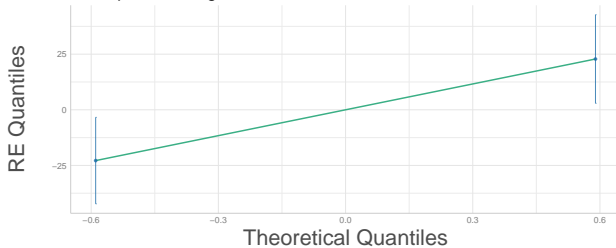
Normality of Residuals

Dots should fall along the line



Normality of Random Effects (plot)

Dots should be plotted along the line



Section S4: Overyielding microbial respiration (H2)

Model summary

```
lmer(bas_over ~ depth + (1|plot), data = df)
```

	Estimate	Std. Error	t-value	p-value
(Intercept)	-0.0142504	0.6264277	-0.0227487	0.9853692
depth	0.1416237	0.0428361	3.3061788	0.0013700

Figure 3 Tukey test - depth

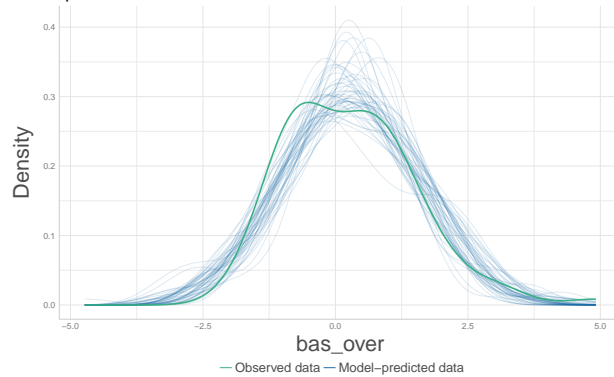
	Sum Sq.	Mean Sq.	f-value	p-value
depth %>% as.factor	9.283579	9.283579	6.564345	0.0120856
Residuals	125.867631	1.414243	NA	NA

	Diff	Lower	Upper	p-value
5-0	0.6391505	0.1434713	1.13483	0.0120856

Model fit

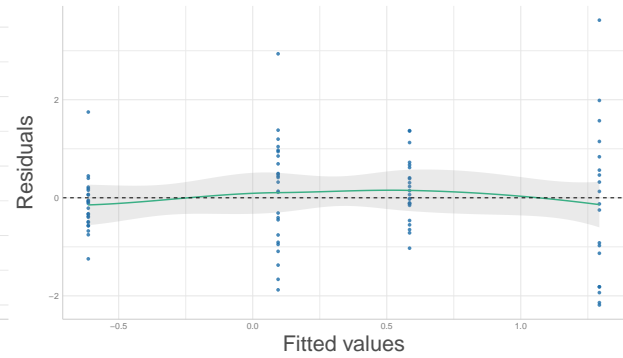
Posterior Predictive Check

Model-predicted lines should resemble observed data line



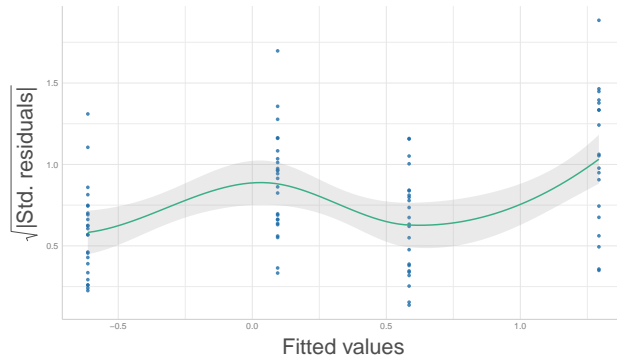
Linearity

Reference line should be flat and horizontal



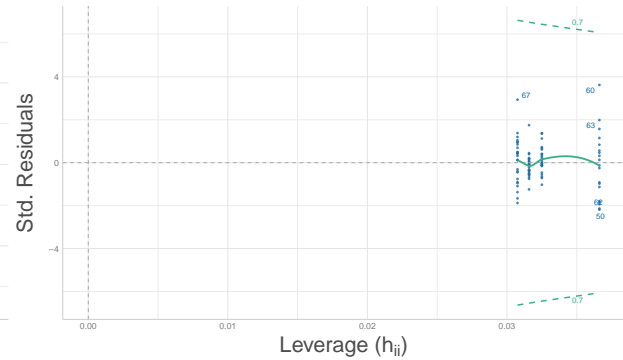
Homogeneity of Variance

Reference line should be flat and horizontal



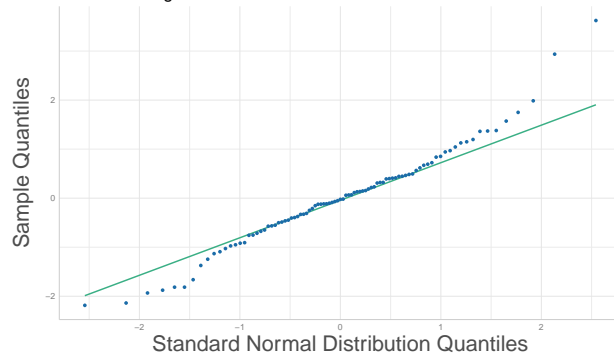
Influential Observations

Points should be inside the contour lines



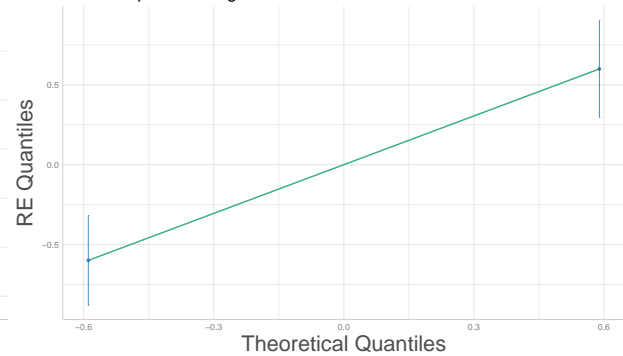
Normality of Residuals

Dots should fall along the line



Normality of Random Effects (plot)

Dots should be plotted along the line



Section S5: Overyielding microbial biomass (H2)

Model summary

```
lmer(cmic_over ~ depth + (1|plot), data = df)
```

	Estimate	Std. Error	t-value	p-value
(Intercept)	128.57173	29.616232	4.341259	0.0161693
depth	-30.13394	8.433534	-3.573110	0.0005736

Figure 3 Tukey test - depth

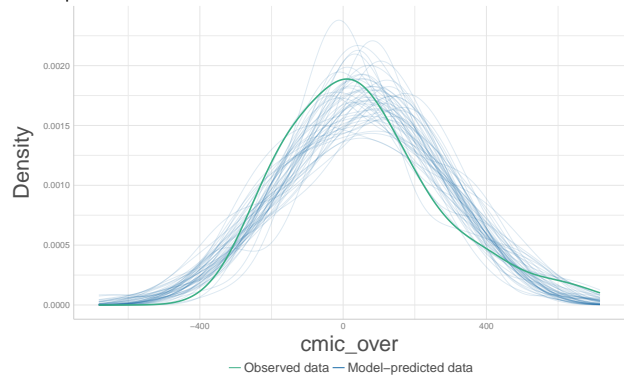
	Sum Sq.	Mean Sq.	f-value	p-value
depth %>% as.factor	516533.2	516533.20	12.77892	0.000569
Residuals	3597445.0	40420.73	NA	NA

	Diff	Lower	Upper	p-value
5-0	-150.7629	-234.5623	-66.96356	0.000569

Model fit

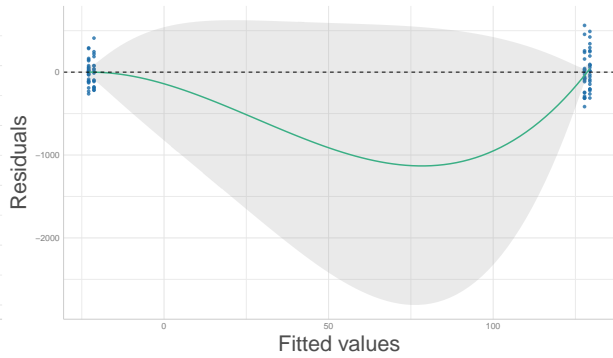
Posterior Predictive Check

Model-predicted lines should resemble observed data line



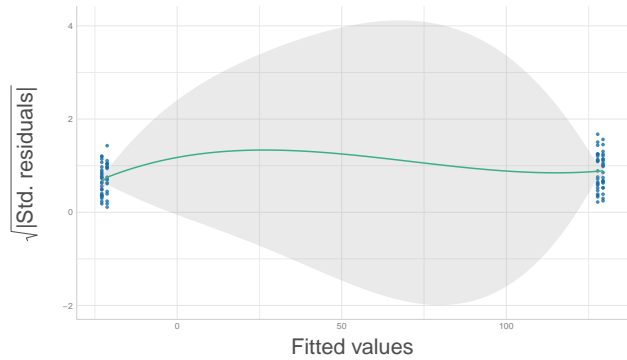
Linearity

Reference line should be flat and horizontal



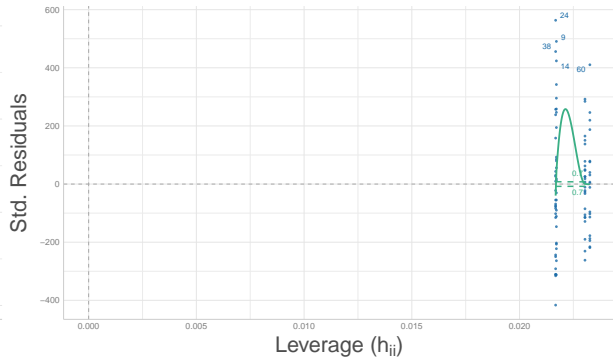
Homogeneity of Variance

Reference line should be flat and horizontal



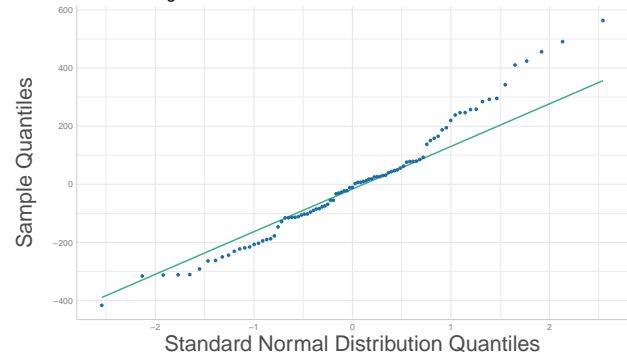
Influential Observations

Points should be inside the contour lines



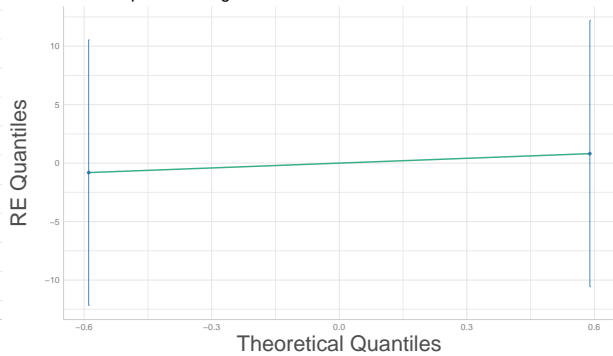
Normality of Residuals

Dots should fall along the line



Normality of Random Effects (plot)

Dots should be plotted along the line



Section S6: Spatial distribution of microbial respiration overyielding (H3)

Model summary

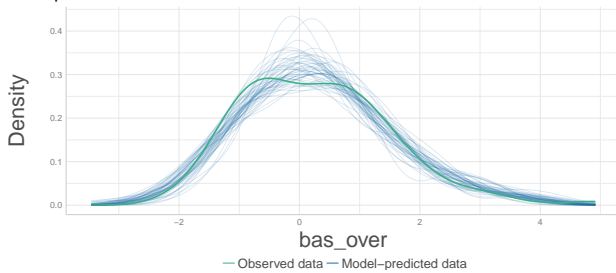
```
lmer(bas_over ~ dist.T1.center * depth + (1|plot), data = df)
```

	Estimate	Std. Error	t-value	p-value
(Intercept)	-0.0229950	0.6296411	-0.0365208	0.9766871
dist.T1.center	-0.7741122	0.1876610	-4.1250569	0.0000853
depth	0.1445341	0.0236760	6.1046629	0.0000000
dist.T1.center:depth	-0.3759578	0.0541292	-6.9455595	0.0000000

Model fit

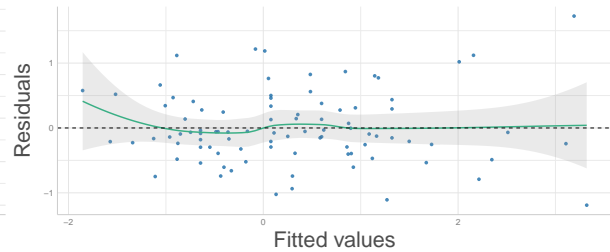
Posterior Predictive Check

Model-predicted lines should resemble observed data line



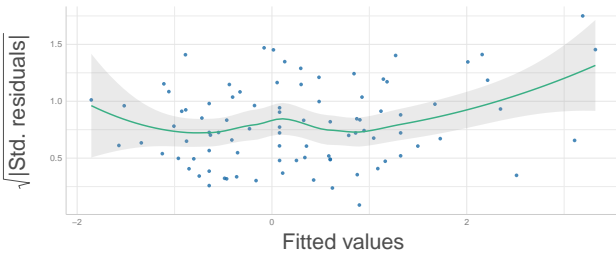
Linearity

Reference line should be flat and horizontal



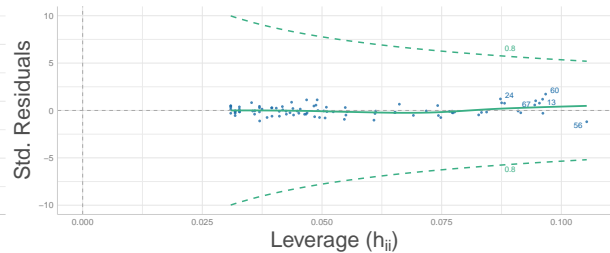
Homogeneity of Variance

Reference line should be flat and horizontal



Influential Observations

Points should be inside the contour lines



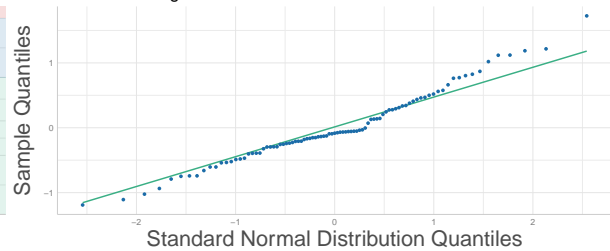
Collinearity

High collinearity (VIF) may inflate parameter uncertainty



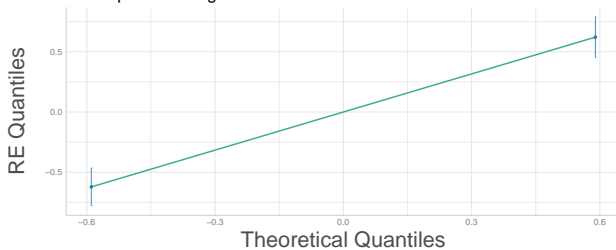
Normality of Residuals

Dots should fall along the line



Normality of Random Effects (plot)

Dots should be plotted along the line



Section S7: Spatial distribution of microbial biomass overyielding (H3)

Model summary

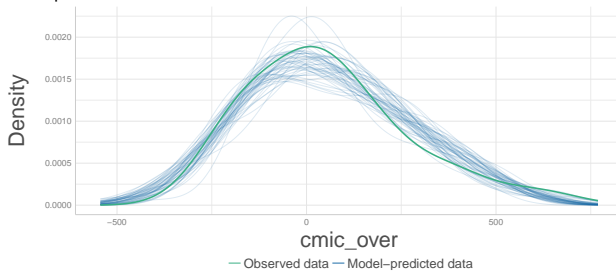
```
lmer(cmic_over ~ dist.T1.center * depth + (1|plot), data = df)
```

	Estimate	Std. Error	t-value	p-value
(Intercept)	123.62549	28.254908	4.375363	0.0930928
dist.T1.center	-452.50479	34.902000	-12.965010	0.0000000
depth	-28.51567	4.402464	-6.477206	0.0000000
dist.T1.center:depth	30.01283	10.067663	2.981112	0.0037344

Model fit

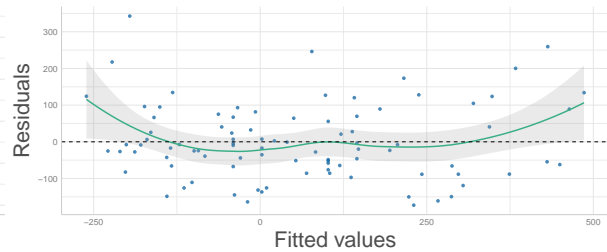
Posterior Predictive Check

Model-predicted lines should resemble observed data line



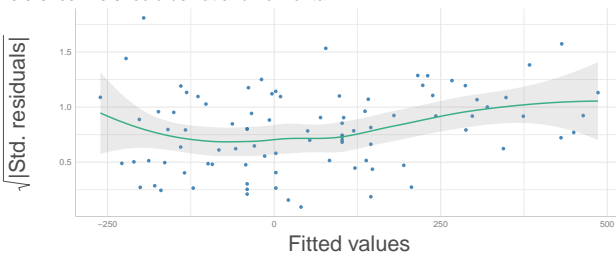
Linearity

Reference line should be flat and horizontal



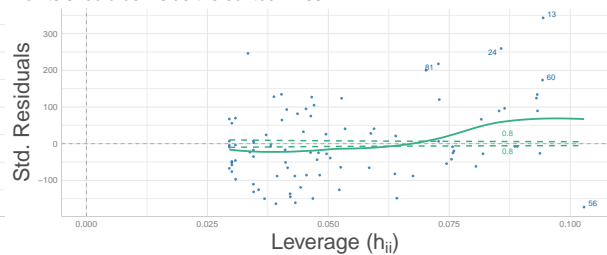
Homogeneity of Variance

Reference line should be flat and horizontal



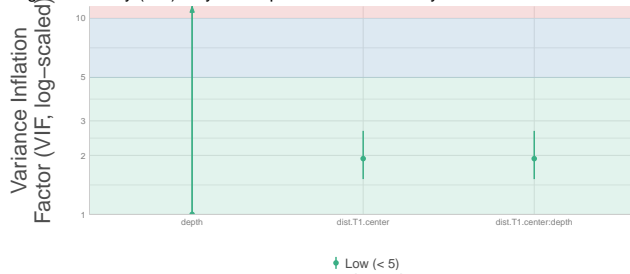
Influential Observations

Points should be inside the contour lines



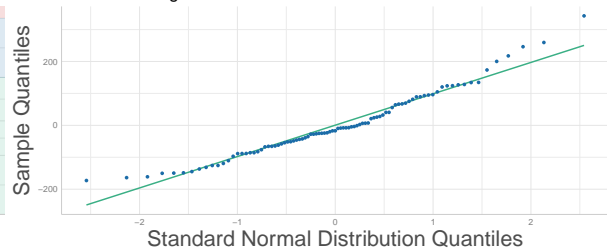
Collinearity

High collinearity (VIF) may inflate parameter uncertainty



Normality of Residuals

Dots should fall along the line



Normality of Random Effects (plot)

Dots should be plotted along the line

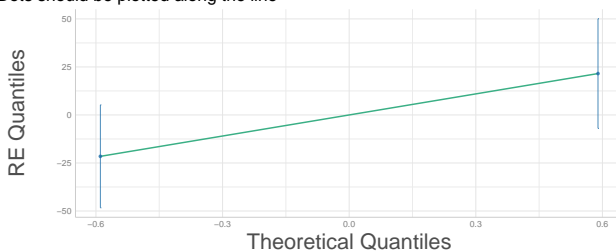


Figure S2: Abiotic and biotic drivers of soil microbial biomass and respiration

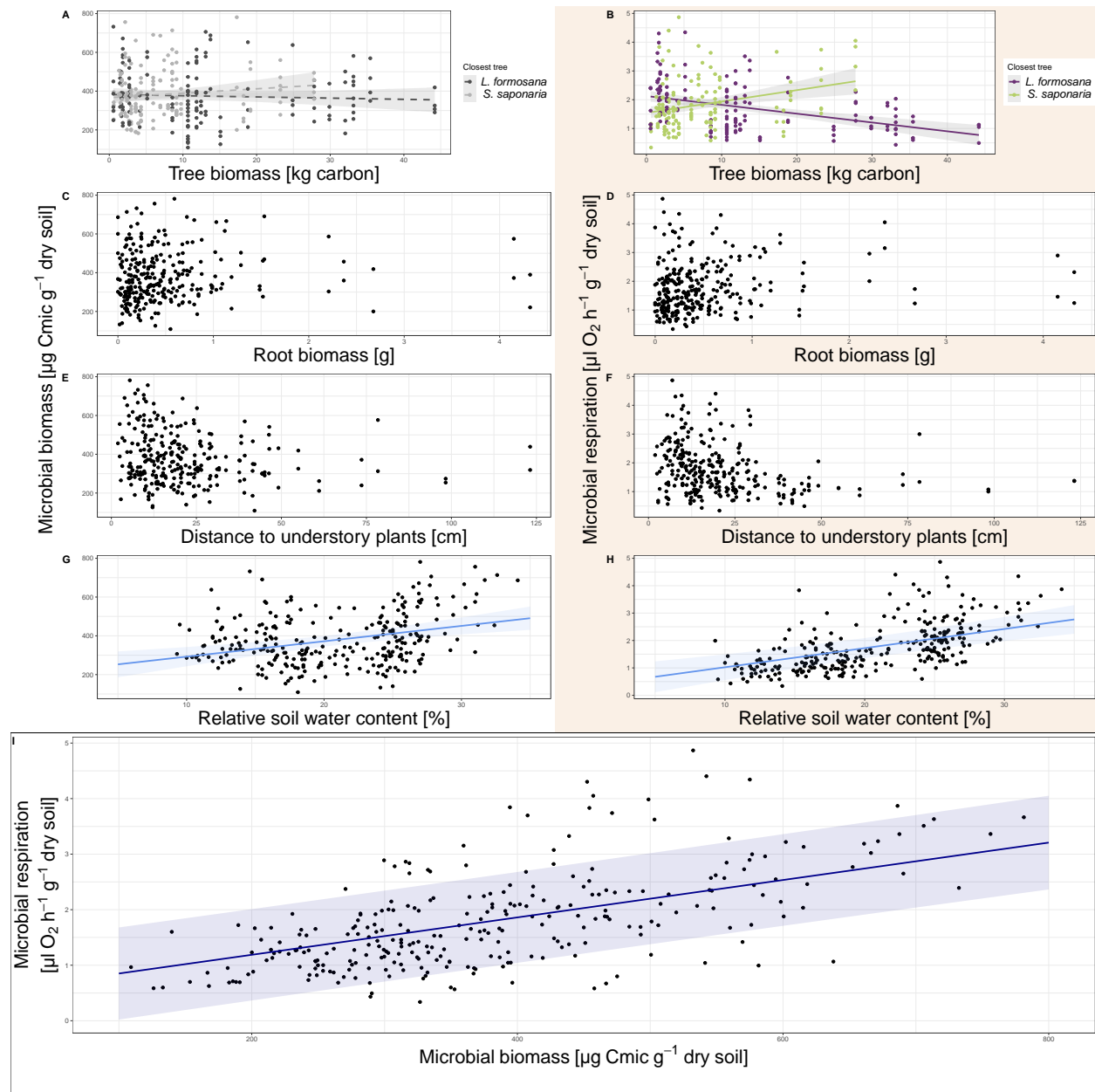


Figure S2: Overview of small scale drivers of microbial biomass and respiration. Effects of tree size and species identity on microbial biomass (A) and respiration (B). Effects of root biomass and distance to understory plants were non-significant on microbial biomass (C, E, respectively) or respiration (D, F, respectively). Positive effect of relative soil water content on microbial biomass (G) and respiration (H). Positive correlation of microbial biomass and respiration (I). Significant effects in colour.