Supplementary material III-S8

The assumptions of the linear models fitted in our analyses were tested using the "check_model" function from the R package performance.

Models Hypothesis H1

Soil historical carbon concentration model

Summary

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.038	0.000	1.000
CURV_PL	0.357	0.084	4.258	0.000
SLOPE	0.175	0.084	2.090	0.038

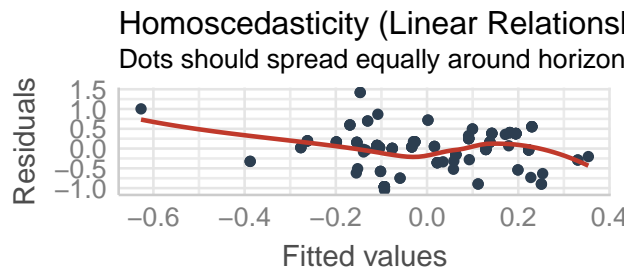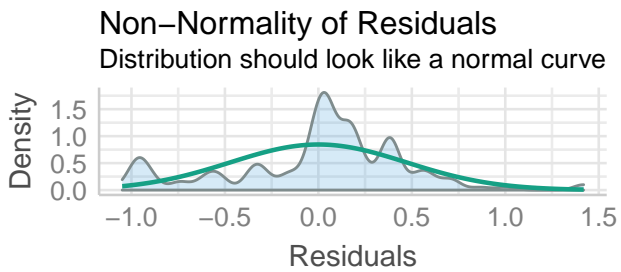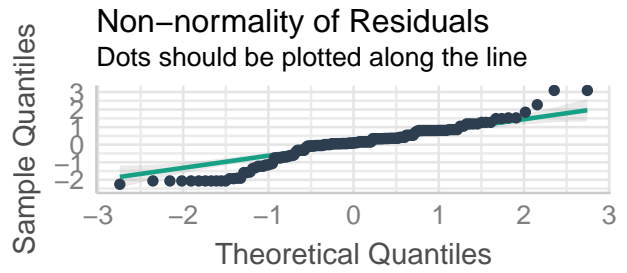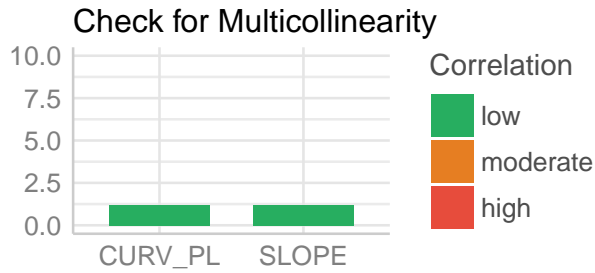**Model statistical hypotheses**

```
## Loading required namespace: qqplotr
```

```
## 'geom_smooth()' using formula 'y ~ x'
## 'geom_smooth()' using formula 'y ~ x'
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```
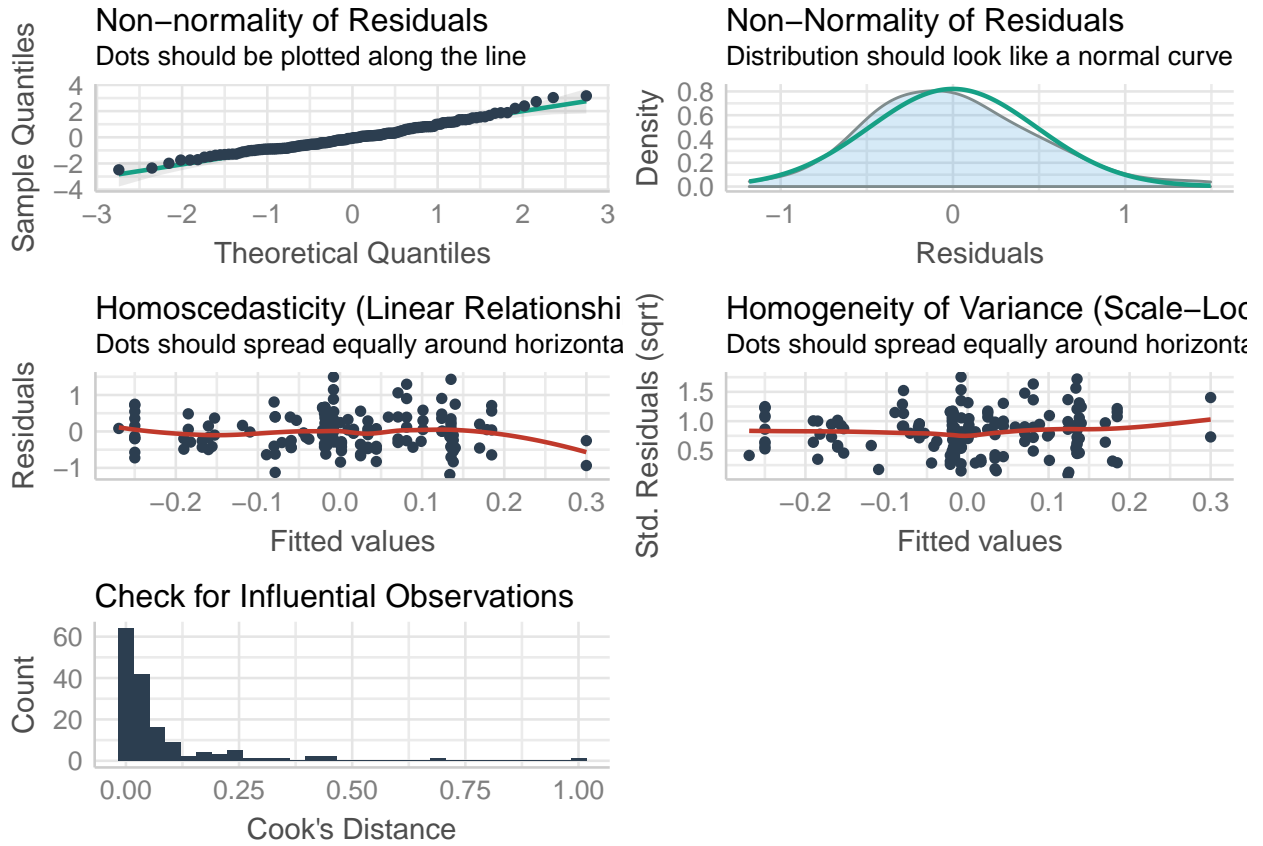
Check for Multicollinearity

Non−normality of Residuals
Dots should be plotted along the line

Non−Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationship)
Dots should spread equally around horizon

Homogeneity of Variance (Scale−Location)
Dots should spread equally around horizontal

Check for Influential Observations

Tree diversity effects on carbon concentration model

Summary

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.039	0.00	1.000
Soil.C.2010	0.236	0.079	2.99	0.003

Model statistical hypotheses

Non−normality of Residuals
Dots should be plotted along the line

Non−Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationshi
Dots should spread equally around horizonta

Homogeneity of Variance (Scale−Lo
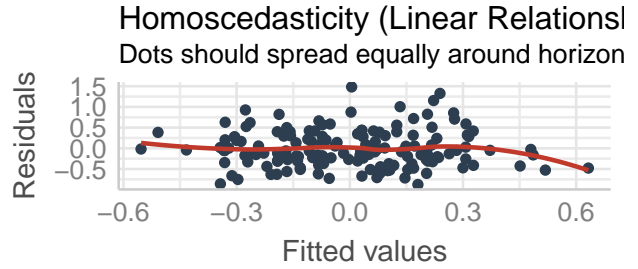Dots should spread equally around horizonta

Check for Influential Observations

Tree functional traits effects on carbon concentration model

Summary

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.037	0.000	1.000
CURV_PL	0.236	0.095	2.482	0.014
CN.litterfall	-0.218	0.081	-2.701	0.008
ENL	0.344	0.106	3.228	0.002
TSP.RD	0.206	0.103	2.010	0.046
TSP.FRic.RD	-0.135	0.084	-1.613	0.109
RD	-0.286	0.101	-2.829	0.005
AM.ECM	-0.155	0.093	-1.659	0.099
Soil.C.2010	0.294	0.080	3.673	0.000

Model statistical hypotheses

Check for Multicollinearity

Non−normality of Residuals
Dots should be plotted along the line

Non−Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationsł
Dots should spread equally around horizon

Homogeneity of Variance (Scale−Loc
Dots should spread equally around horizonta

Check for Influential Observations
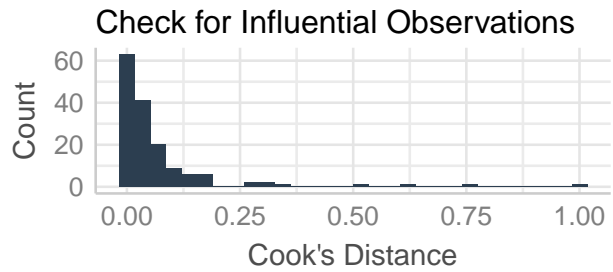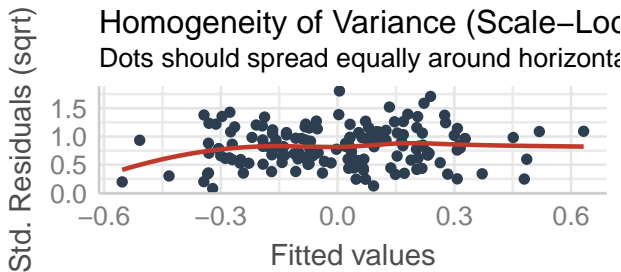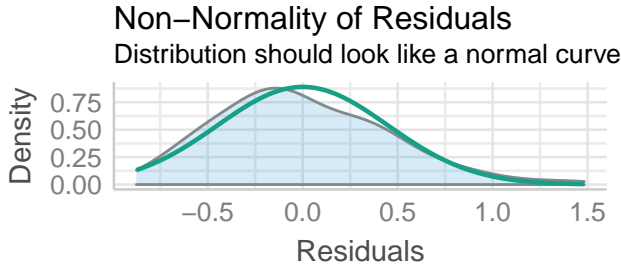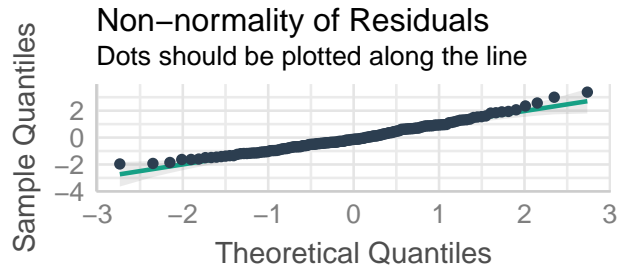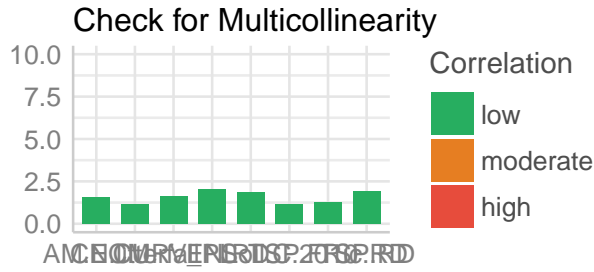
Models Hypothesis H2

Tree diversity effects on microbial biomass

Summary

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.040	0.000	1.000
Sp.rich	0.202	0.079	2.544	0.012

Model statistical hypotheses

Non−normality of Residuals
Dots should be plotted along the line

Non−Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationshi
Dots should spread equally around horizonta

Homogeneity of Variance (Scale−Lo
Dots should spread equally around horizonta

Check for Influential Observations
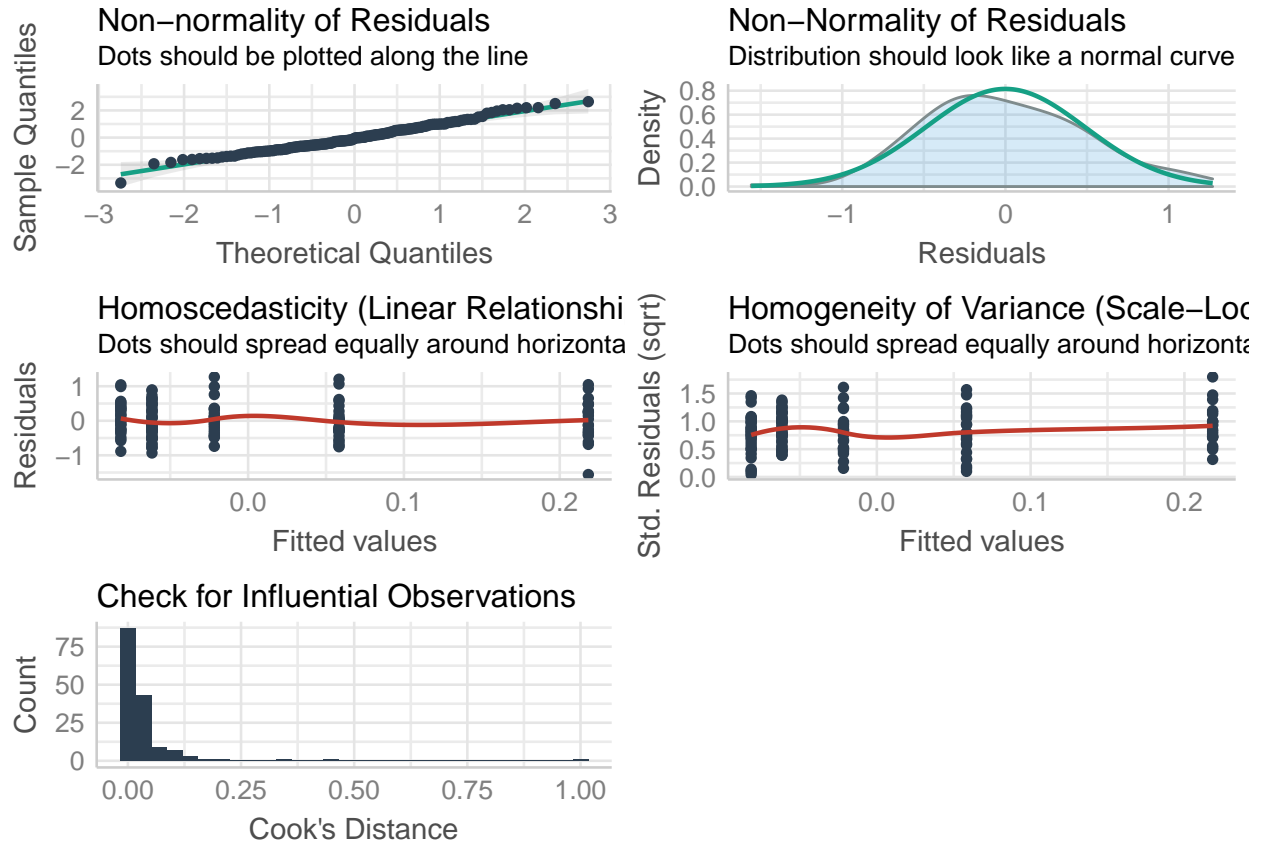
Tree functional traits effects on microbial biomass

Summary

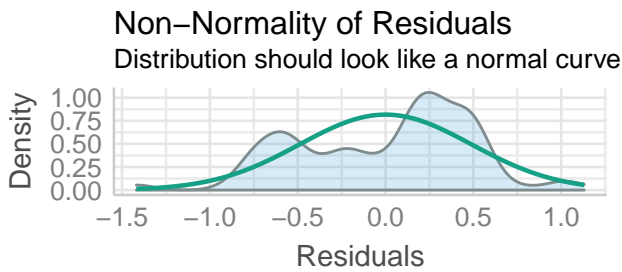|	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.037	0.000	1.000
ENL	0.177	0.087	2.037	0.043
TSP.SRL	0.223	0.103	2.176	0.031
TSP.RD	0.308	0.116	2.643	0.009
TSP.AM.ECM	-0.145	0.085	-1.695	0.092
FDis.SRL	-0.216	0.102	-2.124	0.035
FDis.AM.ECM	0.153	0.103	1.488	0.139
RD	-0.349	0.100	-3.494	0.001

Model statistical hypotheses

Check for Multicollinearity

Non−normality of Residuals
Dots should be plotted along the line

Non−Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationship)
Dots should spread equally around horizontal

Homogeneity of Variance (Scale−Location)
Dots should spread equally around horizontal

Check for Influential Observations

Models Hypothesis H3

Tree diversity and traits effects on environmental conditions

Temperature

Species richness model

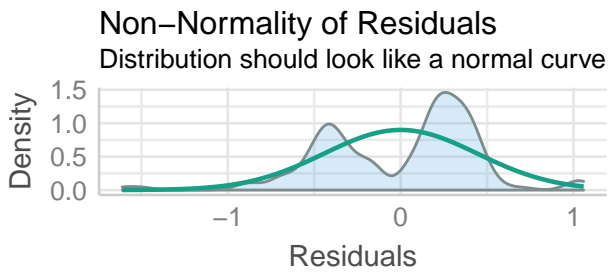|	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.040	0.000	1.000
Sp.rich	-0.208	0.082	-2.534	0.012
homo.hetero	0.128	0.086	1.484	0.140

Check for Multicollinearity

Non−normality of Residuals
Dots should be plotted along the line

Non−Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationsh
Dots should spread equally around horizon

Homogeneity of Variance (Scale−Loc
Dots should spread equally around horizonta

Check for Influential Observations
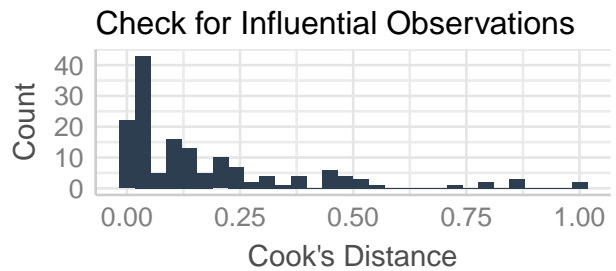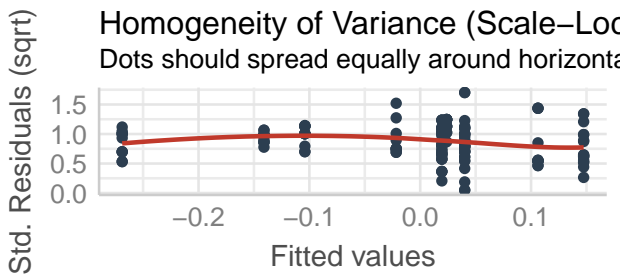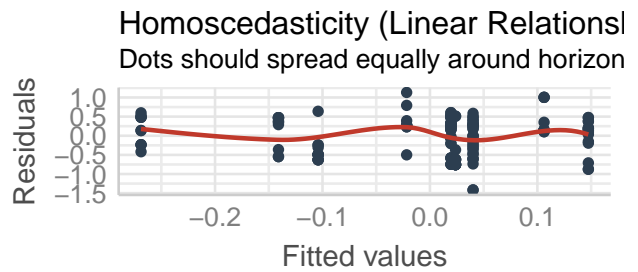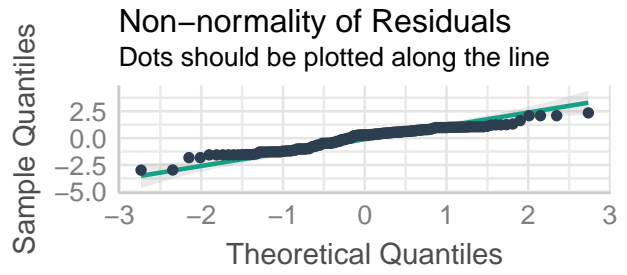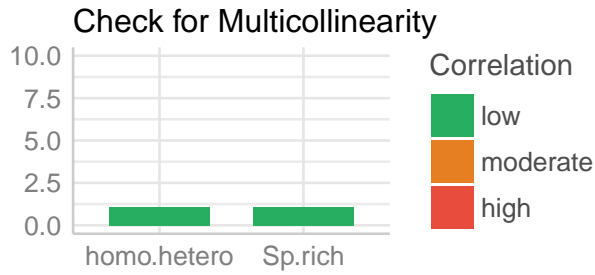
Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.036	0.000	1.000
neigh.biomass	-0.113	0.078	-1.452	0.149
ENL	-0.406	0.078	-5.207	0.000

### Check for Multicollinearity

Non−normality of Residuals
Dots should be plotted along the line

Non−Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationshi
Dots should spread equally around horizonta

Homogeneity of Variance (Scale−Loc
Dots should spread equally around horizonta

Check for Influential Observations

Soil relative humidity

Species richness model

(No variable selected)

Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.037	0.000	1.000
CN.litterfall	-0.247	0.077	-3.192	0.002
TSP.SRL	-0.290	0.088	-3.301	0.001
FDis.SRL	0.111	0.076	1.454	0.148
SRL	-0.145	0.087	-1.656	0.100

Check for Multicollinearity
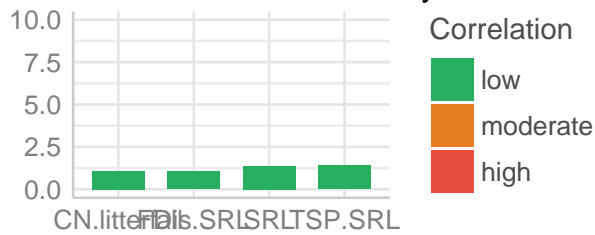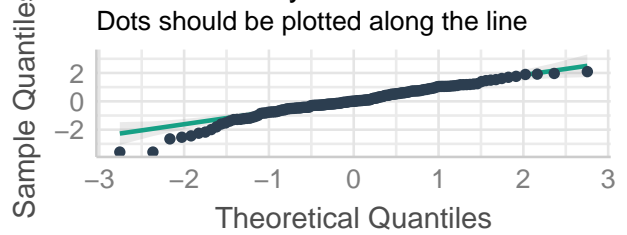
Non-normality of Residuals
Dots should be plotted along the line

Non-Normality of Residuals
Distribution should look like a normal curve
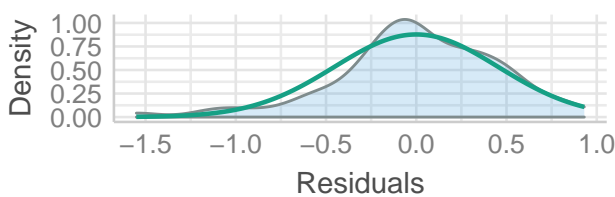
Homoscedasticity (Linear Relationship)
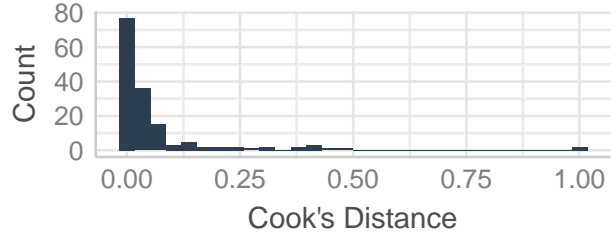Dots should spread equally around horizontal
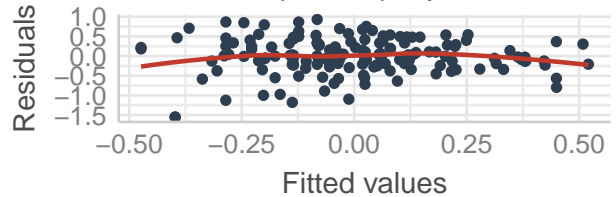
Homogeneity of Variance (Scale-Location)
Dots should spread equally around horizontal
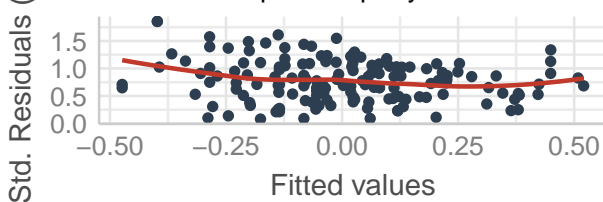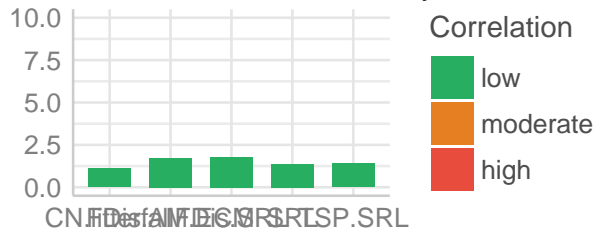
Check for Influential Observations

Soil nitrogen
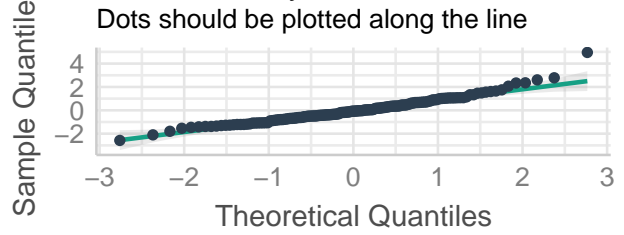
Species richness model

(No variable selected)

Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.039	0.000	1.000
CN.litterfall	-0.189	0.082	-2.300	0.023
TSP.SRL	-0.135	0.093	-1.460	0.146
FDis.SRL	-0.253	0.104	-2.422	0.017
FDis.AM.ECM	0.149	0.104	1.442	0.151
SRL	0.214	0.092	2.318	0.022

Check for Multicollinearity

Non–normality of Residuals
Dots should be plotted along the line
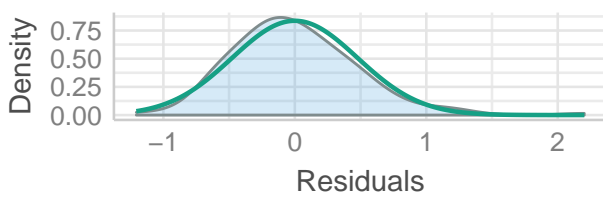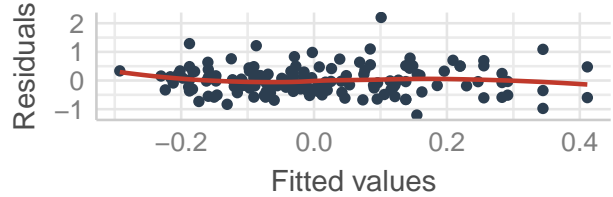

Non–Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationshi
Dots should spread equally around horizonta

Homogeneity of Variance (Scale–Loc
Dots should spread equally around horizonta
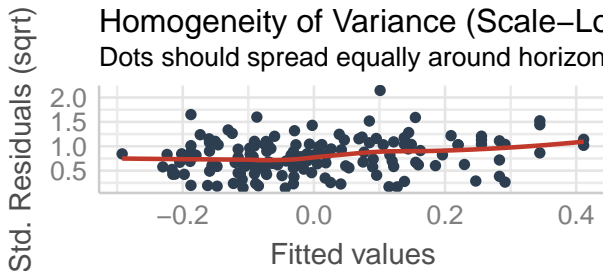
Check for Influential Observations
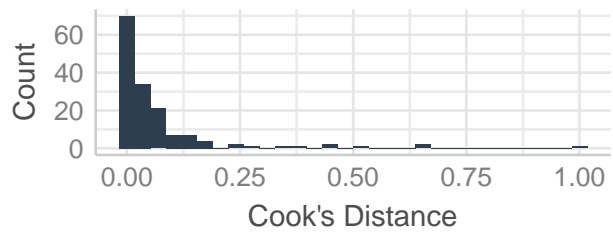
Soil phosphorus

Species richness model

(No variable selected)

Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.037	0.000	1.000
CN.litterfall	-0.186	0.080	-2.309	0.022
neigh.biomass	0.149	0.080	1.866	0.064
FDis.RD	-0.446	0.096	-4.622	0.000
RD	0.408	0.097	4.214	0.000
AM.ECM	-0.127	0.082	-1.552	0.123

Check for Multicollinearity

Non–normality of Residuals
Dots should be plotted along the line

Non–Normality of Residuals
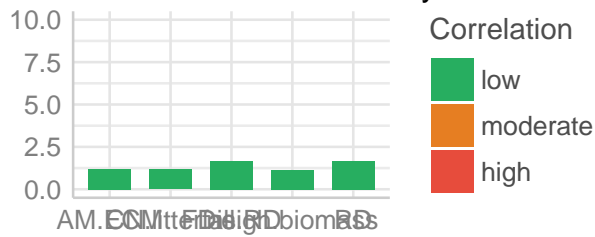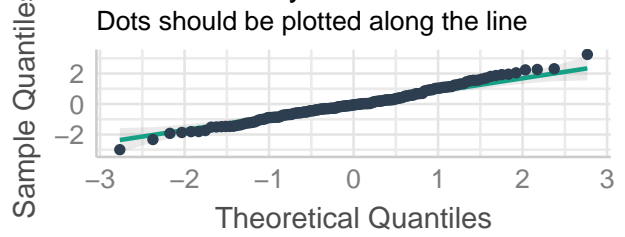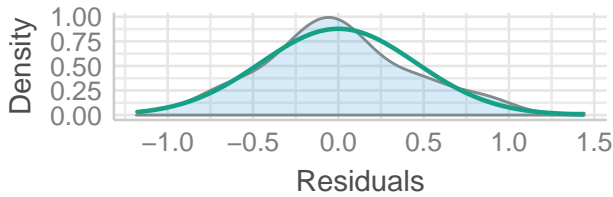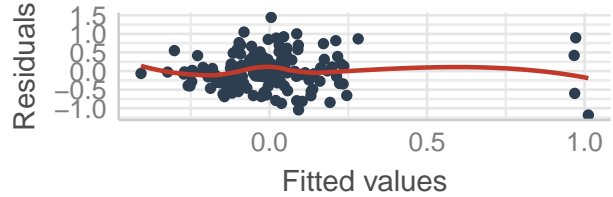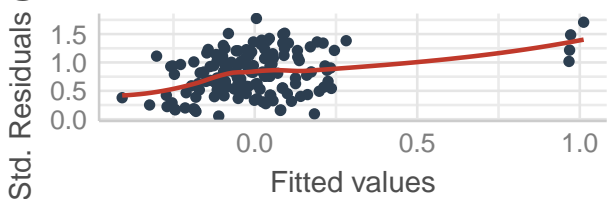Distribution should look like a normal curve

Homoscedasticity (Linear Relationship)
Dots should spread equally around horizontal

Homogeneity of Variance (Scale–Location)
Dots should spread equally around horizontal

Check for Influential Observations
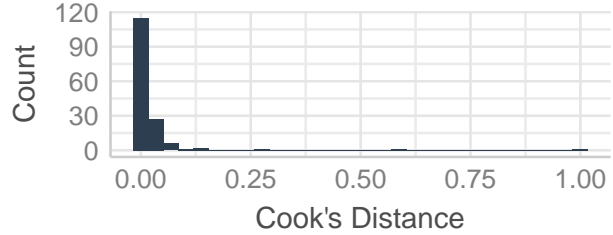
Plant abundance

Species richness model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.040	0.000	1.000
Sp.rich	-0.129	0.083	-1.559	0.121
homo.hetero	0.135	0.087	1.545	0.124
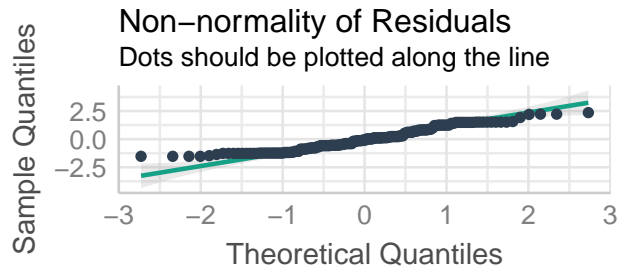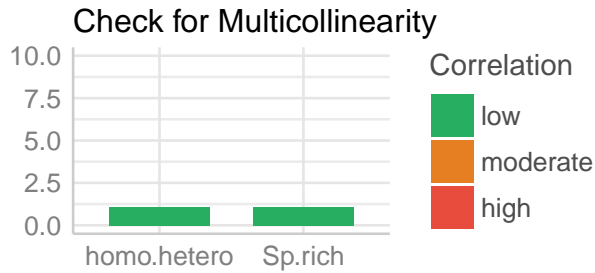
Check for Multicollinearity

Non−normality of Residuals
Dots should be plotted along the line

Non−Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationsł
Dots should spread equally around horizon

Homogeneity of Variance (Scale−Loc
Dots should spread equally around horizonta

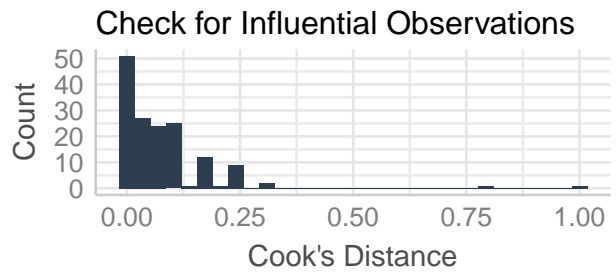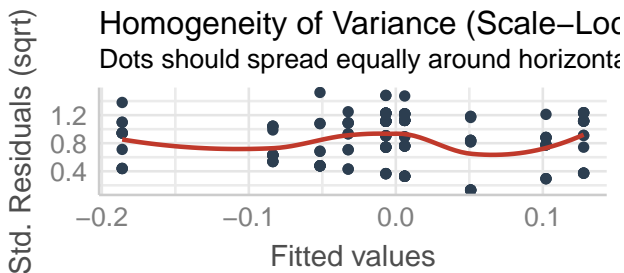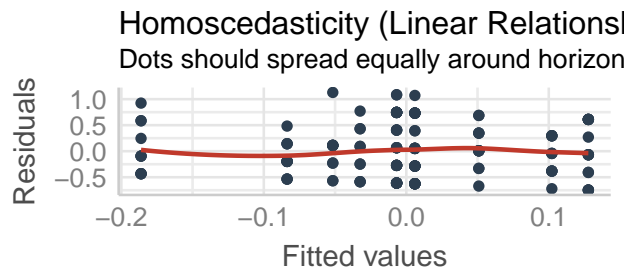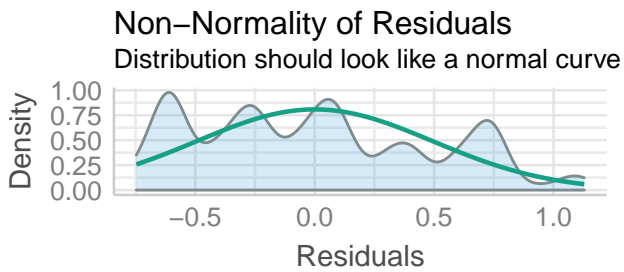## Check for Influential Observations

Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.036	0.000	1.000
CN.litterfall	-0.305	0.085	-3.591	0.000
ENL	-0.472	0.080	-5.909	0.000
TSP.SRL	-0.262	0.105	-2.488	0.014
TSP.RD	-0.212	0.103	-2.055	0.042
TSP.FRic.SRL	0.181	0.076	2.376	0.019

Check for Multicollinearity
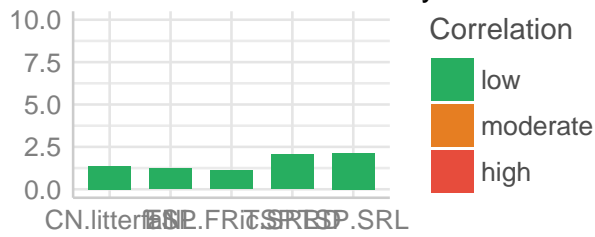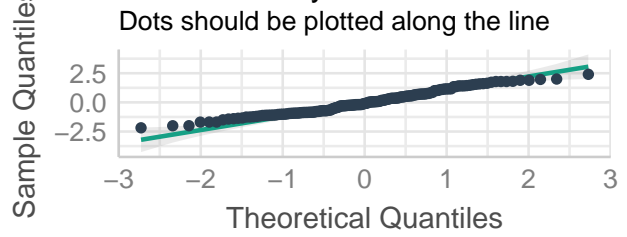
Non−normality of Residuals

Dots should be plotted along the line

Non−Normality of Residuals

Distribution should look like a normal curve
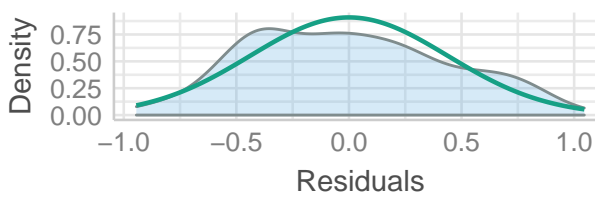
Homoscedasticity (Linear Relationsh

Dots should spread equally around horizon
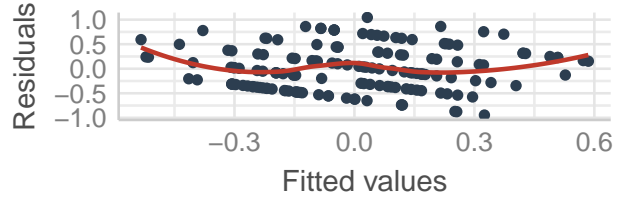
Homogeneity of Variance (Scale−Loc

Dots should spread equally around horizonta

Check for Influential Observations
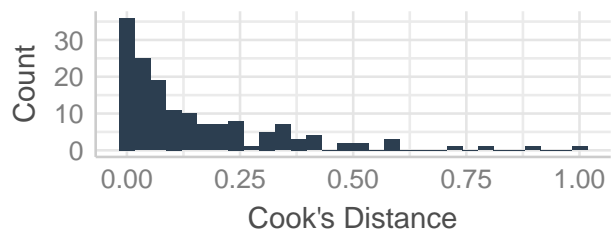
Root biomass

Species richness model

(No variable selected)

Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.035	0.000	1.000
C.litterfall	-0.218	0.091	-2.393	0.018
ENL	-0.389	0.091	-4.275	0.000
AM.ECM	0.237	0.079	3.022	0.003

## Check for Multicollinearity

Non-normality of Residuals
Dots should be plotted along the line

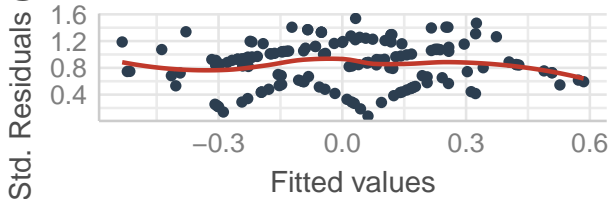## Non-Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationship
Dots should spread equally around horizontal

Homogeneity of Variance (Scale-Lo
Dots should spread equally around horizonta

Check for Influential Observations

Litter abundance

Species richness model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.04	0.000	1.000
Sp.rich	0.168	0.08	2.098	0.038
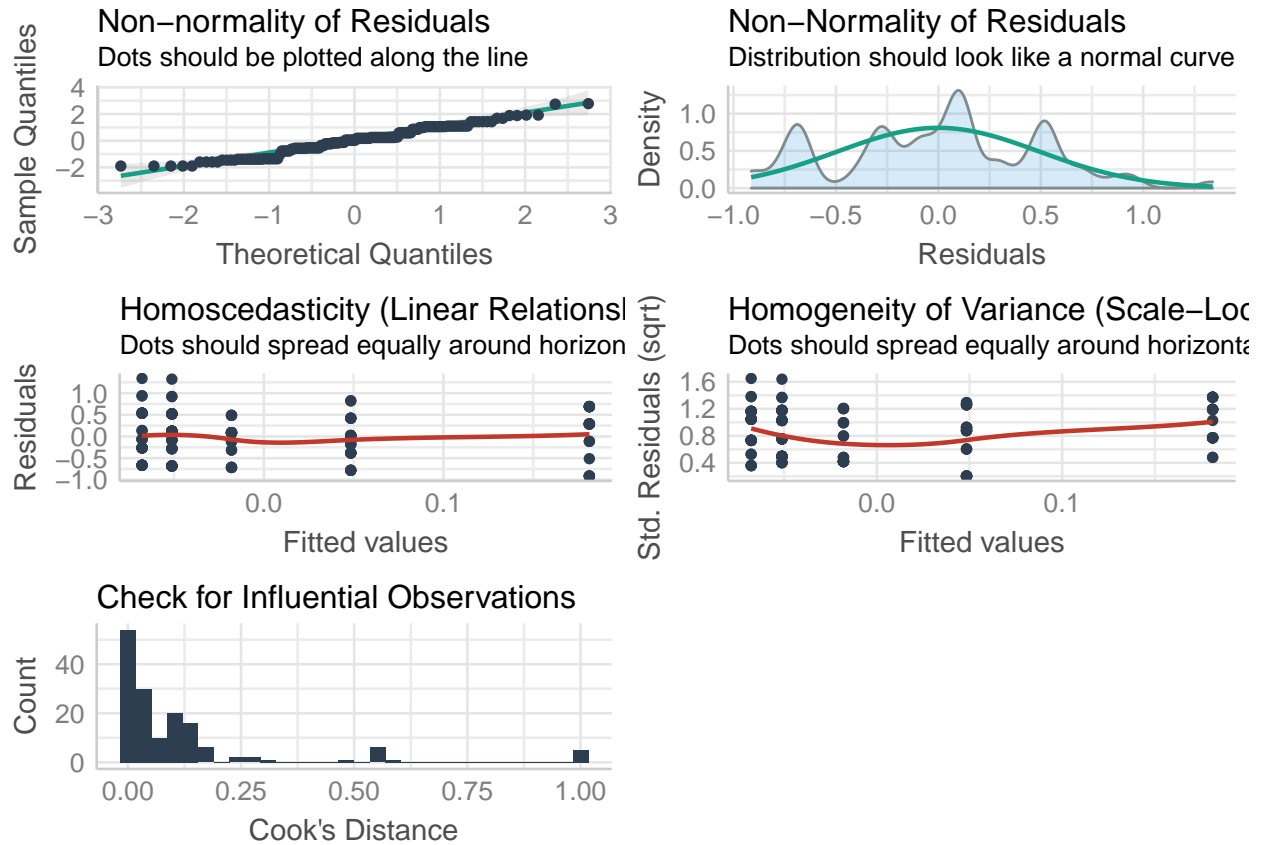
Non−normality of Residuals
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Non−Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationsh
Dots should spread equally around horizon

Homogeneity of Variance (Scale−Loc
Dots should spread equally around horizonta

Check for Influential Observations

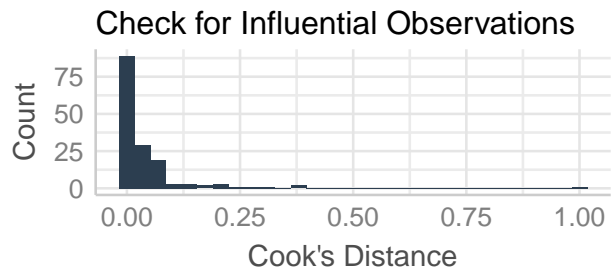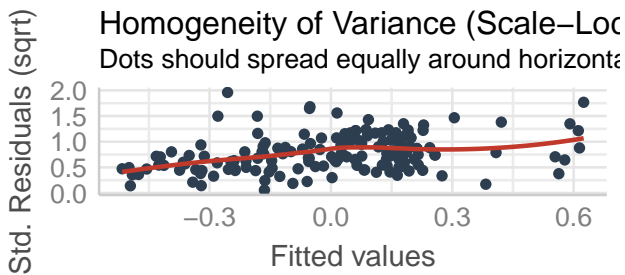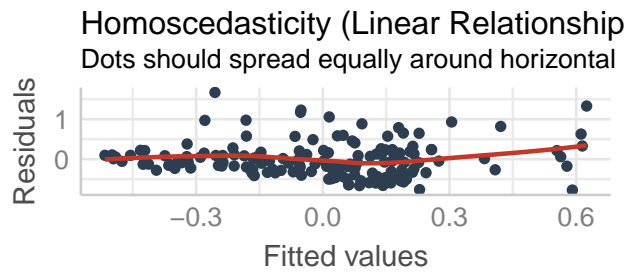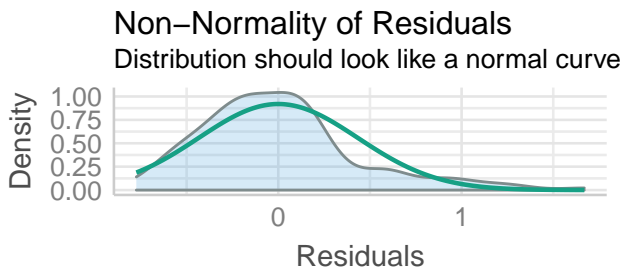Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.037	0.000	1.000
CN.litterfall	-0.153	0.090	-1.698	0.092
ENL	-0.294	0.084	-3.502	0.001
TSP.SRL	-0.365	0.116	-3.135	0.002
TSP.RD	-0.254	0.115	-2.206	0.029
TSP.AM.ECM	-0.205	0.087	-2.358	0.020
TSP.FRic.RD	0.120	0.087	1.391	0.166
FDis.SRL	0.217	0.083	2.620	0.010

Check for Multicollinearity
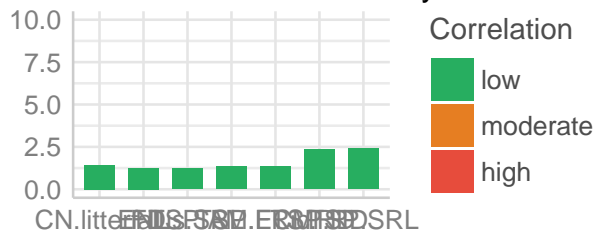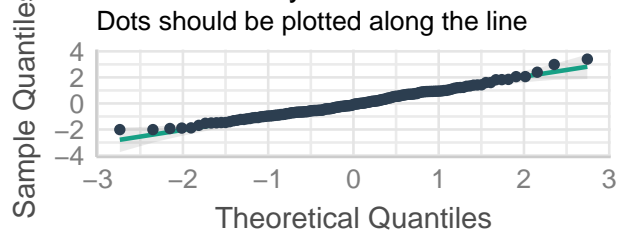
Non−normality of Residuals
Dots should be plotted along the line

Non−Normality of Residuals
Distribution should look like a normal curve
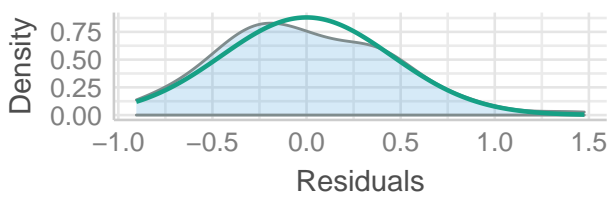
Homoscedasticity (Linear Relationship)
Dots should spread equally around horizontal
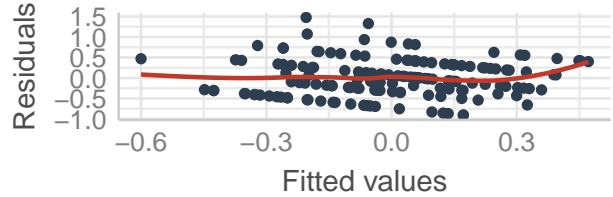
Homogeneity of Variance (Scale−Location)
Dots should spread equally around horizontal
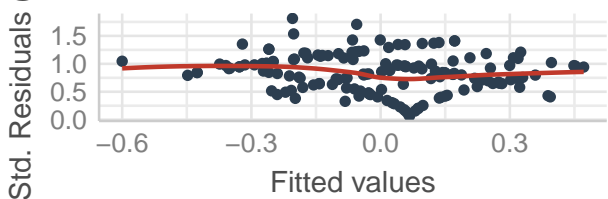
Check for Influential Observations
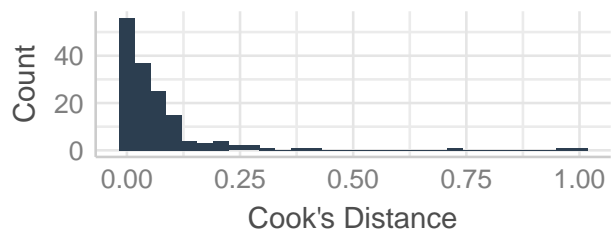
Litter CN

Species richness model

(No variable selected)

Trait model

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.036	0.000	1.000
CN.litterfall	0.233	0.077	3.046	0.003
TSP.biomass	-0.116	0.076	-1.523	0.130
ENL	-0.306	0.089	-3.440	0.001
TSP.FRic.RD	0.159	0.077	2.065	0.041
FDis.AM.ECM	0.133	0.081	1.641	0.103
AM.ECM	0.369	0.080	4.612	0.000

Check for Multicollinearity

Non−normality of Residuals
Dots should be plotted along the line

Non−Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationshi
Dots should spread equally around horizonta

Homogeneity of Variance (Scale−Loc
Dots should spread equally around horizonta

Check for Influential Observations

Environmental effects on microbial biomass

	Estimate	Std Error	t-value	p-value
(Intercept)	0.000	0.033	0.000	1.000
Soil.humidity	-0.221	0.066	-3.334	0.001
temperature	-0.379	0.072	-5.282	0.000
Soil.N.2018	0.385	0.066	5.846	0.000
litter.CN	0.239	0.068	3.494	0.001
litter.ab	0.117	0.070	1.669	0.097

Check for Multicollinearity

Non−normality of Residuals
Dots should be plotted along the line

Non−Normality of Residuals
Distribution should look like a normal curve

Homoscedasticity (Linear Relationsh
Dots should spread equally around horizon

Homogeneity of Variance (Scale−Loc
Dots should spread equally around horizonta
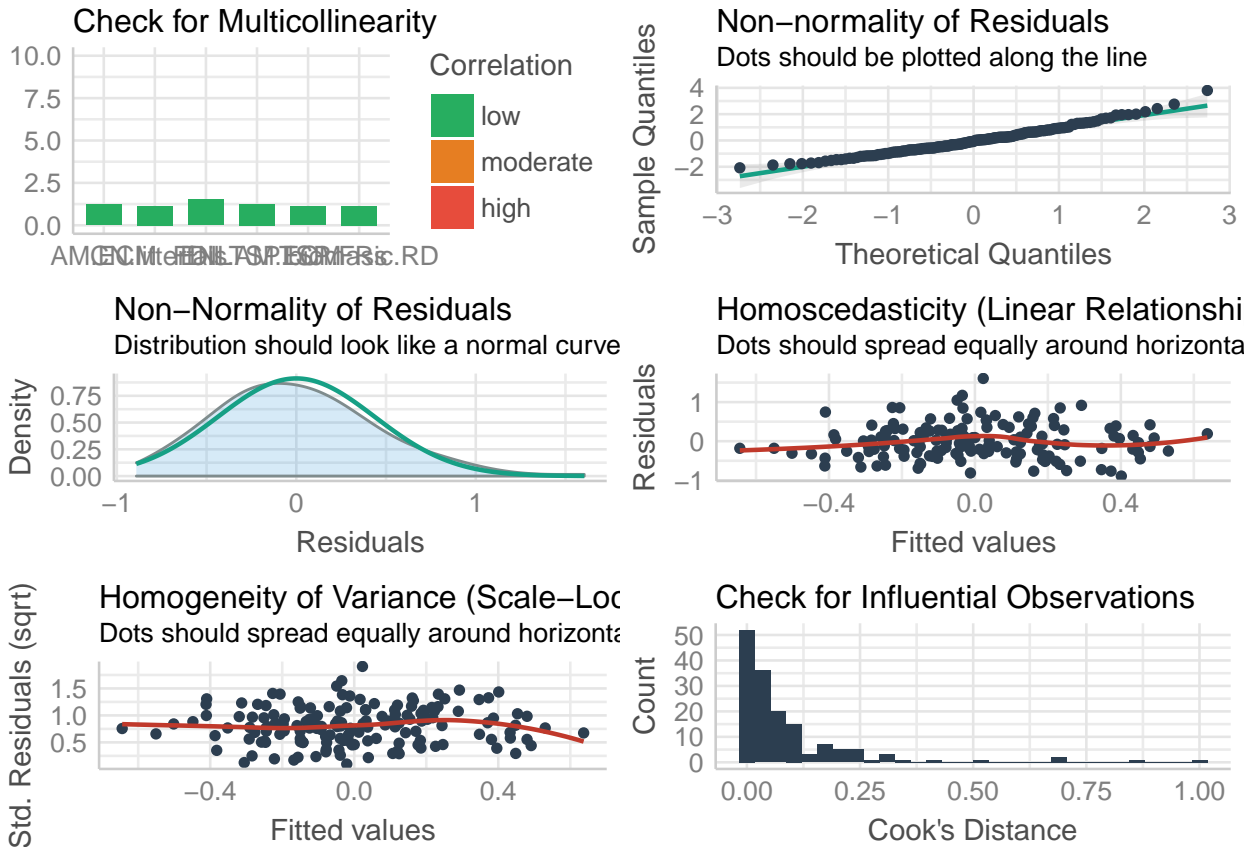

Check for Influential Observations