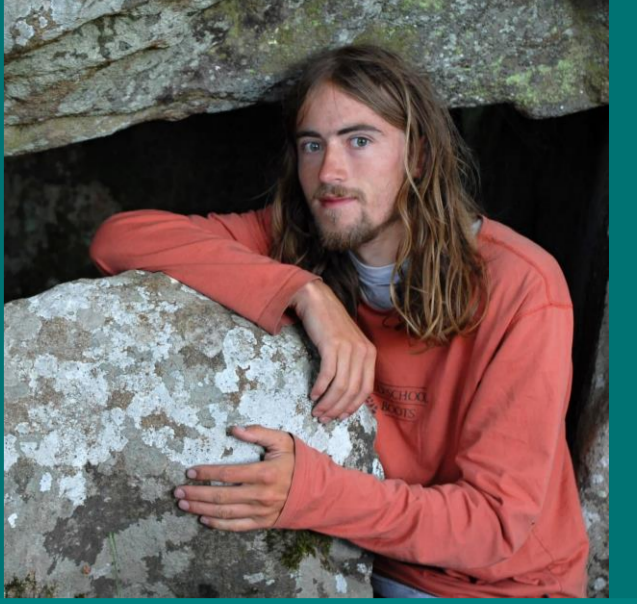


Scale matters: Disentangling drivers of fine-scale and regional species richness pattern in temperate forest understorey



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Intro

„Herb layer host most of the plant diversity in the temperate forests. While main determinants of the herb layer diversity are well known, relatively little is known about scale dependency of the importance of these factors.

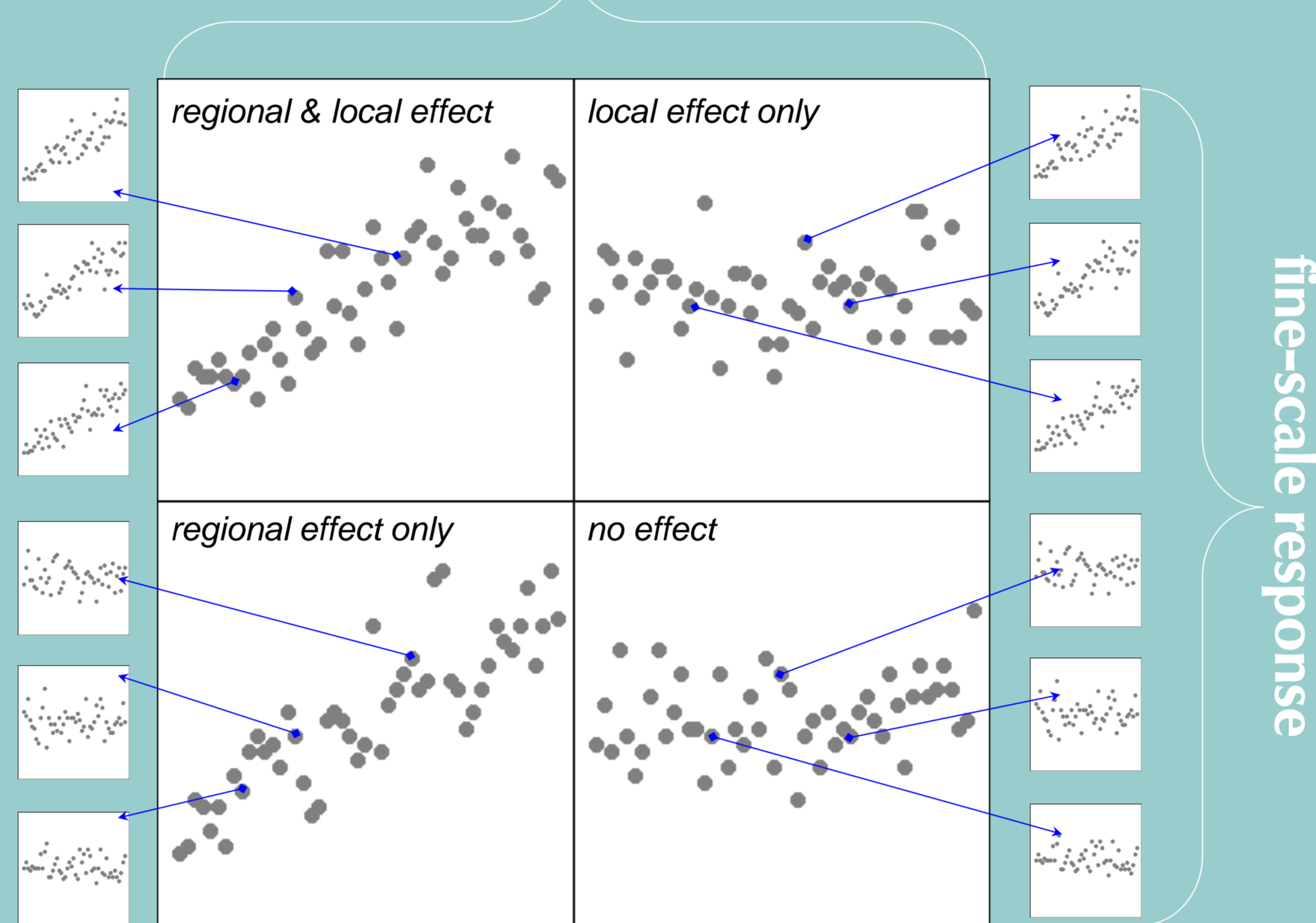
Study focus on the two important environmental factors affecting herb layer diversity in temperate forests: soil pH and understorey light.

We explored deciduous forest herb layer diversity in at two spatial scales: landscape scale (grain 100m²; extend 500 km²) and local scale (grain 1m²; extend 100m²).“

Aims

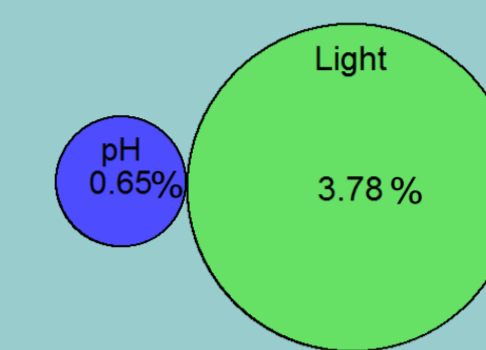
- To identify key factors related to forest floor herb diversity
- To compare forest herb layer diversity driving factors on regional and local scale

landscape-scale response



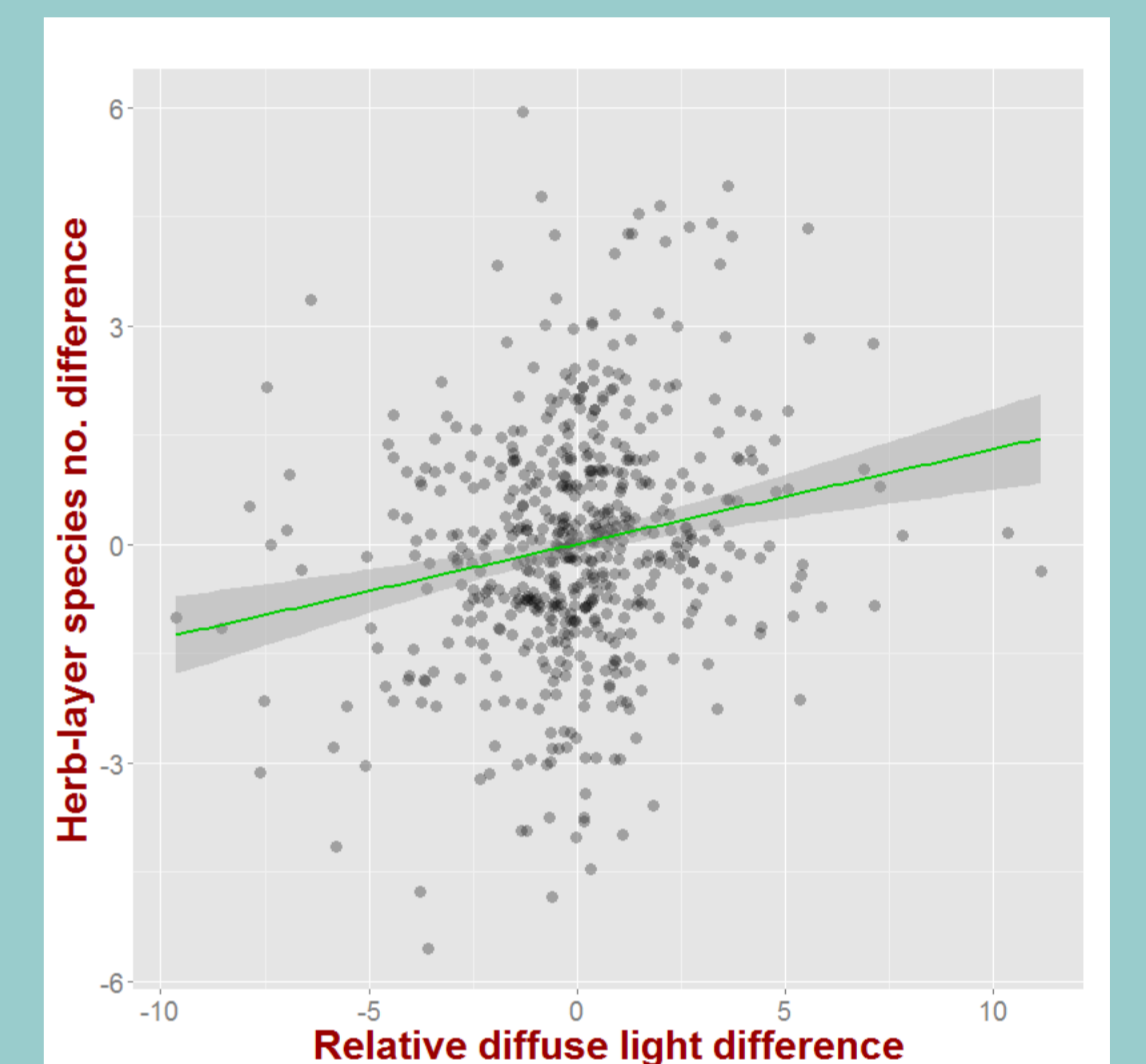
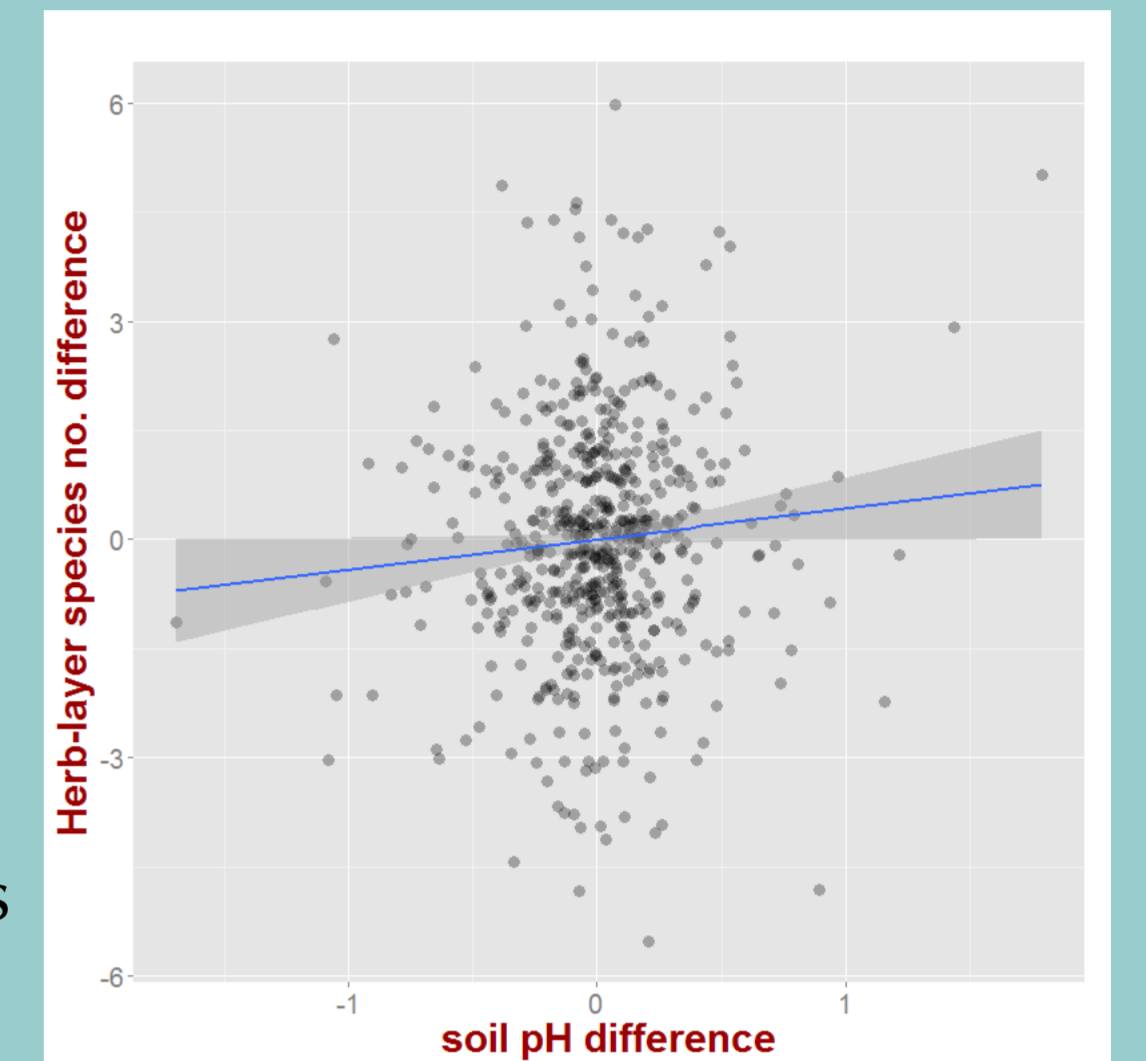
Hypothetical combination of scale-dependent diversity response to various factors

Results: fine-scale



Soil pH effect is insignificant ($p=0.17$)

Light contributes weakly to diversity pattern on fine scale ($p < 0.001$)



Methods

Set of **115 plots** is distributed within 500 km² area of České Středohoří mts, Czech Republic. Oak-hornbeam and beech dominated termophilous to mesic forests are prevailing in studied area.

Stratified random sampling design was based on soil type, SAGA wetness index and potential solar radiation using ArcGIS 9.2. Non-natural (eg. coniferous) plantations were excluded.

Each square-shaped 100 m² plot contain five 1 m² subplots (575 total) with following measurements:

- Soil **pH** (H₂O), samples of upper 5 cm A horizon
- Herb layer **species number** counted for both plots and subplots
- Light** as relative diffuse and direct radiation assessed by hemispherical image analysis using Gap Light Analyzer software
- Soil C, N, P, K, Ca content and topographic indices assessed only for whole-plot level

Data analysis

Mixed-effect data analysis of fine scale diversity pattern (subplot diversity and environmental scores centered within plot) using function *lmer* from *lme4* library in R 2.15.2, plots treated as random effect, light and pH as fixed effects.

Regional scale diversity was analysed using poisson family *glm* in R. Stepwise regression used AIC criterion for building full model.

Results: landscape-scale

Variable	Direction	Residual deviance	Explained deviance	p (>Ch)
pH	+	460.47	19.7%	<0.001
Ca	+	498.05	13.1%	<0.001
P	-	511.56	10.7%	<0.001
Topographic slope	-	518.51	9.5%	<0.001
C/N	-	531.78	7.2%	<0.001
Diffuse light	+	536.80	6.3%	<0.001
C org.	-	554.06	3.3%	<0.001
Direct light	+	555.89	3.0%	<0.001
SAGA Wetness index	+	560.33	2.2%	<0.001
K	+	567.85	0.9%	0.022
N	-	570.30	0.5%	0.095
Null model	0	573.09	-	-

Single effects on diversity, sorted by deviance, only factors with $p > 0.1$ displayed.

Variable	Conditional direction	Residual deviance	Explained deviance
Null model		573.09	-
pH	+	460.47	19.7%
Topographic slope	-	419.51	26.8%
Diffuse light	+	382.32	33.3%
P	-	361.52	36.9%
Ca	+	346.86	39.5%
SAGA Wetness index	-	344.04	40.0%
C org.	-	334.65	41.6%
N	+	321.35	43.9%

Full model: cumulative effects of diversity predictors in order as selected by stepwise regression. Model $p < 0.001$.

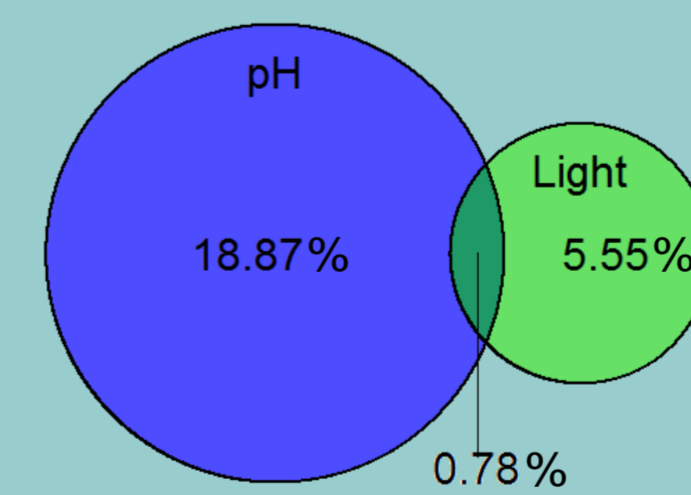
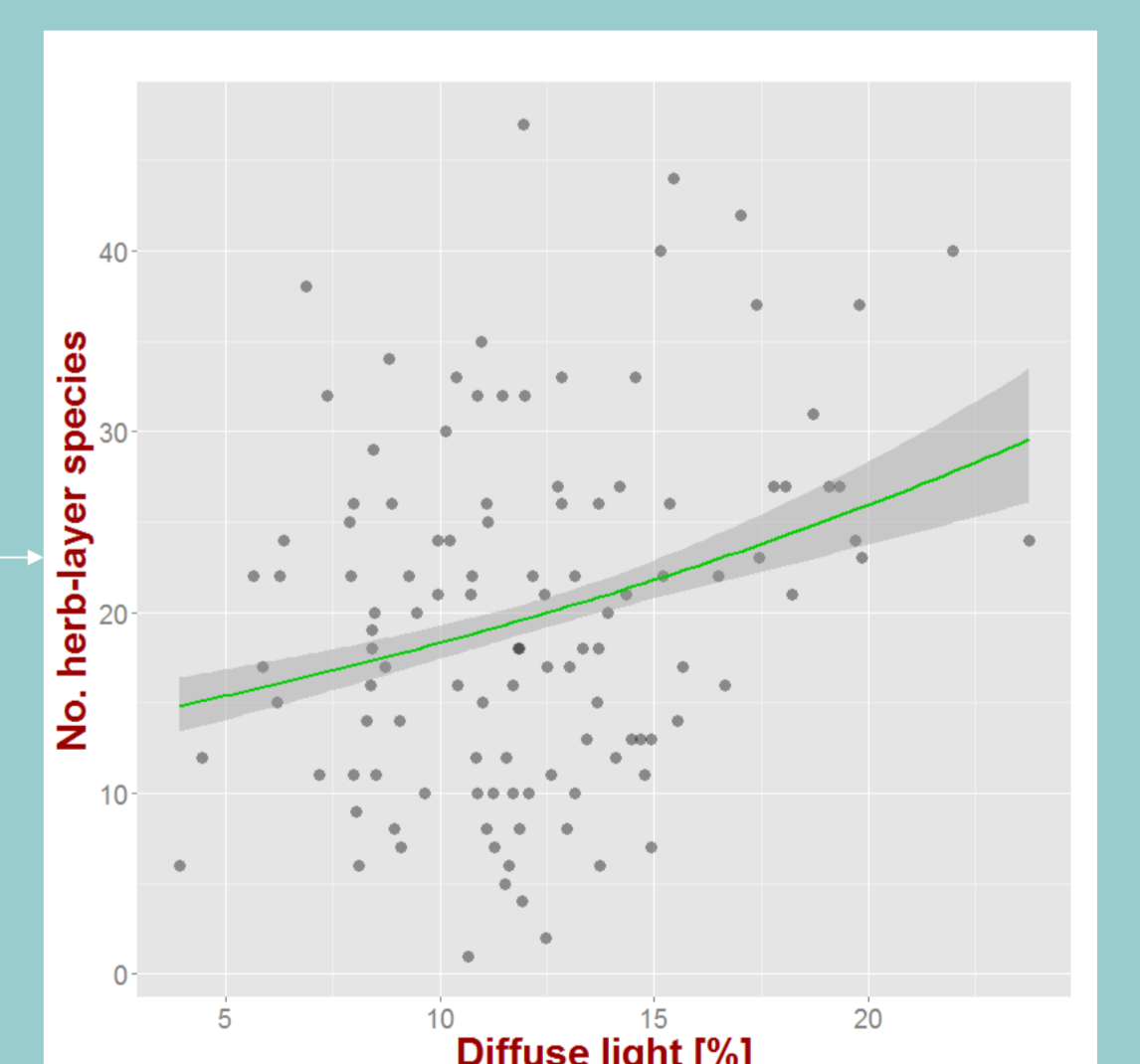
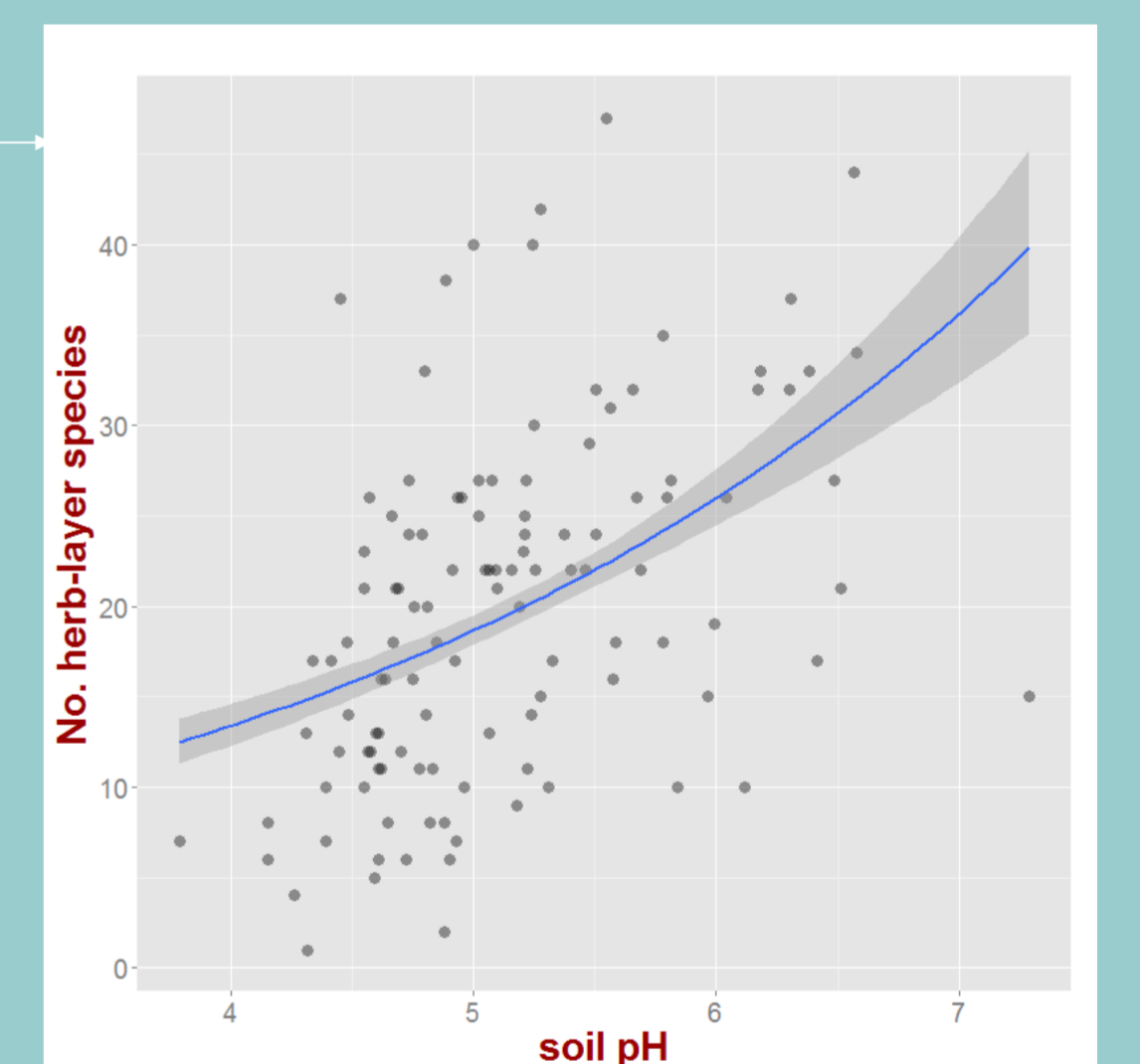


Diagram of effect sizes for soil pH and diffuse light on diversity (from model with only pH and light as predictors)



Conclusions

- Soil reaction** is the strongest predictor of forest herb layer diversity on regional scale, prior to other soil, light or topographical properties, but insignificant on fine scale.
- Light availability** influence diversity considerably on both scales.
- Fine-scale pattern** is poorly predictable as low no. of individuals, disturbances, biotic or other processes influence diversity.

The effect size of soil pH and light on herb layer diversity is reversed between landscape and within-plot scale.

This suggests that forest community assembly is driven by hierarchical process: species occurring in the plot are filtered from the regional species pool according to soil pH, but their distribution within the plot is driven by light availability under varying canopy.