## Combining spatial and phylogenetic eigenvector filtering in trait analyses

## **Supplementary material**

Ingolf Kühn<sup>1,3,\*</sup>, Michael P. Nobis<sup>2</sup>, Walter Durka<sup>1</sup>

1) UFZ, Centre for Environmental Research – UFZ, Dept. Community Ecology, Theodor-Lieser-Str. 4, 06120 Halle, Germany

2) Swiss Federal Research Institute WSL, Research Unit Biodiversity and Conservation Biology, Zuercherstrasse 111, 8903 Birmensdorf, Switzerland

3) Virtual Institute Macroecology, Theodor-Lieser-Str. 4, 06120 Halle, Germany

\* corresponding author: Ingolf.Kuehn@ufz.de, Phone: ++49/345/558-5311

## **Supplementary Material:**

Table S1: Correlation matrix of eigenvectors selected by spatial and spatio-phylogenetic (spatio-phylo) filtering. Absolute values greater than 0.2 are indicated in bold, those smaller than 0.1 in grey.

		spatio-phylo							
	Filter	P4	P27	P3	P5	P94	P147		
spatial	<b>S</b> 3	-0.139	-0.093	0.209	0.288	0.039	0.010		
	S49	-0.085	-0.043	-0.035	0.010	0.071	0.050		
	<b>S</b> 8	0.081	-0.005	-0.095	-0.017	-0.097	0.012		
	S35	-0.081	-0.037	-0.075	0.046	-0.089	-0.044		
	S57	0.080	-0.022	-0.053	0.070	-0.134	0.020		
	S10	0.023	0.007	0.052	-0.035	0.065	-0.010		
	S40	0.045	0.061	-0.044	-0.002	-0.003	0.018		
	S51	0.075	-0.100	0.051	0.084	-0.101	0.062		
	S17	-0.024	-0.066	-0.085	-0.074	-0.033	0.020		

Table S2: Correlation matrix of eigenvectors for combining spatial and spatially structured phylogenetic (spatio-phylo) filters in one model (both). Due to the lacking correlations between orthogonal spatial or orthogonal spatio-phylogenetic filters, these values are not shown. Absolute values smaller than 0.1 in grey.

		spatio-phylo					
	Filter	P32	P45	P4	P27		
spatial	<b>S</b> 3	-0.178	0.050	-0.139	-0.093		
	S35	0.046	-0.020	-0.081	-0.037		

	A B BB							
AA 1		AE 2	3		BI	BA 4	B 5	BB
Species\Branch	Α	AA	AB	В	BA	BB	BBA	BBB
Species 1	1	1	0	0	0	0	0	0
Species 2	1	0	1	0	0	0	0	0
Species 3	0	0	0	1	1	0	0	0
Species 4	0	0	0	1	0	1	1	0
Species 5	0	0	0	1	0	1	0	1

Figure S1: Representation of a binary phylogenetic tree in a species by phylogenetic branch matrix, using phylogenies in CAIC format, i.e. different letters represents different branches at each node.



Figure S2 Moran's *I* correlograms of residual autocorrelation of the different models explaining average onset of flowering in Switzerland: no filters (a), spatial filters (b), spatially structured phylogenetic filters (c), both filters simultaneously (d), residuals of pure phylogenetic filters on the traits (e) and sequential phylogenetic and spatial filtering (f); see methods for details. Significant coefficients are depicted as closed circles (P <0.05; in black after Bonferroni correction, in grey without correction), insignificant autocorrelation as open circles.



Figure S3 Moran's *I* correlograms of residual autocorrelation of the different models explaining average onset of flowering in Switzerland as in Fig. S1, but excluding calcareous substrate from the predictors: no filters (a), spatial filters (b), spatially structured phylogenetic filters (c), both filters simultaneously (d), residuals of pure phylogenetic filters on the traits (e) and sequential phylogenetic and spatial filtering (f); see methods for details.