Supplementary Figures: captions

Supplementary Figure 1. Observed vs. model-predicted values (left) and observed vs. residuals (right) of transfer function models of bryophytes for depth to the water table (DWT) and pH.

Supplementary Figure 2. Observed vs. model-predicted values (left) and observed vs. residuals (right) of transfer function models of vascular plants for depth to the water table (DWT) and pH.

Supplementary Figure 3. Observed vs. model-predicted values (left) and observed vs. residuals (right) of transfer function models of testate amoeba presence/absence data for depth to the water table (DWT) and pH.

Supplementary Figure 4. Observed vs. model-predicted values (left) and observed vs. residuals (right) of transfer function models of testate amoeba percentages for depth to the water table (DWT) and pH.

Supplementary Figure 5. Observed vs. model-predicted values (left) and observed vs. residuals (right) of transfer function models of bryophytes and vascular plants for depth to the water table (DWT) and pH.

Supplementary Figure 6. Observed vs. model-predicted values (left) and observed vs. residuals (right) of transfer function models of testate amoebae presence/absence data and bryophytes for depth to the water table (DWT) and pH.

Supplementary Figure 7. Observed vs. model-predicted values (left) and observed vs. residuals (right) of transfer function models of testate amoeba presence/absence data and vascular plants for depth to the water table (DWT) and pH.

Supplementary Figure 8. Observed vs. model-predicted values (left) and observed vs. residuals (right) of transfer function models of testate amoeba presence/absence data, bryophytes and vascular plants for depth to the water table (DWT) and pH.

Supplementary Figure 9. Observed vs. model-predicted values (left) and observed vs. residuals (right) of transfer function models of testate amoeba percentages and bryophytes for depth to the water table (DWT) and pH.

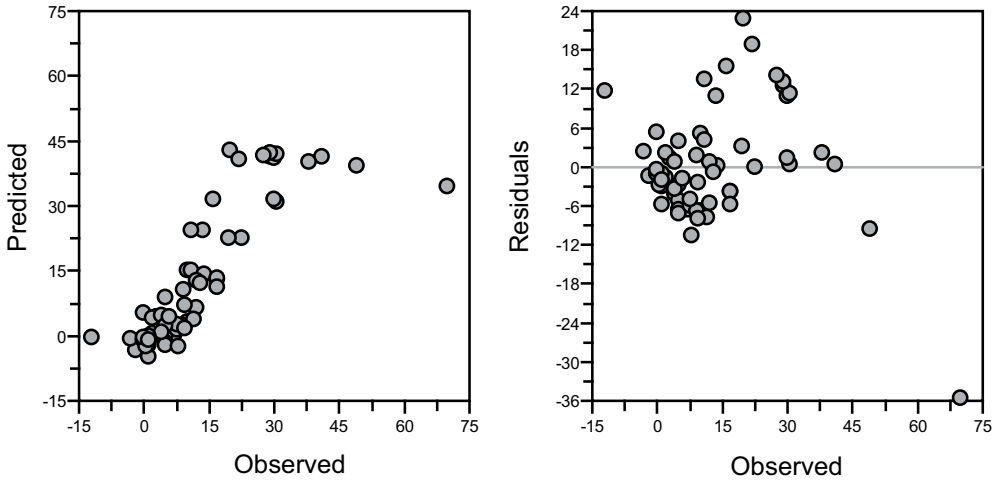
Supplementary Figure 10. Observed vs. model-predicted values (left) and observed vs. residuals (right) of transfer function models of testate amoeba percentages and vascular plants for depth to the water table (DWT) and pH.

Supplementary Figure 11. Observed vs. model-predicted values (left) and observed vs. residuals (right) of transfer function models of testate amoeba percentages, bryophytes and vascular plants for depth to water table (DWT) and pH.

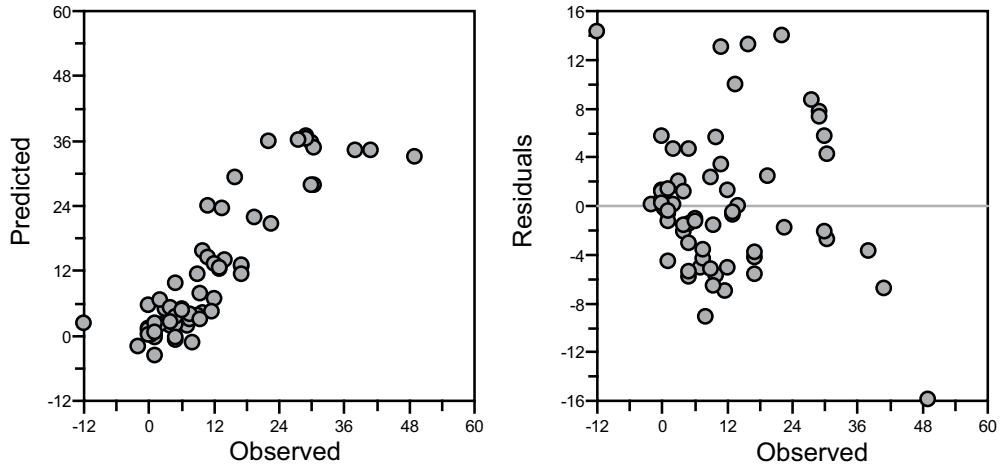
Supplementary Figure 12. Reconstruction of depth to the water table (DWT, A and C) and pH (B and D) from a 1000 year record from Mauntschas mire, Engadine, Switzerland (van der Knaap et al., 2011), plotted against sample depth (A and B) and age (C and D), using raw and filtered percentage (%) and presence/absence (1/0) testate amoeba-based transfer functions. Black lines = raw %, red = filtered %, blue = raw 1/0, green = filtered 1/0.

MOSSES

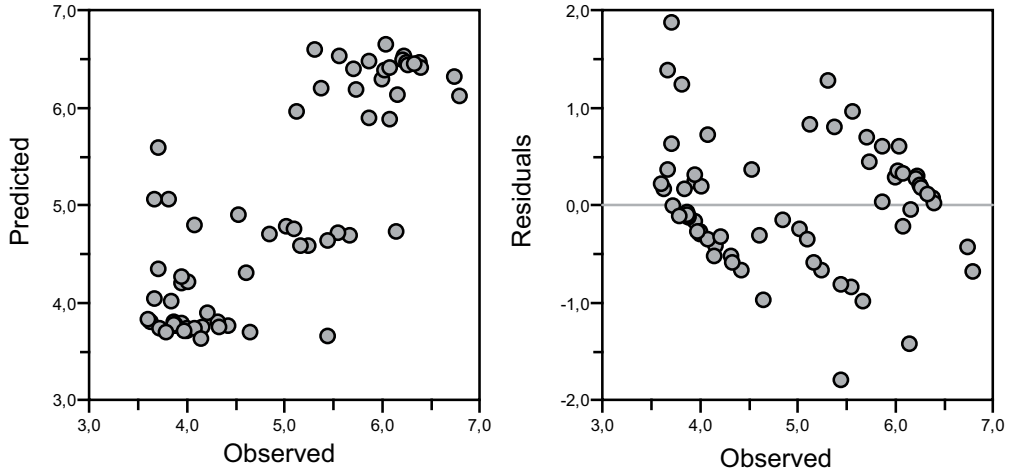
DWT raw



DWT filtered



pH raw



pH filtered

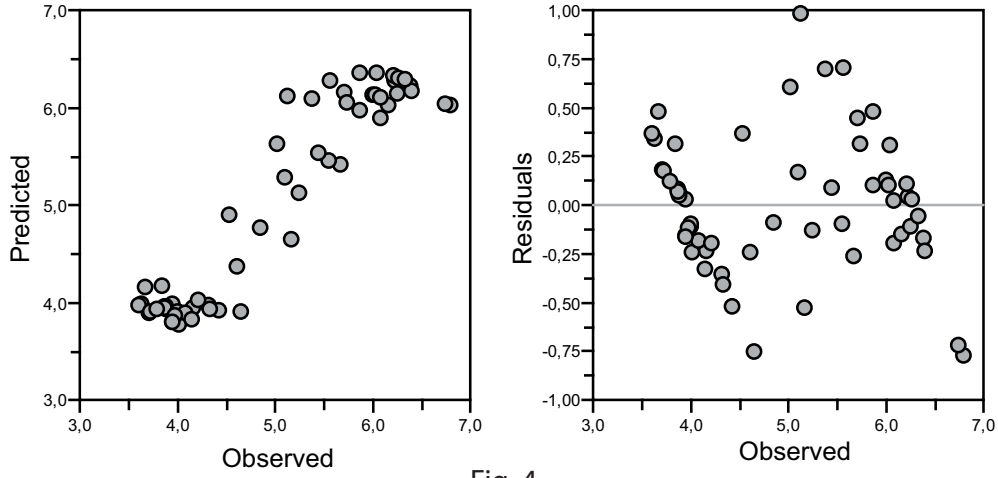


Fig. 4

VASCULAR PLANTS

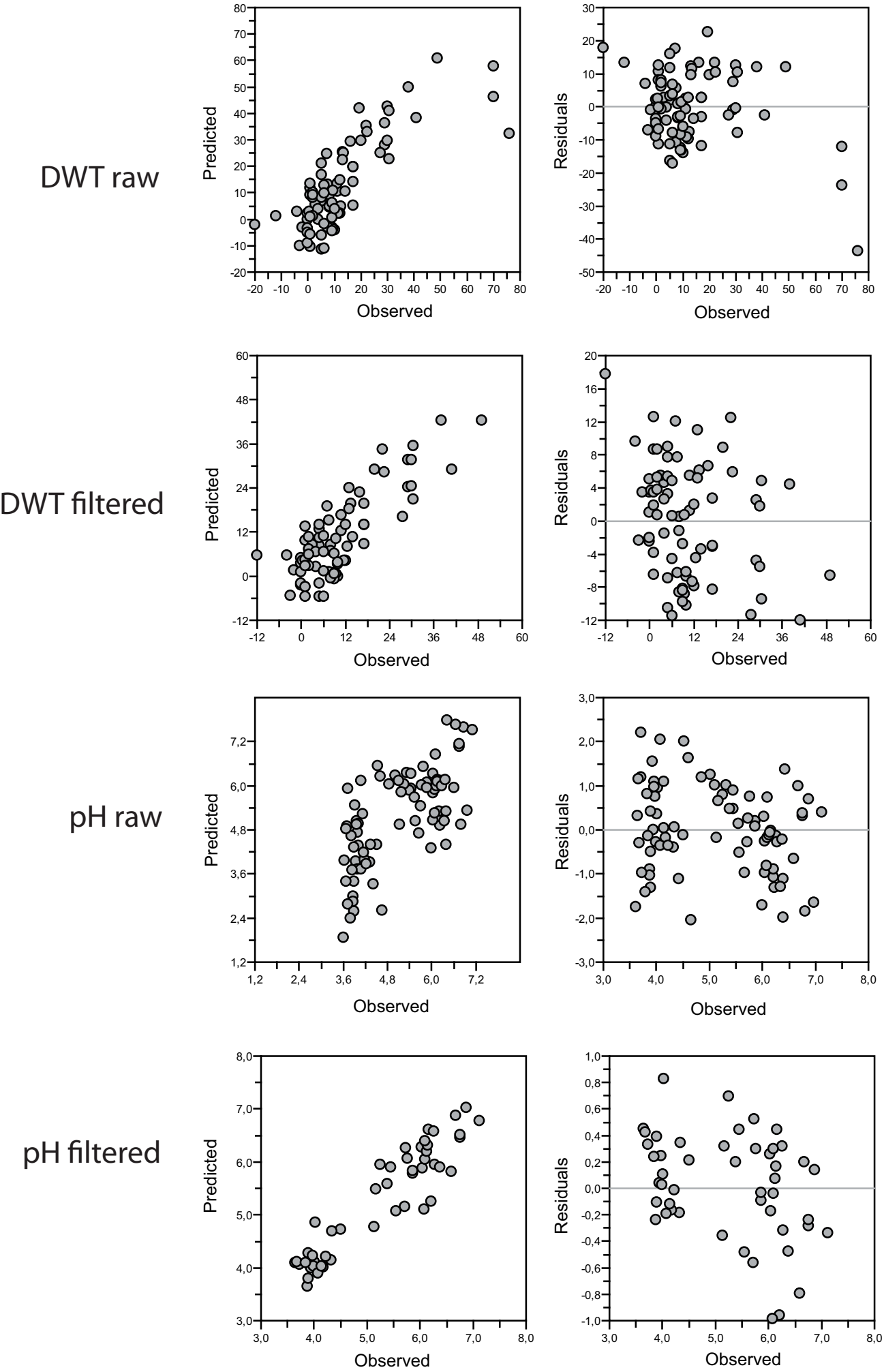
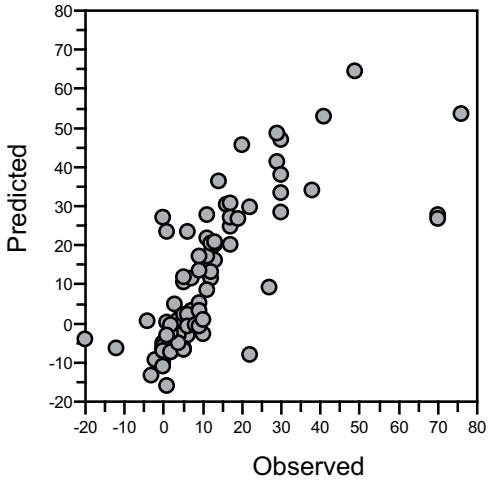
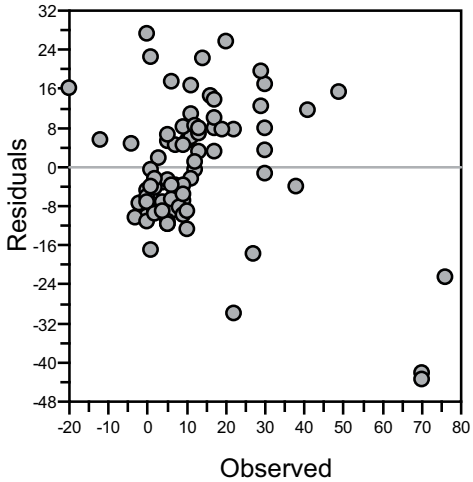


Fig. 5

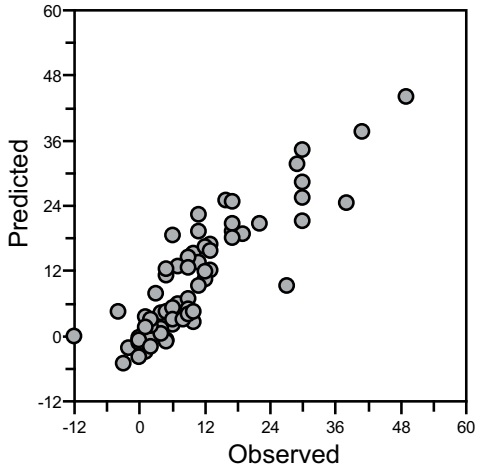
TESTATE AMOEBAE 1/0

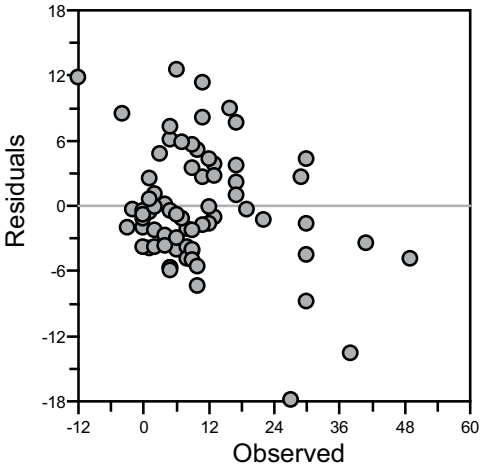
DWT raw



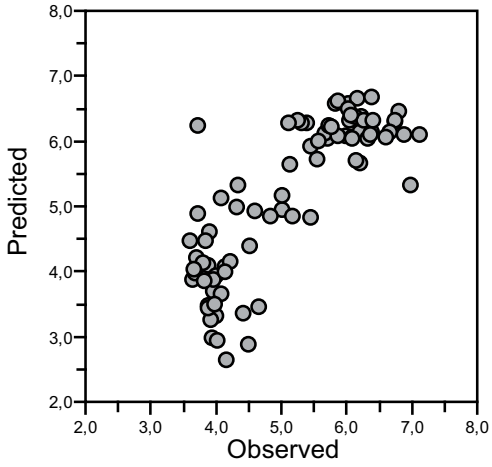


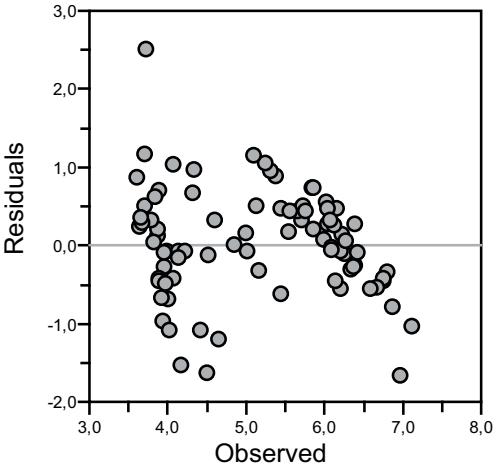
DWT filtered



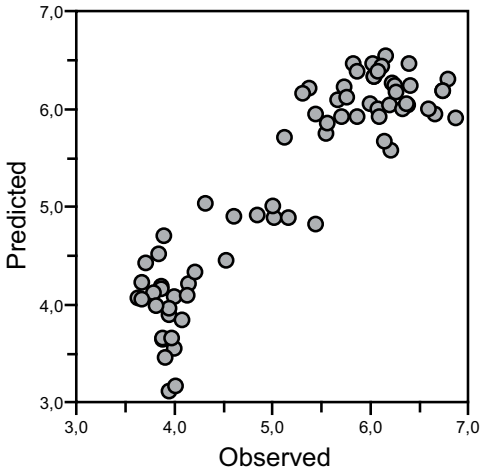


pH raw





pH filtered



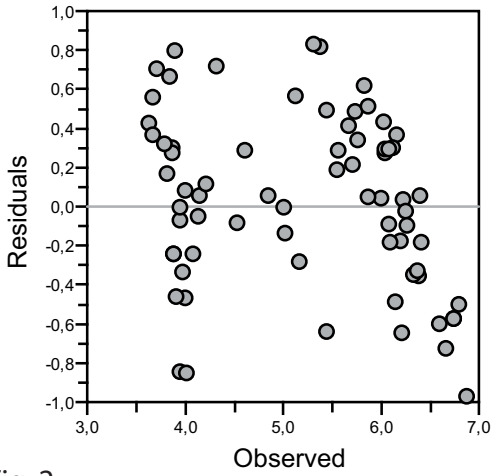
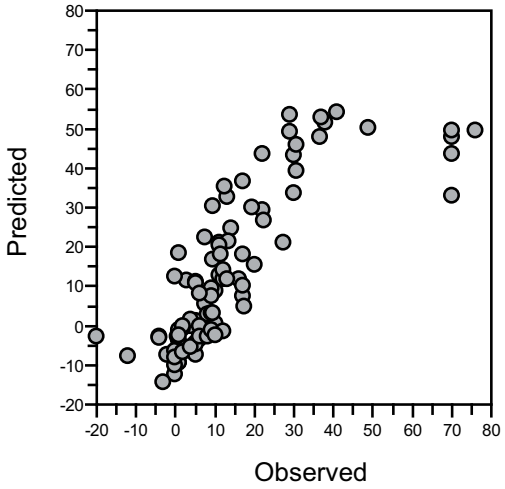


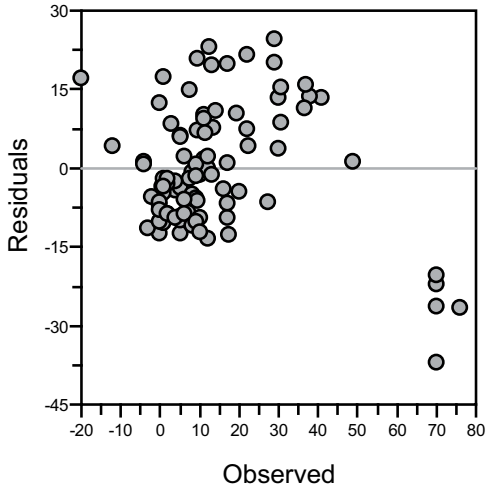
Fig. 2

Supplemental Material (Online Only)

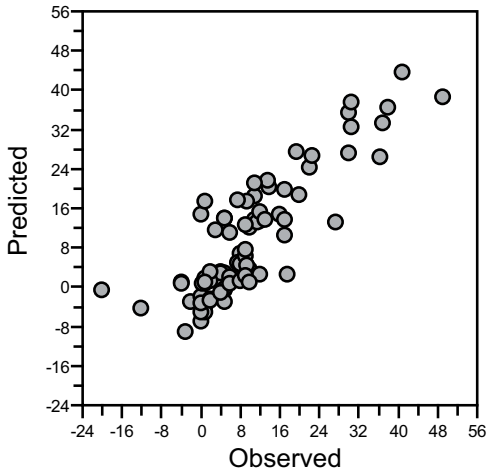
TESTATE AMOEBAE %

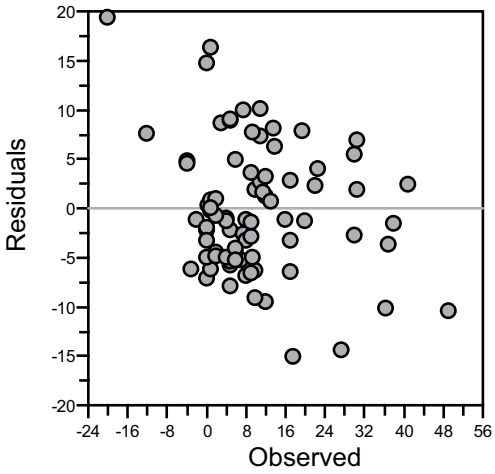
DWT raw



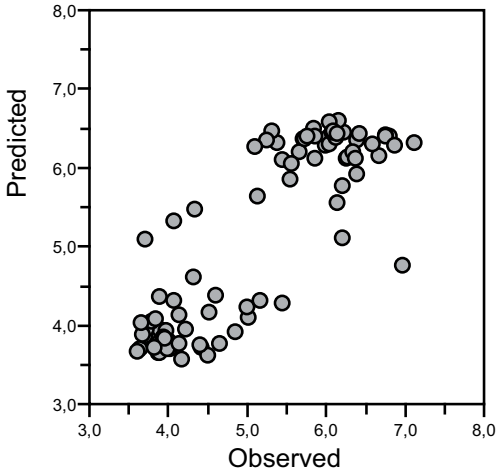


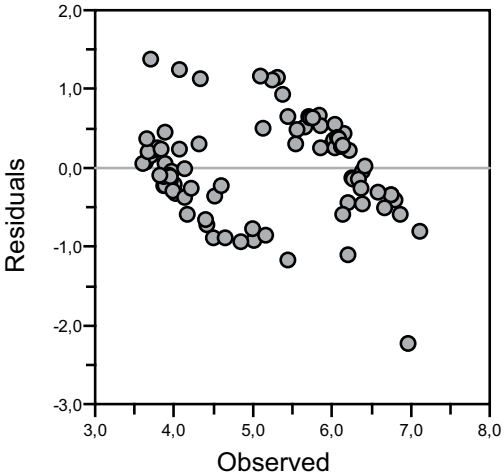
DWT filtered



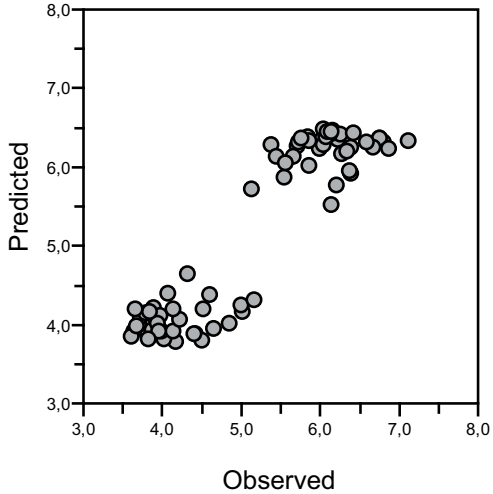


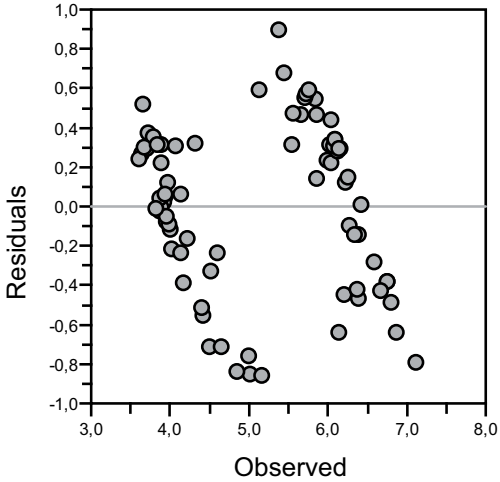
pH raw





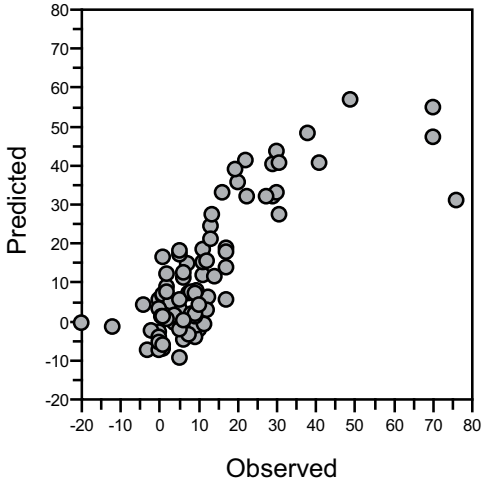
pH filtered

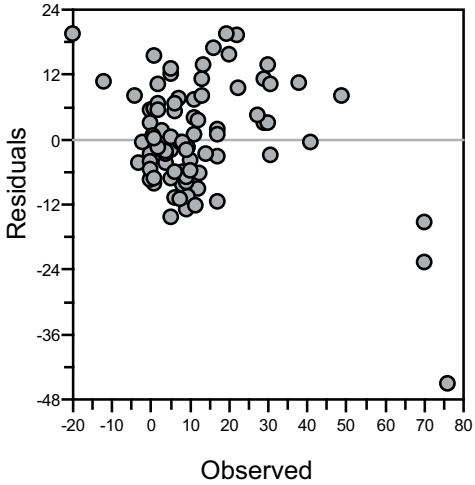




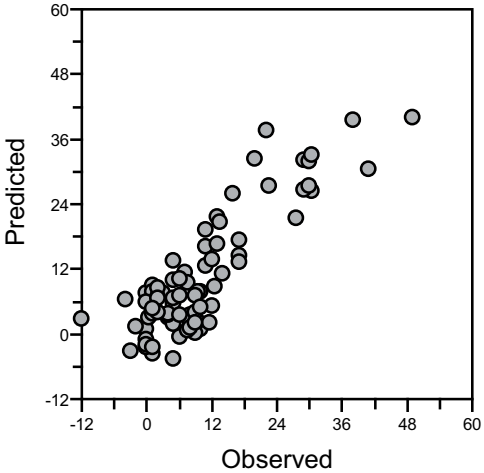
MOSSES & VASCULAR PLANTS

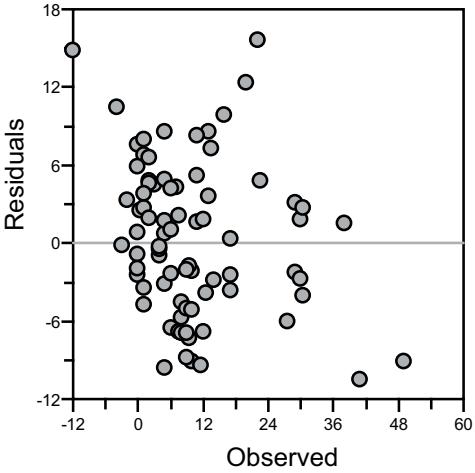
DWT raw



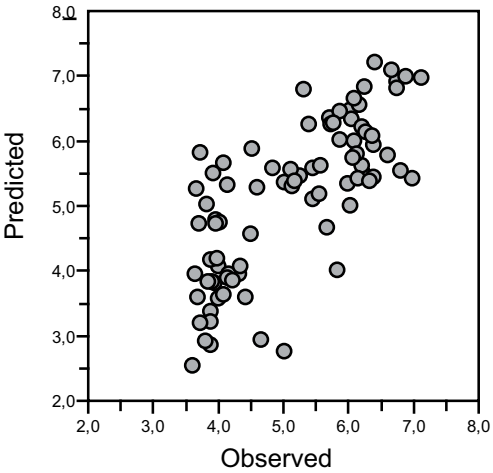


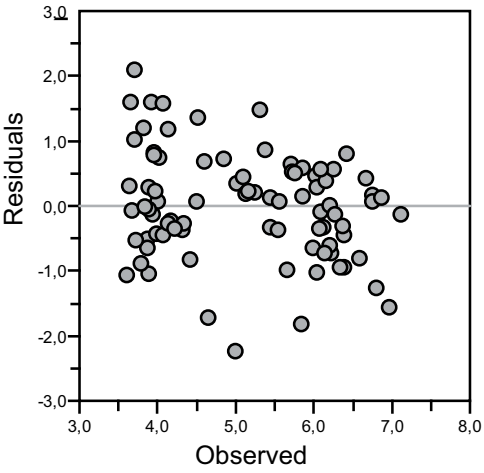
DWT filtered



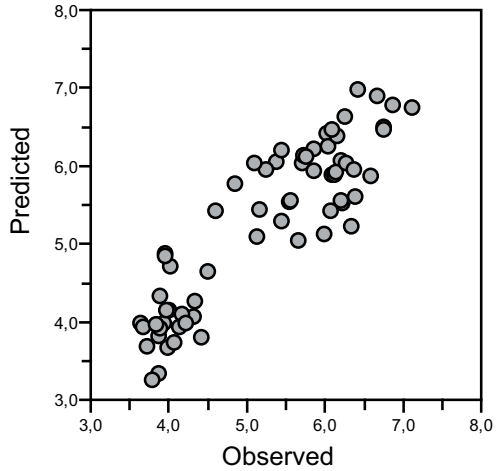


pH raw





pH filtered



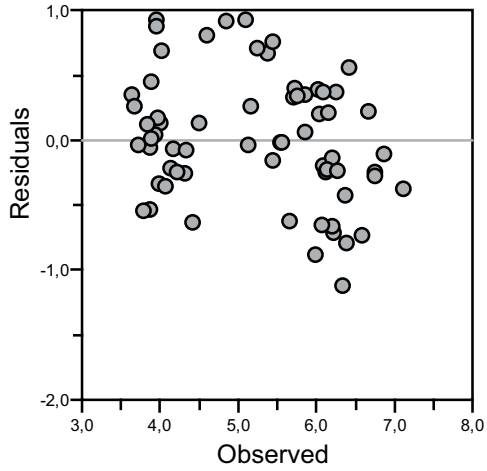


Fig. 3

TESTATE AMOEBAE 1/0 & MOSSES

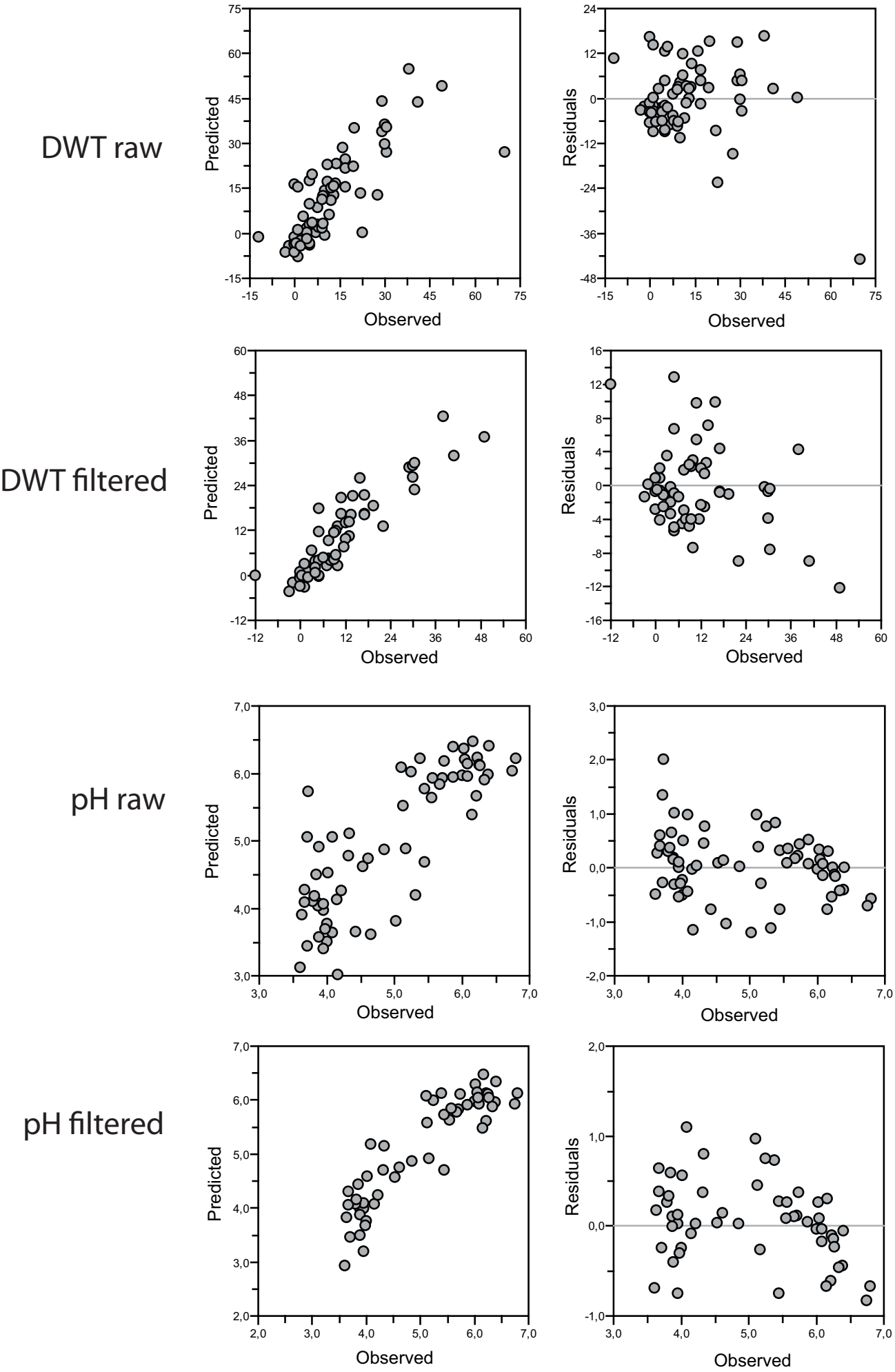


Fig. 6

TESTATE AMOEBAE 1/0 & VASCULAR PLANTS

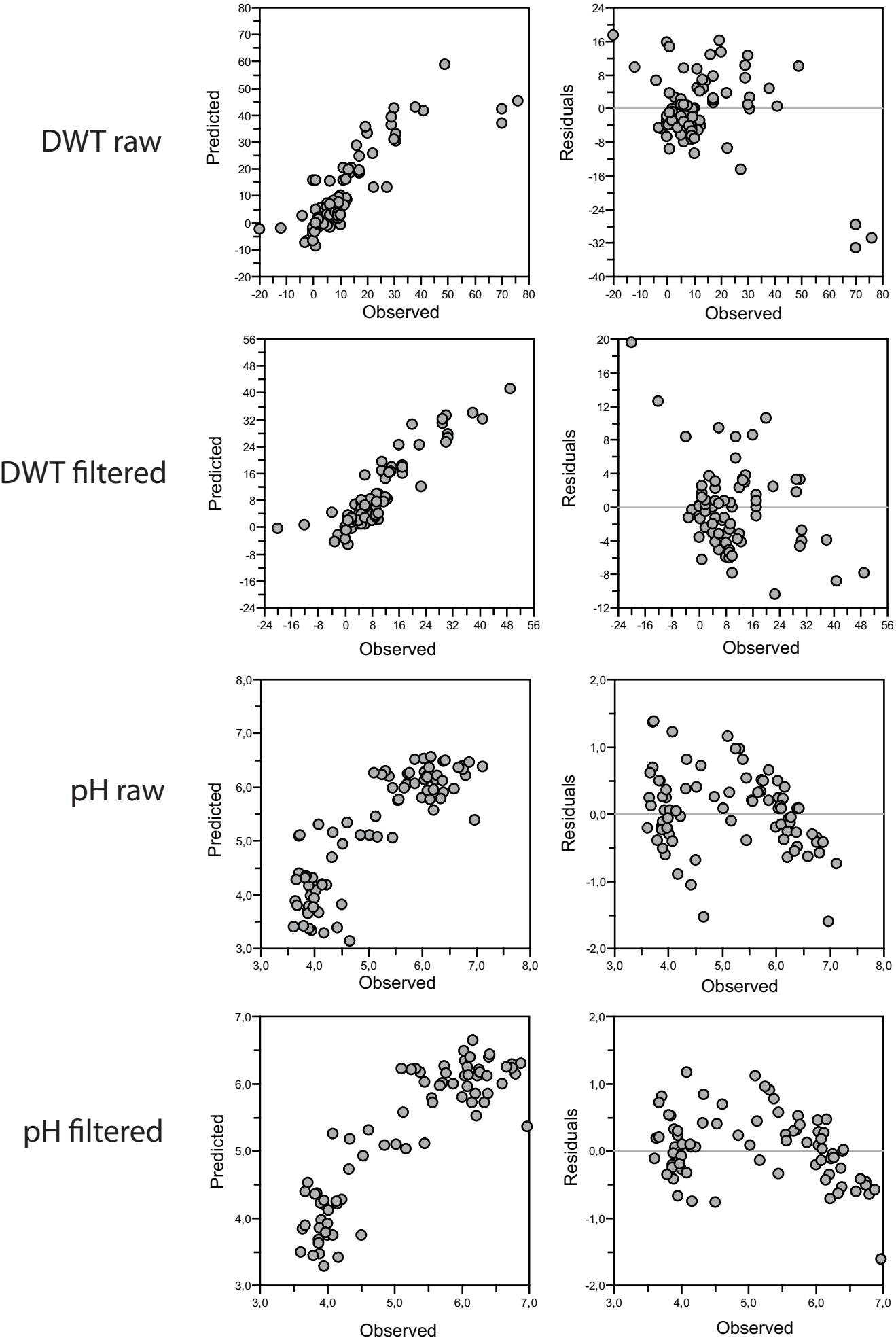


Fig. 8

TESTATE AMOEBAE 1/0, MOSSES & VASCULAR PLANTS

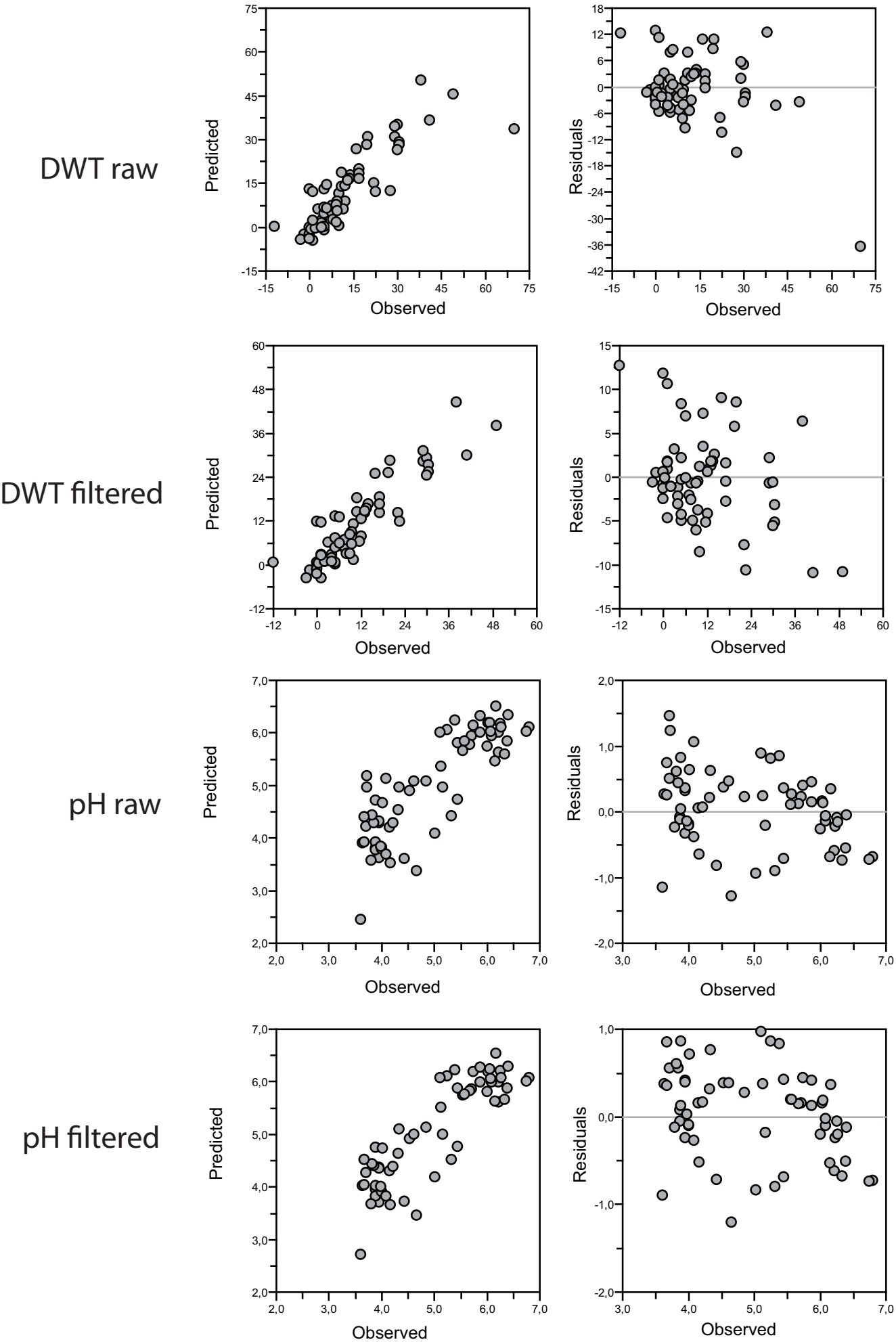


Fig. 7

TESTATE AMOEBAE % & MOSSES

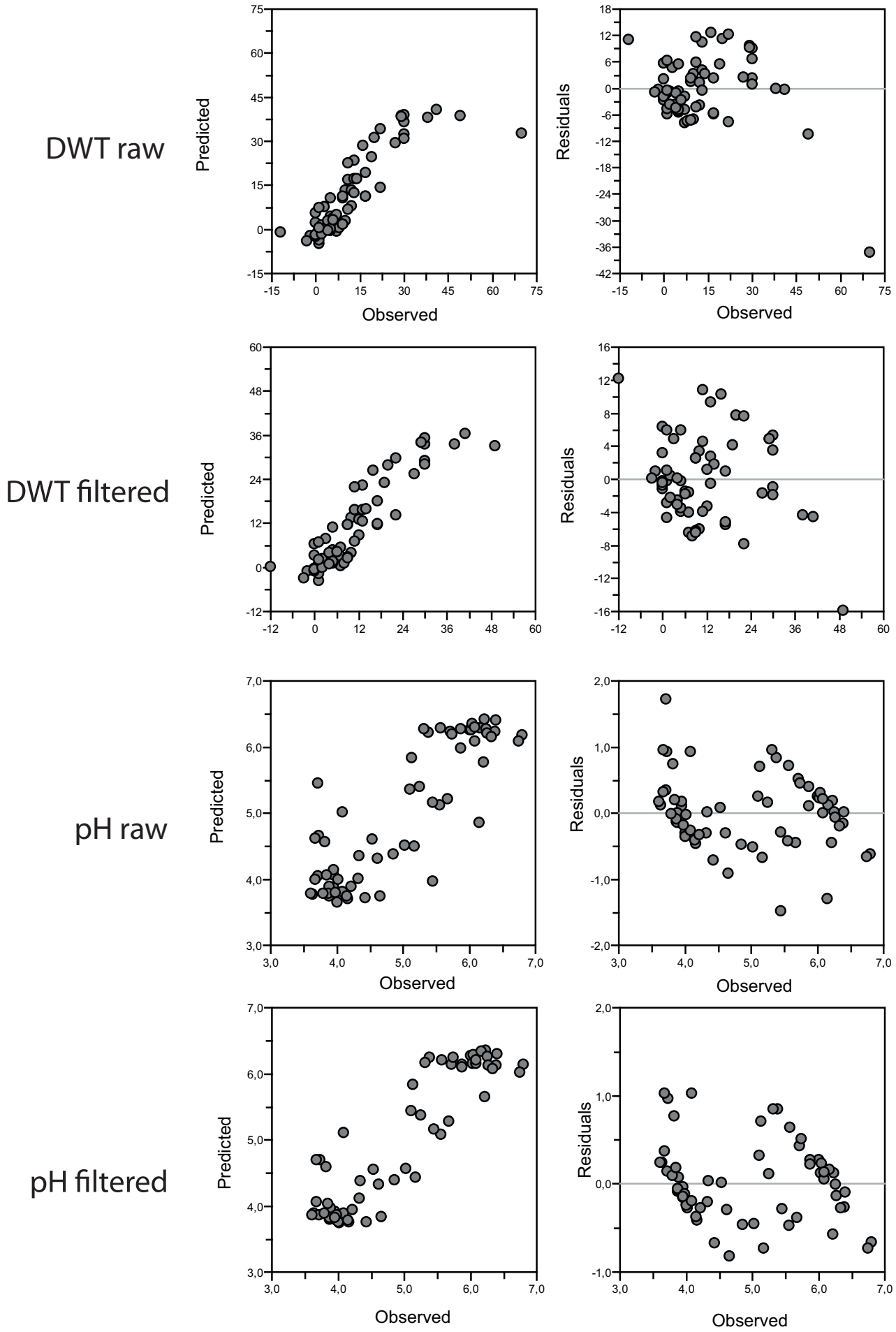


Fig. 9

TESTATE AMOEBAE % & VASCULAR PLANTS

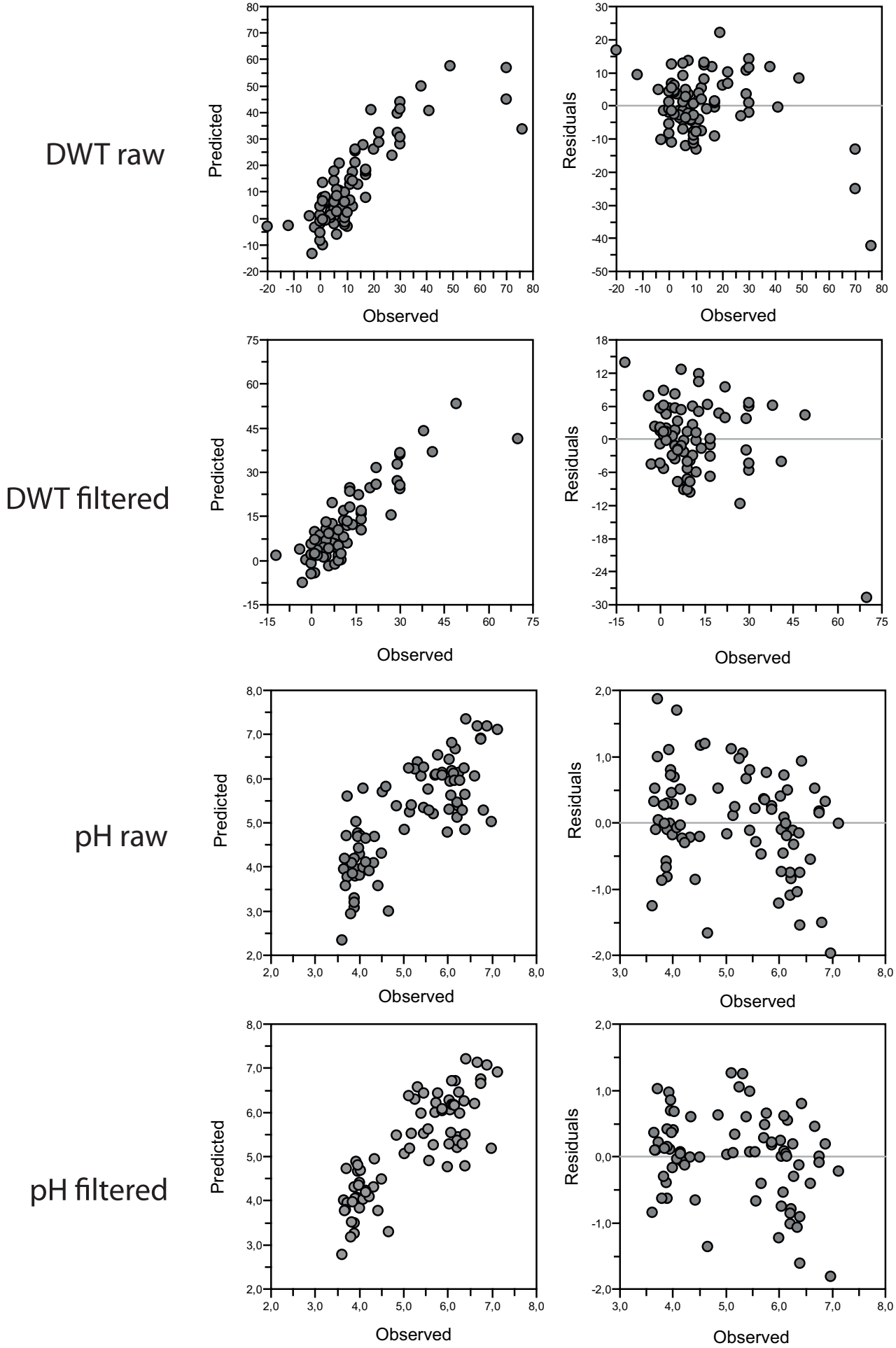


Fig. 10

TESTATE AMOEBAE % , MOSSES AND VASCULAR PLANTS

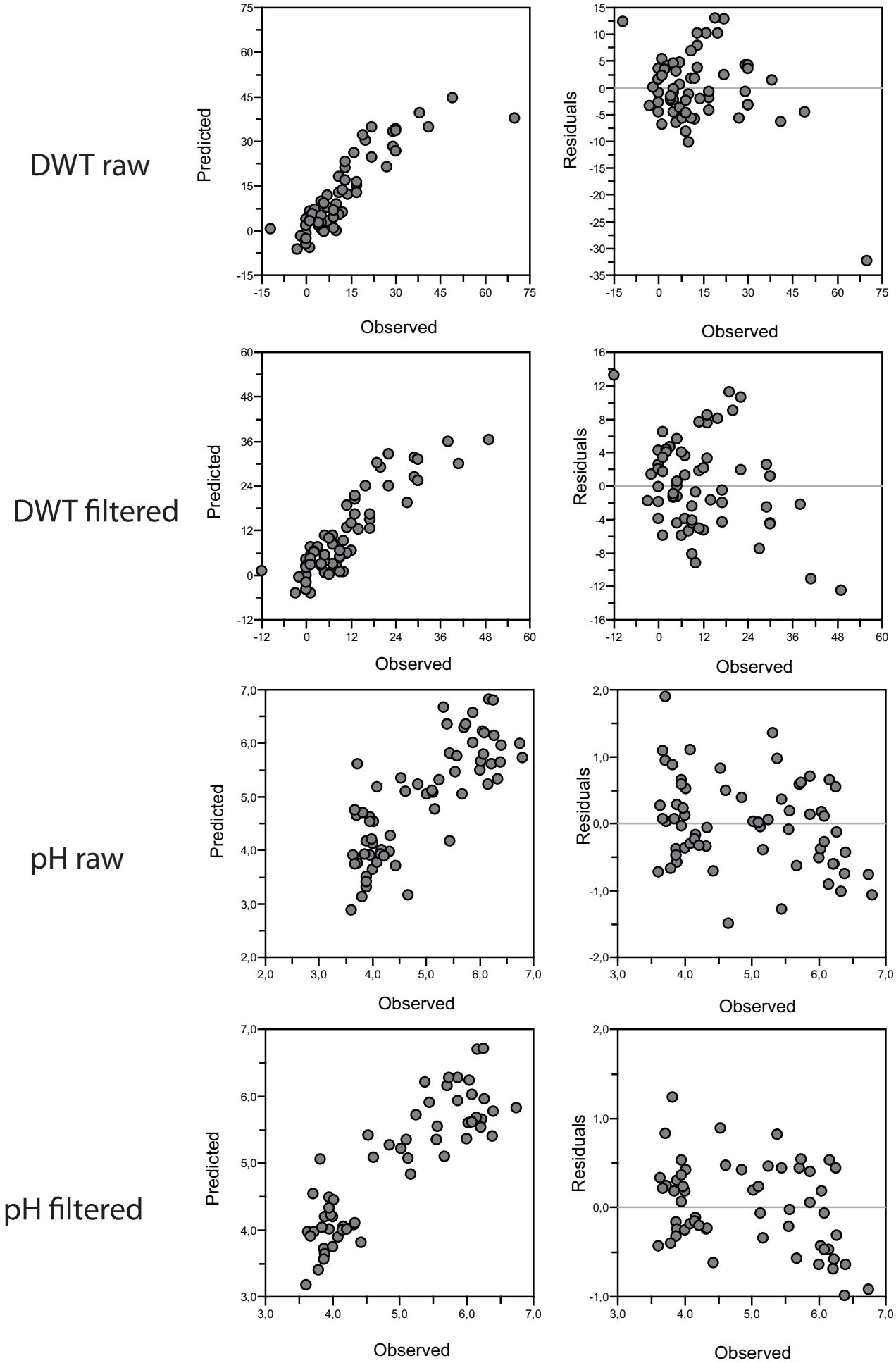
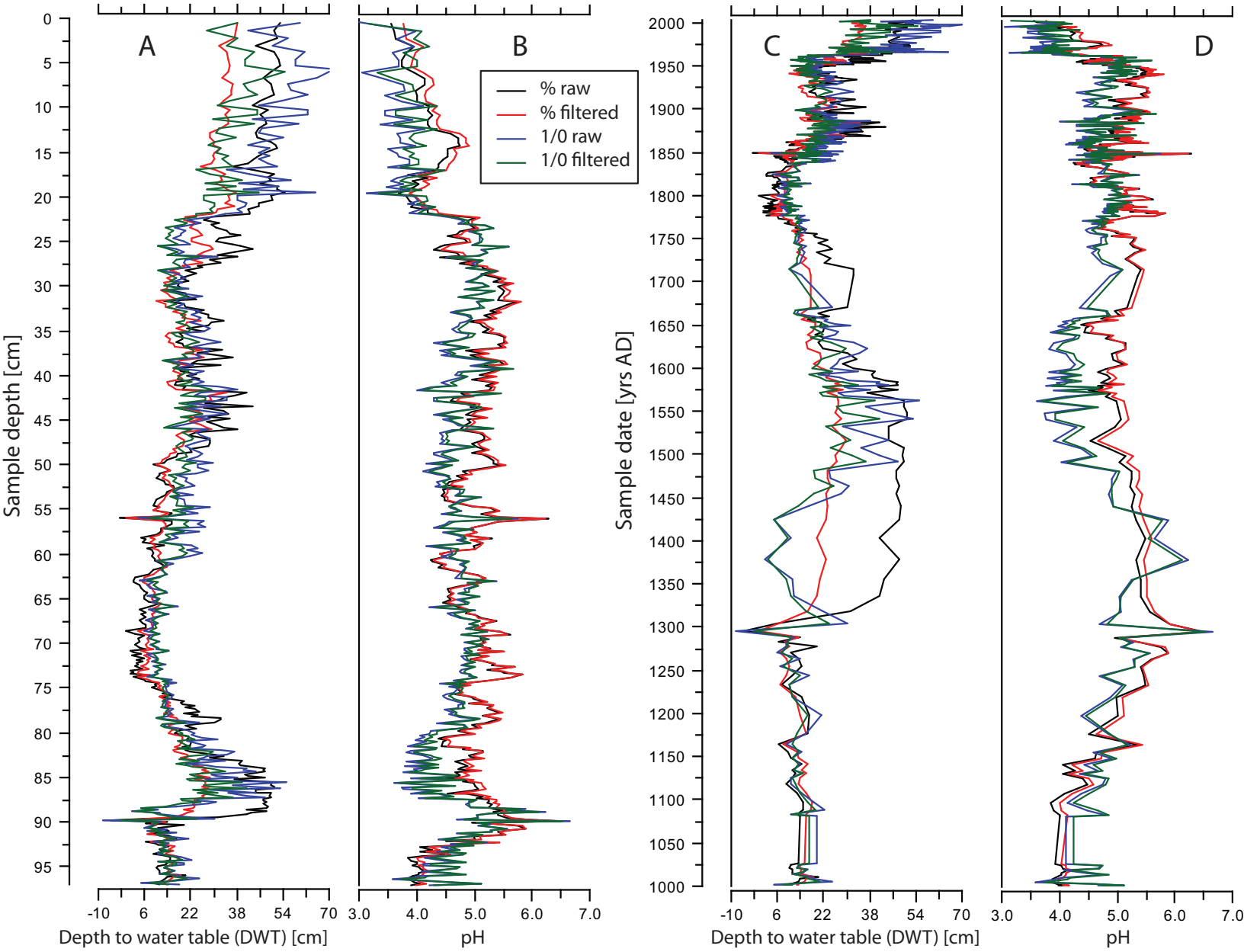


Fig. 11

Supplemental Material (Online Only)



Supplementary table 1. Summary performance indicators of the transfer function models (classical weighted averaging) for depth to the water table (DWT) and pH in peatlands of the Eastern Swiss Alps (Engadine valley). For each group of models (singly proxy, combined with presence-absence data, combined including testate amoeba percentage data) and for either raw of filtered models, the best values for r^2_{boot}, Maximum Bias $_{Boot}$, and RMSEP are indicated by undelined numbers both for raw and filtered models, the best of the two are bolded (taking into consideration exact values). The best models overall for DWT and pH are indicated in grey background. Raw: unfiltered models, filtered: filtered models (with removal of rare species and outlier samples, see text for details).

		DWT [cm]		pH	
		Raw	Filtered	Raw	Filtered
Models on individual groups					
Bryophytes presence/absence	r^2_{Boot}	0.71	0.79	0.67	0.89
	Maximum Bias $_{Boot}$	35.6	16.2	0.56	0.75
	RMSEP	9.0	6.2	0.71	0.37
	Number of samples	65	62	65	58
	Number of species	12	12	12	11
Vascular plants presence/absence	r^2_{Boot}	0.62	0.66	0.46	0.87
	Maximum Bias $_{Boot}$	26.6	17.8	1.20	**0.28**
	RMSEP	11.5	7.4	1.08	0.45
	Number of samples	82	77	82	49
	Number of species	30	30	30	30
Testate amoebae presence/absence	r^2_{Boot}	0.53	0.71	0.67	0.83
	Maximum Bias $_{Boot}$	36.1	34.8	0.96	0.60
	RMSEP	13.2	8.0	0.70	0.46
	Number of samples	93	74	93	71
	Number of species	69	69	69	69
Testate amoebae percentages	r^2	0.65	0.73	0.73	0.86
	Maximum Bias	26.5	19.4	1.01	0.80
	RMSEP	12.2	6.8	0.62	0.43

	Number of samples	93	81	93	78
	Number of species	69	68	69	69
Multi-group models with presence/absence data only *					
	r^2_{Boot}	0.64	0.74	0.55	0.80
	Maximum Bias $_{Boot}$	27.7	14.8	0.77	0.92
Bryophytes & vascular plants	RMSEP	10.8	6.3	0.90	0.53
	Number of samples	82	78	82	65
	Number of species	42	42	42	42
	r^2_{Boot}	0.62	0.83	0.68	0.82
	Maximum Bias $_{Boot}$	43.1	12.2	0.65	0.75
Testate amoebae & bryophytes	RMSEP	9.9	5.2	0.62	0.47
	Number of samples	65	57	65	54
	Number of species	83	83	83	83
	r^2_{Boot}	0.71	0.81	0.75	0.79
	Maximum Bias $_{Boot}$	30.5	19.6	0.84	0.71
Testate amoebae & vascular plants	RMSEP	9.3	5.3	0.58	0.52
	Number of samples	82	75	82	76
	Number of species	106	106	106	106
	r^2_{Boot}	0.73	0.81	0.70	0.75
	Maximum Bias $_{Boot}$	36.5	12.7	0.71	0.73
Testate amoebae, bryophytes & vascular plants	RMSEP	7.6	5.4	0.59	0.52
	Number of samples	65	63	65	62
	Number of species	105	105	105	103
Multi-group models with testate amoeba percentages data *					

Testate amoebae % & bryophytes (100/0)	r^2_{Boot}	0.66	0.78	0.70	**0.94**
	Maximum Bias $_{Boot}$	39.2	11.0	0.66	0.69
	RMSEP	9.1	5.3	0.61	**0.27**
	Number of samples	65	52	65	45
	Number of species	81	81	81	75
Testate amoebae % & vascular plants (100/0)	r^2_{Boot}	0.64	0.73	0.68	0.90
	Maximum Bias $_{Boot}$	29.6	19.4	1.03	0.76
	RMSEP	11.0	5.7	0.70	0.37
	Number of samples	82	64	82	63
	Number of species	106	102	106	102
Testate amoebae %, bryophytes & vascular plants (100/0)	r^2_{Boot}	0.68	0.87	0.71	0.92
	Maximum Bias $_{Boot}$	38.4	15.3	0.68	0.67
	RMSEP	8.7	4.3	0.60	0.30
	Number of samples	65	50	65	46
	Number of species	105	105	105	103

* For models based on presence-absence data, using 0/1 or 0/100 coding does not modify the model performance. In models combining percentage and binary data 0/100 coding of binary data is used.

Supplementary table 2. Comparison of transfer function models (classical weighted averaging) performance indicators of raw (unfiltered) models for depth to the water table (DWT) based on testate amoeba (TA), bryophyte (Bryo), vascular plant (Vasc) data, and combinations of these from peatlands of the Eastern Swiss Alps (Engadine valley). The best models for each category are underlined, best models per transformation of binary data option are indicated in grey shading and best models overall are in bold.

		DWT [cm]				pH			
		Transformation of binary data				Transformation of binary data			
		1/0	(100/n)/0	100/0 #	%	1/0	(100/n)/0	100/0 #	%
Models on individual groups									
Bryo	$r^2_{(boot)}$	0.71	<u>0.71</u>	0.71	n.a.	0.67	0.68	0.66	
	Max Bias $_{(boot)}$	35.6	35.5	35.9	n.a.	<u>0.56</u>	0.60	0.69	
	RMSEP	9.0	<u>8.7</u>	8.7	n.a.	0.71	0.69	0.73	
Vasc	$r^2_{(boot)}$	0.62	0.61	0.62	n.a.	0.46	0.38	0.43	
	Max Bias $_{(boot)}$	26.6	**<u>21.9</u>**	25.8	n.a.	1.20	1.37	1.35	
	RMSEP	11.5	12.0	11.7	n.a.	1.08	1.18	1.14	
TA	$r^2_{(boot)}$	0.53	0.61	0.54	0.65	0.67	0.72	0.68	<u>0.73</u>
	Max Bias $_{(boot)}$	36.1	35.8	36.3	26.5	0.96	1.02	0.96	1.01
	RMSEP	13.2	11.0	12.9	12.2	0.70	<u>0.62</u>	0.68	0.62
Multi-group models without percentage data									
Bryo & Vasc	$r^2_{(boot)}$	0.64	0.64	0.64		0.55	0.59	0.54	

	Max Bias $_{(boot)}$	27.7	28.4	28.3	0.77	0.88	0.79
	RMSEP	10.8	11.0	10.9	0.90	0.83	0.93
TA & Bryo	$r^2_{(boot)}$	0.62	0.72	0.61	0.68	**0.75**	0.68
	Max Bias $_{(boot)}$	43.1	38.9	43.6	0.65	0.64	0.64
	RMSEP	9.9	8.0	9.7	0.62	**0.56**	0.62
TA & Vasc	$r^2_{(boot)}$	0.71	0.72	0.72	0.75	0.66	0.72
	Max Bias $_{(boot)}$	30.5	28.2	29.0	0.84	0.97	1.13
	RMSEP	9.3	9.3	9.2	0.58	0.71	0.69
TA, Bryo & Vasc	$r^2_{(boot)}$	0.73	0.69	0.73	0.70	0.69	0.70
	Max Bias $_{(boot)}$	36.5	31.5	37.2	0.71	0.97	0.72
	RMSEP	7.6	9.8	7.7	0.59	0.68	0.58
Multi-group models with TA percentages data							
TA % & Bryo	$r^2_{(boot)}$	0.66	0.72	0.74	0.70	0.75	0.66
	Max Bias $_{(boot)}$	39.2	38.8	37.2	0.66	0.64	0.60
	RMSEP	9.1	8.0	7.9	0.61	0.56	0.78
TA % & Vasc	$r^2_{(boot)}$	0.6	0.72	0.69	0.6	0.66	0.58

		4			8		
	Max Bias $_{(boot)}$	29.6	28.8	26.8	1.03	0.96	0.49
	RMSEP	11.0	8.7	10.1	0.70	0.66	0.92
	$r^2_{(boot)}$	0.68	0.68	**0.77**	0.71	0.68	0.57
TA %, Bryo & Vasc	Max Bias $_{(boot)}$	38.4	31.8	32.3	0.68	0.97	**0.48**
	RMSEP	8.7	9.9	**7.1**	0.60	0.68	0.87

#: 0/1 and 0/100 models are identical except when combined with TA % data

Supplementary table 3. Summary performance indicators of the LOSO (Leave One Site Out) validation of raw (unfiltered) transfer function models (classical weighted averaging) for depth to the water table (DWT) and pH in peatlands of the Eastern Swiss Alps (Engadine valley). The best models for each category are underlined, best models per transformation of binary data option are indicated in grey shading and best models overall are in bold. Note that WA is not neccessarily the best-performing transfer function technique and other models with the same data may have more predictive power.

		DWT [cm]				pH			
		Transformation of binary data				Transformation of binary data			
		1/0	(100/n)/0	100/0 #	%	1/0	(100/n)/0	100/0 #	%
Models on individual groups									
	r^2	0.64	0.63			0.53	0.54		
Bryophytes	Maximum Bias	35.2	35.4			**0.55**	0.57		
	RMSEP	11.0	11.3			0.84	0.83		
	r^2	0.41	0.45			0.00	0.00		
Vascular plants	Maximum Bias	25.0	24.2			2.39	2.16		
	RMSEP	15.2	14.2			1.66	1.62		
	r^2	0.52	0.56		0.59	0.66	0.66		0.65
Testate amoebae	Maximum Bias	37.8	37.6		29.2	1.05	1.13		1.17
	RMSEP	13.8	11.8		12.18	0.67	0.67		0.69
Multi-group models without percentage data									
	r^2	0.50	0.53			0.12	0.24		
Bryophytes & vascular plants	Maximum Bias	27.9	30.7			2.00	1.67		
	RMSEP	13.2	13.4			1.22	1.10		
	r^2	0.62	0.66			0.69	0.65		
Testate amoebae & bryophytes	Maximum Bias	41.6	38.5			0.67	0.61		
	RMSEP	10.1	9.7			**0.60**	0.64		
	r^2	0.65	0.64			0.66	0.40		
Testate amoebae & vascular plants	Maximum Bias	32.5	31.7			1.17	1.44		
	RMSEP	9.9	10.0			0.64	0.87		

	r^2	0.64	0.59		0.65	0.47	
Testate amoebae, bryophytes & vascular plants	Maximum Bias	33.0	34.1		1.16	1.37	
	RMSEP	10.2	11.6		0.65	0.83	
Multi-group models with testate amoeba percentages data							
	r^2	0.62	0.68	0.69	0.68	**0.69**	0.66
Testate amoebae % & bryophytes	Maximum Bias	37.0	36.0	36.0	0.65	0.59	0.58
	RMSEP	10.2	9.6	9.5	0.64	0.61	0.65
	r^2	0.60	**0.70**	0.58	0.67	0.53	0.25
Testate amoebae % & vascular plants	Maximum Bias	29.2	27.5	**26.7**	1.16	1.35	1.77
	RMSEP	11.9	**9.2**	11.4	0.66	0.75	1.02
	r^2	0.60	0.65	0.61	0.67	0.55	0.34
Testate amoebae %, bryophytes & vascular plants	Maximum Bias	29.2	30.1	28.6	1.16	1.31	1.66
	RMSEP	11.8	10.7	11.1	0.66	0.75	0.93

#: 0/1 and 0/100 models are identical except when combined with TA % data