

Appendix D. Detailed results on the phylogenetic and functional beta diversity.

TABLE D1. Same as Table 1, but only for the small plant-neighborhood scales of $r = 1$ to 50m. The proportion of variation (R^2) explained by the five ecological process hypotheses: random placement hypotheses, habitat filtering hypothesis, dispersal limitation hypothesis, the combined habitat and dispersal hypothesis, and independent placement hypothesis. The proportion of variation explained by a model is calculated by $1 - \text{SSE}/\text{SST}$, where $\text{SSE} = \sum_r [D_{\text{obs}}(r) - D_{\text{pre}}(r)]^2$ and $\text{SST} = \sum_r [D_{\text{obs}}(r) - \text{mean}(D_{\text{obs}})]^2$, in which $D_{\text{pre}}(r)$ is the predicted phylogenetic or functional $D_{\text{pw}}(r)$, and $D_{\text{obs}}(r)$ is the observed phylogenetic and functional $D_{\text{pw}}(r)$. Note that R^2 yields negative values if the intercept only model (i.e., the mean value of $D_{\text{obs}}(r)$ averaged over all r) fits better than the model.

		Random placement	Dispersal	Habitat	Habitat and Dispersal	Independent placement
Large trees						
Phylogenetic	CBS	8.0	92.2	43.2	91.5	98.0
D_{pw}	Wabikon	-375.0	-94.1	-372.9	41.1	94.7
Functional	CBS	93.8	84.7	14.5	86.5	93.8
D_{pw}	Wabikon	-97.6	76.4	-49.3	71.0	95.2
Species	CBS	-138.7	83.5	-8.4	80.6	93.5
D_{pw}	Wabikon	-93.9	62.3	-28.3	77.4	97.1
Small trees						
Phylogenetic	CBS	-26.4	93.4	-6.7	33.1	92.8
D_{pw}	Wabikon	-154.9	84.8	-492.0	-359.2	90.4
Functional	CBS	-76.4	63.6	20.3	64.3	97.2
D_{pw}	Wabikon	-68.4	93.2	-107.3	-93.7	98.6
Species	CBS	-37.4	90.0	9.6	57.3	95.7
D_{pw}	Wabikon	-60.7	97.9	-39.4	-32.6	98.5

TABLE D2. Same as Table D1, but only for immediate within-habitat scales of $r = 51$ to 150m . The proportion of variation (R^2) explained by the five ecological process hypotheses: random placement hypotheses, habitat filtering hypothesis, dispersal limitation hypothesis, the combined habitat and dispersal hypothesis, and independent placement hypothesis. The proportion of variation explained by a model is calculated by $1 - \text{SSE}/\text{SST}$, where $\text{SSE} = \sum_r [D_{\text{obs}}(r) - D_{\text{pre}}(r)]^2$ and $\text{SST} = \sum_r [D_{\text{obs}}(r) - \text{mean}(D_{\text{obs}})]^2$, in which $D_{\text{pre}}(r)$ is the predicted phylogenetic or functional $D_{\text{pw}}(r)$, and $D_{\text{obs}}(r)$ is the observed phylogenetic and functional $D_{\text{pw}}(r)$. Note that R^2 yields negative values if the intercept only model (i.e., the mean value of $D_{\text{obs}}(r)$ averaged over all r) fits better than the model.

		Random placement	Dispersal	Habitat	Habitat and Dispersal	Independent placement
Large trees						
Phylogenetic	CBS	89.1	90.3	51.0	90.9	97.7
D_{pw}	Wabikon	-524.6	-227.9	-558.8	26.1	98.2
Functional	CBS	92.2	81.1	14.6	83.6	92.2
D_{pw}	Wabikon	17.1	71.8	-78.1	76.4	98.8
Species	CBS	-105.0	77.4	-28.6	72.8	92.0
D_{pw}	Wabikon	24.6	51.9	-43.5	80.7	99.3
Small trees						
Phylogenetic	CBS	58.0	97.1	-47.5	24.5	96.8
D_{pw}	Wabikon	-217.1	27.4	-1249.5	-1067.8	77.3
Functional	CBS	-40.3	-24.3	33.5	75.1	97.8
D_{pw}	Wabikon	82.4	82.2	-191.1	-186.9	97.7
Species	CBS	42.6	67.8	0.3	75.9	96.8
D_{pw}	Wabikon	83.6	95.5	-70.3	-64.6	97.7

TABLE D3. Same as Table D2, but only for larger scales of $r = 151$ to 250m . The proportion of variation (R^2) explained by the five ecological process hypotheses: random placement hypotheses, habitat filtering hypothesis, dispersal limitation hypothesis, the combined habitat and dispersal hypothesis, and independent placement hypothesis. The proportion of variation explained by a model is calculated by $1 - \text{SSE}/\text{SST}$, where $\text{SSE} = \sum_r [D_{\text{obs}}(r) - D_{\text{pre}}(r)]^2$ and $\text{SST} = \sum_r [D_{\text{obs}}(r) - \text{mean}(D_{\text{obs}})]^2$, in which $D_{\text{pre}}(r)$ is the predicted phylogenetic or functional $D_{\text{pw}}(r)$, and $D_{\text{obs}}(r)$ is the observed phylogenetic and functional $D_{\text{pw}}(r)$. Note that R^2 yields negative values if the intercept only model (i.e., the mean value of $D_{\text{obs}}(r)$ averaged over all r) fits better than the model.

		Random placement	Dispersal	Habitat	Habitat and Dispersal	Independent placement
Large trees						
Phylogenetic	CBS	-16.9	11.2	94.4	93.1	99.6
D_{pw}	Wabikon	-73.9	-156.0	57.4	97.0	99.9
Functional	CBS	9.0	17.2	97.5	97.6	98.8
D_{pw}	Wabikon	97.3	87.1	99.4	99.6	100.0
Species	CBS	-118.2	-97.5	91.9	98.5	98.9
D_{pw}	Wabikon	95.7	93.3	95.6	99.0	100.0
Small trees						
Phylogenetic	CBS	75.1	54.7	98.6	61.4	99.5
D_{pw}	Wabikon	-5374.1	-5685.0	-1657.8	16.3	86.5
Functional	CBS	67.8	24.8	96.6	60.5	99.8
D_{pw}	Wabikon	-158.0	-233.1	22.1	56.3	98.7
Species	CBS	76.5	22.5	96.4	59.9	99.8
D_{pw}	Wabikon	76.1	58.0	99.1	75.4	99.3

TABLE D4. Same as Table D2, but only for small scales of $r = 1$ to 20m. The proportion of variation (R^2) explained by the five ecological process hypotheses: random placement hypotheses, habitat filtering hypothesis, dispersal limitation hypothesis, the combined habitat and dispersal hypothesis, and independent placement hypothesis. The proportion of variation explained by a model is calculated by $1 - \text{SSE}/\text{SST}$, where $\text{SSE} = \sum_r [D_{obs}(r) - D_{pre}(r)]^2$ and $\text{SST} = \sum_r [D_{obs}(r) - \text{mean}(D_{obs})]^2$, in which $D_{pre}(r)$ is the predicted phylogenetic or functional $D_{pw}(r)$, and $D_{obs}(r)$ is the observed phylogenetic and functional $D_{pw}(r)$. Note that R^2 yields negative values if the intercept only model (i.e., the mean value of $D_{obs}(r)$ averaged over all r) fits better than the model.

		Random placement	Dispersal	Habitat	Habitat and Dispersal	Independent placement
Large trees						
Phylogenetic	CBS	6.6	93.1	36.6	89.8	97.8
D_{pw}	Wabikon	-245.1	1.0	-268.0	47.4	94.1
Functional	CBS	94.6	87.4	14.2	86.4	94.6
D_{pw}	Wabikon	-69.3	81.1	-33.1	69.2	94.5
Species	CBS	-99.1	86.9	-4.9	80.8	94.2
D_{pw}	Wabikon	-68.4	73.0	-17.1	75.5	96.4
Small trees						
Phylogenetic	CBS	-22.8	93.5	-5.6	34.0	93.0
D_{pw}	Wabikon	-129.3	95.4	-373.6	-257.3	93.1
Functional	CBS	-54.8	81.0	18.7	66.9	97.5
D_{pw}	Wabikon	-50.9	94.8	-81.9	-65.5	99.2
Species	CBS	-29.7	93.3	9.8	57.6	95.9
D_{pw}	Wabikon	-45.3	98.7	-28.8	-18.8	99.1

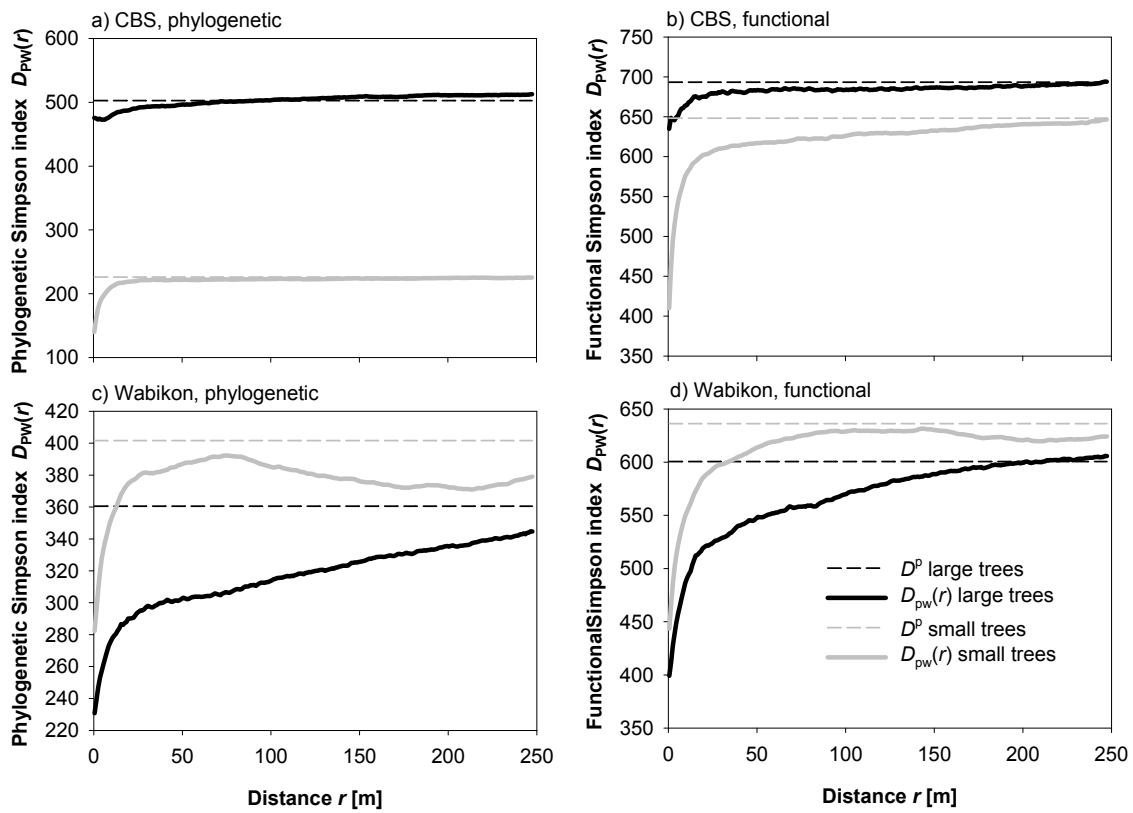


FIG. D1. The pattern of functional and phylogenetic beta diversity for the two forests and the two size classes.

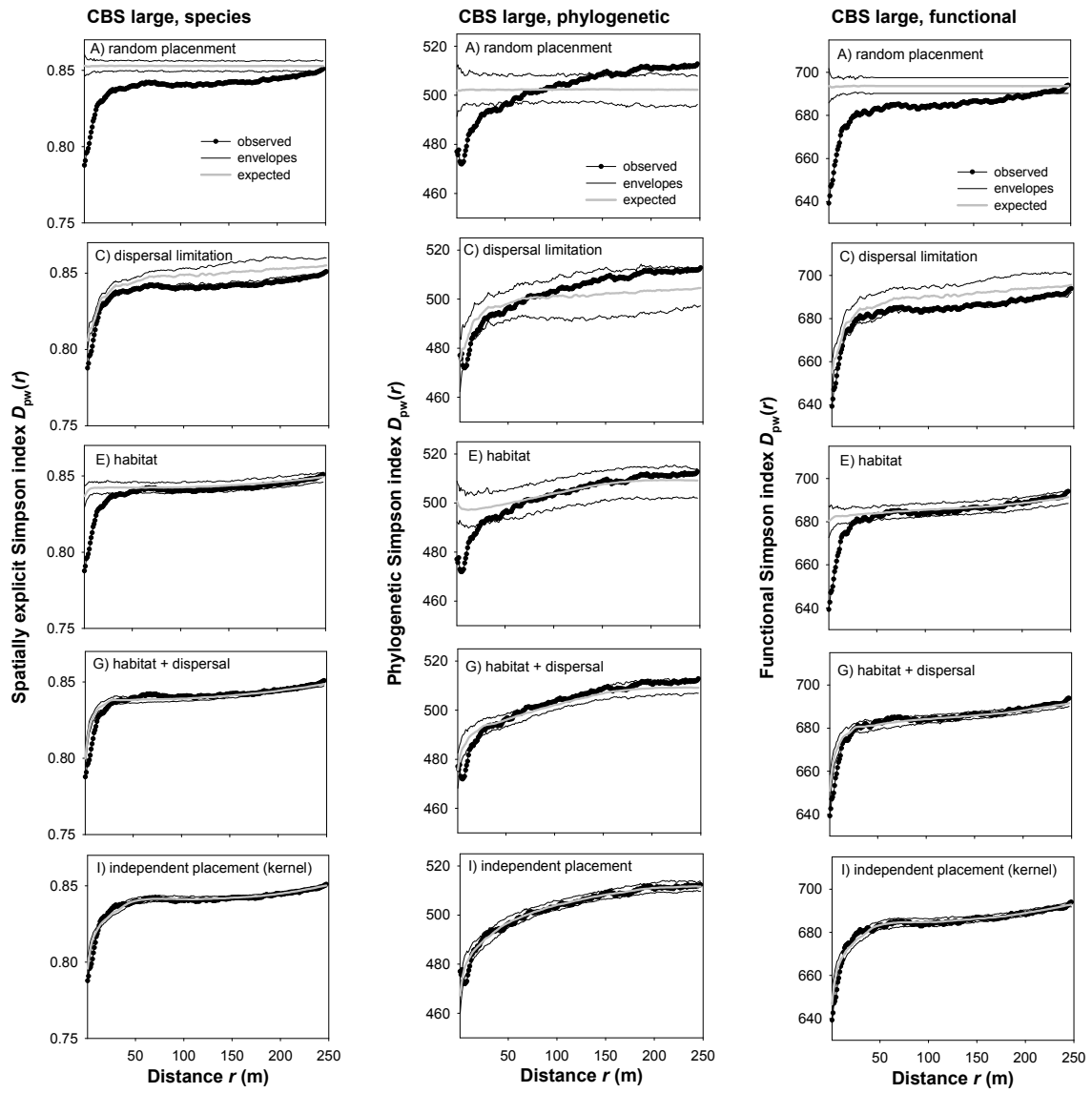


FIG. D2. Summary of results for large trees at the CBS forest.

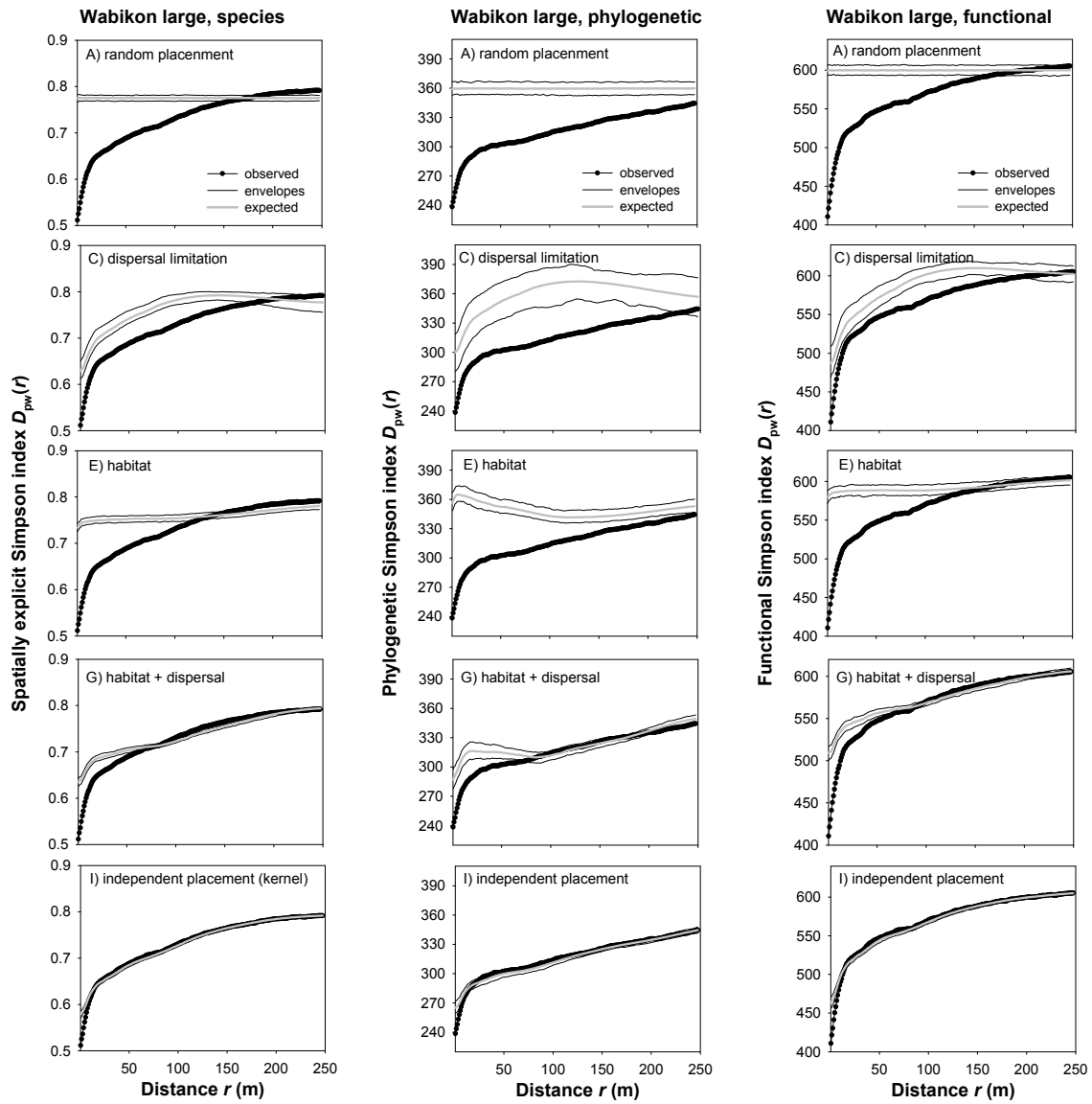


FIG. D3. Summary of results for large trees at the Wabikon forest.

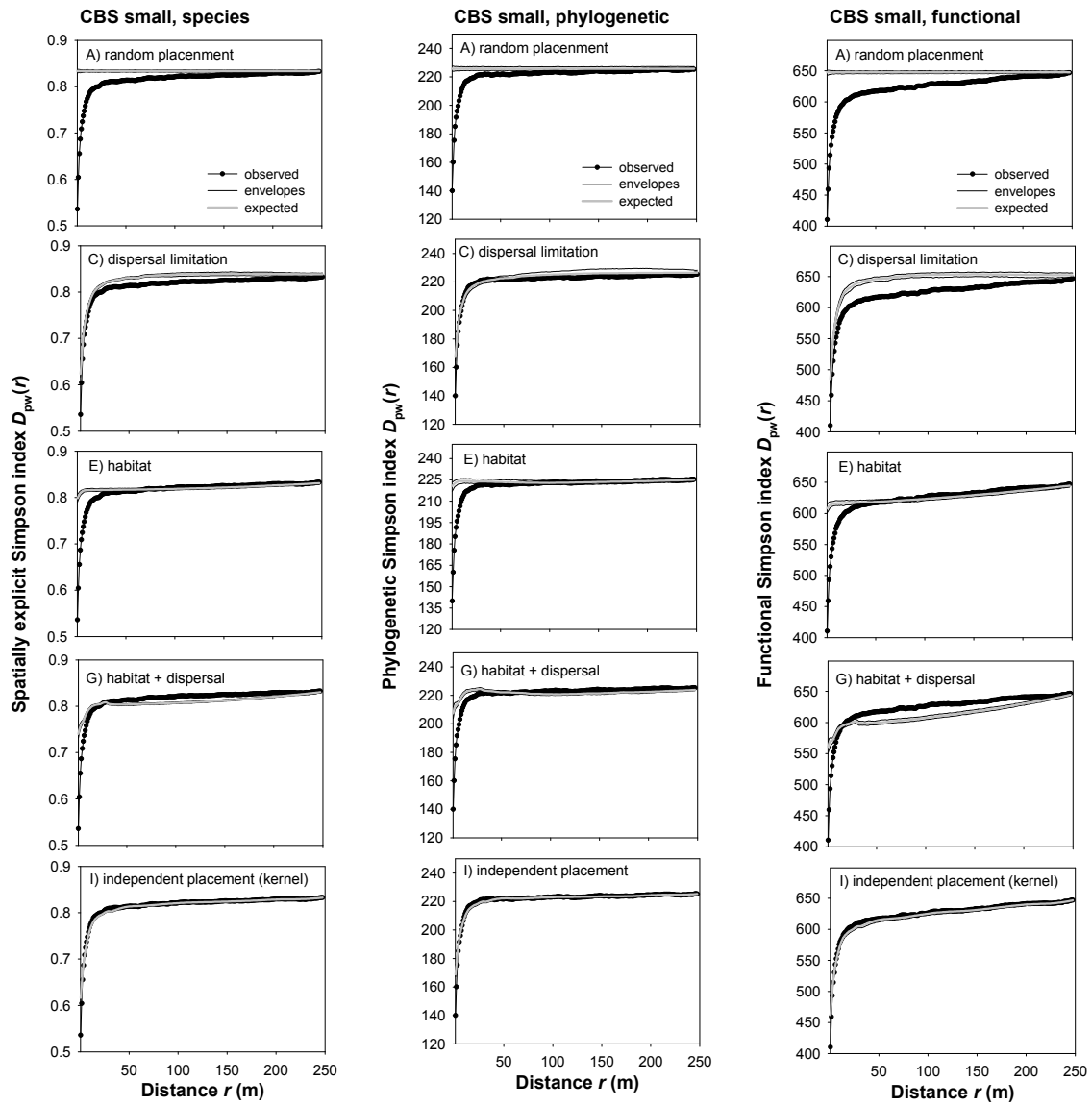


FIG. D4. Summary of results for small trees at the CBS forest.

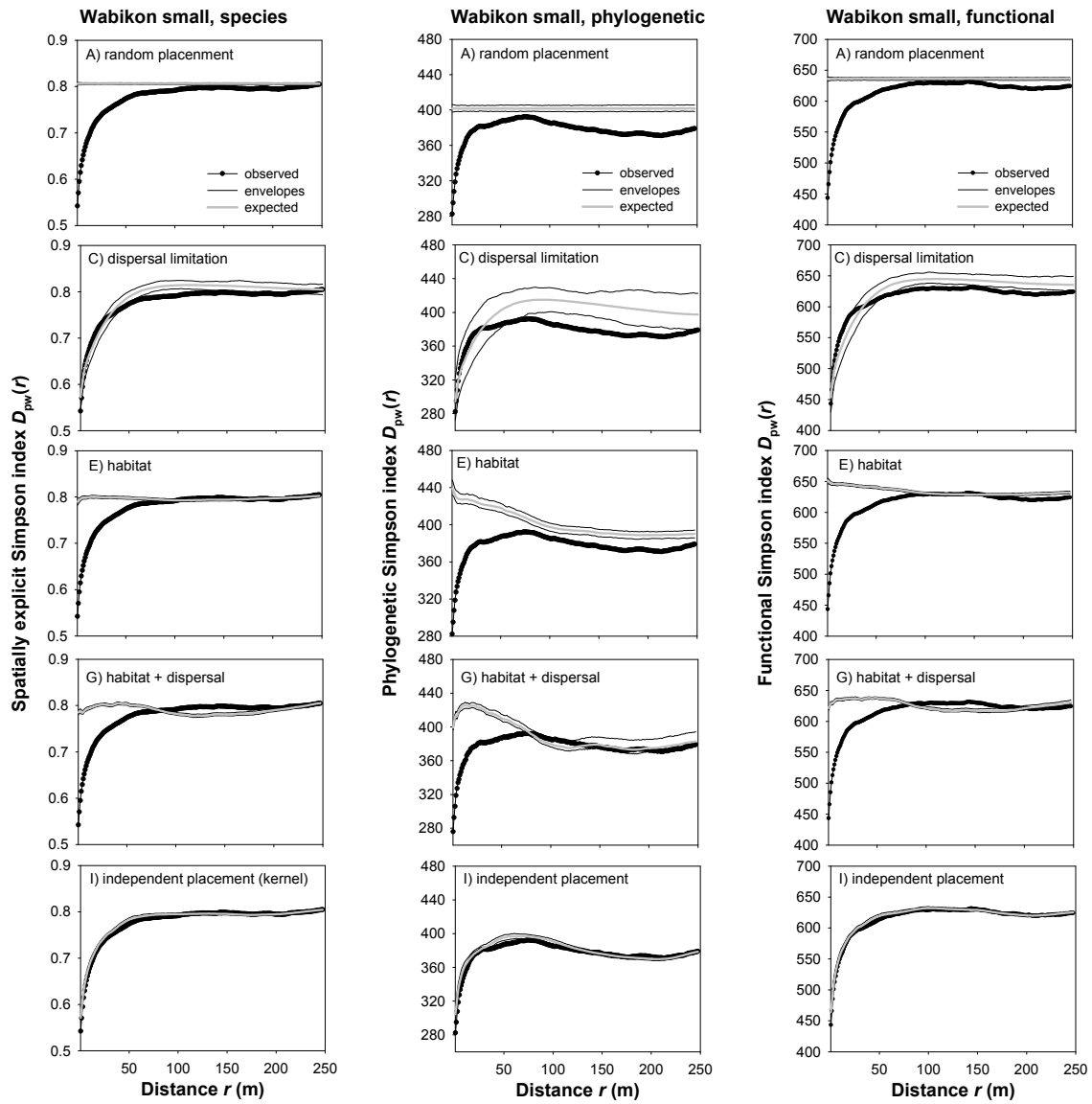


FIG. D5. Summary of results for small trees at the Wabikon forest.

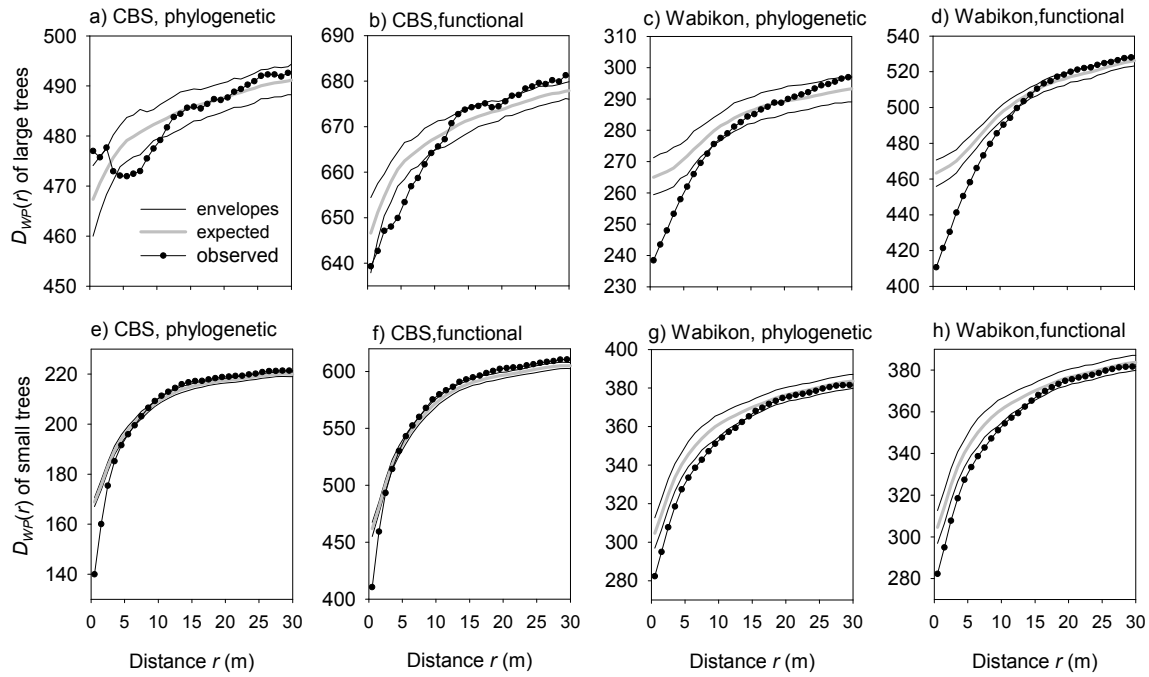


FIG. D6. Summary of results for the independent placement hypothesis at small distances of 1-30m. The gray line is the average beta diversity $D_{wp}(r)$ estimated from the 99 null communities corresponding to the independent placement hypothesis, the solid black lines are the minimal and maximal values of $D_{wp}(r)$ estimated from the 99 null communities and the closed disks are the observed $D_{wp}(r)$. The results show that two nearby individuals are on average more closely related than expected by independent placement.