Do priority effects outweigh environmental filtering in a guild of dominant freshwater macroinvertebrates? DOI: 10.1098/rspb.2018.0205

Appendix I – Data handling and model specification

1. Data processing to make models.

All data processing before constructing different models (described in the main text) was performed in R (R Core Team 2016) in order to ensure replicability. The data file contains the data which already excludes outlet points (all designated as point number 1 within a catchment, which is why such labeled points are lacking in the dataset). The "sampling bout" column was excluded from all analyses as there were other ways to refine the data while capturing this information; within the data file, information from sampling points is listed blockwise with the first sampling bout first, then a block of data from the second sampling bout, etc.

Total Nitrogen was excluded from the analysis because it was highly correlated with Total Phosphorus and thus redundant, and total organic carbon (TOC) was excluded for being highly correlated to dissolved organic carbon (DOC), and thus redundant. Two more land use variables were excluded from the point-level measures because these land use types had only surrounded the outlets and were zero for all other points.

```
> datatouse <- datatouse[,c(-10, -12, -30, -31)]
```

The estimates of abundance – which had been binned by orders of magnitude, refer to the list of variable names for information on this measure – were transformed to presence/absence information for analysis.

```
> datatouse$G..pulex.est[datatouse$G..pulex.est > 0] <- 1

> datatouse$G..fossarum.est[datatouse$G..fossarum.est > 0] <- 1

> datatouse$G..roeseli.est[datatouse$G..roeseli.est > 0] <- 1

> datatouse$G..pulex.est.prev[datatouse$G..pulex.est.prev > 0] <- 1

> datatouse$G..fossarum.est.prev[datatouse$G..fossarum.est.prev > 0] <- 1

> datatouse$G..roeseli.est.prev[datatouse$G..roeseli.est.prev > 0] <- 1
```

Data was subsetted to fit each model as follows:

S model, spatial random effects only using sampling bouts 2-4

Point and catchment identifiers were retained along with the presence and absence of all three species, but no other data was included in this model. Points where amphipod occurrence were not assessed (primarily due to the stream bed being dry) were excluded, and then the subset of points from the second to fourth sampling bouts was specified.

```
> data_random <- datatouse[,c(1,2,5,6,7)]
```

```
> data_random <- data_random [which(complete.cases(data_random)),]
```

```
> data_random24 <- data_random [112:390,]
```

For the ‘HMSC’ model (Ovaskainen *et al.* 2017), only a Y matrix (responses) and Π matrix (random effects) were needed.

```
> Ymatrix_S <- as.matrix(data_random24[,3:5])
```

```
> Pimatrix_S <- as.data.frame(data_random24[,1:2])
```

SP model, spatial random effects plus previous amphipod occurrence using sampling bouts 2-4

Point and catchment identifiers were retained along with the presence and absence of all three species at the current sampling bout, and the presence and absence of all three species at the previous sampling bout. Points where amphipod occurrence were not assessed in the current bout (primarily due to the stream bed being dry) were excluded. We used the complete case argument to exclude data from the first sampling bout, where data about amphipod occurrence at the previous sampling point by definition did not exist.

```
> data_amphi_only <- datatouse[,c(1,2,5,6,7,30,31,32)]
```

```
> data_amphi_only <- data_amphi_only[which(complete.cases(data_amphi_only)),]
```

For the ‘HMSC’ model, a Y matrix (responses) and Π matrix (random effects) were defined. The data on species occurrence at the previous sampling bout was placed into the covariate matrix X.

```
> Ymatrix_SP <- as.matrix(data_amphi_only[,3:5])
```

```
> Pimatrix_SP <- as.data.frame(data_amphi_only[,1:2])
```

```
> Xmatrix_SP <- as.matrix(data_amphi_only[,6:8])
```

SE model, spatial random effects plus environmental covariates using sampling bouts 2-4

The only variables excluded from this model were the information on previous occurrence of amphipod species. The dataset was reduced by only considering complete cases, because the ‘HMSC’ package does not handle NA’s in the covariate matrices.

```
> data_envonly <- datatouse[,c(-30, -31, -32)]
```

```
> data_envonly <- data_envonly[which(complete.cases(data_envonly)),]
```

For the ‘HMSC’ model, a Y matrix (responses) and Π matrix (random effects) were defined. The data on environmental conditions was placed into the covariate matrix X. The subset of points from the second to fourth sampling bouts was specified as the matrices were created.

```
> Ymatrix_SE <- as.matrix(data_envonly[108:367,5:7])

> Pimatrix_SE <- as.data.frame(data_envonly[108:367,1:2])

> Xmatrix_SE <- as.matrix(data_envonly[108:367,c(-1, -2, -5, -6, -7)])
```

Diversity measures (richness and Shannon diversity) were calculated using the ‘vegan’ package (Oksanen *et al.* 2012) to try to estimate habitat complexity, and these two variables were added to the X matrix before the model was run.

```
> Xhabitats <- Xmatrix_SE[,8:17]

> Shannonmicrohab <- diversity(Xhabitats, "shannon")

> habrichness <- specnumber(Xhabitats)

> Xmatrix_SE <- cbind(Xmatrix_SE, Shannonmicrohab, habrichness)
```

SPE model, spatial random effects plus previous amphipod occurrence and environmental covariates using sampling bouts 2-4

Point and catchment identifiers were retained along with the presence and absence of all three species at the current sampling bout, and the presence and absence of all three species at the previous sampling bout, and environmental data. We used the complete case argument to exclude data from the first sampling bout, where data about amphipod occurrence at the previous sampling point by definition did not exist. This further reduced the dataset considering that so many variables had to have recorded information for each sampling point and missing a value from any one of these variables would result in the point being excluded, however, it was also necessary the ‘HMSC’ package does not handle NA’s in the covariate matrices.

```
> data_manip <- datatouse[which(complete.cases(datatouse)),]
```

For the ‘HMSC’ model, a Y matrix (responses) and Π matrix (random effects) were defined. The data on environmental conditions and data on previous amphipod occurrence were both placed into the covariate matrix X.

```
> Ymatrix_SPE <- as.matrix(data_manip[,5:7])

> Pimatrix_SPE <- as.data.frame(data_manip[,1:2])

> Xmatrix_SPE <- as.matrix(data_manip[,c(-1,-2,-5,-6,-7)])
```

Diversity measures for habitat complexity were calculated and appended to the X matrix as described above.

SE_{Full} model, spatial random effects plus environmental covariates in all four sampling bouts

The only variables excluded from this model were the information on previous occurrence of amphipod species. The dataset was reduced by only considering complete cases, because the 'HMSC' package does not handle NA's in the covariate matrices.

```
> data_envonly <- datatouse[,c(-30, -31, -32)]
```

```
> data_envonly <- data_envonly[which(complete.cases(data_envonly)),]
```

For the 'HMSC' model, a Y matrix (responses) and Π matrix (random effects) were defined. The data on environmental conditions was placed into the covariate matrix X.

```
> Ymatrix_SEFull <- as.matrix(data_envonly[,5:7])
```

```
> Pimatrix_SEFull <- as.data.frame(data_envonly[,1:2])
```

```
> Xmatrix_SEFull <- as.matrix(data_envonly[,c(-1, -2, -5, -6, -7)])
```

Diversity measures for habitat complexity were calculated and appended to the X matrix as described above.

2. Model specification.

Model specification is described below for the *SPE* model, but all models are specified similarly so this structure could be adjusted by including only the relevant matrices. In all cases, data was scaled (centered and standardized) when they are formed into an HMSC data object. Because we are working with binary presence/absence data, the probit link is used in the underlying GLM framework of the model. We ran 200000 iterations of each model, with a burn-in of the first half of this (100000 iterations), and then thinned the posterior samples by a factor of 100 to retain 1000 samples.

```
> data_SPE <- as.HMSCdata(Y = Ymatrix_4SPE, X = Xmatrix_SPE, Random =
Pimatrix_SPE,  scaleX = TRUE, interceptX=FALSE)
```

```
> model_SPE <- hmsc(data_SPE, family = "probit", niter = 200000, nburn =
100000, thin = 100)
```

3. Comparison of results from all models.

Results from the *S*, *SPE*, and SE_{Full} models are presented in the main text. For comparison, The *SP* model using only spatial random effects and information about amphipod occurrence (n=256) explained 52% of the variation in the dataset, suggesting that this information was largely redundant with information about sampling location (which had explained 51% of the variation in a dataset of 390 observations). Adding environmental covariates (land use, water chemistry, and microhabitat) rather than prior occurrence information (the *SE* model, n=260) explained 65% of the variation in species occurrences. However, neither of these models explained as much variation as the *SPE* model, which had a Tjur's R^2 of 0.71.

Table S1. Proportion of variance explained by factors with strong directional effects (+ or -) on the occurrence of species in four different hierarchical joint species distribution models described above. Only factors having this strong effect (defined as the 95% central credible interval of the association between the factor and the species presence/absence being nonoverlapping with zero) for the given species in at least one of the models are included in the table. Factors without a strong directional effect for a given model are indicated with "n.s.", and factors not included in a given model are indicated by "N/A". The random effects associated with catchment and sampling point are included for reference for all species and models and highlighted in gray to differentiate them from the effects of measured covariates.

	SP model	*SE* model	*SPE* model	SE_{Full} model
(A) ***G. pulex***				
Catchment	0.452	0.453	0.501	0.445
Point	0.003	0.004	0.002	0.003
G. pulex previous presence (+)	0.005	N/A	0.020	N/A
Arable land at point (+)	n.s.	0.014	0.013	0.015
Area of leaves (-)	n.s.	0.014	0.012	0.017
Orchard at point (-)	n.s.	0.010	n.s.	n.s.
(B) ***G. fossarum***				
Catchment	0.297	0.224	0.001	0.026
Point	0.004	0.020	0.002	0.074
Latitude (+)	n.s.	n.s.	0.112	0.135
G. fossarum previous presence (+)	0.124	N/A	0.075	N/A
Orchard in catchment (+)	n.s.	n.s.	0.067	n.s.
Dissolved organic carbon (-)	n.s.	0.025	0.056	0.023
Previous drying (-)	n.s.	0.020	n.s.	0.018
Area of moss, algae, macrophytes (-)	n.s.	n.s.	n.s.	0.017
Area of leaves (+)	n.s.	0.018	n.s.	n.s.
(C) ***G. roeseli***				
Catchment	0.508	0.555	0.634	0.566
Point	0.001	0.001	0.001	0.001
G. pulex previous presence (+)	0.006	N/A	0.004	N/A
Industrial/commercial at point (+)	n.s.	0.005	0.003	0.003
Area of leaves (-)	n.s.	0.008	n.s.	n.s.

4. Results from SPE Model

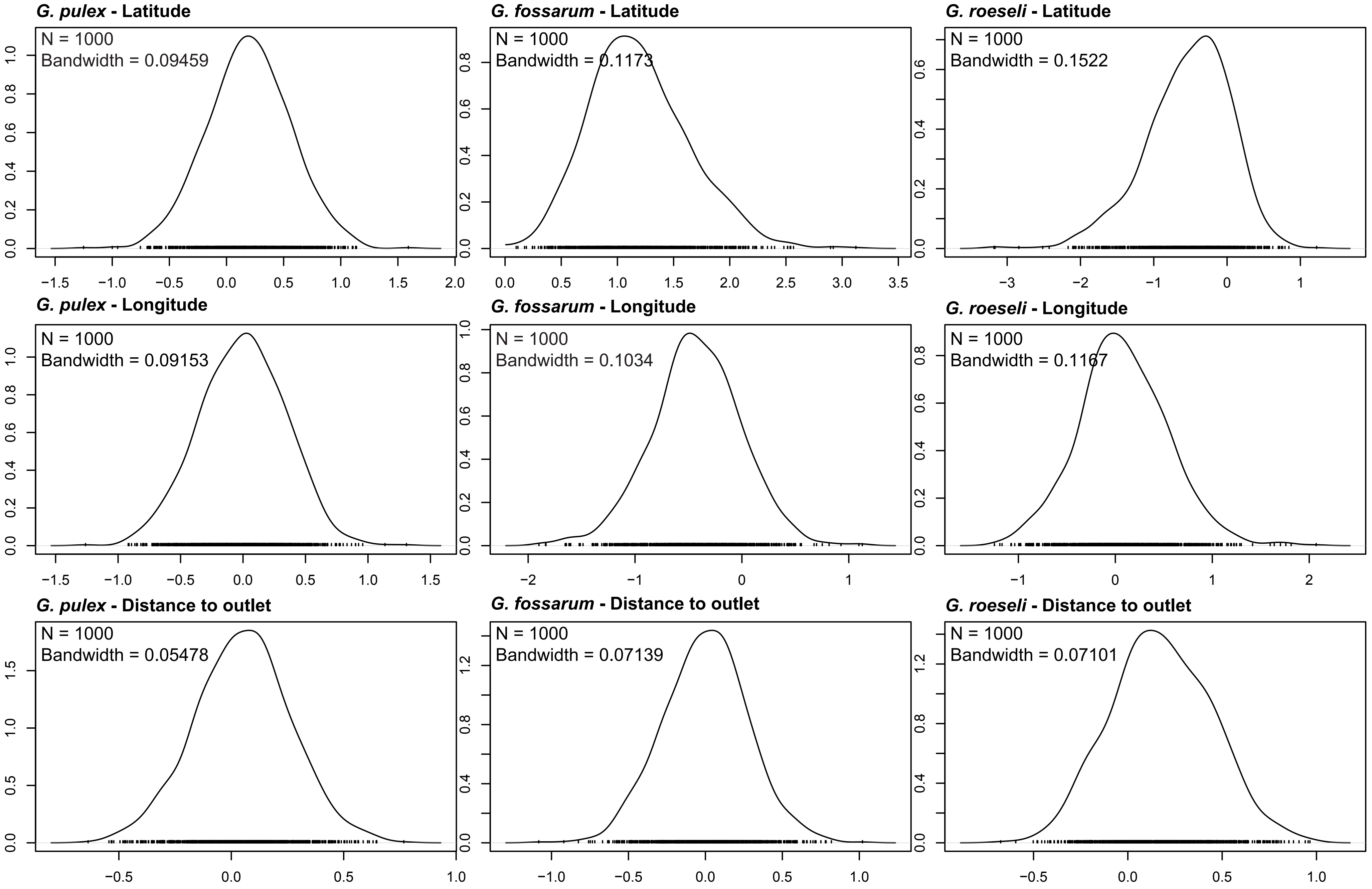
Figure S1 (following pages). Densities of the posterior distributions of associations between all explanator variables included in the 'SPE' model (described above) and the occurrence of the three amphipod species.

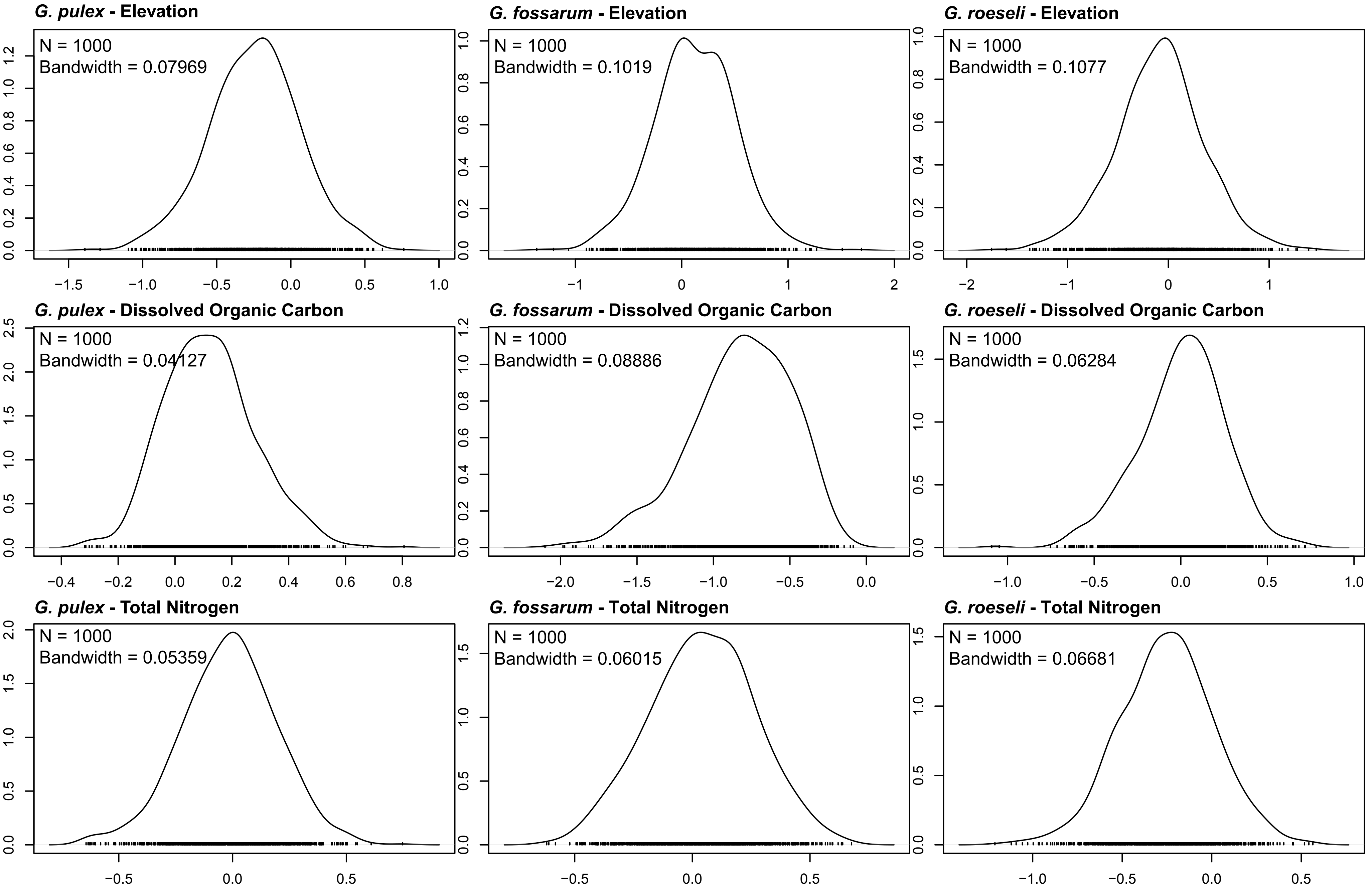
References

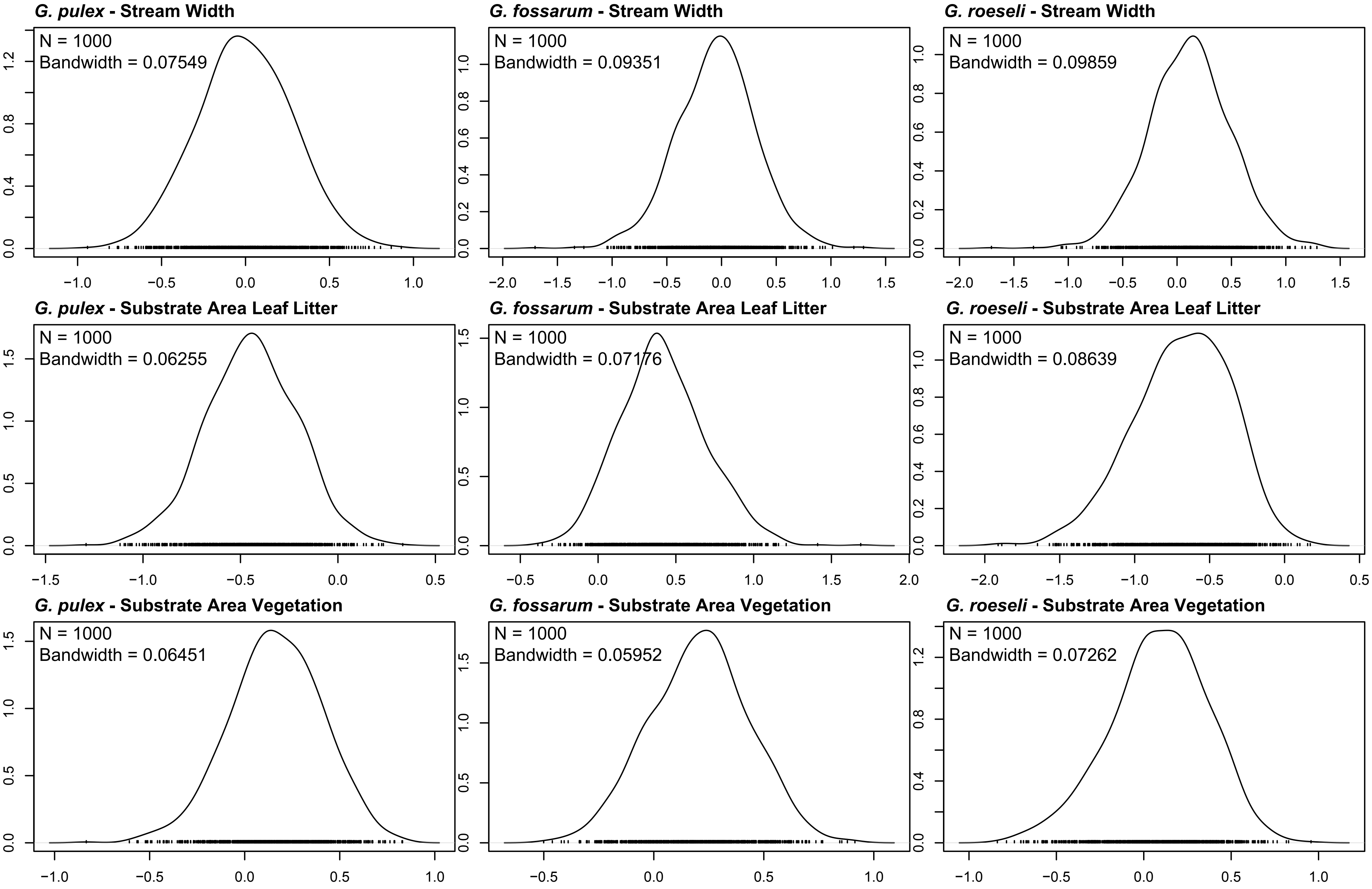
1.Oksanen, J., Blanchet, F.G., Kindt, R., Legendre, P., Minchin, P.R., O'Hara, R.B., *et al.* (2012). vegan: Community Ecology Package

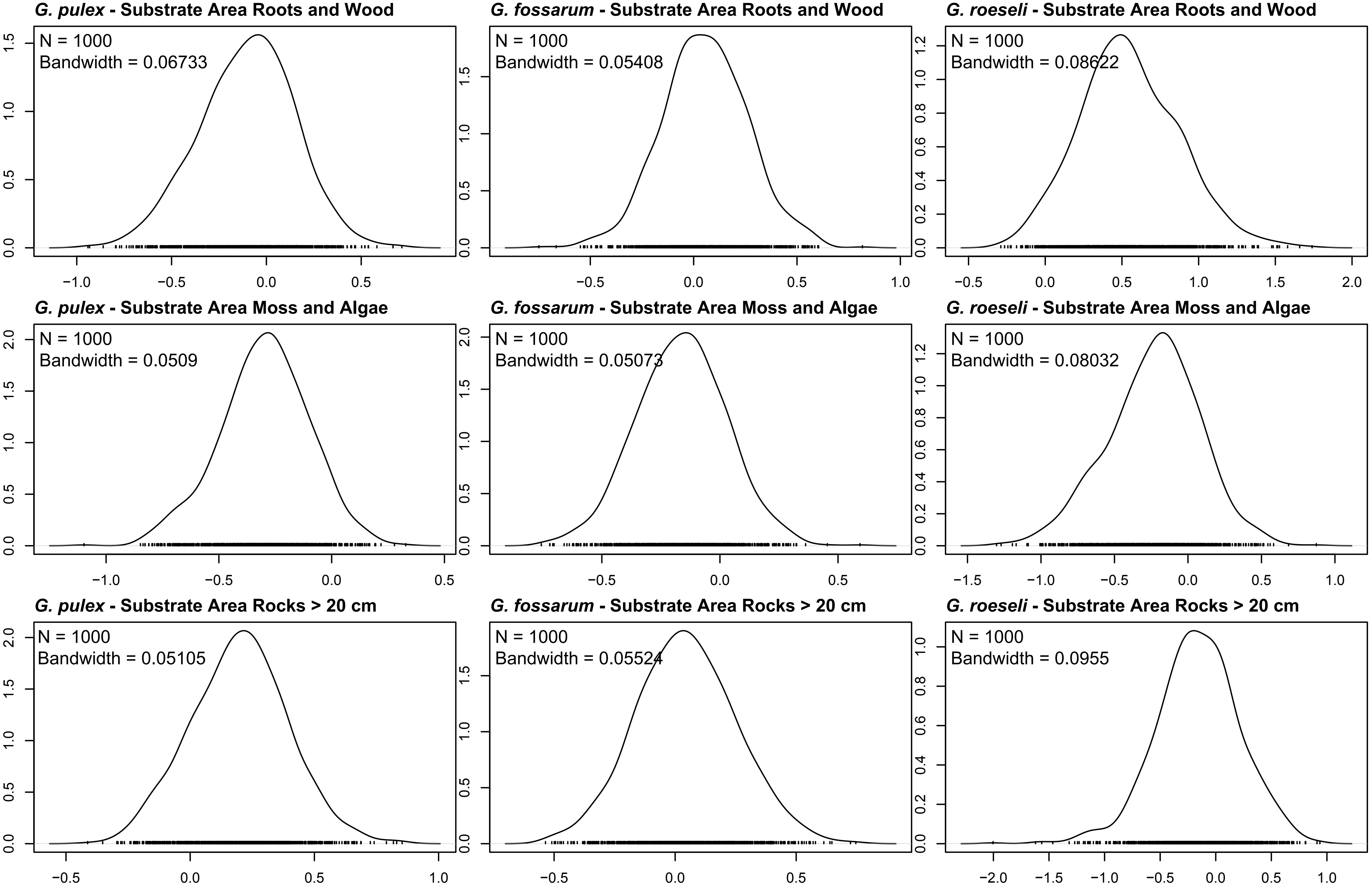
2.Ovaskainen, O., Tikhonov, G., Norberg, A., Blanchet, F.G., Duan, L., Dunson, D., *et al.* (2017). How to make more out of community data ? A conceptual framework and its implementation as models and software. *Ecol. Lett.*, 20, 561–576

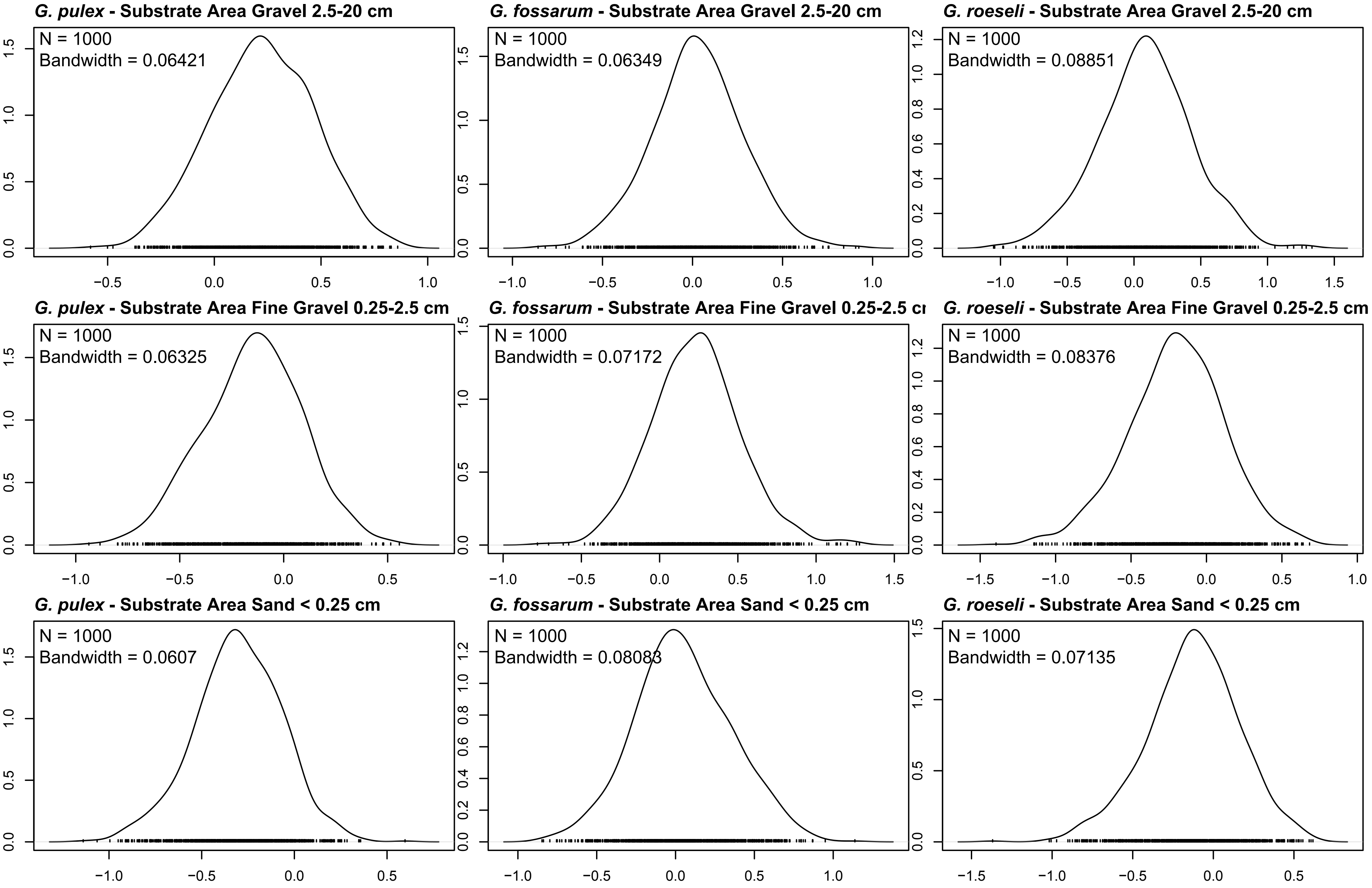
3.R Core Team. (2016). R: A Language and Environment for Statistical Computing


G. pulex - Latitude
N = 1000
Bandwidth = 0.09459
G. fossarum - Latitude
N = 1000
Bandwidth = 0.1173
G. roeseli - Latitude
N = 1000
Bandwidth = 0.1522
G. pulex - Longitude
N = 1000
Bandwidth = 0.09153
G. fossarum - Longitude
N = 1000
Bandwidth = 0.1034
G. roeseli - Longitude
N = 1000
Bandwidth = 0.1167
G. pulex - Distance to outlet
N = 1000
Bandwidth = 0.05478
G. fossarum - Distance to outlet
N = 1000
Bandwidth = 0.07139
G. roeseli - Distance to outlet
N = 1000
Bandwidth = 0.07101
0.0
0.2
0.4
0.6
0.8
1.0
1.5
0.5
1.2
−1.5
−1.0
−0.5
2.0
2.5
3.0
3.5
−3
−2
−1
0
1
2

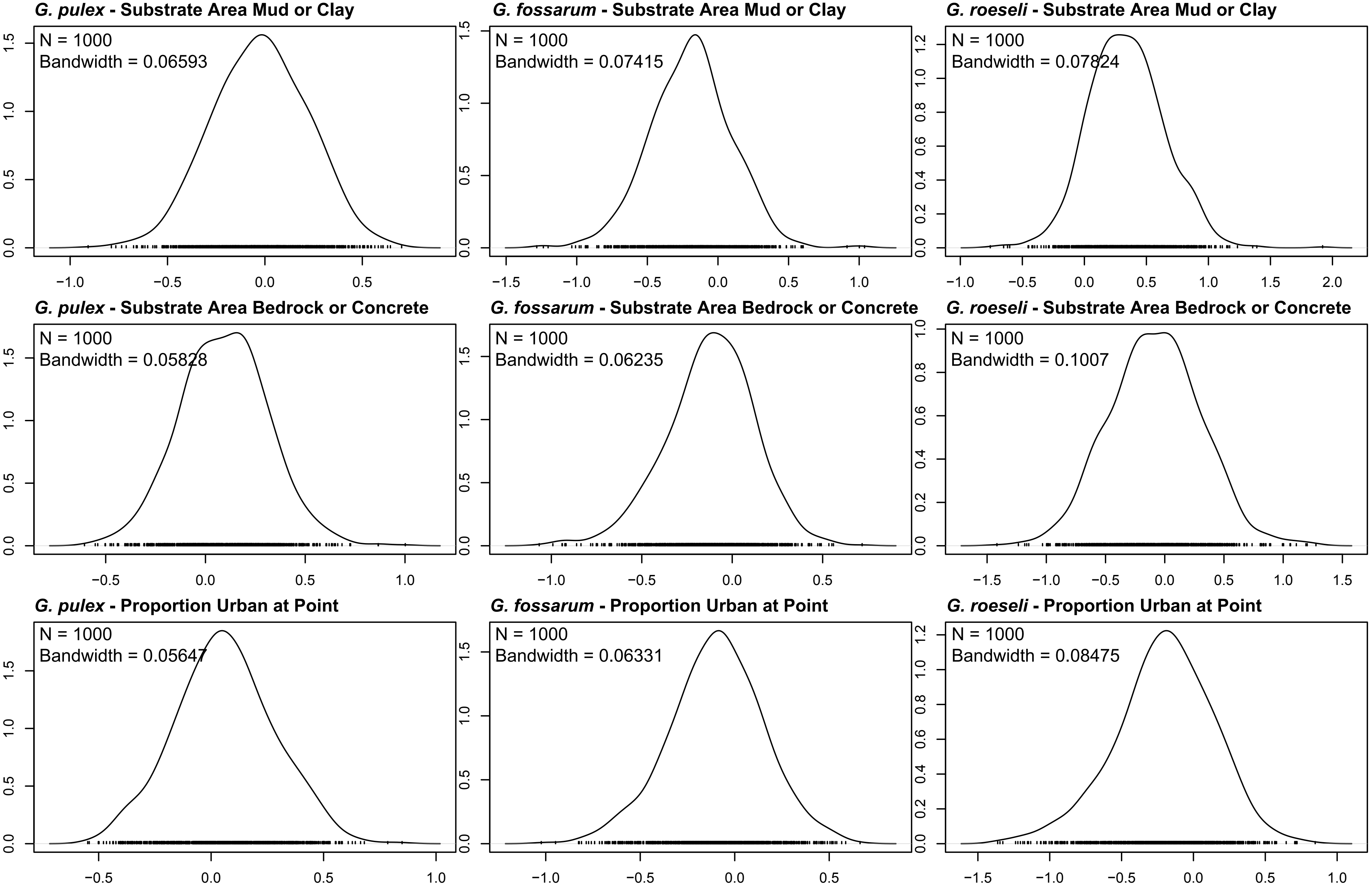

G. pulex - Elevation
N = 1000
Bandwidth = 0.07969
0.0
0.2
0.4
0.6
0.8
1.0
1.2
−1.5
−1.0
−0.5
0.0
0.5
1.0
G. fossarum - Elevation
N = 1000
Bandwidth = 0.1019
0.0
0.2
0.4
0.6
0.8
1.0
−1
0
1
2
G. roeseli - Elevation
N = 1000
Bandwidth = 0.1077
0.0
0.2
0.4
0.6
0.8
1.0
−2
−1
0
1
G. pulex - Dissolved Organic Carbon
N = 1000
Bandwidth = 0.04127
0.0
0.5
1.0
1.5
2.0
2.5
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
G. fossarum - Dissolved Organic Carbon
N = 1000
Bandwidth = 0.08886
0.0
0.2
0.4
0.6
0.8
1.0
1.2
−2.0
−1.5
−1.0
−0.5
0.0
G. roeseli - Dissolved Organic Carbon
N = 1000
Bandwidth = 0.06284
0.0
0.5
1.0
1.5
−1.0
−0.5
0.0
0.5
1.0
G. pulex - Total Nitrogen
N = 1000
Bandwidth = 0.05359
0.0
0.5
1.0
1.5
2.0
−0.5
0.0
0.5
G. fossarum - Total Nitrogen
N = 1000
Bandwidth = 0.06015
0.0
0.5
1.0
1.5
−0.5
0.0
0.5
G. roeseli - Total Nitrogen
N = 1000
Bandwidth = 0.06681
0.0
0.5
1.0
1.5
−1.0
−0.5
0.0
0.5


G. pulex - Stream Width
N = 1000
Bandwidth = 0.07549
0.0
0.4
0.8
1.2
−1.0
−0.5
0.0
0.5
1.0
G. fossarum - Stream Width
N = 1000
Bandwidth = 0.09351
0.0
0.2
0.4
0.6
0.8
1.0
−2.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
G. roeseli - Stream Width
N = 1000
Bandwidth = 0.09859
0.0
0.2
0.4
0.6
0.8
1.0
−2.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
G. pulex - Substrate Area Leaf Litter
N = 1000
Bandwidth = 0.06255
0.0
0.5
1.0
1.5
−1.5
−1.0
−0.5
0.0
0.5
G. fossarum - Substrate Area Leaf Litter
N = 1000
Bandwidth = 0.07176
0.0
0.5
1.0
1.5
−0.5
0.0
0.5
1.0
1.5
2.0
G. roeseli - Substrate Area Leaf Litter
N = 1000
Bandwidth = 0.08639
0.0
0.2
0.4
0.6
0.8
1.0
−2.0
−1.5
−1.0
−0.5
0.0
0.5
G. pulex - Substrate Area Vegetation
N = 1000
Bandwidth = 0.06451
0.0
0.5
1.0
1.5
−1.0
−0.5
0.0
0.5
1.0
G. fossarum - Substrate Area Vegetation
N = 1000
Bandwidth = 0.05952
0.0
0.5
1.0
1.5
−0.5
0.0
0.5
1.0
G. roeseli - Substrate Area Vegetation
N = 1000
Bandwidth = 0.07262
0.0
0.4
0.8
1.2
−1.0
−0.5
0.0
0.5
1.0


G. pulex - Substrate Area Roots and Wood
N = 1000
Bandwidth = 0.06733
0.0
0.5
1.0
1.5
−1.0
−0.5
0.0
0.5
G. fossarum - Substrate Area Roots and Wood
N = 1000
Bandwidth = 0.05408
0.0
0.5
1.0
1.5
−0.5
0.0
0.5
1.0
G. roeseli - Substrate Area Roots and Wood
N = 1000
Bandwidth = 0.08622
0.0
0.2
0.4
0.6
0.8
1.0
1.2
−0.5
0.0
0.5
1.0
1.5
2.0
G. pulex - Substrate Area Moss and Algae
N = 1000
Bandwidth = 0.0509
0.0
0.5
1.0
1.5
2.0
−1.0
−0.5
0.0
0.5
G. fossarum - Substrate Area Moss and Algae
N = 1000
Bandwidth = 0.05073
0.0
0.5
1.0
1.5
2.0
−0.5
0.0
0.5
G. roeseli - Substrate Area Moss and Algae
N = 1000
Bandwidth = 0.08032
0.0
0.2
0.4
0.6
0.8
1.0
1.2
−1.5
−1.0
−0.5
0.0
0.5
1.0
G. pulex - Substrate Area Rocks > 20 cm
N = 1000
Bandwidth = 0.05105
0.0
0.5
1.0
1.5
2.0
−0.5
0.0
0.5
1.0
G. fossarum - Substrate Area Rocks > 20 cm
N = 1000
Bandwidth = 0.05524
0.0
0.5
1.0
1.5
−0.5
0.0
0.5
G. roeseli - Substrate Area Rocks > 20 cm
N = 1000
Bandwidth = 0.0955
0.0
0.2
0.4
0.6
0.8
1.0
−2.0
−1.5
−1.0
−0.5
0.0
0.5
1.0



G. pulex - Substrate Area Gravel 2.5-20 cm
N = 1000
Bandwidth = 0.06421
0.0
0.5
1.0
1.5
-0.5
0.0
0.5
1.0
G. fossarum - Substrate Area Gravel 2.5-20 cm
N = 1000
Bandwidth = 0.06349
0.0
0.5
1.0
1.5
-1.0
-0.5
0.0
0.5
1.0
G. roeseli - Substrate Area Gravel 2.5-20 cm
N = 1000
Bandwidth = 0.08851
0.0
0.2
0.4
0.6
0.8
1.0
1.2
-1.0
-0.5
0.0
0.5
1.0
1.5
G. pulex - Substrate Area Fine Gravel 0.25-2.5 cm
N = 1000
Bandwidth = 0.06325
0.0
0.5
1.0
1.5
-1.0
-0.5
0.0
0.5
G. fossarum - Substrate Area Fine Gravel 0.25-2.5 c
N = 1000
Bandwidth = 0.07172
0.0
0.5
1.0
1.5
-1.0
-0.5
0.0
0.5
1.0
1.5
G. roeseli - Substrate Area Fine Gravel 0.25-2.5 cm
N = 1000
Bandwidth = 0.08376
0.0
0.2
0.4
0.6
0.8
1.0
1.2
-1.5
-1.0
-0.5
0.0
0.5
1.0
G. pulex - Substrate Area Sand < 0.25 cm
N = 1000
Bandwidth = 0.0607
0.0
0.5
1.0
1.5
-1.0
-0.5
0.0
0.5
G. fossarum - Substrate Area Sand < 0.25 cm
N = 1000
Bandwidth = 0.08083
0.0
0.2
0.4
0.6
0.8
1.0
1.2
-1.0
-0.5
0.0
0.5
1.0
G. roeseli - Substrate Area Sand < 0.25 cm
N = 1000
Bandwidth = 0.07135
0.0
0.5
1.0
1.5
-1.5
-1.0
-0.5
0.0
0.5



G. pulex **- Substrate Area Mud or Clay**

G. fossarum **- Substrate Area Mud or Clay**

G. roeseli **- Substrate Area Mud or Clay**

G. pulex **- Substrate Area Bedrock or Concrete**

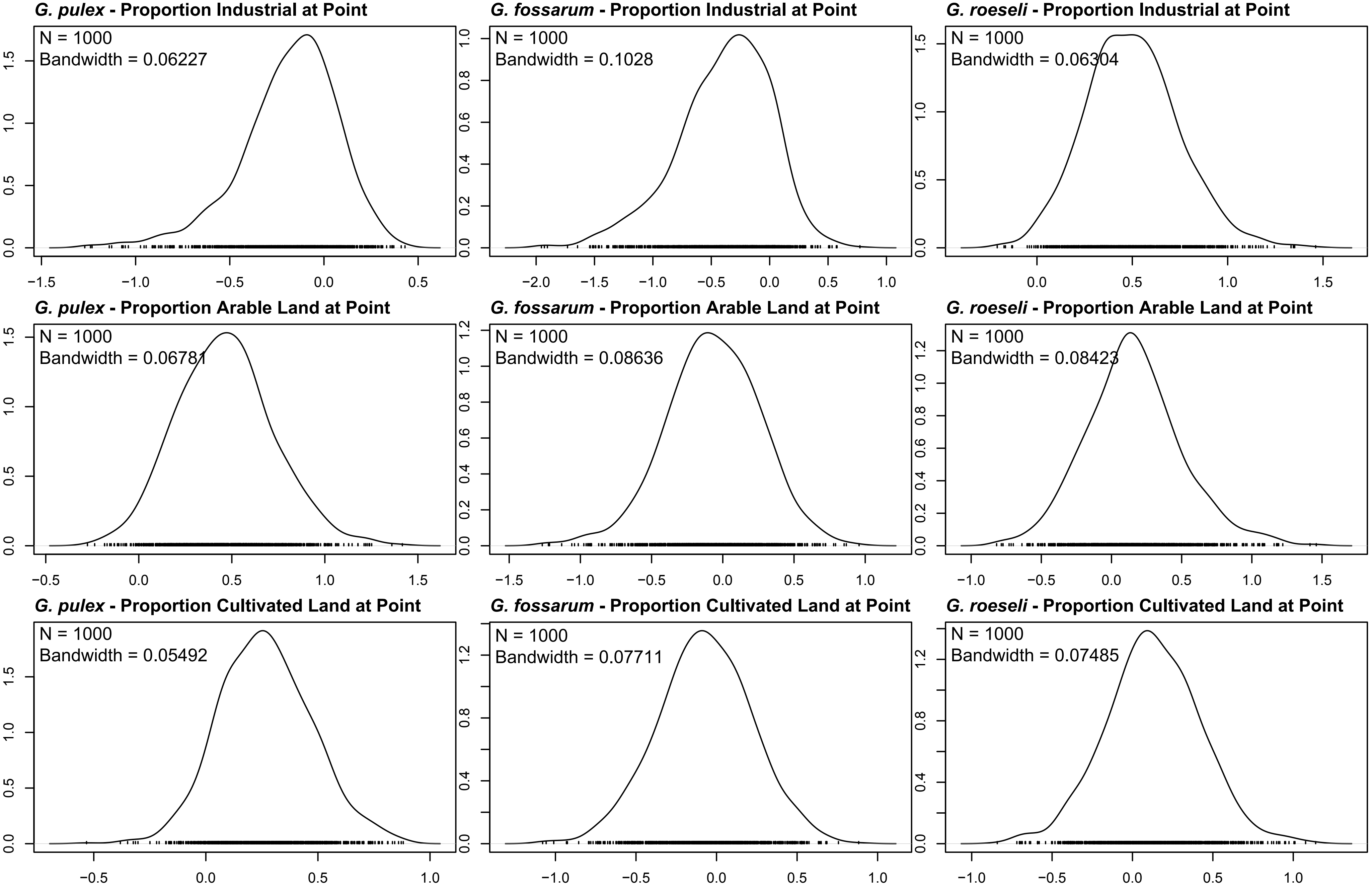
G. fossarum **- Substrate Area Bedrock or Concrete**

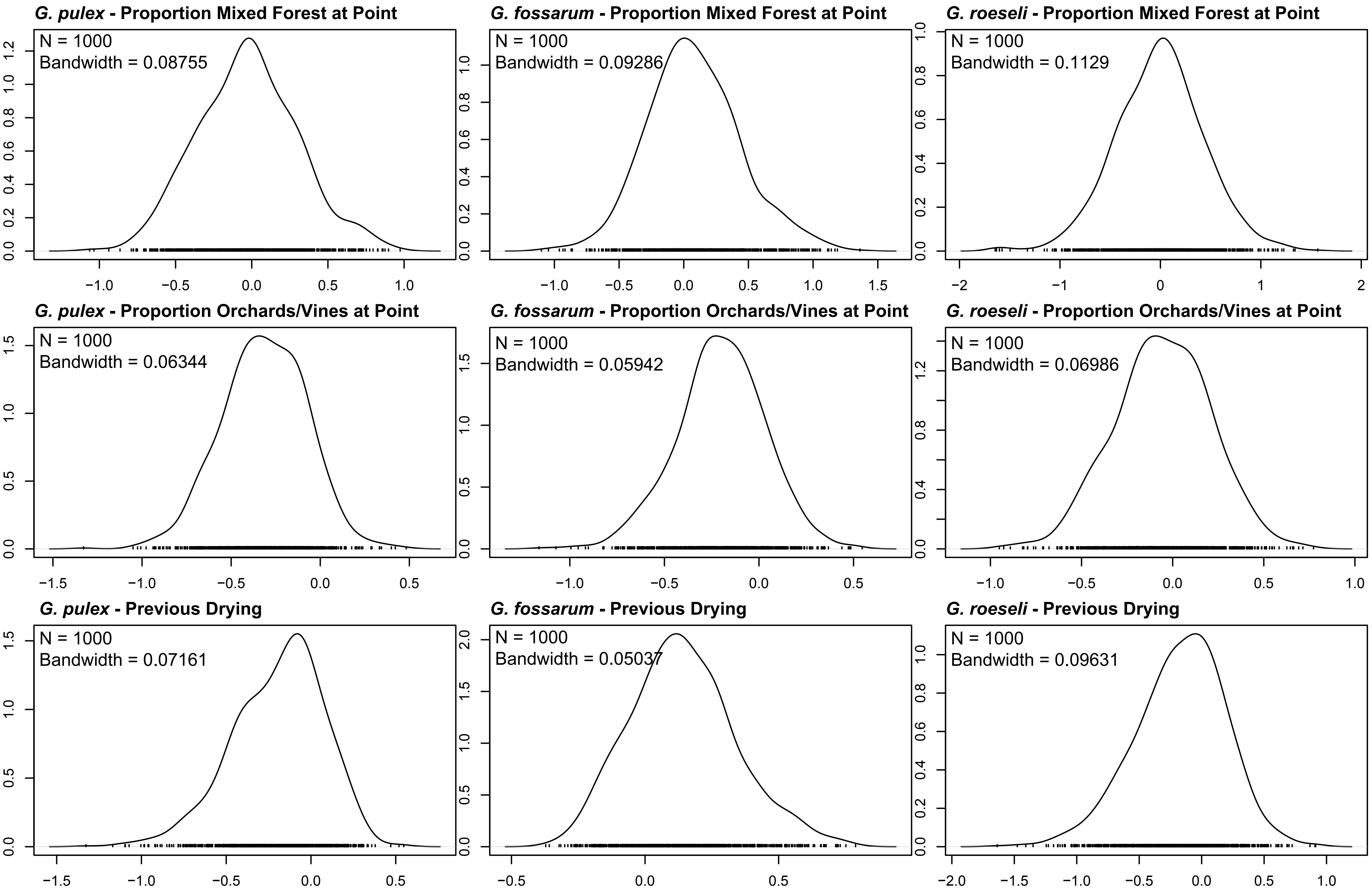
G. roeseli **- Substrate Area Bedrock or Concrete**

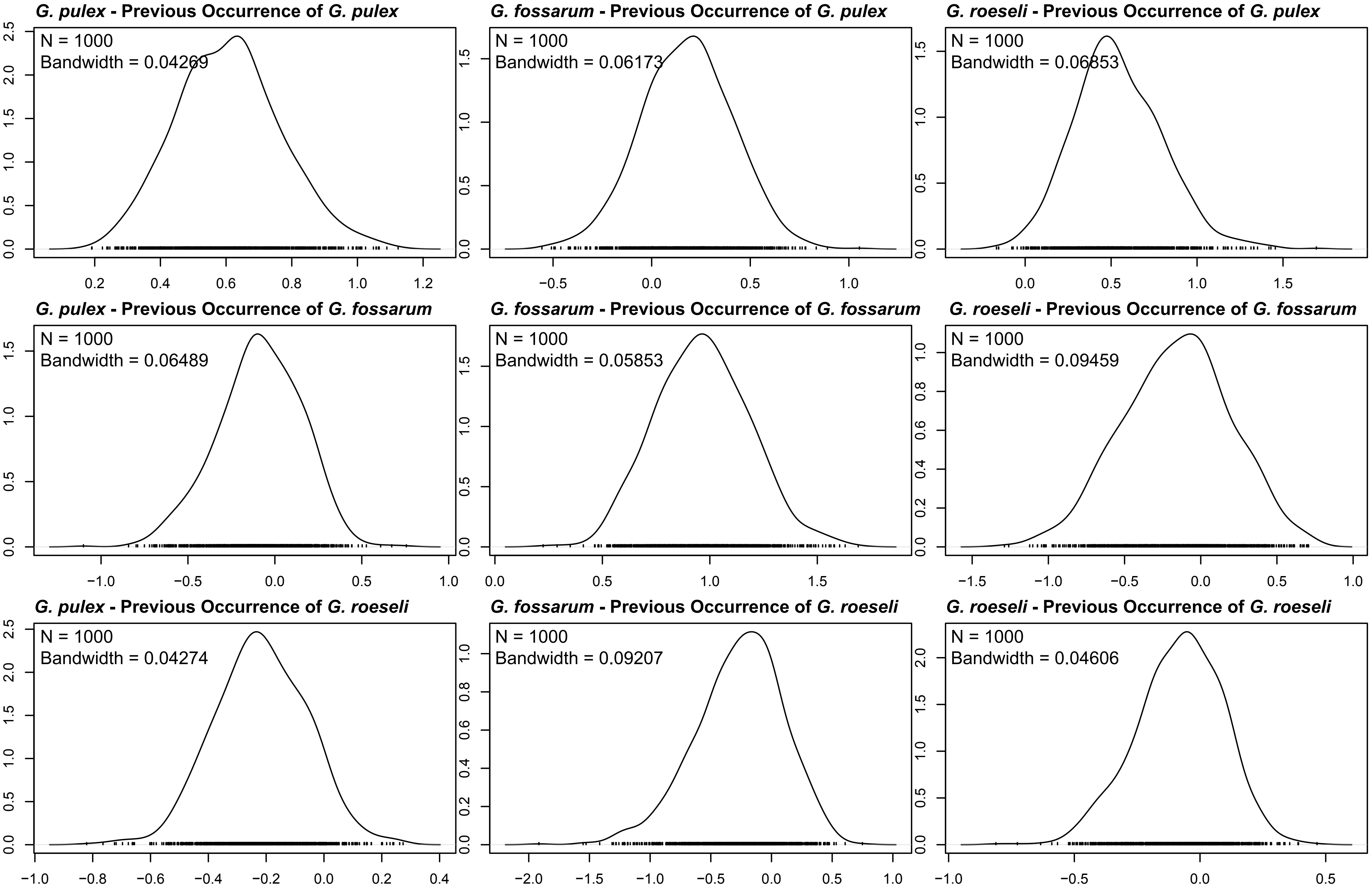
G. pulex **- Proportion Urban at Point**

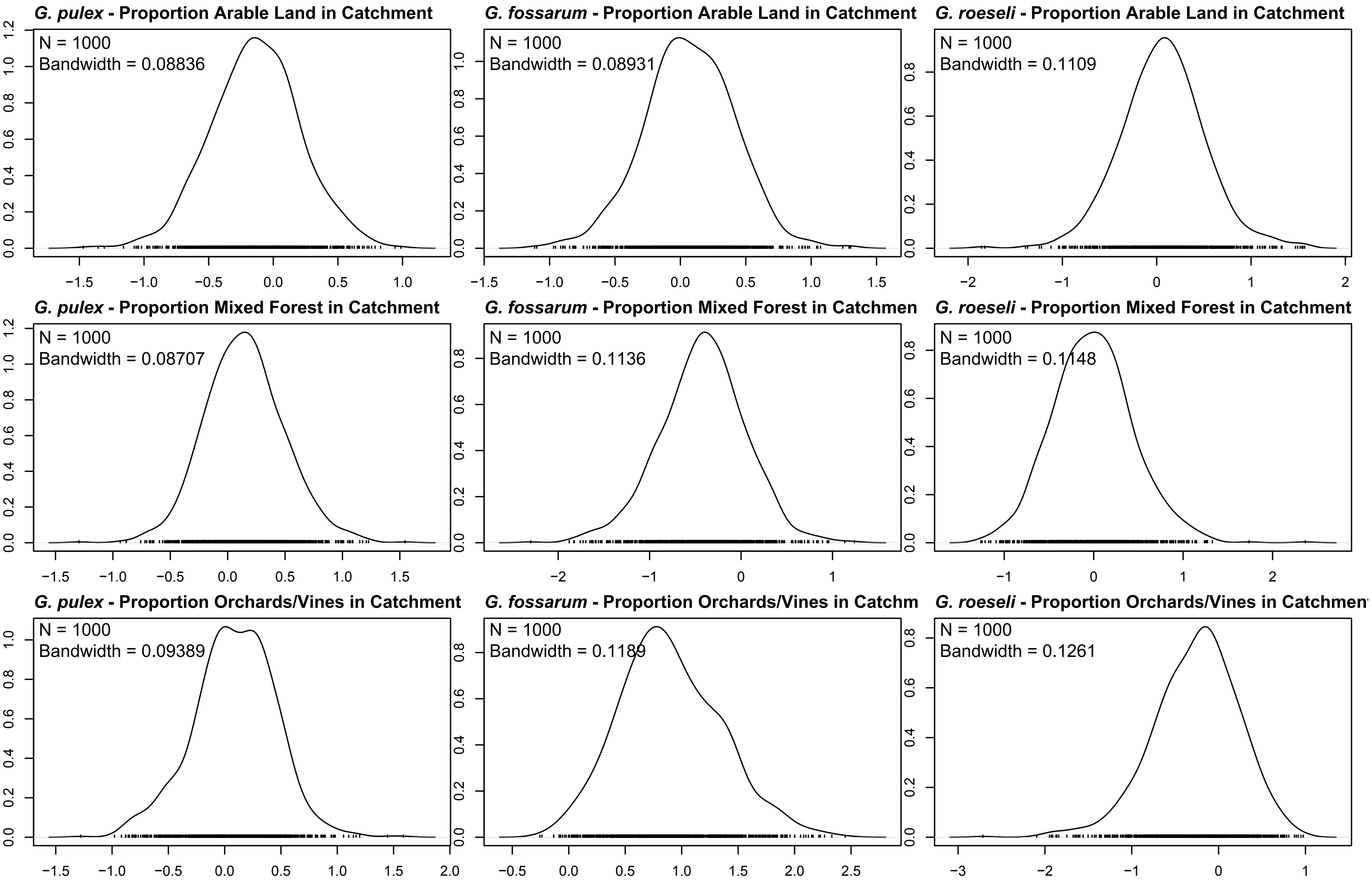
G. fossarum **- Proportion Urban at Point**

G. roeseli **- Proportion Urban at Point**


G. pulex - Proportion Industrial at Point
N = 1000
Bandwidth = 0.06227
G. fossarum - Proportion Industrial at Point
N = 1000
Bandwidth = 0.1028
G. roeseli - Proportion Industrial at Point
N = 1000
Bandwidth = 0.06304
G. pulex - Proportion Arable Land at Point
N = 1000
Bandwidth = 0.06781
G. fossarum - Proportion Arable Land at Point
N = 1000
Bandwidth = 0.08636
G. roeseli - Proportion Arable Land at Point
N = 1000
Bandwidth = 0.08423
G. pulex - Proportion Cultivated Land at Point
N = 1000
Bandwidth = 0.05492
G. fossarum - Proportion Cultivated Land at Point
N = 1000
Bandwidth = 0.07711
G. roeseli - Proportion Cultivated Land at Point
N = 1000
Bandwidth = 0.07485


G. pulex - Proportion Mixed Forest at Point
N = 1000
Bandwidth = 0.08755
0.0
0.2
0.4
0.6
0.8
1.0
1.2
−1.0
−0.5
0.0
0.5
1.0
G. fossarum - Proportion Mixed Forest at Point
N = 1000
Bandwidth = 0.09286
0.0
0.2
0.4
0.6
0.8
1.0
−1.0
−0.5
0.0
0.5
1.0
1.5
G. roeseli - Proportion Mixed Forest at Point
N = 1000
Bandwidth = 0.1129
0.0
0.2
0.4
0.6
0.8
1.0
−2
−1
0
1
2
G. pulex - Proportion Orchards/Vines at Point
N = 1000
Bandwidth = 0.06344
0.0
0.5
1.0
1.5
−1.5
−1.0
−0.5
0.0
0.5
G. fossarum - Proportion Orchards/Vines at Point
N = 1000
Bandwidth = 0.05942
0.0
0.5
1.0
1.5
−1.0
−0.5
0.0
0.5
G. roeseli - Proportion Orchards/Vines at Point
N = 1000
Bandwidth = 0.06986
0.0
0.4
0.8
1.2
−1.0
−0.5
0.0
0.5
1.0
G. pulex - Previous Drying
N = 1000
Bandwidth = 0.07161
0.0
0.5
1.0
1.5
−1.5
−1.0
−0.5
0.0
0.5
G. fossarum - Previous Drying
N = 1000
Bandwidth = 0.05037
0.0
0.5
1.0
1.5
2.0
−0.5
0.0
0.5
G. roeseli - Previous Drying
N = 1000
Bandwidth = 0.09631
0.0
0.2
0.4
0.6
0.8
1.0
−2.0
−1.5
−1.0
−0.5
0.0
0.5
1.0


G. pulex - Previous Occurrence of G. pulex
N = 1000
Bandwidth = 0.04269
0.0 0.5 1.0 1.5 2.0 2.5
0.2 0.4 0.6 0.8 1.0 1.2
G. fossarum - Previous Occurrence of G. pulex
N = 1000
Bandwidth = 0.06173
0.0 0.5 1.0 1.5
−0.5 0.0 0.5 1.0
G. roeseli - Previous Occurrence of G. pulex
N = 1000
Bandwidth = 0.06853
0.0 0.5 1.0 1.5
0.0 0.5 1.0 1.5
G. pulex - Previous Occurrence of G. fossarum
N = 1000
Bandwidth = 0.06489
0.0 0.5 1.0 1.5
−1.0 −0.5 0.0 0.5 1.0
G. fossarum - Previous Occurrence of G. fossarum
N = 1000
Bandwidth = 0.05853
0.0 0.5 1.0 1.5
0.0 0.5 1.0 1.5
G. roeseli - Previous Occurrence of G. fossarum
N = 1000
Bandwidth = 0.09459
0.0 0.2 0.4 0.6 0.8 1.0
−1.5 −1.0 −0.5 0.0 0.5 1.0
G. pulex - Previous Occurrence of G. roeseli
N = 1000
Bandwidth = 0.04274
0.0 0.5 1.0 1.5 2.0 2.5
−1.0 −0.8 −0.6 −0.4 −0.2 0.0 0.2 0.4
G. fossarum - Previous Occurrence of G. roeseli
N = 1000
Bandwidth = 0.09207
0.0 0.2 0.4 0.6 0.8 1.0
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
G. roeseli - Previous Occurrence of G. roeseli
N = 1000
Bandwidth = 0.04606
0.0 0.5 1.0 1.5 2.0
−1.0 −0.5 0.0 0.5


G. pulex **- Proportion Arable Land in Catchment**

G. fossarum **- Proportion Arable Land in Catchment**

G. roeseli **- Proportion Arable Land in Catchment**

G. pulex **- Proportion Mixed Forest in Catchment**

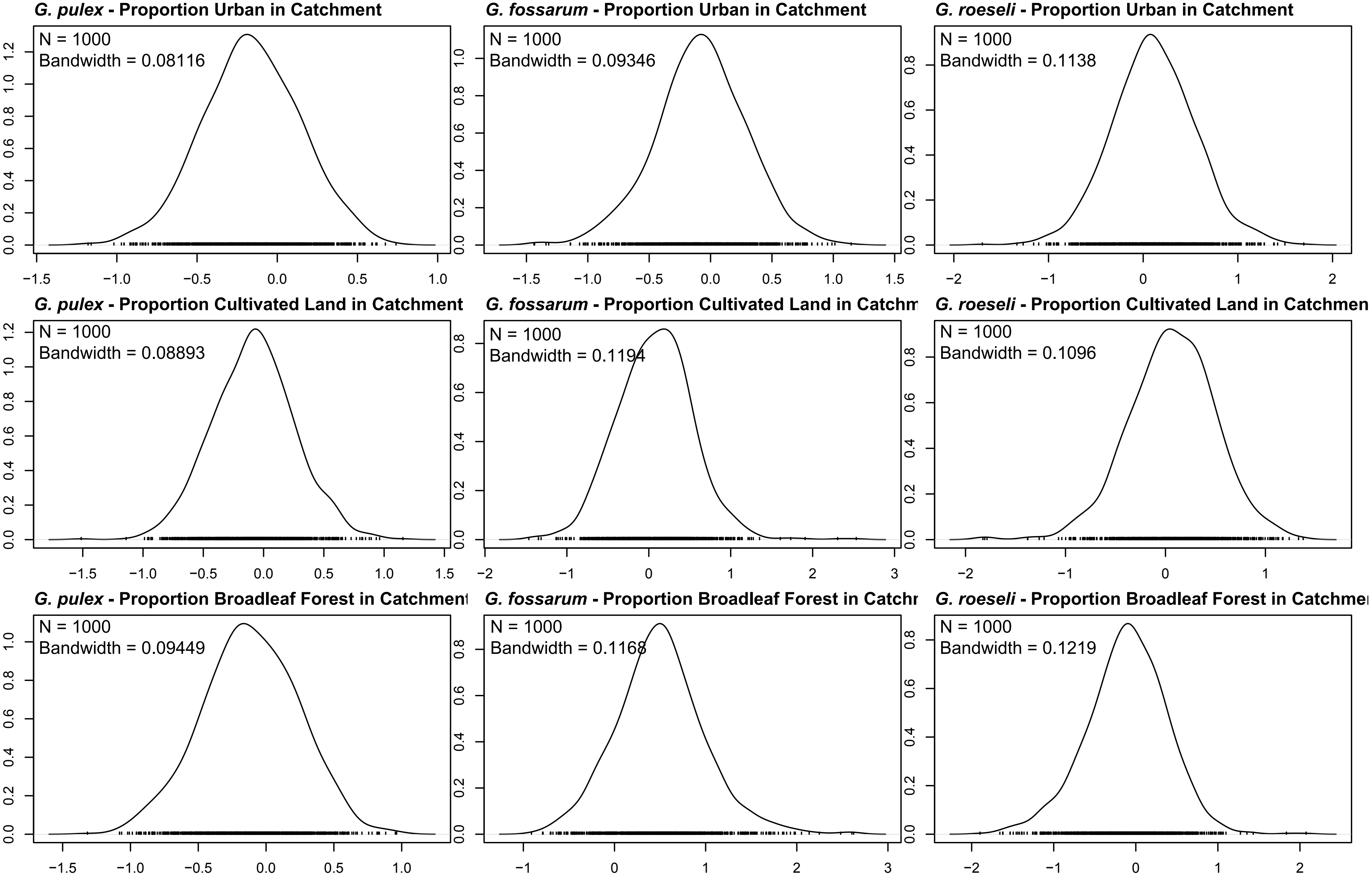
G. fossarum **- Proportion Mixed Forest in Catchmen**

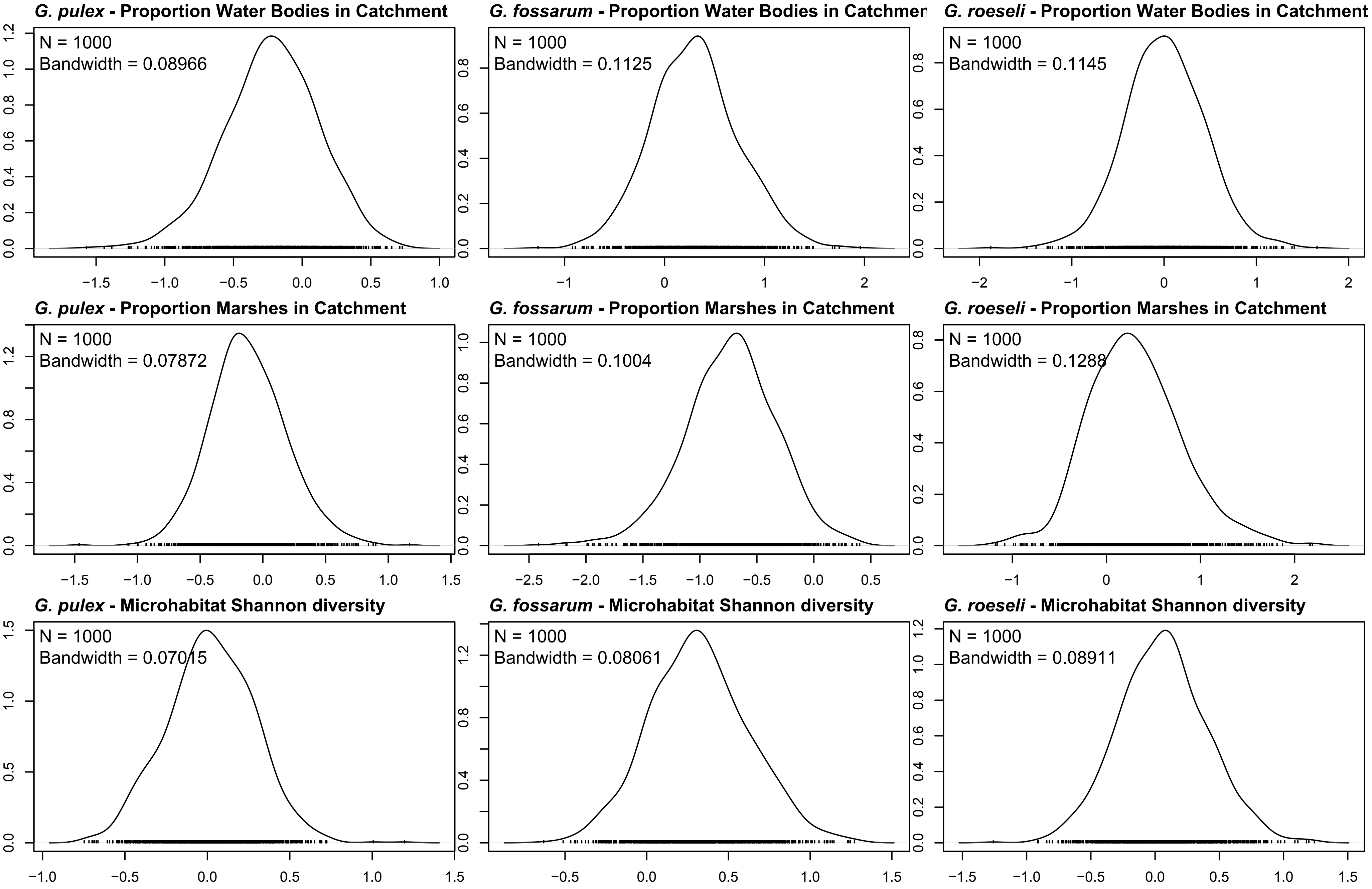
G. roeseli **- Proportion Mixed Forest in Catchment**

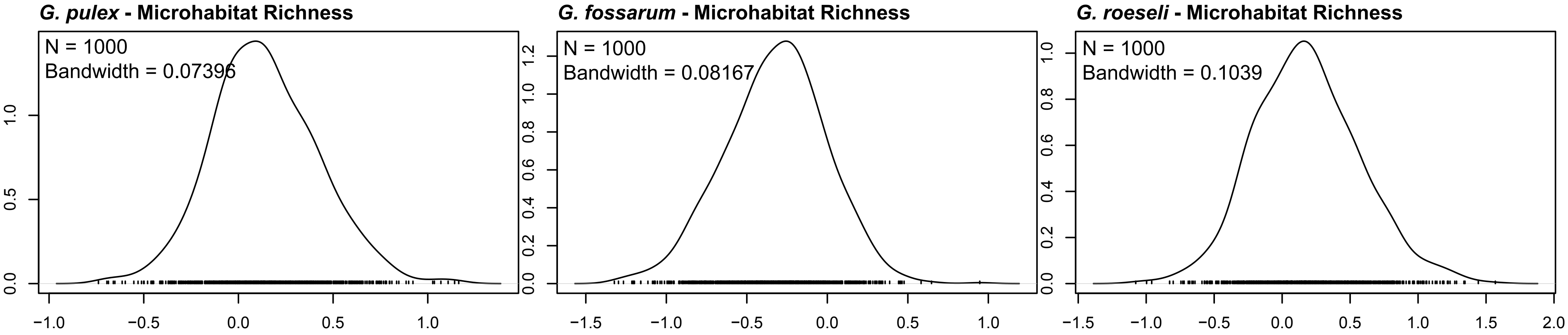
G. pulex **- Proportion Orchards/Vines in Catchment**

G. fossarum **- Proportion Orchards/Vines in Catchm**

G. roeseli **- Proportion Orchards/Vines in Catchmen**


G. pulex - Proportion Urban in Catchment
N = 1000
Bandwidth = 0.08116
0.0
0.2
0.4
0.6
0.8
1.0
1.2
−1.5
−1.0
−0.5
0.0
0.5
1.0
G. fossarum - Proportion Urban in Catchment
N = 1000
Bandwidth = 0.09346
0.0
0.2
0.4
0.6
0.8
1.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
G. roeseli - Proportion Urban in Catchment
N = 1000
Bandwidth = 0.1138
0.0
0.2
0.4
0.6
0.8
−2
−1
0
1
2
G. pulex - Proportion Cultivated Land in Catchment
N = 1000
Bandwidth = 0.08893
0.0
0.2
0.4
0.6
0.8
1.0
1.2
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
G. fossarum - Proportion Cultivated Land in Catchm
N = 1000
Bandwidth = 0.1194
0.0
0.2
0.4
0.6
0.8
−2
−1
0
1
2
3
G. roeseli - Proportion Cultivated Land in Catchmen
N = 1000
Bandwidth = 0.1096
0.0
0.2
0.4
0.6
0.8
−2
−1
0
1
G. pulex - Proportion Broadleaf Forest in Catchment
N = 1000
Bandwidth = 0.09449
0.0
0.2
0.4
0.6
0.8
1.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
G. fossarum - Proportion Broadleaf Forest in Catchr
N = 1000
Bandwidth = 0.1168
0.0
0.2
0.4
0.6
0.8
−1
0
1
2
3
G. roeseli - Proportion Broadleaf Forest in Catchmer
N = 1000
Bandwidth = 0.1219
0.0
0.2
0.4
0.6
0.8
−2
−1
0
1
2


G. pulex - Proportion Water Bodies in Catchment
N = 1000
Bandwidth = 0.08966
0.0 0.2 0.4 0.6 0.8 1.0 1.2
−1.5 −1.0 −0.5 0.0 0.5 1.0
G. fossarum - Proportion Water Bodies in Catchmer
N = 1000
Bandwidth = 0.1125
0.0 0.2 0.4 0.6 0.8
−1 0 1 2
G. roeseli - Proportion Water Bodies in Catchment
N = 1000
Bandwidth = 0.1145
0.0 0.2 0.4 0.6 0.8
−2 −1 0 1 2
G. pulex - Proportion Marshes in Catchment
N = 1000
Bandwidth = 0.07872
0.0 0.4 0.8 1.2
−1.5 −1.0 −0.5 0.0 0.5 1.0 1.5
G. fossarum - Proportion Marshes in Catchment
N = 1000
Bandwidth = 0.1004
0.0 0.2 0.4 0.6 0.8 1.0
−2.5 −2.0 −1.5 −1.0 −0.5 0.0 0.5
G. roeseli - Proportion Marshes in Catchment
N = 1000
Bandwidth = 0.1288
0.0 0.2 0.4 0.6 0.8
−1 0 1 2
G. pulex - Microhabitat Shannon diversity
N = 1000
Bandwidth = 0.07015
0.0 0.5 1.0 1.5
−1.0 −0.5 0.0 0.5 1.0 1.5
G. fossarum - Microhabitat Shannon diversity
N = 1000
Bandwidth = 0.08061
0.0 0.4 0.8 1.2
−0.5 0.0 0.5 1.0 1.5
G. roeseli - Microhabitat Shannon diversity
N = 1000
Bandwidth = 0.08911
0.0 0.2 0.4 0.6 0.8 1.0 1.2
−1.5 −1.0 −0.5 0.0 0.5 1.0 1.5


G. pulex - Microhabitat Richness
N = 1000
Bandwidth = 0.07396
0.0
0.5
1.0
−1.0
−0.5
0.0
0.5
1.0
G. fossarum - Microhabitat Richness
N = 1000
Bandwidth = 0.08167
0.0
0.2
0.4
0.6
0.8
1.0
1.2
−1.5
−1.0
−0.5
0.0
0.5
1.0
G. roeseli - Microhabitat Richness
N = 1000
Bandwidth = 0.1039
0.0
0.2
0.4
0.6
0.8
1.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0