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BIOL 591 Quantifying Community Structure

QUANTIFYING COMMUNITY STRUCTURE

A cluster analysis was performed on selected fish community data from the Willamette River. Data, obtained from samples representing 50 km reaches of the river, were initially rarified using EcoSim, using the size of the smallest raw sample (300-349, N = 170) as the target abundance level for the rarefaction. The rarefied data set is given in Table 1.

The rarefied data were then subjected to cluster analysis using PC-ORD (also BioDiversity Professional, but both gave identical results). The Bray-Curtis (Sorensen) coefficient was used as the distance coefficient, with the Group Average selected as the linkage method. The distance coefficients were converted to similarity coefficients by subtracting the distances from 100. The Bray-Curtis similarity matrix is presented in Table 2. Note that one sample, 400-450, had very little in common with any other sample, with highest similarity values of 4 compared to two samples, 300-349 and 350-399; it was deleted from further analysis. The cluster analysis was repreated using the smaller data set. Omission of 400-450 had no effect on distance measures and cluster groupings. Two groups were identified, a lower river group consisting of samples 0-50 through 250-299 and an upper river group consisting of samples 300-349 and 350-399. The cluster dendrogram is provided in Figure 1.

The statistical significance of the cluster groupings was examined with an exact permutation test using RTNDST6, a component of MEANSIM6. The two-group classification is statistically significant (p = 0.036).

There is some logic to the classification, as one would expect a system as big as the Willamette River to have important differences in physical, chemical, and biotic characteristics from headwaters to mouth. Nevertheless, the truncated data set limits the utility of the current classification obtained. Incorporating more samples would increase the spatial resolution of the current analysis and lead to a more robust classification that offers more meaningful insights into the biogeography and ecology of the Willamette River ecosystem.

Table 1. Rarified data matrix for Willamette River fish data.

Species	0-49	50-99	100-149	150-199	200-249	250-299	300-349	350-399	400-450
Brook_trout	0	0	0	0	0	0	0	0	2
Coho_salmon	0	0	0	0	0	0	0	0	17
Mottled_sculpin	0	0	0	0	0	0	4	30	0
Rainbow_trout	0	0	0	0	0	1	13	12	0
Cutthroat_trout	0	0	0	0	1	3	7	0	15
Sand_roller	0	0	0	0	0	0	0	0	0
Paiute_sculpin	0	0	2	0	1	3	12	30	0
Leopard_dace	0	0	4	2	3	0	0	0	0
Longnose_dace	0	0	3	3	2	4	5	5	0
Redside_shiner	1	19	5	28	7	4	0	0	0
Mountain_whitefish	0	5	6	15	39	41	87	33	0
Mountain_sucker	0	11	16	13	22	12	0	1	0
Torrent_sculpin	0	0	1	2	2	3	3	2	0
Speckled_dace	0	0	1	1	4	6	3	3	0
Chinook_salmon	3	0	0	0	2	8	0	6	0
Chiselmouth	1	17	19	17	7	4	0	0	0
Peamouth	3	0	2	1	1	0	7	0	0
Bluegill	0	0	0	0	1	0	0	0	0
Reticulate_sculpin	1	1	0	0	1	3	0	0	136
Largescale_sucker	66	39	51	65	64	65	22	46	0
Northern_pikeminnow	41	74	59	21	13	13	6	2	0
Common_carp	26	2	1	0	0	0	0	0	0
Prickly_sculpin	3	2	0	2	0	0	1	0	0
Largemouth_bass	5	0	0	0	0	0	0	0	0
Smallmouth_bass	15	0	0	0	0	0	0	0	0
American_shad	3	0	0	0	0	0	0	0	0
Banded_killifish	0	0	0	0	0	0	0	0	0
Pacific_lamprey	1	0	0	0	0	0	0	0	0
Yellow_perch	1	0	0	0	0	0	0	0	0
Yellow_bullhead	0	0	0	0	0	0	0	0	0
Goldfish	0	0	0	0	0	0	0	0	0

Table 2. Bray-Curtis similarity matrix for Willamette River fish data.

Sample	0-49	50-99	100-149	150-199	200-249	250-299	300-349	350-399	400-450
0-49	100	51	57	54	49	49	19	30	1
50-99	51	100	81	67	49	45	20	28	1
100-149	57	81	100	71	63	57	25	36	0
150-199	54	67	71	100	75	70	30	41	0
200-249	49	49	63	75	100	88	45	54	1
250-299	49	45	57	70	88	100	51	59	4
300-349	19	20	25	30	45	51	100	56	4
350-399	30	28	36	41	54	59	56	100	0
400-450	1	1	0	0	1	4	4	0	100

Table 3. Output from RTNDST6 test of statistical significance of cluster analysis groupings.

```
Run ID = Wilammette River Fish Data
 Number of sites =     8


 Groups =     Lower     Upper
 Sizes  =      6         2

 Matrix of mean similarities:
            Lower   Upper
 Lower     61.686  36.569
 Upper      0.000  55.887

 Number of between and within similarities = 12.00000    16.00000

 Weighted within-groups mean similarity, Wbar =     60.2
 Unweighted within-groups mean =     61.3
 Between-groups mean similarity, Bbar =  36.6

 Observed ratio, M = Bbar/Wbar = 0.607
 Observed difference, (Wbar-Bbar) =  23.7

 The number of possible unique permutations is only   28.0
 Permutation test using     1000 randomly-sampled permutations would be
invalid.

Proceeding with exact permutation test.


Exact permutation test finished

 Number of possible permutations =         28

 Number of cases with [ M < (Observed M)] =       0
 For M, exact P-value = 0.357E-01

 Number of cases with [(Wbar-Bbar) > Observed (Wbar-BBar)] =       0
 For (Wbar-Bbar), exact P-value = 0.357E-01
```

```
                         Distance (Objective Function)
         0.008           0.150           0.292           0.435
0.577
          |-------+-------+-------+-------+-------+-------+-------+-------+
                         Information remaining (%)
     100.000          75.000          50.000          25.000           0.000
          |-------+-------+-------+-------+-------+-------+-------+-------+
0-49      ---------------------------------------|
                                                 |
50-99     -|                                     |-----------------------|
           |-------------|                       |                       |
100-149   -|             |                       |                       |
                         |-----------------------|                       |
150-199   -----|         |                                               |
               |---------|                                               |
200-249   |    |                                                         |
          |----|                                                         |
250-299   |                                                              |
                                                                         |
300-349   --------------------------|                                    |
                                    |------------------------------------|
350-399   --------------------------|
```

Figure 1. Dendrogram of Willamette River fish data. Two groups are apparent, a lower river group (in red) and an upper river group (in blue). According to an exact permutation test, the grouping is statistically significant (p = 0.036).