

Appendix A

To assess the effect of habitat on species relative abundance we used Senecal 2008 data that sampled in five different habitat types (backwater, shoal, riffle, run, and pool). We were interested in seeing if fish assemblage structure was likely to vary if differing habitat types were sampled since we do not know which habitats were sampled historically. We hypothesized that pools were likely targeted historically so were specifically interested in whether pools were different from other habitat types. The permutational multivariate analysis of variance found significant differences between the habitats ($F_{4,169} = 7.02$, $p < 0.001$, $R^2 = 0.14$), despite substantial overlap in community composition for all habitat types (Fig. 1.1). Given the lack of clear patterns between habitats and the very low amount of variation explained by the permutational multivariate analysis of variance we did not use any habitat correction factor in our analyses.

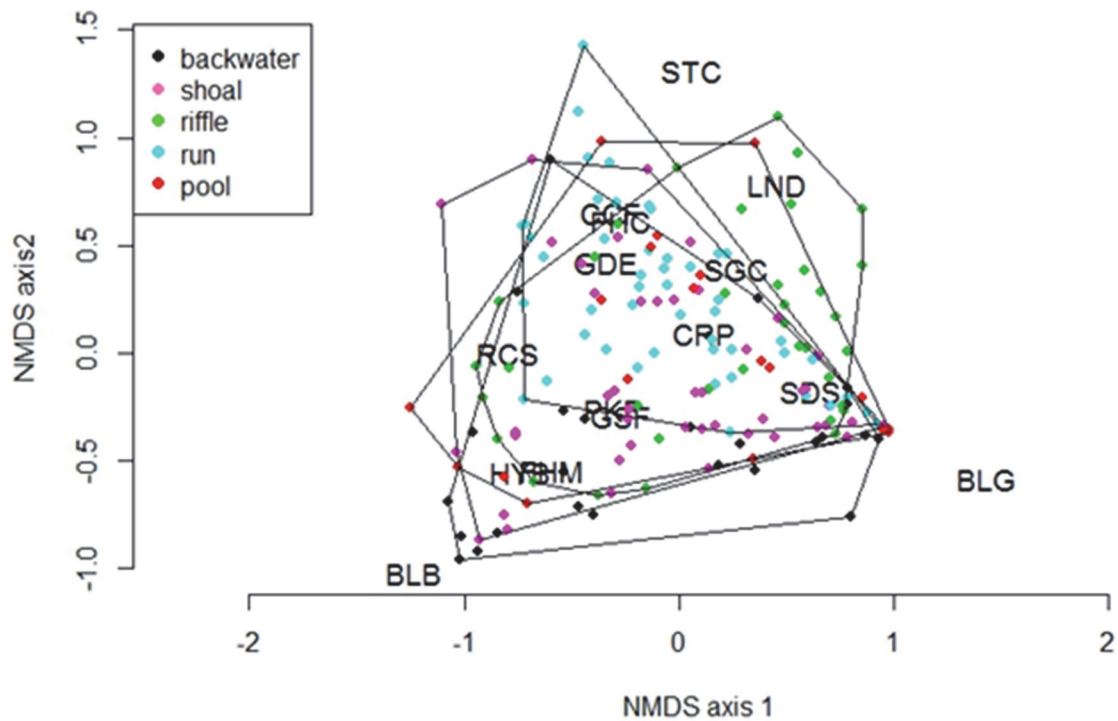


FIG. A1. Nonmetric multidimensional scaling plot (stress = 0.14) of fish community composition for each 2008 sampling event color coded by habitat type sampled. Samples from the same habitat type are boxed together. Species codes are BLB = black bullhead, BLG = bluegill, CCF = channel catfish, CRP = common carp, GDE = goldeye, GSF = green sunfish, FHC = flathead chub., FHM = fathead minnow, HYB = *Hybognathus* sp. (plains and western silvery minnow), LND = longnose dace, PKF = plains killifish, RCS = river carpsucker, SDS = sand shiner, SGC = sturgeon chub, and STC = stonecat.