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Taxonomic Resolution of Benthic Macroin-
Vertebrate communities in bioassessments:
Question and context determine strategy

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Taxonomic Resolution of benthic Macroinvertebrate Communities in Bioassessments: Questions and Context determine strategy

MANAGEMENT PERSPECTIVE

Benthic macroinvertebrates are commonly used in the bioassessment of lakes and streams. Although there has been substantial debate among benthologists carrying out bioassessments about design, field sampling, laboratory processing of samples, and data analysis, one of the most contentious issues has been *taxonomic resolution*: to what level (from phylum to species) should macroinvertebrates be identified? This paper examines which level is most appropriate for various types of studies. Often for bioassessment purposes family level is sufficient, this has considerable implications for large scale monitoring programmes, and must be considered if any national biomonitoring programme is developed.

Make recommendations on current large scale biomonitoring programmes (e.g., Fraser R., Great Lakes) as to appropriate taxonomic level for biomonitoring.

Key Words: taxonomic resolution, benthic communities, bioassessment

Résolution taxinomique pour les communautés de macroinvertébrés benthiques dans les évaluations biologiques : les questions posées et le contexte déterminent la stratégie

SOMMAIRE À L'INTENTION DE LA DIRECTION

Les macroinvertébrés benthiques sont fréquemment utilisés dans l'évaluation biologique des lacs et des cours d'eau. Les benthologues qui effectuent des évaluations biologiques ont largement débattu des protocoles, de l'échantillonnage sur le terrain, du traitement des échantillons en laboratoire et de l'analyse des données, mais l'une des questions les plus controversées est celle de la *résolution taxinomique* : jusqu'à quel niveau (du phylum aux espèces) doit-on identifier les macroinvertébrés? Dans cet article, nous examinons quel est le niveau d'identification approprié pour différentes sortes d'études. Il est fréquent que, pour les besoins d'une évaluation biologique, une identification au niveau de la famille soit suffisante, ce qui a des conséquences importantes pour les programmes de surveillance à grande échelle et doit être pris en considération dans tout programme de biosurveillance national.

Faire des recommandations pour les programmes actuels de biosurveillance à grande échelle (p. ex. ceux du Fraser et des Grands Lacs) concernant le niveau taxinomique approprié pour la biosurveillance.

Mots-clés : résolution taxinomique, communautés benthiques, évaluation biologique

**Taxonomic Resolution of Benthic Macroinvertebrate Communities in
Bioassessments: Question and Context Determine Strategy**

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Benthic macroinvertebrates are commonly used in bioassessments of lakes and streams. Although there has been substantial debate among benthologists carrying out bioassessments about design, field sampling, laboratory processing of samples, and data analysis, one of the most contentious issues has been *taxonomic resolution*: to what level (from phylum to species) should macroinvertebrates be identified? A position argued for more than 25 years is that the substantial variation among species within genera and families in their ecology and, in particular, their response to various kinds of pollution exposure, makes it important to monitor individual species if we are to adequately assess changes in aquatic ecosystems (e.g. Resh and Unzicker 1975). These benthologists support identification to the "lowest practicable level", which is usually genus or species, depending on the lifestage of the organisms collected and the number of times a particular site is sampled. An alternative view is held by some ecologists in both the marine (e.g. Warwick 1988) and freshwater (e.g. Bowman and Bailey 1998) benthic contexts, who have repeatedly found little effect of varying taxonomic resolution (from genus/species to family or even phylum level) on multivariate descriptions of variation among communities, particularly in the contrast between reference communities and those exposed to some type of pollution. They argue that identification of organisms to family level (or even higher) provides sufficient resolution for sensitive and accurate bioassessments.

What is the question?

The necessary level of taxonomic resolution always depends on the purpose(s) of a study. It is obvious that if the physiology, toxicological response, population dynamics or secondary production need to be estimated for a particular species or group of species, any necessary effort needed to insure accurate species level identification must be expended. This may include detailed analysis of several life stages of the organisms from the same site, including rearing of individuals in field or laboratory cages

if required. Even crude calculations of secondary production made by pooling taxa are of dubious value if estimates of ecosystem processes like total community production are desired (Lenat and Resh 2000). Conservation biology (e.g. biodiversity, conservation status of species) studies usually demand species level identifications as well. A survey of New York State lakes and streams to determine the current status and ranges within the state of endangered and threatened freshwater mussels would be of little use if only the abundance of "Unionidae" at each site was estimated.

If bioassessment, then what?

Bioassessment generally involves sampling of the benthic macroinvertebrate community at each of a set of sites, and comparison of the community structure and composition at a test site with those occurring at reference sites (Reynoldson *et al.* 1997). Detection of a difference between a test site and the reference condition will depend on sampling effort, natural variability and the magnitude of differences considered to represent unacceptable damage (Norris 1996), as well as the degree to which variability among reference communities can be explained by variation in environmental features (Bailey *et al.* 1998). For bioassessment, taxonomic resolution must be sufficient to reliably identify truly degraded test sites with little chance of mistakenly passing or failing a test site. It is clear that genus or species level identification of the invertebrates in a community will add at least some amount of information to the description of that community, relative to a family level description. The key questions to be considered in determining the necessary taxonomic resolution for a particular bioassessment study are:

- 1) Does genus/species identification add significant information to our description of variation among benthic macroinvertebrate communities?
- 2) Is deviation from reference condition easier to detect with genus/species identification?

3) Are there sufficient resources available to the project to insure that sample maintenance and data quality is sufficient?

1. Does genus/species identification add significant information?

There are a variety of methods used to evaluate a test site in a bioassessment, and therefore a variety of approaches are needed to answer this question. In particular contexts, the varying sensitivities of each within a group of species found in the study area may make them ideal as indicators (e.g. *Ceraclea spp.* Lenat and Resh 2000; Resh and Unsicker 1975). They should be identified to species and their abundance in a test site compared to the variability among reference sites. At the community level, however, where the estimated tolerances of genera or species to some specific or general stressor is often integrated into an index (e.g. Hilsenhoff 1987), the value of genus/species identification is less clear. We calculated the variability of several tolerance indices used in the United States Environmental Protection Agency Rapid Bioassessment Protocol (Barbour *et al.* 1999) among taxa from genus to order level. At the genus level, the variance among genera within each family was calculated and an average variance across all families determined, as well as the mean index value for each family. At the family level, the average within order variance was calculated, as well as the mean for each order. Finally, the variance among index values for the 6 insect Orders analyzed was calculated. It is clear that with the exception of the MidAtlantic Coastal Streams index, there is as much or more variation among families within orders and orders within the Insecta as there is among genera within families (Table 1). A substantial component of the genus tolerance information would be retained by just using the average tolerance for family members and applying this to calculation of an aggregated biotic index for a community of macroinvertebrates identified only to family level.

Wiscardi!

Many benthologists describe communities, and particularly variation among communities, with multivariate statistical techniques. Such techniques do not rely on tolerance indices to summarize the composition of a community, but are based on quantifying the difference between any two communities by comparing the relative (or absolute) abundance (or biomass) of each taxon present in each of the two communities, and aggregating this set of comparisons into a distance measure (e.g. Bray-Curtis distance). The full set of all paired comparisons between communities for a given study is known as a distance matrix. A "good" ordination of such a matrix will graphically represent it such that very similar communities are close together in ordination space while very different communities are far apart. Repeated analysis of benthic macroinvertebrate community data has shown little change in a multivariate description of community variation at taxonomic levels from genus to order (Furse et al. 1984, Marchant et al. 1995, Norris 1996, Bowman and Bailey 1998; but cf. Hawkins *et al.* 2000). Two communities that are quite similar when compared using genus level data are also quite similar using family or even order level data (Figure 1). So multivariate characterizations of community composition do not seem to be sensitive to taxonomic resolution, at least to family level.

2. Is a deviation from reference conditions easier to detect with genus/species identification?

To some extent, identification of community members to genus or species *must*, by definition, provide us with more information than coarser resolution. Although, as described previously, the amount that variability among communities is enhanced by genus or species identification may be small, it must be determined whether or not the increased information better distinguishes a degraded ecosystem from reference conditions than family identification.

Hawkins *et al.* (2000) found that genus/species data "worked better" than family data in a RIVPACS style analysis of several hundred California streams. They found that with species data,

there was more variation among reference communities (10 species-based versus 7 family-based clusters of similar communities), more of this variation was explained by environmental variation (higher classification success with species versus family predictive models in discriminant models), and most importantly, a clearer distinction between reference and exposed sites was apparent. They concluded that family data will work just as well as species or genus data when there is relatively little taxonomic or ecological diversity within families. Bowman and Bailey (1998) also showed that among the 10 published datasets they analyzed, studies with more genera and species showed lower correlations among distance matrices calculated at different levels of taxonomic resolution.

Although, as Hawkins *et al.* (2000) proposed, samples from communities with greater generic and specific diversity will be more informative when organisms are identified to genus or species than when only family identifications are made, such information may just represent undesirable noise in a bioassessment unless deviation from reference conditions is more evident with genus identification (Figure 2). We need more work on the detectability of the degradation of individual test sites with different degrees of taxonomic resolution.

3. Are the resources available to get accurate and precise data at the genus/species level?

Sometimes the argument for family or coarser level taxonomy is couched in terms of resource savings. Although skilled technicians often point out that the incremental costs for them to identify a group of invertebrates to genus rather than family is very small, the more pertinent question is if real cost savings are possible because the need for highly skilled taxonomic experts is avoided. This does not mean, however, that sampling methods and processing may be more haphazard and sloppy if identifications will only be to the family or order level. Whether identification is to order, family, or genus/species level, resources for housing a reference collection as well as assessing and controlling

the quality of the resulting data must also be in place. Family or even order identifications will require expert verification, particularly if the public is involved in sample collection and initial processing. Such samples will also be readily available if identification to genus or species is desirable in the future. Otherwise, the resulting data will be worth as much as the effort put into confirming its quality. With all of these considerations, the cost difference between family and genus level identification may be small enough that project managers opt for genus identification and err on the side of too much, rather than too little, information.

Often the proponents of "lowest practicable identification" are particularly concerned with missing rare species in the community in a bioassessment. Unfortunately, unless a particular subset of species relevant to a particular study is targeted for identification as present or absent in a community, many of the rare species will be missed in a typical benthic subsampling procedure, constrained by limiting resources. Simulated subsampling of collections from sites in the Fraser River (B.C., Canada) basin that were completely processed and identified to the lowest practicable level showed that only large (500-1000 individuals) subsamples of sites with relatively low diversity (< 30 taxa) and abundance (< 2000 individuals) recovered more than 75% of the taxa actually present in the collection (Figs. 3 and 4). This is similar to the lack of success of Cao et al. (1998) in finding all the taxa in simulated subsamples of a large benthic macroinvertebrate community sample from a site. Thus, if it is deemed critical to develop a full list of all of the taxa present at a site, 1000's of organisms must be identified. Although relative abundance data are not needed from such processing, the cost of identifying all unique taxa in such a large sample may be prohibitive such that it reduces the number of sites that may be visited and assessed in a given sampling year. The proportion of the actual number of taxa estimated varied substantially among subsample sizes (Figs. 3 and 4), but there are very strong

correlations among the various subsample sizes in the estimated richness of a site (Fig. 5). Even subsamples of 50 organisms were able to put the 20 sites considered here on roughly the same gradient of richness as the subsample of 1000 organisms. So genus identification may not be particularly useful at finding all of the taxa, but it will certainly describe a site's richness relative to others rather precisely.

Perhaps the best use of always limiting resources for processing of benthic macroinvertebrate community samples would be to first record community structure and composition (i.e. taxa present and their relative abundance in the community) at the family level based on a subsample of 200-500 organisms. These community data would be used in multivariate analysis of community variation (e.g. Reynoldson et al. 1999) or index calculations (e.g. Barbour et al. 1999) necessary for a bioassessment. Complementary to this characterization of the community, a short list of critical indicator taxa pertinent in the context of a particular study (e.g. species of Hydropsychidae caddisflies in an area with metal mining effluent) should be created, and a reasonably large number of individuals processed in looking for these taxa from each site sampled. The chance of missing a given indicator taxon by this procedure is small, even if the taxon is quite rare. Figure 6 illustrates this with what we call the "1% rule"; if one examines a subsample of 500 individuals, there is less than a 1% chance that a taxon with a relative abundance of at least 1% will be missed. The two-tiered protocol we suggest would be much less resource consuming than either identifying all members of a 200 organism subsample to the lowest practical level (a fruitless task that will miss many taxa and result in no better a characterization of community structure and composition) or identifying all unique taxa from a much larger subsample. It would result in a sensitive, accurate, and efficient bioassessment of a site.

Taxonomic Resolution in Bioassessment Depends on the Ecological Context

There will always be a place in benthic research for the identification of specimens to the species level. Conservation, range definition, productivity and population dynamics studies all, by definition, require species identifications. It also satisfies the soul of the naturalist that lives within most benthologists to be able to name the species of an organism recovered from a lake or stream, and have at least a little insight into its unique features. But in the context of biological assessments, when we require a precise and accurate answer to a basic question... "Is this ecosystem degraded?" ... we must carefully judge when it is worthwhile to expend the extra resources to get good quality genus/species identification of our invertebrate samples. Organisms identified to genus or species must provide a significantly more informative description of the community present at a reference or test site. In other words, there should be substantially more variance among communities identified to genus (however community structure is quantified) than among communities identified only to family. Also, genus identification must enable better detection of a given test site's departure from reference condition, and not just increase ecological noise. If we have prior knowledge of varying sensitivities among species that are present in our study area (e.g. *Ceraclea spp.*), they should be identified and exploited as indicators of departure from reference condition in our study. For a community as a whole, genus or species identification tends to improve our ability to judge test sites in study areas with diverse fauna at the generic level that vary substantially within families in their ecological niches and tolerances. In some cases, even a diverse fauna with little variability among genera within a family in their niches and tolerances will simply add ecological noise to our description of the reference condition, making it harder to detect degraded sites. Finally, regardless of our judgment about the nature of diversity and necessary taxonomic resolution in our study area, we must insure that sufficient resources are directed to the precise and accurate description of the community. If family level

identification is sufficient, we must direct resources to the proper maintenance of samples in case genus/species identifications are warranted in the future. Our always limited resources must be targeted where we can get the most "bang for the buck".

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Table 1. Variability among taxa¹ in ^{Tolerance}indices commonly used to measure the sensitivity of benthic macroinvertebrates to pollution (<http://www.epa.gov/owow/monitoring/rbp/>)

	Among Orders	Among Families	Among Genera
Idaho (index?)	2.08	6.28	1.96
Ohio	0.95	3.21	1.87
North Carolina	3.89	3.33	3.52
Wisconsin	4.25	3.12	3.62
MidAtlantic Coastal Streams	2.91	1.13	4.74

¹Taxa included Coleoptera (Elmidae, Hydrophilidae, Psephenidae), Diptera (Certatopogonidae, Chironomidae), Ephemeroptera (Baetidae, Ephemerellidae, Heptageniidae), Odonata (Gomphidae, Libellulidae), Plecoptera (Chloroperlidae, Nemouridae, Perlidae, Perlodidae), Trichoptera (Brachycentridae, Hydropsychidae, Leptoceridae, Limnephilidae, Polycentropodidae, Psychomiidae). Not all indices were available for all genera.

Figures

Figure 1. The effect of taxonomic resolution on the description of community variability in an ordination may be either large (left) if there is substantial additional information at the generic level relative to the family level, or small (right) if there is little additional information.

Figure 2. Increased taxonomic resolution may make it either easier (left) or harder (right) to detect deviation of a test site from reference conditions.

Figure 3. The average (10 subsamples per point) proportion of actual richness as it relates to the actual richness at a site (20 sites) for subsamples of 50, 100, 200, 500, and 1000 individuals.

Figure 4. The average (10 subsamples per point) proportion of actual richness as it relates to the total number of organisms collected at a site (20 sites) for subsamples of 50, 100, 200, 500, and 1000 individuals.

Figure 5. Correlations in the average (10 subsamples per point) proportion of actual richness estimated with subsamples of 50 (PRICH50), 100 (PRICH100), 200 (PRICH200), 500 (PRICH500), and 1000 (PRICH1000).

Figure 6. The probability of not detecting a given taxon as a function of the relative abundance of the taxon in the community.

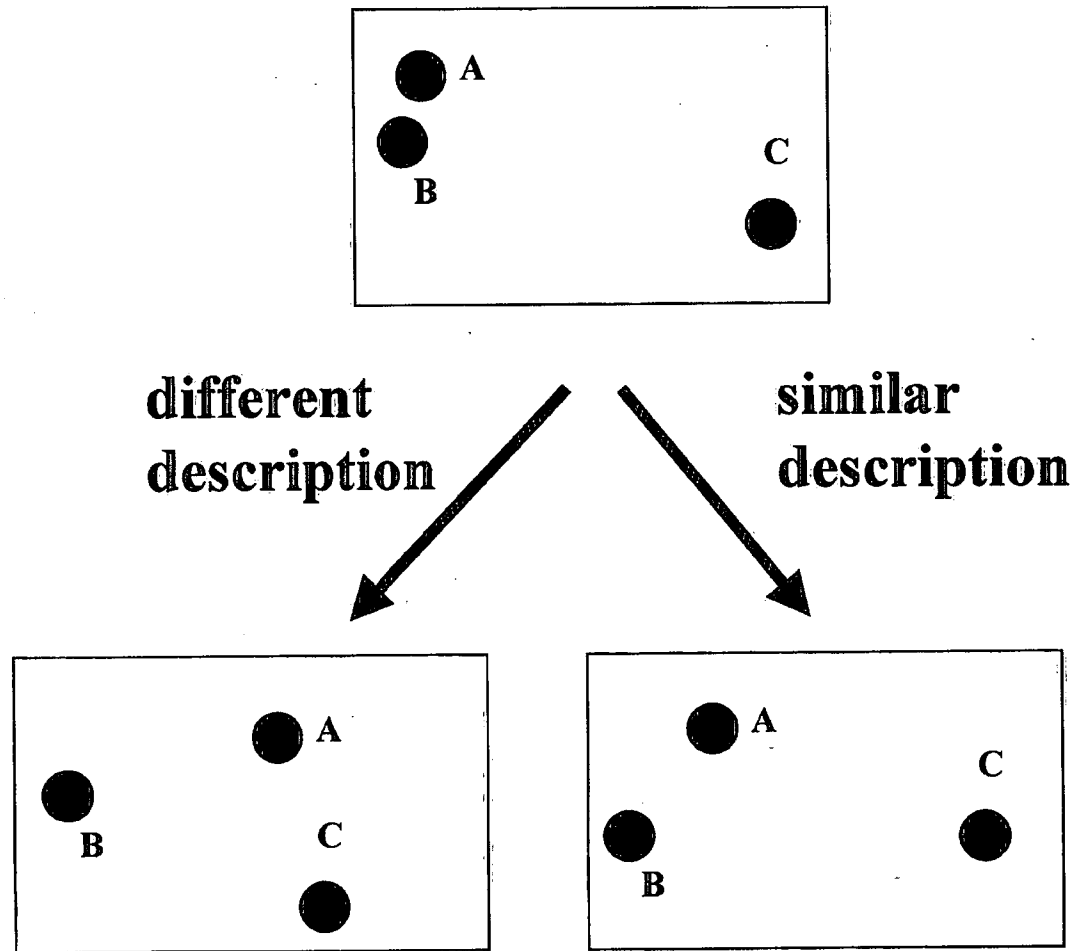


Figure 1.
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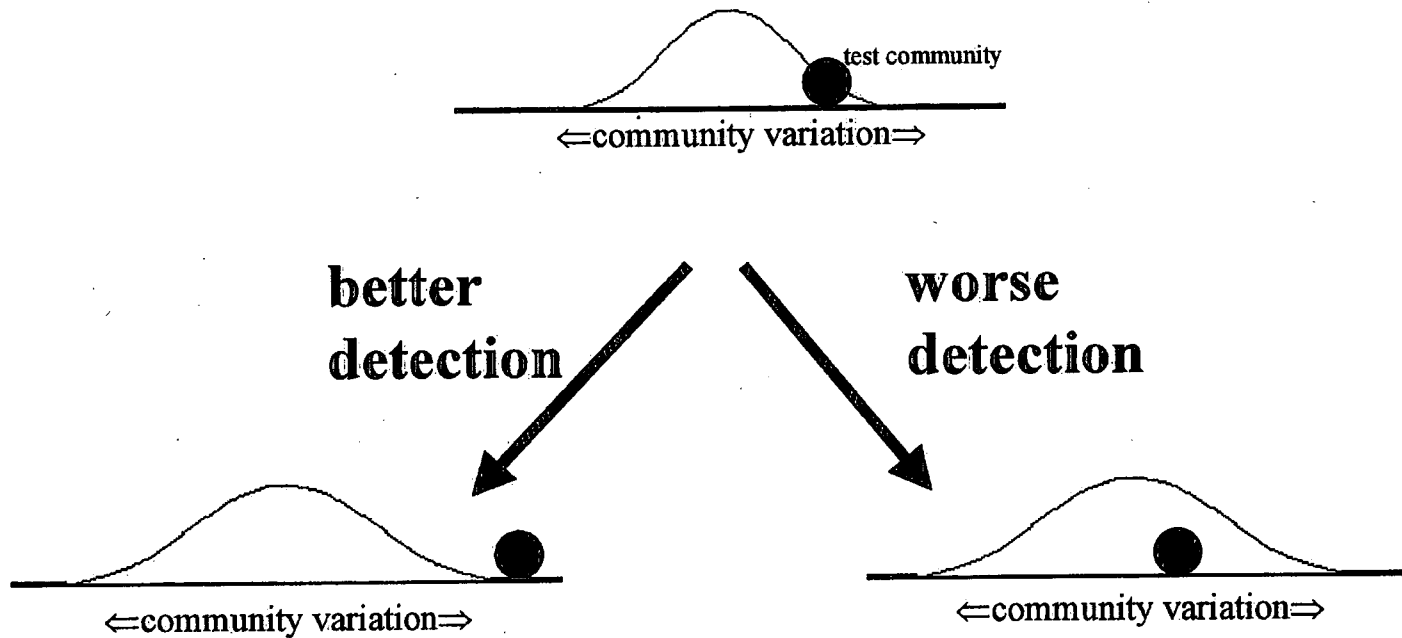


Figure 2.
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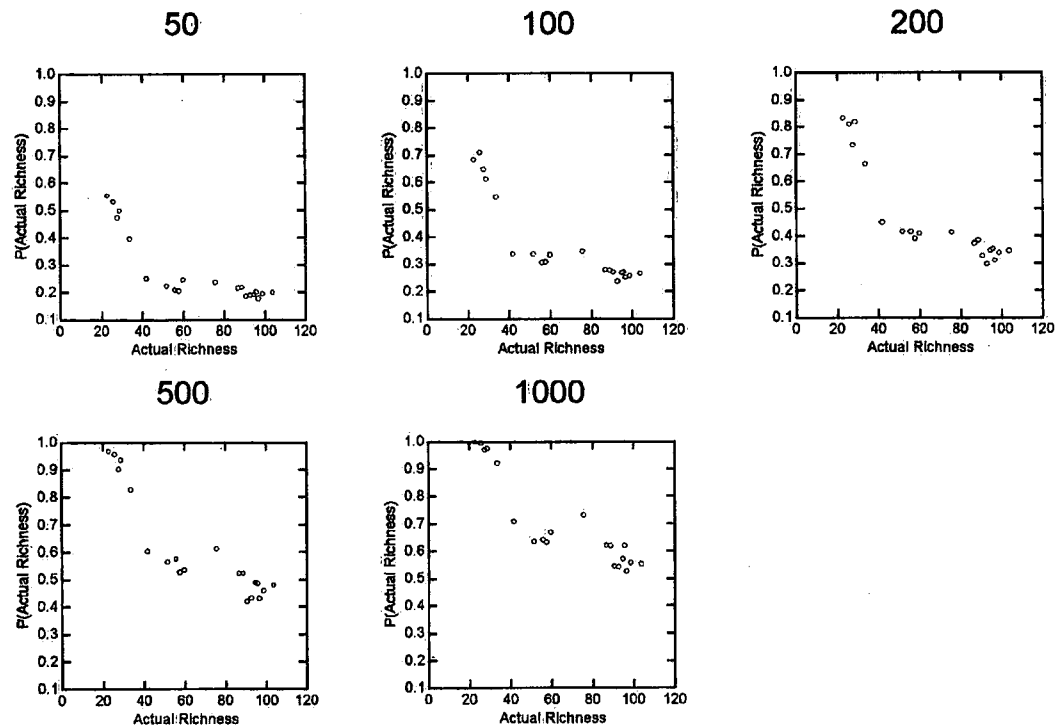


Figure 3.
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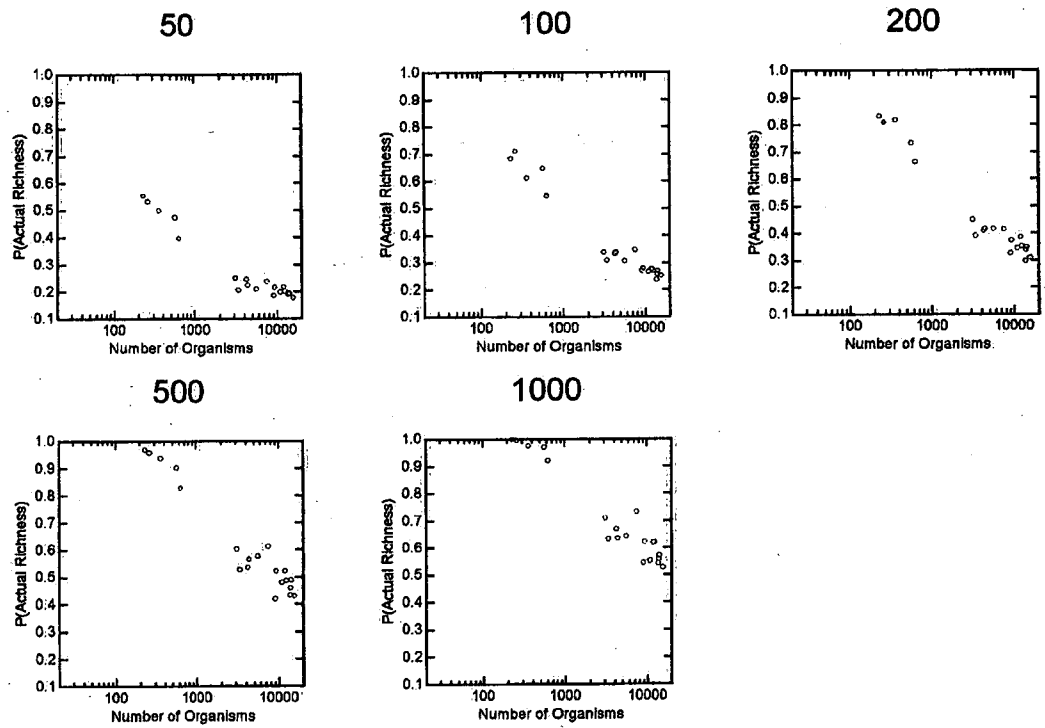


Figure 4.
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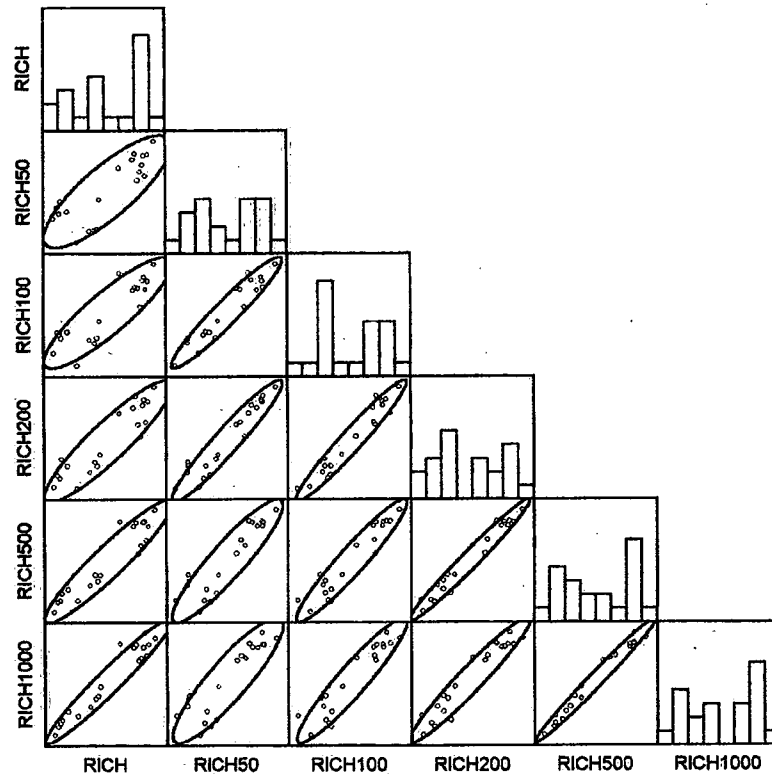


Figure 5.
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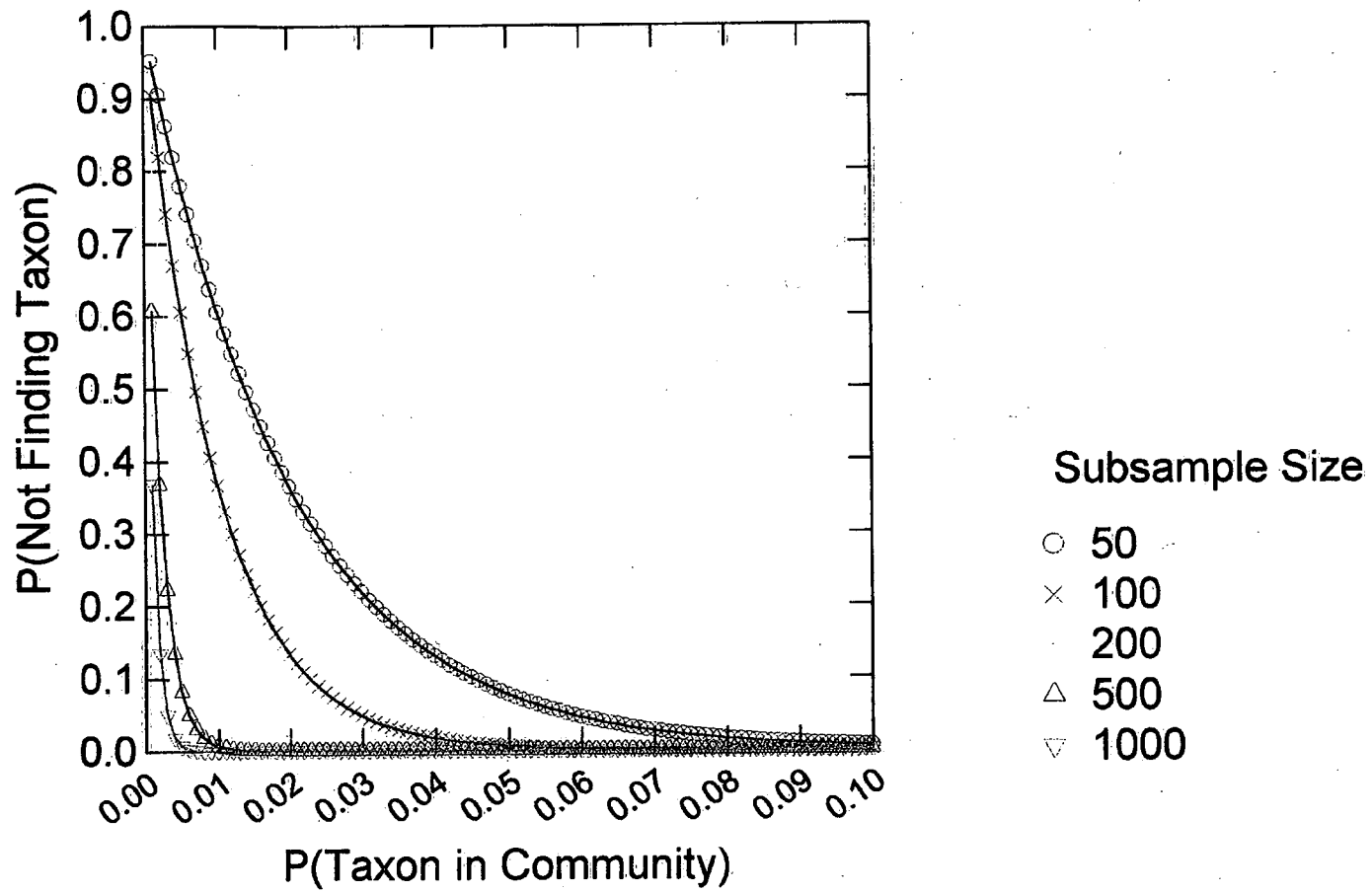


Figure 6.
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