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THE THEORY OF QUANTUM MICROBIOGEOGRAPHY: MECHANISMS OF THE PRIORITY SITE DETERMINATION

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Abstract

The Theory of Quantum Microbiogeography predicts a parsimonious quantum of highly efficacious study sites with regard to sampling of ecologically relevant community types and species of interest approximate beta diversity. Independence of efficacy from diversity, coupled with cohesion of efficacy to diversity, apparently drives these unique outcomes. Specifically, the Gehrt-Mueller Priority Site Determination represents a multi-dimensional approach for biased selection of long term ecologic monitoring sites on the basis of Sabaj efficacy, producing a parsimonious quantum of study sites approximating beta diversity. These approaches are expected to provide a highly quantitative means for assessment of change relative to natural and manmade disturbance, bio-invasion and ecologic restoration.

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Merging Practice with Theory

Table of Contents

List of Figures

List of Tables

Introduction

Rudiments of The Theory of Quantum Microbiogeography originated when several molecular biologists shared a twelve pack of micro-brews along the banks of the Dolores River in far-western Colorado. We were charged with the task of characterizing riparian flora of the lower Dolores in such a manner that change in community composition could be quantitatively assessed during and following restoration efforts. Those were our only instructions, and left to our own devices, we conjured up the unique approaches presented herein.

Considerable dialogue ensued in attempting to address the primary research objective using elements of molecular, rather than ecologic, techniques. Briefly, those techniques chosen were two dimensional gel electrophoresis, Western blotting and molecular genetics. By drawing upon our backgrounds in protein biochemistry, and DNA and RNA sequencing and analysis, we felt facets of the ecosphere not previously known might be revealed. Alternatively, we could simply assert our distorted and myopic view of the world, resulting from years of confinement to the laboratory- drove us over the edge...

Initially, study sites were assessed in a manner somewhat consistent with two dimensional gel electrophoresis and Western blotting. These techniques are used to separate extracted proteins on the basis of charge and molecular weight, and then identify individual proteins using highly specific primary and secondary antibodies. The technique hinges upon the two dimensions of separation (i.e., charge and molecular weight) being largely independent of one another. In attempting to treat study sites as proteins, it was therefore important to separate them in two independent dimensions. Sampling efficacy and biodiversity were selected as the two dimensions of separation, as initial tests indicated they were, in large part, independent of one another *per* simple regression. The Western blot equivalent was represented by those study sites occurring within the 95% confidence intervals of regression analyses.

A thorough review of the literature failed to identify a concept for sampling efficacy deemed sufficient for these purposes. Thus, the Sabaj Efficacy Index was developed to quantitatively assess community efficacy standards, and to be regressed with alpha diversity. Sabaj efficacy was defined in terms of four biotic communities: native, exotic, woody and herbaceous. These communities were assessed within each site using exact sets of confidence interval estimates. Confidence intervals estimated the number of transects required to detect a 25% or greater change in absolute percent cover of each community, with an alpha of 0.10. These estimates were derived from data collected from 39, 80m X 50m (approximately one-square acre) sites distributed throughout the lower Dolores watershed (figure 1). Using the point-intercept method, percent cover of species were estimated using five, 50m transects, perpendicular to the channel bank. Points were evaluated at 10cm intervals, resulting in 500 points per transect and 2500 points per site. Data were then arcsine-square root transformed *per* species, *per* transect. Average percent cover *per* species, *per* site were estimated by averaging estimates across five transects. Then, average, arcsine transformed, absolute percent cover estimates of

species were sequentially combined to derive percent cover estimates of communities. Confidence intervals were established about the means of these community estimates.

Sabaj efficacy was defined as the proportion of communities requiring five transects, with 500 points per transect and 2500 points per site, to detect a 25% or greater change in community composition. The index ranges from zero to one, with zero equaling no efficacy, and one equaling maximum efficacy. Study sites were in part defined by these index values. Sabaj efficacy was used as the predictor on the *X*-axis of regression analyses. Eleven diversity indices representing richness, abundance, dominance and total diversity were used as the response variables on the *Y*-axis of regression analyses. These regressions provided the means to separate study sites in two independent dimensions: efficacy and diversity. The Western blots were represented as those study sites occurring within the 95% confidence intervals of the regression analyses.

Minimum tree distances, derived from Principle Components Analysis (PCA) correlation matrices, are frequently applied to estimate phylogenetic relationships among taxa using sequence data. Minimum tree distance was the molecular genetics technique selected for application in an ecologic context. As with regression, Sabaj efficacy and biodiversity indices were used as variables for PCA correlations. Thus, just as molecular sequencing data are used to estimate phylogenies, community efficacy standards and diversity were used as variables to estimate study site relatedness and parsimony. The PCA correlation matrices were used to develop a novel statistic: the Quinn Cohesion Index (QCI). The QCI estimates the energy of cohesion (i.e., relatedness) occurring between efficacy and diversity, as efficacy increases. The index ranges from zero to one, with zero equaling no cohesion, and one equaling maximum cohesion. In general, the greater the cohesion between efficacy and diversity, the greater the degree of relatedness of study sites on the basis of efficacy and diversity.

Thus, a variety of standard and novel statistical approaches were uniquely applied for derivation of the Gehrt-Mueller Priority Site Determination (GM-PSD) and its underlying mechanism. The GM-PSD is a novel formulation for selection of long term ecologic monitoring sites, based upon efficacious and quantitative sampling of botanic communities and species of interest. The impetus for development of the GM-PSD arose from the desire of the lower Dolores study group, represented by the United States Bureau of Land Management (BLM), The Nature Conservancy (TNC), the Edwin James Society (EJS), the Tamarisk Coalition, and other invested partners, to identify a subset of study sites wherein "it made good sense to expend substantial funds and resources for expanded, long term monitoring of ecologic restoration". The expanded monitoring protocols were envisioned to include assessment of site-specific hydrology, micro-climate, soil chemistry, cattle grazing regimens, soil microbes, and insect, avian, reptilian, amphibian and mammalian communities. Thus, the Edwin James Society Division of Research focused its efforts on developing a novel, efficacious and quantitative means for selection of long term monitoring sites based upon these criteria. Four years of research were invested by the EJS to fully develop the approaches presented. In addition to formulating the GM-PSD, the EJS also revealed the mechanism operating the GM-PSD, and proposes a novel theory driving that mechanism: *The Theory of Quantum*

Microbiogeography. The theory predicts a parsimonious quantum of highly efficacious study sites with regard to sampling of ecologically relevant community types and species of interest approximate beta diversity based upon a quantum duality.

The unique set of approaches suggests quantitative sampling efficacy of ecologically relevant community types, a dominant/ invasive species (tamarisk), and its primary competitor (cottonwood) were captured among a parsimonious quantum of long term monitoring sites. Sampling efficacy of community types was largely independent of diversity, satisfying the requirement for independence concerning the two dimensions of study site separation. Curiously, the relatively narrow overlap between efficacy and diversity (specifically, evenness) appeared to drive the model. This overlap was revealed as the cohesion occurring between the largely independent variables of Sabaj efficacy and nine diversity indices. The Quinn Cohesion Index (QCI) and refined Quinn Cohesion Index (r-QCI) were developed to estimate the force of cohesion between efficacy and diversity. Cohesion apparently enabled selection of priority sites on the basis of efficacy while capturing beta diversity among those sites.

The GM-PSD is a unique microbiogeographical approach wherein key ecosystem variables are captured among a relatively small and parsimonious set of study sites. Seven priority level one sites, and six priority level two sites, occurring along the riparian zone of a watershed extending from western Colorado to eastern Utah were deemed sufficient to characterize all variables of interest. The Dolores River is approximately 400 km in length, about half of which was spanned by the 39 study sites traversing the Slick Rock, Paradox, Mesa and Gateway canyons. As such, the GM-PSD captured a broad range of ecologically meaningful data on a microbiogeographical scale. Parsimony among sites was uniquely determined by assessing study site relatedness using efficacy and diversity as variables in PCA correlation matrices.

The GM-PSD was developed in an attempt to maximize sampling efficacy and capture beta diversity among a parsimonious quantum of study sites. A novel, two-tiered approach was used to derive the GM-PSD. Tier one was defined as community-level efficacy, and tier two as species-level efficacy. Ecologically meaningful community types, relevant to long term study objectives, were identified as native, exotic, woody and herbaceous. Tamarisk (woody, exotic) is a dominant/ invasive species which, upon removal, would most likely be initially replaced by herbaceous/ native and herbaceous/ exotic vegetation. Eventually, woody/ native species are expected to succeed portions of the initial herbaceous communities. It is also important to note for purposes of analyses that woody and herbaceous are mutually exclusive community types; as are native and exotic. However, these two mutually exclusive community groupings overlap with one another.

Next, species of interest (*Tamarix chinensis* and *Populus deltoides*) were chosen as the second tier related to efficacy. Tamarisk is an invasive species dominating the lower Dolores riparian zone. As tamarisk mortality increases due to defoliation by the biocontrol (*Diorhabda carinulata*), and mechanical/ chemical treatments, it is anticipated cottonwood will be actively planted in an attempt to restore native communities. Cottonwood is not

expected to replace tamarisk naturally, as altered hydrology resulting from impoundment and removal of 40 to 50 percent of Dolores river surface water (Richards & Leib 2011) prevent optimal seed deposition, germination and root establishment. Altered hydrology essentially abolished the competitive advantage of cottonwood over tamarisk, allowing for large-scale tamarisk invasion.

Timed releases of water from the McPhee dam and/ or installation of reach-level impoundments could, to some extent, restore the ability of cottonwood to naturally reproduce. If natural flows were restored during the timing of cottonwood seed dispersal, germination and root establishment, and we can quantitatively assess tamarisk and cottonwood populations with regard to resource partitioning, then competitive interactions between these species could be evaluated. The same approach for species was used to evaluate transect number requirements for community types, except a 40% confidence limit was chosen. Thus, tier two requirements for selection of long term priority sites mandated the ability to detect 40% or greater change in percent cover of tamarisk and/ or cottonwood, using five transects, with 500 points per transect and 2500 points per site.

Often, investigators analyze and report percent cover estimates as relative percent covers. Relative percent cover is also used for those diversity indices calculating abundance. However, a means by which absolute percent cover estimates could be assessed parametrically might impart a variety of advantages. Concerning the lower Dolores riparian corridors, significant areas (i.e., patches and bands) of barren ground occurred between areas (i.e., patches or bands) of plant cover. Individual species, community types, and barren ground tended to occur as bands, rather than patches within these riparian corridors. The conversion of absolute percent cover estimates to relative percent cover estimates obscures impacts of barren ground contributions from harsh or disturbed environments. Investigators have attempted to address this issue in a manner of ways, such as including barren ground as an equivalent cover type to living community types in abundance models (Hoffman et al. 1983; Cole & Bayfield 1993; Gibson et al. 2004; Porensky et al. 2011). However, issues might arise when attempting to compare relative percent covers between study sites, yearly estimates, ecosystems, and studies where barren ground contributions vary.

A model wherein absolute percent cover estimates were implemented seemed superior to these other approaches. Barren ground occurrences become substantial in arid and semi-arid climes, high altitude regions, lake shores, coastlines, islands, disturbed soils, and steeped slopes. Use of absolute percent cover estimates also allows for direct comparison to other studies reporting absolute cover. Relative cover estimate comparisons between studies becomes problematic, insomuch as absolute cover estimates can vary significantly, even when the relative covers are approximately equal. As such, when considering the implications of comparing long term monitoring data over decades or centuries, use of absolute cover estimates enhances the ability to make these comparisons. Although data our data were presented as arcsine transformed, absolute percent cover estimates, the simple back-transformation, using transect-level estimates, produces raw data for individual species and community types. Given there were many

advantages observed in using arcsine transformed data, evaluation of long term ecosystem dynamics using transformed data might prove beneficial.

Confidence intervals were established about the means of system variables. Thus, non-parametric data almost always produce confidence interval estimates that are statistically flawed. Use of these estimates with non-parametric data can lead to erroneous conclusions and impaired environmental management strategies. Thus, considerable effort was expended to identify the types of frequency distributions produced for variables of interest. Using arcsine transformed data, frequency distributions for species, community types, barren ground, Sabaj efficacy and diversity indices were assessed. Typically, normal data are used with parametric statistics. However other distributions are appropriate when means and variances obey assumptions of normality.

The GM-PSD was derived following careful evaluation of these distributions. The complex formulation appeared to capture beta diversity while maximizing sampling efficacy of ecologically relevant communities and species of interest. In short, as demonstrated via r-QCI, site-level parsimony relative to efficacy and diversity were maximized among a quantum of study sites. The GM-PSD also achieved one of the primary goals of the research affiliates: i.e., a **rapid monitoring protocol**. The reductionist/ minimalist approaches of the GM-PSD revealed just 13 sites were required to quantify all ecosystem variables of interest.

Several members of the research group expressed reservations concerning the point-intercept method, indicating a desire to use ocular estimates of percent cover from one-meter square quadrats for long term, rapid monitoring of the ecosystem. However, the GM-PSD revealed just 13 sites were required using the point intercept method as described. Labor, effort and costs would be substantially reduced, while accuracy and precision markedly increased compared to use of an ocular quadrat method utilizing 39 or more sites. Furthermore, in regression analyses of data from a related study (unpublished data), accuracy and precision were reduced for mid-range (i.e., about 40% to 80%) ocular estimates of percent cover compared to the point-intercept method. Thus, ocular estimates of percent cover may preclude use of parametric statistics, as the actual frequency distribution of species remains unknown.

As monitoring personnel are likely to change over the years, the point intercept method also ensures continuity of percent cover estimates over time. Sabaj-Stahl (unpublished data) compared the point intercept and quadrat methods for estimation of lichen percent cover on rock surfaces. Eight students participated in estimating lichen percent covers. Estimates using the ocular quadrat method varied considerably from student to student, but were highly consistent using the point intercept method. Errors concerning the point-intercept method were generally restricted to species-level identifications and "burn-out" associated with extended periods of monitoring. Thus, it is important to have an experienced lead field biologist, familiar with regional flora, on site at all times when field crews are making species identifications. It would also be preferable to rotate crew members among specific tasks to obviate burn-out associated with prolonged, continuous use of the point-intercept method.

The occurrence of beta diversity among a parsimonious quantum of highly efficacious, long term monitoring sites identified by the GM-PSD provided motivation to seek out the mechanism driving the outcomes. Specifically, we wanted to understand how a biased selection of study sites, based upon sampling efficacy of ecologically relevant community types and species of interest, also resulted in approximation of beta diversity among those sites. Identification of that mechanism permitted development of The Theory of Quantum Microbiogeography. The novel theory revealed sampling efficacy was maximized and mean ecosystem diversity approximated among a parsimonious quantum of priority sites. The independence of efficacy from diversity, coupled with the cohesion of efficacy to diversity, appeared to drive these processes.

Several novel concepts with related statistical procedures are introduced. The Sabaj Efficacy Index estimates efficacious sampling of ecologically relevant community types. The index was named in honor of Alice and Kevin Sabaj-Stahl (deceased; 1994 & 2001, respectively). Fogleman richness estimates sample size-dependent, arcsine transformed species richness. The index was named in honor of Jim Fogleman, PhD (Denver University). The Gehrt-Mueller Priority Site Determination estimates the number of sites required for efficacious sampling of ecologically relevant community types and species of interest. The formulation was named in honor of Kevin and Jo Ann Gehrt (Oshkosh, WI, USA), and Peter Mueller (Project Director; The Nature Conservancy). The McIsaac Paradox describes the apparent conundrum of the occurrence of beta diversity among the parsimonious quantum of efficacious study sites. The paradox was named in honor of Hugh McIsaac (Denver University). The Quinn Cohesion Index and refined Quinn Cohesion Index estimate the force of cohesion between efficacy and diversity with increasing efficacy. The indices were named in honor of Tom Quinn, PhD (Denver University).

Methods

Thirty-nine monitoring sites were selected by the Edwin James Society (EJS) Division of Research, in cooperation with the Dolores River Restoration Partnership (DRRP), the Tamarisk Coalition (TC) and the United States Bureau of Land Management (BLM), within riparian corridors of the lower Dolores (figure 1). Sites were chosen with respect to tamarisk density (i.e., low, medium and high stem density) and stand age (i.e., early-, mid- and old-growth). Density and age estimates were made in advance via on-ground assessments by the TC. Candidate sites were evaluated on-ground by EJS, BLM, and TC biologists. Study sites consisted of an 80 x 50 meter quadrat (approximately one acre plot) parallel to the channel bank. GPS coordinates and four photo-points were taken for each site. Site monuments (one wooden stake, one rebar stake) were painted blaze orange and established at the two monitoring plot corners furthest from water's edge. In rare cases, site conditions precluded monument positioning in this manner, and stakes were established at the two corners nearest water's edge. Clark Tate (formerly of the TC) expended considerable effort in assuring the site selection process was representative of the lower Dolores riparian ecosystem.

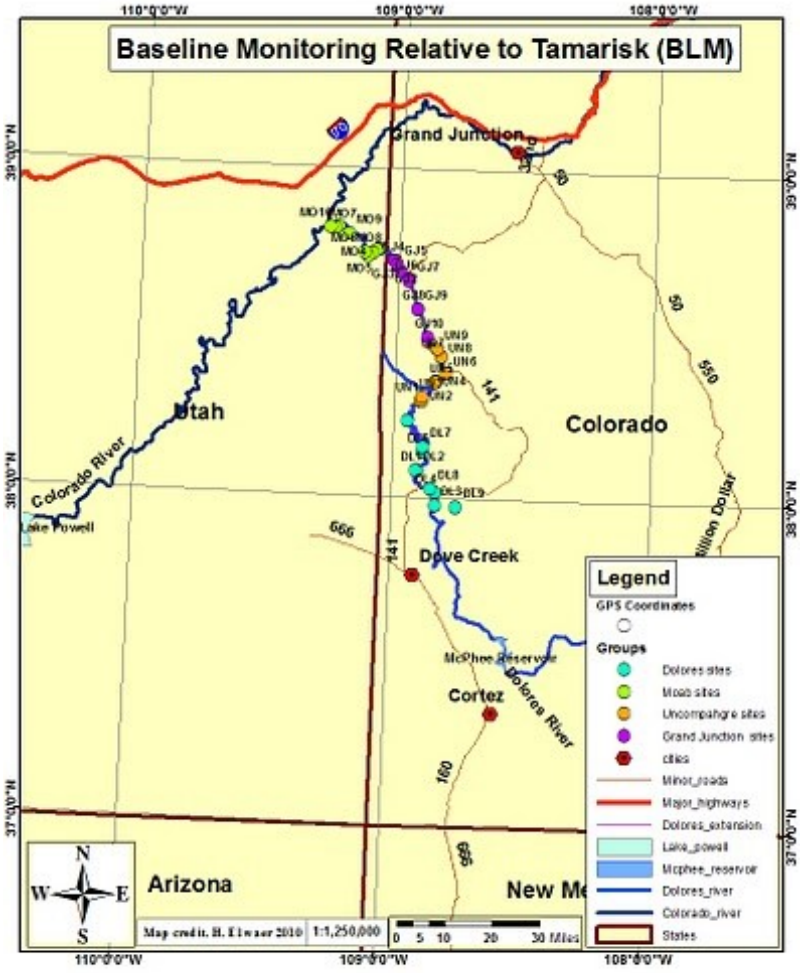


Figure 1. *39 study sites located in riparian corridors of the lower Dolores watershed. The sites generally extend from Slick Rock, CO downstream to the confluence with the Colorado River near Moab, UT. (Map was created by Environus Associates contract field biologist Hisham El waer, MS).*

During the first week of August 2010, five, 50-meter transects perpendicular to the channel bank were established in a stratified random design within each study plot by randomly placing each transect within 16-meter intervals. Vegetation was evaluated at ten centimeter intervals along each transect, resulting in 500 points per transect and 2500 points per site. Each species intersecting the point was recorded. Percent cover of individual species and community types (i.e., native, exotic, woody and herbaceous) were estimated for each transect by dividing the number of occurrences of that species or community type along each transect by the total number (500) of points assessed.

Absolute percent cover estimates of individual species were converted to proportions, then arcsine-square root transformed in Microsoft Excel®. Species estimates were sequentially combined to yield percent cover estimates of community types. The arcsine transformation was performed for each absolute percent cover estimate of each species along each transect, rather than on a site-level, resulting in average absolute percent cover estimates of individual taxa. The approach allowed for calculation of site-level standard deviations using transect-level transformed data, which were required for determination of sampling effort using the equation described below.

In a few instances, total cover proportions exceeded one when species overlap saturated transects. Proportions greater than 1.00 could not be arcsine transformed, thus a proportion of one was used, representing saturation. Arcsine transformed data were used in conjunction with an equation for determination of sampling efficacy (Elzinga et al. 2001).The form of the equation used for efficacy calculations was: $ESS = \frac{((Z\alpha)^2 * (s)^2)}{B * \bar{X}}$; where *ESS* is estimated sample size, *Zα* the standard normal deviate, *s* the standard deviation, *B* the desired confidence interval width, and $\bar{X}$ the sample mean.

A *Zα* of 1.64 (alpha level = 0.10) and confidence interval widths of 0.25 for community types, and 0.40 for individual species were applied. These confidence interval widths permitted minimum detection of change over time in percent cover of 25% and 40%, respectively. Estimated sample sizes were converted to corrected sample sizes using the sample size correction table from Elzinga et al. (2001) for point in time parameter estimates with a tolerance probability of 0.90. Elzinga et al. (2001) created the table using the algorithm reported by Kupper and Hafner (1989).

Sabaj efficacy outcomes for individual species and community types were derived using the equation given above. Sabaj efficacy was defined as the proportion of transects required to detect a minimum 25% change in community types. The index ranges from 0.00 (no efficacy) to 1.00 (maximal efficacy). Potential dependencies of efficacy with diversity were tested using simple linear regression, logistic regression, and multiple regression (PCA correlation). The variables used in the regressions were the various diversity indices compared to the Sabaj Efficacy Index for each of the 39 sites.

The confidence interval equation described above, using confidence interval widths of 25%, was also applied to estimate the ability to measure other ecosystem variables. In

essence, the equation can be used to estimate confidence intervals for the mean of any system variable.

Figure 1 was created using software provided to Hisham El waer, MS by the Denver University Department of Geography.

Figure 2 was created using software provided by: http://www.kevinotto/RSS/templates/Anderson-DarlingNormalityTestCalculator.xls.

Tables 1 and 2 were created using software provided by: http://jumk.de/statistic-calculator/.

Figures 3 through 11, and figures 15 through 28 were created using PAST software (Hammer et al. 2001).

Tables 3 through 8, and figures 12, 13, 14 were created using Microsoft Excel® 2010 software.

Efficacy calculations were performed using Excel software. All other statistical calculations were performed using PAST software (Hammer et al. 2001).

The Fogleman's Richness Index was developed to assess richness using the arcsine transformation. The Fogleman's Richness Index was calculated by dividing the number of taxa in a particular site by all taxa identified from all sites. Then, these proportions were arcsine transformed.

The Gehrt-Mueller Priority Site Determination (GM-PSD) is a multi-dimensional procedure for selection of long term monitoring sites. Priority-level one and two sites were identified by applying a consistent rationale. Concerning priority-level one sites, the first step was defined by selecting sites wherein 25% confidence intervals were sufficient to estimate change in all four community types. The second step involved choosing among those sites produced from step one, wherein either change of tamarisk and/ or cottonwood could be estimated with 40% confidence intervals.

Concerning priority-level two criteria, the GM-PSD was altered to accommodate sites that were not as efficacious as priority-level one sites, but nonetheless provided a wealth of information. These were defined by applying two sets of standards. One subset of priority-level two sites adhered to the 25% confidence intervals established for the four communities, but they fell short of adhering to the 40% efficacy standard for tamarisk and/ or cottonwood. The second subset of sites obeyed the 25% confidence intervals for three of four community types, as well as the 40% intervals for tamarisk and/ or cottonwood.

The combination of priority-level one and two sites represented the Gehrt-Mueller Priority Site Determination for the lower Dolores watershed. Additional priority levels (III, IV, V, and so on) were derived, but not presented, as they were not required for this particular application of the GM-PSD. The GM-PSD is highly plastic, thus sampling effort, sampling

techniques, alpha levels, confidence intervals, community types, and species of interest can be adjusted to address specific study objectives.

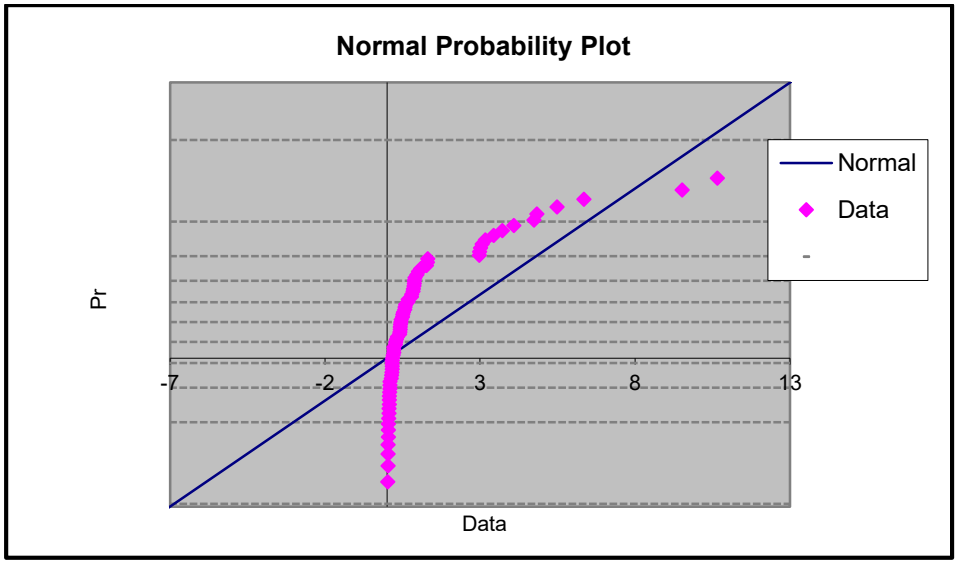
The Quinn Cohesion Index (QCI) was derived from the PCA correlation matrices in figures 15 through 25, excluding Fisher's alpha (figure 22) and Fogleman's S (figure 24). QCI is an approximation of the cohesion between the variables used in the PCA. The index ranges from zero (no cohesion) to one (maximum cohesion). Uniformly distributed data were applied for both variables, and the *X*-axis variable was discrete and categorical. The index was based upon the minimum line distances of the PCA scatter plots. QCI is defined as the proportion of diversity indices with zero line breaks *per* Sabaj efficacy group/ sum of diversity indices used *per* Sabaj efficacy group in the PCA correlation matrices; divided by the proportion of the number of line breaks *per* Sabaj efficacy-diversity index pairing, to the sum of all line breaks in all PCA correlation matrices plus unity (one) (table 8). Data points were plotted as three point moving averages.

The refined Quinn Cohesion Index (r-QCI) was derived from the PCA correlation matrices, using only those indices shown to a) have linear relationships with efficacy *per* linear regression (using the two-tailed p-value) and b) contribute significant information *per* the Akaike Relative Likelihood method. Simpson's dominance, Berger-Parker's dominance, Buzas & Gibson's evenness, and Pielou's J were selected as shown in table 8. The index is an approximation of the cohesion between the variables used in the PCA. As with the QCI, the r-QCI ranges from zero (no cohesion) to one (maximum cohesion). Data points were plotted as three point moving averages. The r-QCI was regressed with, where Sabaj efficacy was the *X*-axis variable and r-QCI the *Y*-axis variable.

Results

Distributions of Taxa, Community Types, Sabaj Efficacy & Diversity Indices

Figure 2: Anderson-Darling Test for Normality of Taxa



14.10176	AD test statistic
14.24072	AD* test statistic
<0.0005	P-value

The Anderson-Darling test for normality was performed using arcsine transformed data for all taxa surveyed among the 39 study sites. Absolute, average percent cover of each taxon across all sites was used. The species distribution was not normal.

Table 1: Descriptive Statistics, Tests for Uniformity & Normality of Taxa

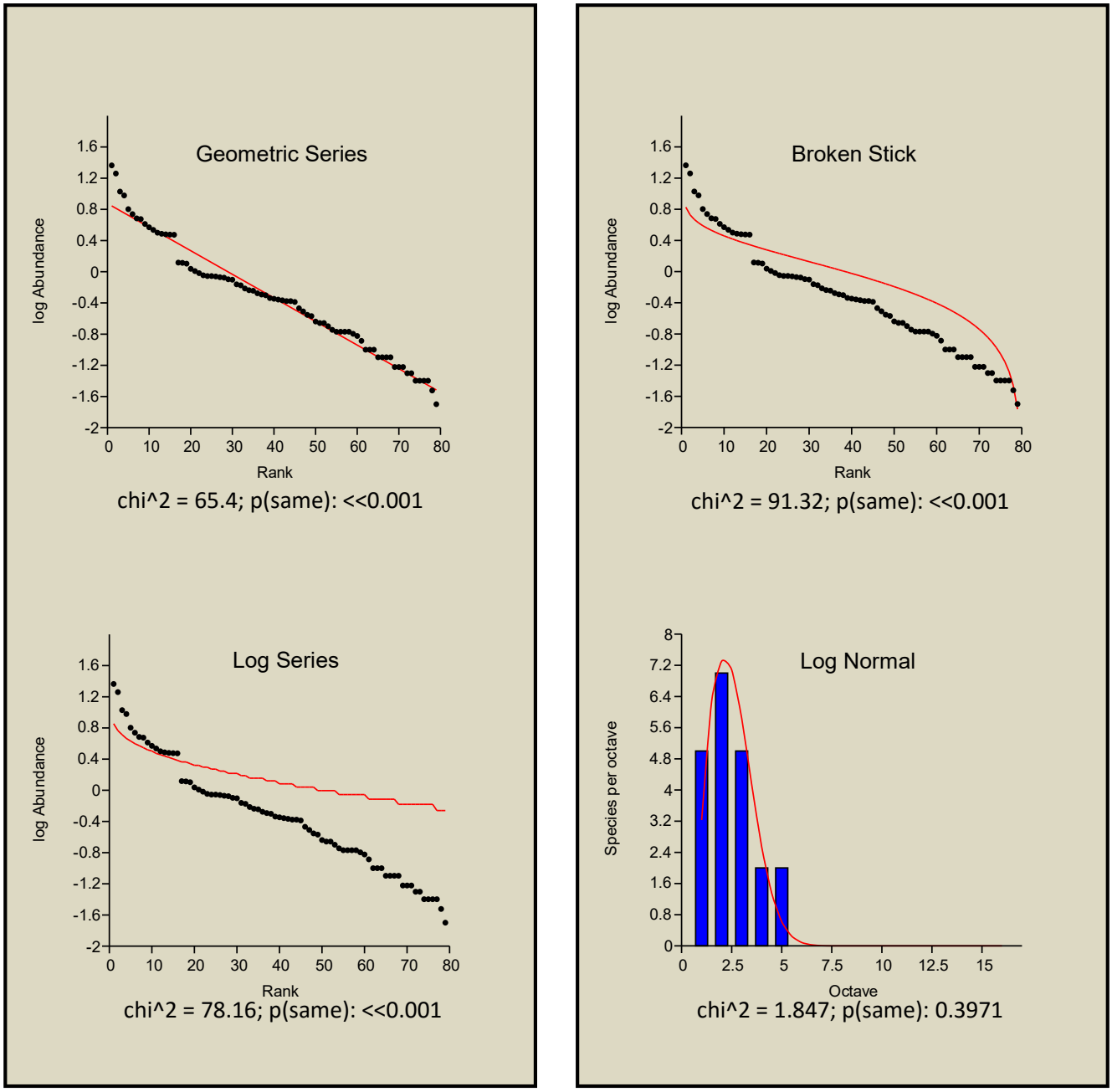
Arithmetic mean (average): 1.713 **|** Geometric mean: 0.462 **|** Harmonic mean: 0.163
Median: 0.45 **|** Mode: 0.04; 0.08; 0.17 **|** Minimum: 0.02 **|** Maximum: 23.13 **|** Max./Min.: 1156.5
Range: 23.11 **|**Quantil Q_{25}: 0.15 **|**Quantil Q_{75}: 1.09 **|** Interquartile range: 0.94
Number of values: 79 **|** Different values: 62
Mean deviation from the median: 1.54 **|** Median absolute deviation: 0.37
Variance: 13.611 **|** Standard deviation: 3.689

Chi-square-test (X^2) for uniform distribution: 619.78 | Degrees of freedom: 78
Significant difference from the uniform distribution 99% or more (p (same) < 0.01).

Kolmogorov-Smirnov test for normal distribution: 7.879
Significant difference from the normal distribution 99% or more (p (same) < 0.01).

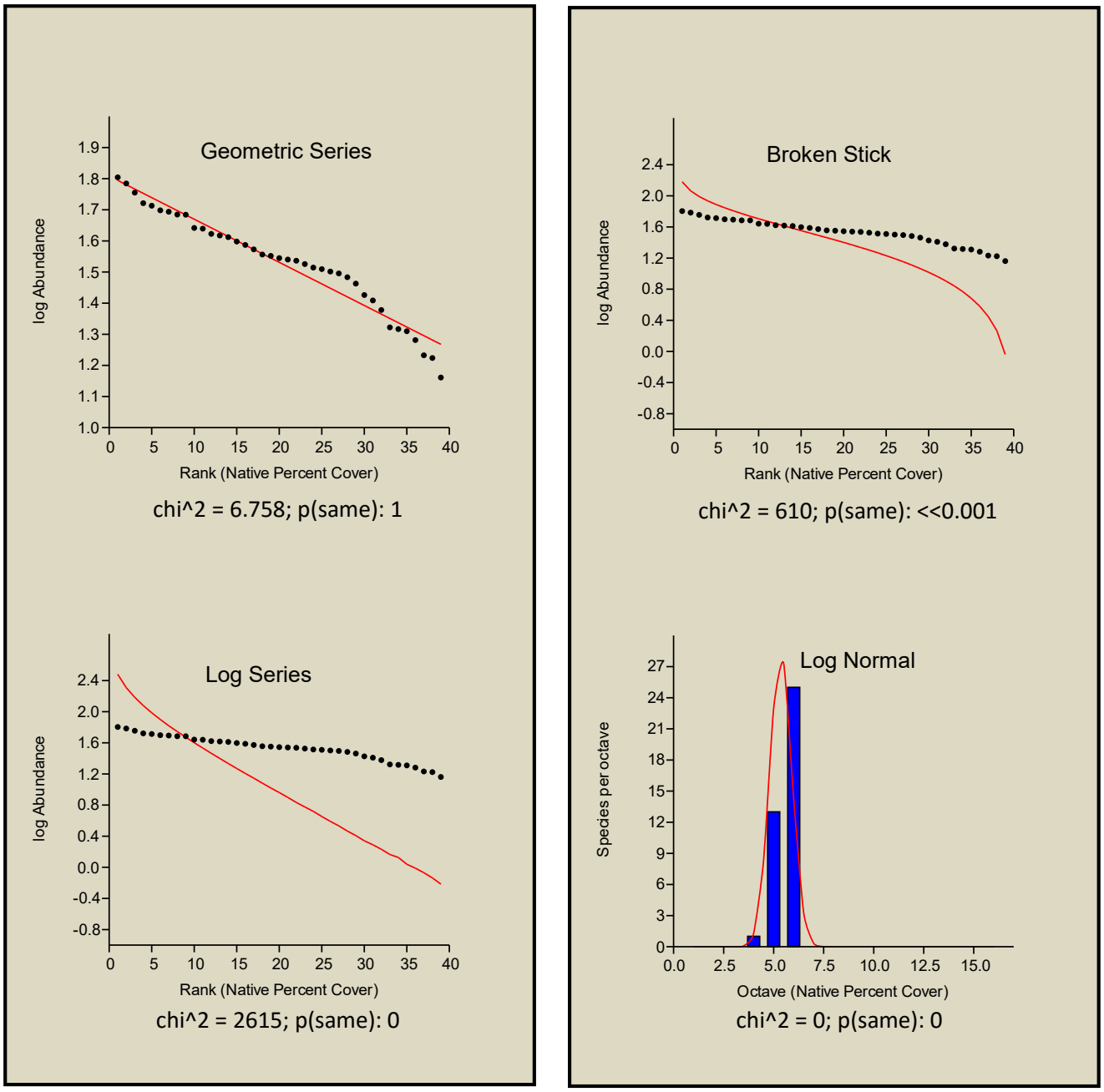
Descriptive statistics, tests for uniformity and normality were performed using arcsine transformed data for all taxa surveyed among the 39 sites. Absolute, average percent cover of each taxon across all sites was used. The species distribution was not uniform or normal.

Figure 3: Abundance Models of Taxa.



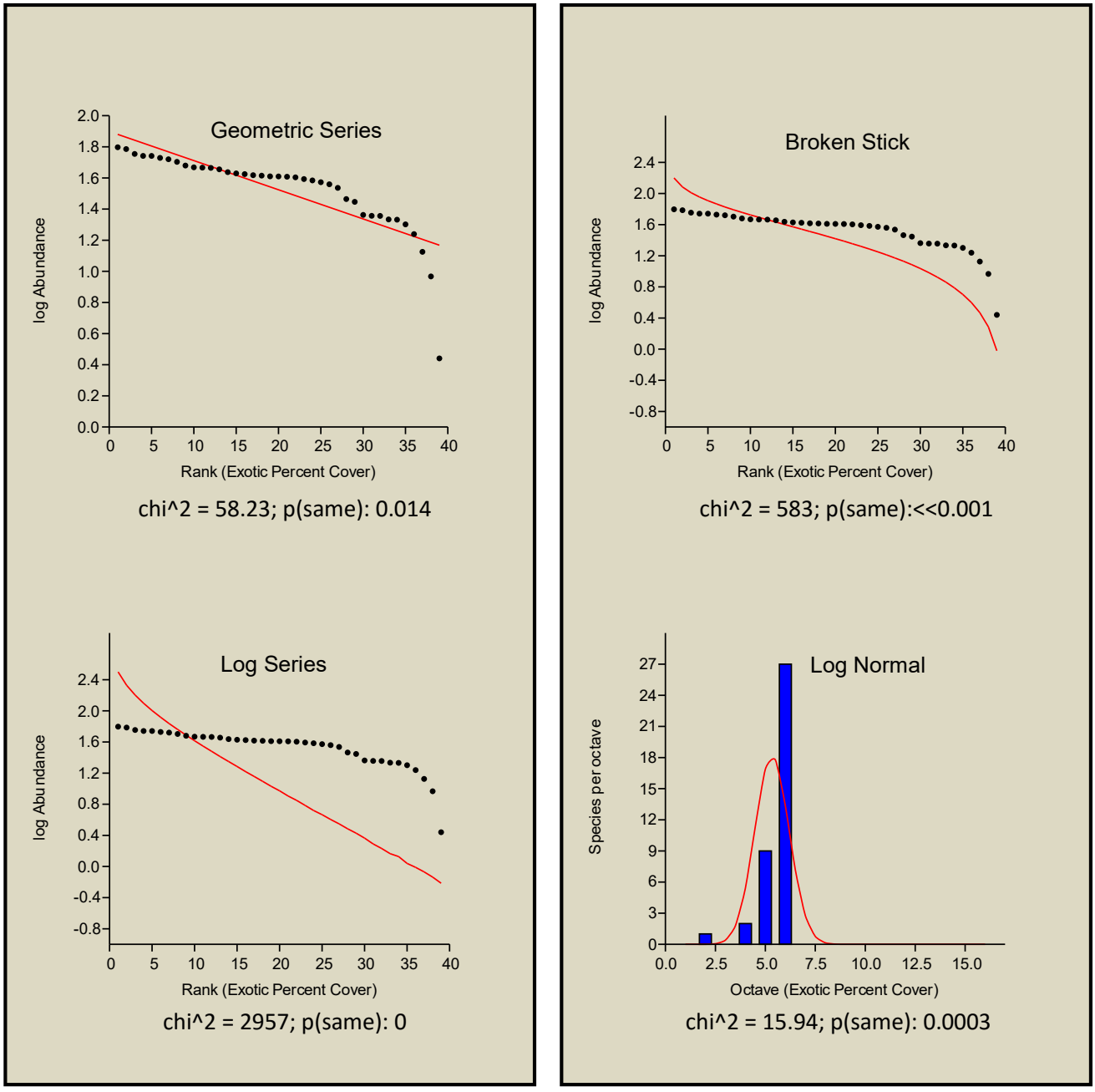
All models were tested using arcsine transformed data for all taxa surveyed among the 39 study sites. Absolute, average percent cover of each taxon across all sites was used. The species distribution was log normal.

Figure 4: Abundance Models for Native Species Mean Percent Cover.



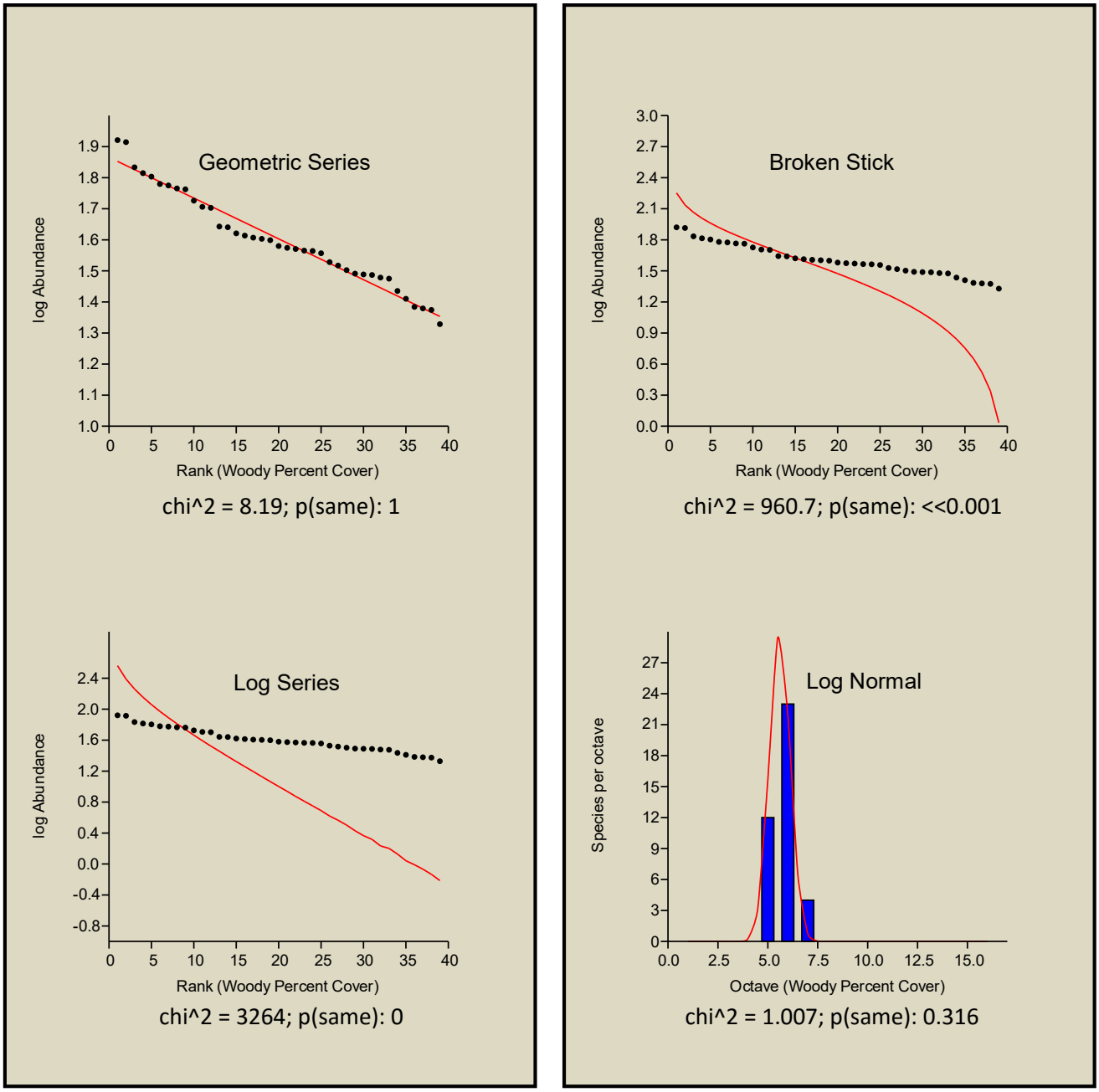
All models were tested using arcsine transformed data for all native taxa surveyed among the 39 study sites. Absolute, average percent cover of each taxon across all sites was used. Those taxa were summed within each site to generate native percent cover estimates. The 39 estimates of native percent cover were used for model tests. The native species distribution was geometric.

Figure 5: Abundance Models for Exotic Species Mean Percent Cover.



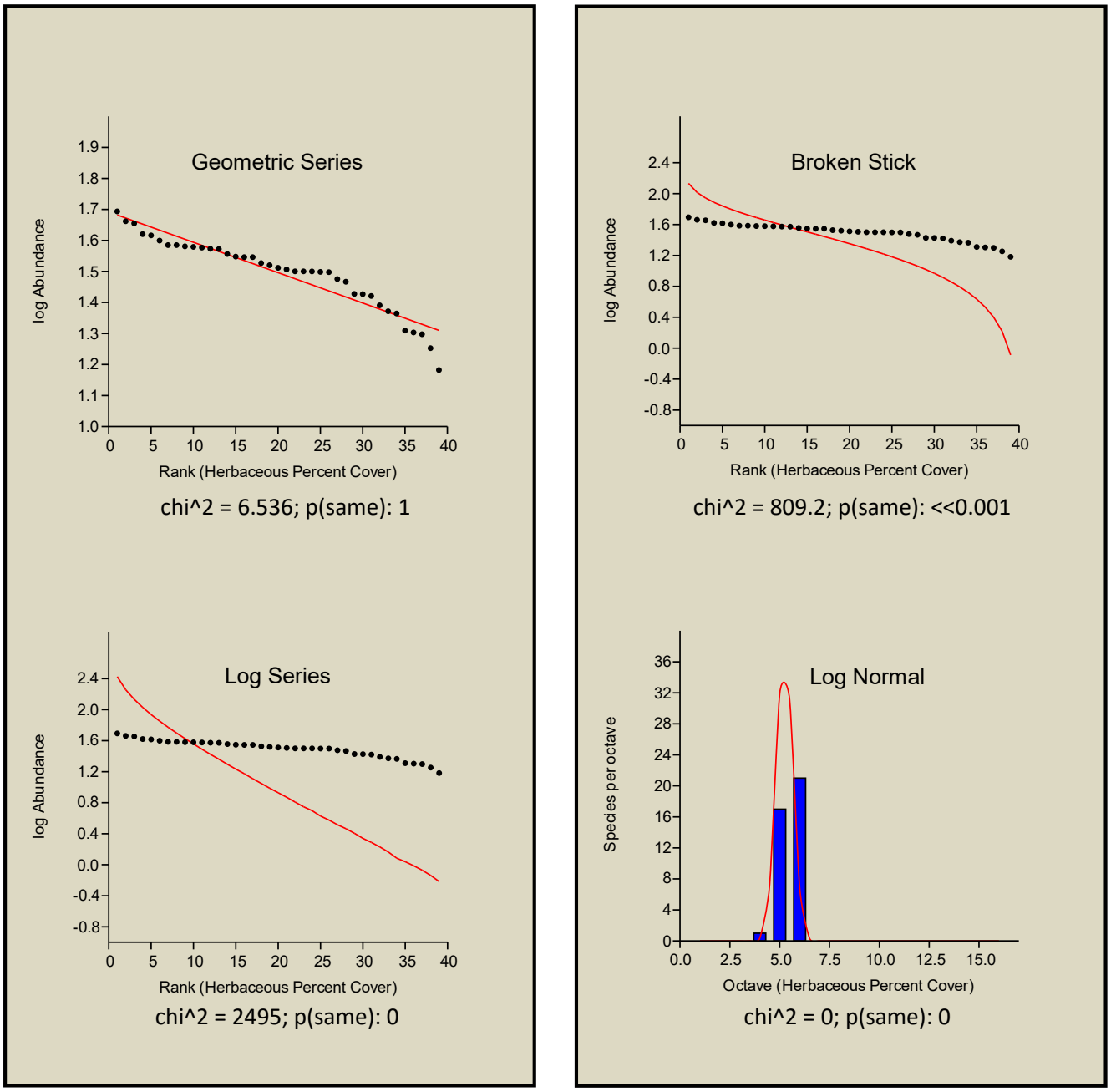
All models were tested using arcsine transformed data for all exotic taxa surveyed among the 39 study sites. Absolute, average percent cover of each taxon across all sites was used. Those taxa were summed within each site to generate exotic percent cover estimates. The 39 estimates of exotic percent cover were used for model tests. The exotic species distribution approached a geometric series, but did not conform to any of the four types.

Figure 6: Abundance Models for Woody Species Mean Percent Cover.



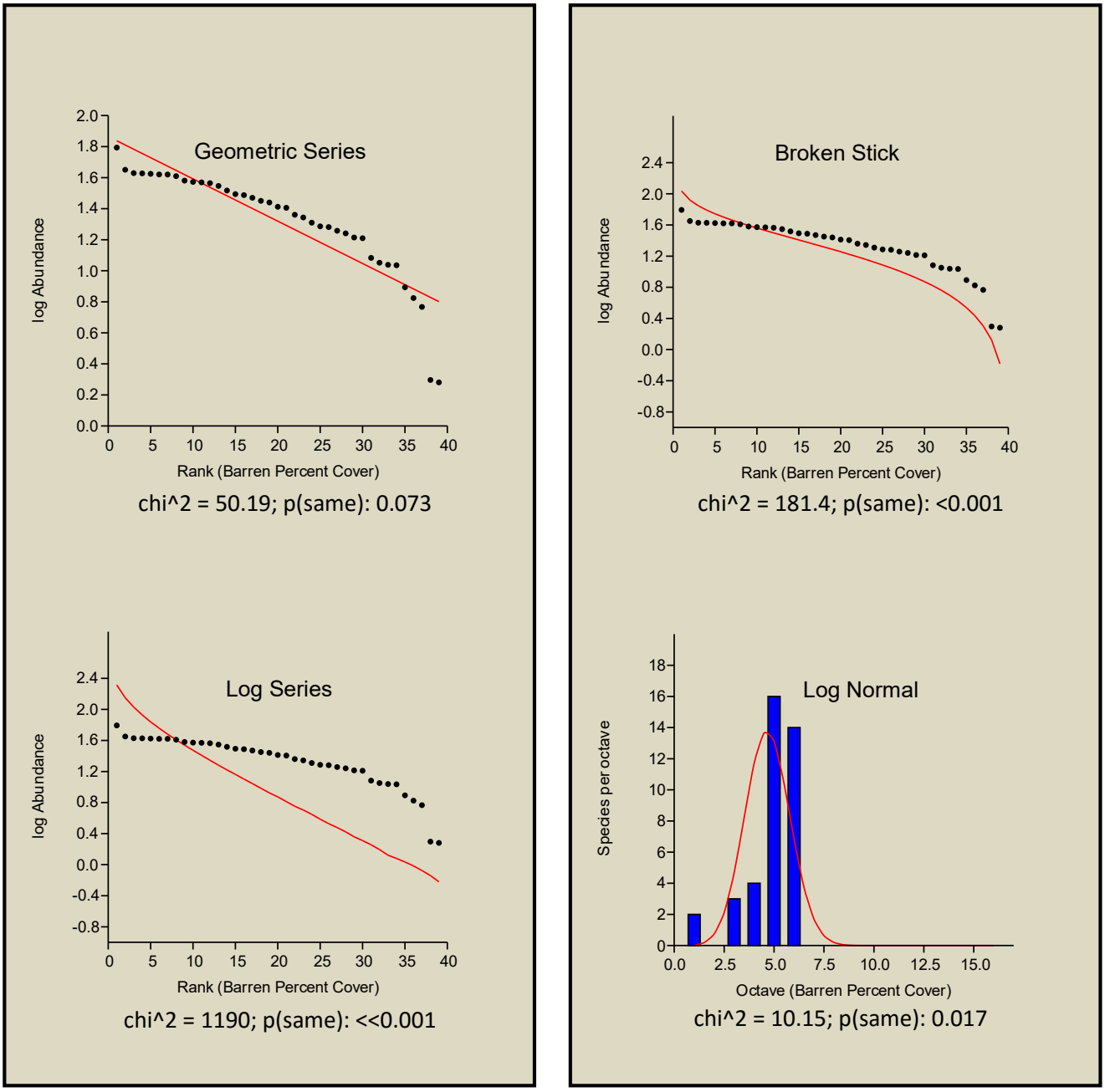
All models were tested using arcsine transformed data for all woody taxa surveyed among the 39 study sites. Absolute, average percent cover of each taxon across all sites was used. Those taxa were summed within each site to generate woody percent cover estimates. The 39 estimates of woody percent cover were used for model tests. The woody species distribution was geometric and log normal.

Figure 7: Abundance Models for Herbaceous Species Mean Percent Cover.



All models were tested using arcsine transformed data for all herbaceous taxa surveyed among the 39 study sites. Absolute, average percent cover of each taxon across all sites was used. Those taxa were summed within each site to generate herbaceous percent cover estimates. The 39 estimates of herbaceous percent cover were used for model tests. The herbaceous species distribution was geometric.

Figure 8: Abundance Models for Barren Ground Mean Percent Cover.



All models were tested using arcsine transformed data for all barren ground (i.e., no plant cover) surveyed among the 39 study sites. Absolute, average percent cover of barren ground across all sites was used, and was calculated (derived) by subtracting the sum of native and exotic absolute percent cover estimates from 100. The barren ground distribution was geometric, and also approached log normal. Barren ground is an abiotic ecosystem component.

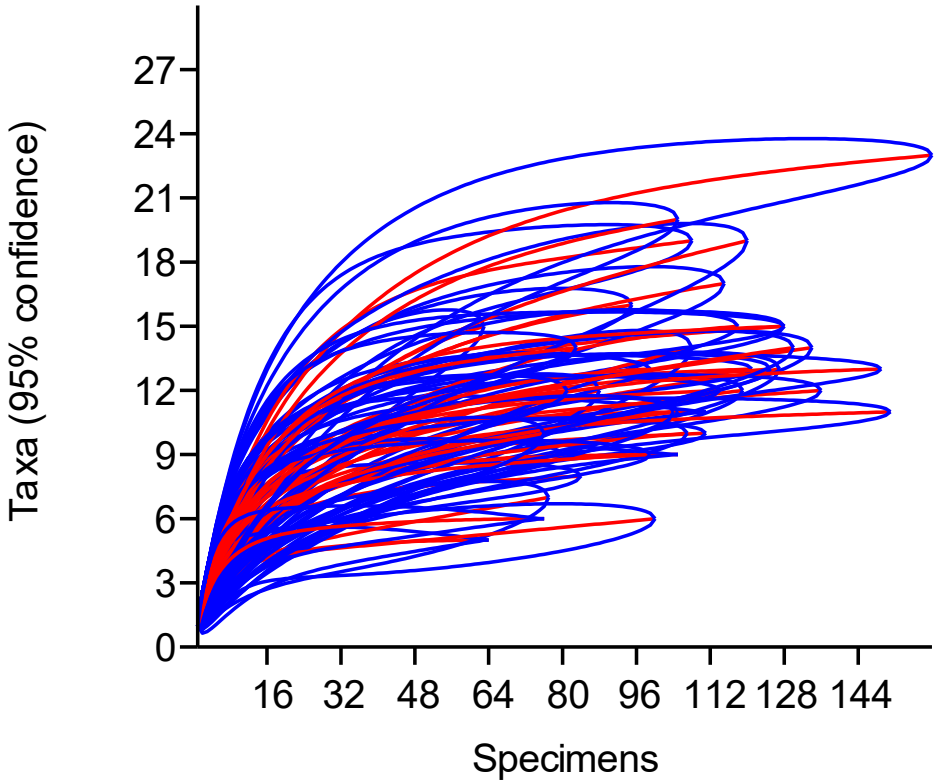
Table 2: Chi-Squared Tests of Uniformity for Efficacy & Diversity.

Sabaj Efficacy:	Chi-square-test (X^2) for uniform distribution: 7.399 | Degrees of freedom: 38 No significant difference from the uniform distribution.
Dominance:	Chi-square-test (X^2) for uniform distribution: 0.557 | Degrees of freedom: 38 No significant difference from the uniform distribution.
Shannon's H:	Chi-square-test (X^2) for uniform distribution: 1.769 | Degrees of freedom: 38 No significant difference from the uniform distribution.
Eveness (e^H/ S):	Chi-square-test (X^2) for uniform distribution: 0.412 | Degrees of freedom: 38 No significant difference from the uniform distribution.
Billouin's Index:	Chi-square-test (X^2) for uniform distribution: 1.540 | Degrees of freedom: 38 No significant difference from the uniform distribution.
Menhinick's Index:	Chi-square-test (X^2) for uniform distribution: 4.077 | Degrees of freedom: 38 No significant difference from the uniform distribution.
Margalef's Index:	Chi-square-test (X^2) for uniform distribution: 11.528 | Degrees of freedom: 38 No significant difference from the uniform distribution.
Equitability J:	Chi-square-test (X^2) for uniform distribution: 0.106 | Degrees of freedom: 38 No significant difference from the uniform distribution.
Fisher's Alpha:	Chi-square-test (X^2) for uniform distribution: 32.073 | Degrees of freedom: 38 No significant difference from the uniform distribution.
Berger-Parker's:	Chi-square-test (X^2) for uniform distribution: 0.784 | Degrees of freedom: 38 No significant difference from the uniform distribution.
Fogleman's S:	Chi-square-test (X^2) for uniform distribution: 29.557 | Degrees of freedom: 38 No significant difference from the uniform distribution.
Log S:	Chi-square-test (X^2) for uniform distribution: 0.586 | Degrees of freedom: 38 No significant difference from the uniform distribution.

Arcsine transformed, absolute percent cover data were used to calculate Sabaj efficacy and all diversity indices. Dominance was defined as Simpson's dominance for the second category in the table. Evenness was defined as Buzas & Gibson's evenness for the fourth category in the table. Sabaj efficacy and all diversity indices conformed to uniform distributions. Tests for normality (data not shown) were negative for all values. p (same) > 0.05 for all uniformity tests.

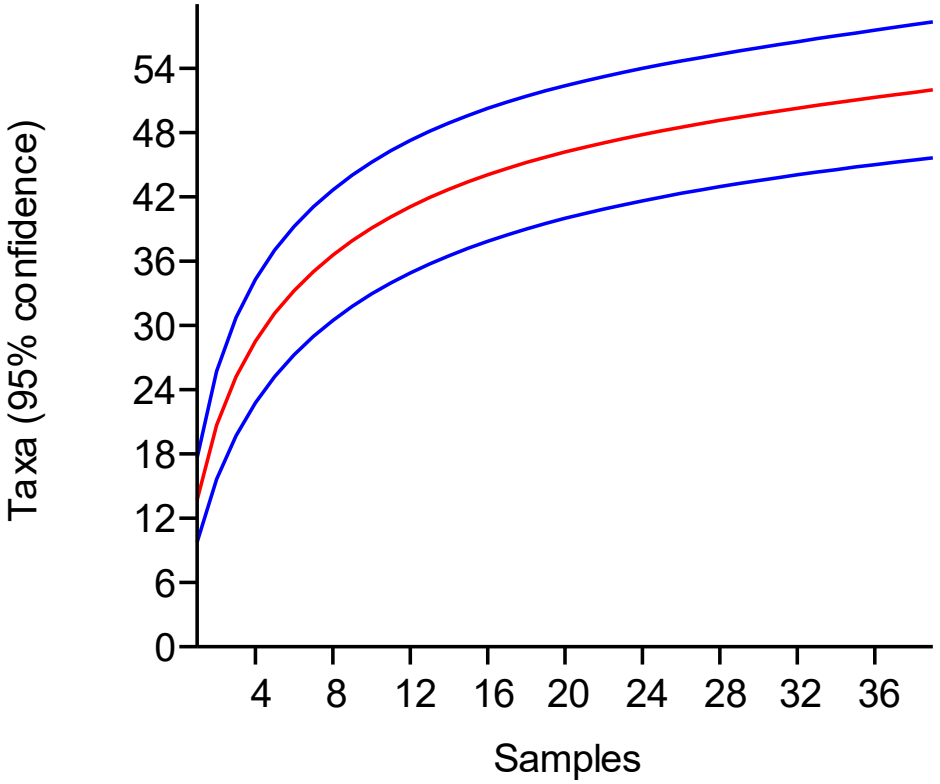
Individual Rarefaction, Sample Rarefaction & SHE Analysis

Figure 9: Individual Rarefaction.



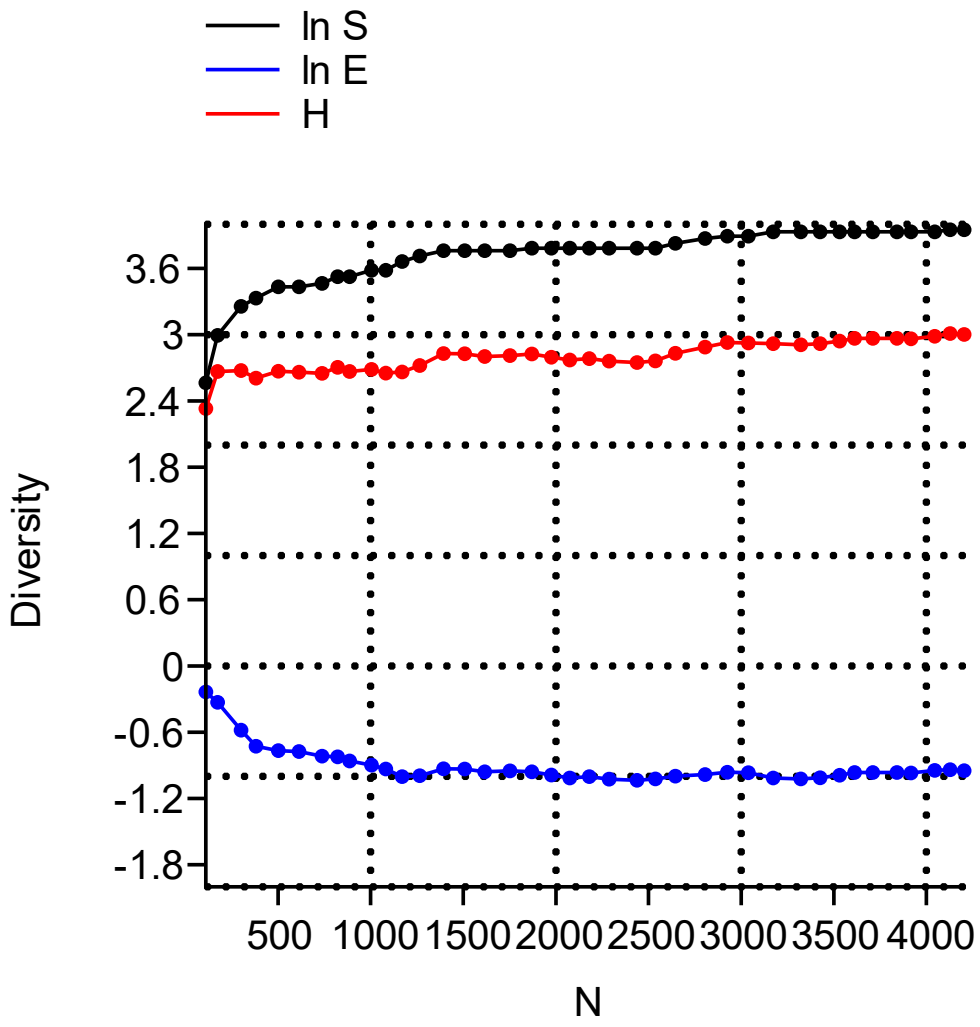
Individual rarefaction was calculated using arcsine transformed, absolute mean percent cover for all taxa within each site. The method estimates how the number of species in a sample changes with the number of individuals. The chart presents the change in richness with increasing number of individuals per study site.

Figure 10: Sample Rarefaction.



Sample rarefaction was calculated using arcsine transformed, absolute mean percent cover data for all taxa across all sites. The method estimates the number of species observed for different numbers of samples. The sample range is from zero to 39 (i.e., the maximum number of samples in the dataset). Sample rarefaction under-estimated the total number of taxa (i.e., 79) from the dataset and the asymptote was not reached for number of taxa. Richness was therefore under-estimated for the ecosystem, largely a consequence of missing rare species.

Figure 11: SHE Analysis.



SHE analysis was conducted using arcsine transformed data for absolute, mean percent cover of all taxa across all sites. SHE analysis examines the relationship between richness (S), Shannon-Wiener diversity (H), and evenness (Pielou J) (E). SHE analyzes the contributions of S and E to changes in diversity with increasing sampling effort (N). Note the pattern exhibited in the chart was indicative of a log normal species distribution.

Efficacy Standards for Community Types, Species & Diversity Indices

Table 3: Percent Cover Estimates & Sampling Effort Required for Community Types.

	Absolute Percent Cover Estimates					# of Transects Required for Efficacious Sampling				
Site	Native	Exotic	Woody	Herb	Barren	Native	Exotic	Woody	Herb	Barren
GJ1	35.63	29.15	30.98	33.65	35.22	5	5	5	5	5
GJ2	23.88	21.56	27.25	17.89	18.11	6	8	6	5	5
GJ3	48.39	40.76	59.55	29.90	10.85	5	5	5	5	29
GJ4	29.03	53.55	33.74	49.40	17.42	8	5	6	5	15
GJ5	51.64	40.55	60.21	33.11	7.82	5	5	6	8	53
GJ6	38.64	38.41	41.06	35.99	22.95	12	12	11	9	15
GJ7	33.55	55.19	50.82	37.95	11.26	8	5	5	5	39
GJ8	16.74	46.57	24.21	41.72	36.70	6	5	5	5	5
GJ9	14.49	43.38	40.09	20.11	42.13	15	6	6	9	6
GJ10	49.40	45.25	63.58	31.66	5.85	5	5	5	6	45
MO1	20.73	46.36	36.64	32.49	32.91	6	9	6	5	9
MO2	21.00	47.83	36.05	35.31	31.17	11	5	6	5	12
MO3	41.43	21.46	23.68	39.76	37.12	5	9	9	5	5
MO4	56.89	22.70	43.92	37.42	20.41	5	5	5	5	11
MO5	30.43	55.13	43.69	38.44	25.47	6	6	11	5	23
MO6	35.99	50.52	65.28	20.39	16.22	6	12	8	12	33
MO7	52.62	37.40	68.17	23.53	12.10	6	11	8	5	88
MO8	32.68	41.47	36.75	37.35	25.85	5	5	5	5	8
MO9	20.41	62.71	53.22	29.29	19.32	8	16	12	6	61
MO10	34.69	46.19	39.69	41.32	19.12	5	5	5	5	9
UC1	17.08	41.18	30.09	31.46	41.74	9	5	5	5	5
UC2	32.32	56.76	50.46	38.44	10.92	5	5	5	5	18
UC3	49.92	52.49	82.10	24.59	1.98	5	6	5	5	140
UC4	31.73	40.73	40.46	32.10	27.54	5	5	5	5	8
UC5	37.38	20.03	23.95	35.16	42.60	5	6	8	5	5
UC6	60.89	22.73	57.90	26.77	16.38	6	17	8	11	44
UC7	31.29	39.18	32.89	37.74	29.54	5	9	9	5	9
UC8	26.68	42.58	37.51	31.65	30.74	12	6	5	5	6
UC9	34.38	61.05	58.28	35.16	6.67	13	11	5	6	50
UC10	63.70	42.12	83.35	26.36	1.91	5	5	5	5	215
DL1	43.81	27.96	25.71	45.18	28.23	5	5	12	5	8
DL2	40.93	17.35	37.20	23.15	41.72	5	6	5	5	5
DL3	35.06	2.76	30.80	15.21	62.18	5	215	5	5	5
DL4	39.61	23.04	41.77	19.84	37.36	5	12	5	15	5
DL5	43.59	34.36	31.81	45.91	22.05	5	5	5	5	5
DL6	19.11	40.19	29.86	31.63	40.70	5	5	6	5	5
DL7	48.32	9.28	38.02	26.72	42.40	5	6	5	5	5
DL8	41.94	13.35	21.31	38.09	44.72	5	29	8	5	6
DL9	25.63	36.27	30.68	31.52	38.09	5	9	6	6	8

Arcsine transformed data for absolute percent cover of taxa were used to calculate cover estimates per site and efficacious sampling effort. Confidence intervals were used to estimate the number of transects required to detect a minimum 25% change per cover type (using 500 points per transect; 2500 points per site). GJ=Grand Junction sites; MO = Moab sites; UC = Uncompahgre sites; DL = Dolores sites. Green = priority level one; purple = priority level two.

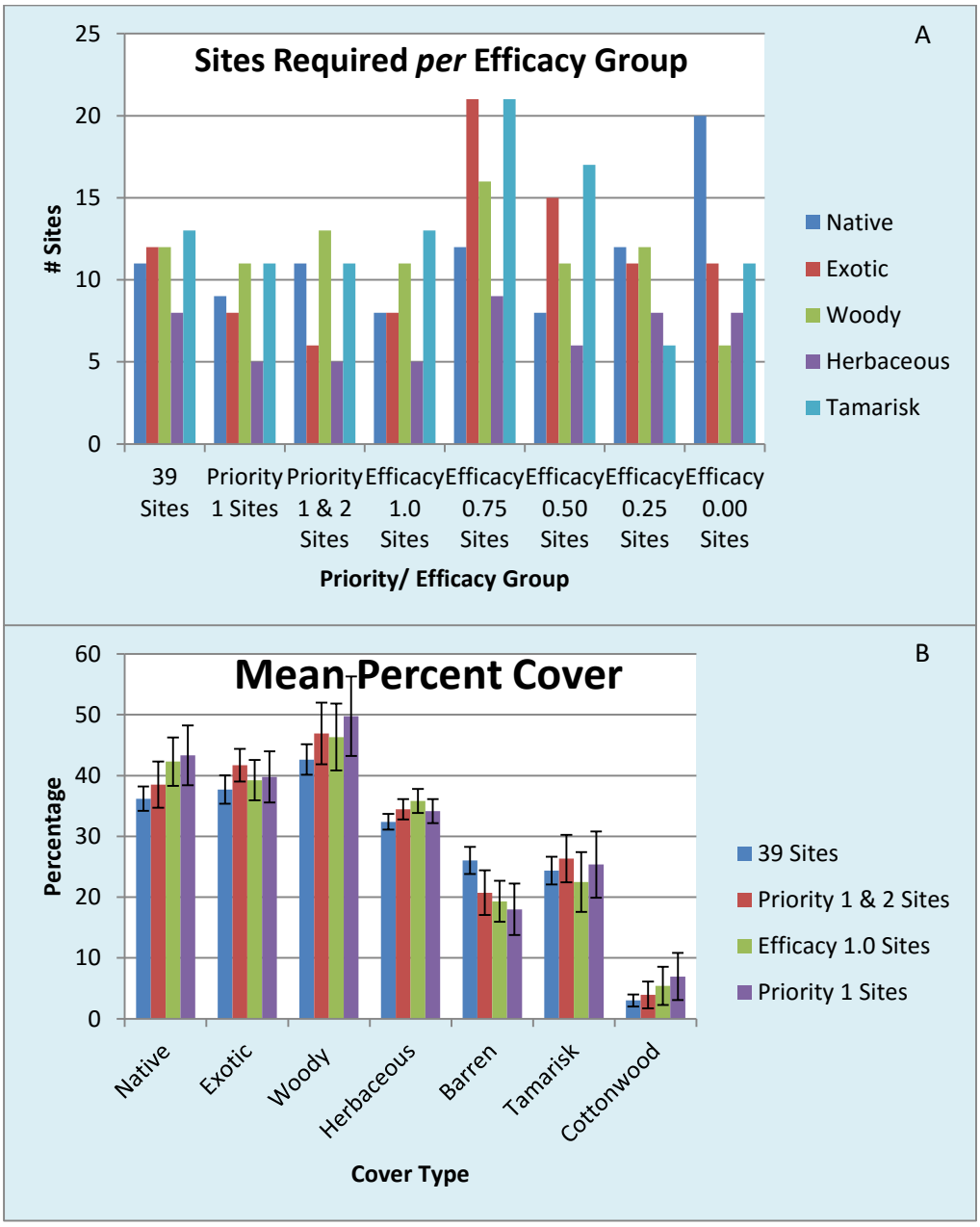
Table 4: Sampling Effort Required per Species:

	Number of Transects Required for Efficacious Sampling					
Site	Tamarisk	Knapweed	Willow	Cheatgrass	NM Privet	Cottonwood
GJ1	5	5	5			
GJ2	6					
GJ3	5	5		5		
GJ4		5				
GJ5	5		5	5		
GJ6		5				
GJ7	5	5		6		
GJ8	5			5		
GJ9	5					
GJ10	5				5	
MO1		5				
MO2	5	5		5		
MO3		5	5			
MO4		5				5
MO5		5	5			
MO6	6				5	
MO7						
MO8		5				
MO9						
MO10	5	5	5			5
UC1	5	5				
UC2	5				6	
UC3	5	5			5	
UC4	5			5		
UC5				5		
UC6			6		5	
UC7	6	6				
UC8	5					
UC9	5	5				
UC10	5		5		5	
DL1		5	5			
DL2			5			
DL3						
DL4			5			
DL5		5	5		5	
DL6	5	5		6		
DL7		5			5	
DL8						
DL9	6	5				

Tamarisk = Tamarix chinensis; Knapweed = Acroptilon repens; Willow = Salix exigua; Cheatgrass = Bromus tectorum; NM Privet = Forestiera neomexicana; Cottonwood = Populus deltoides wislizeni

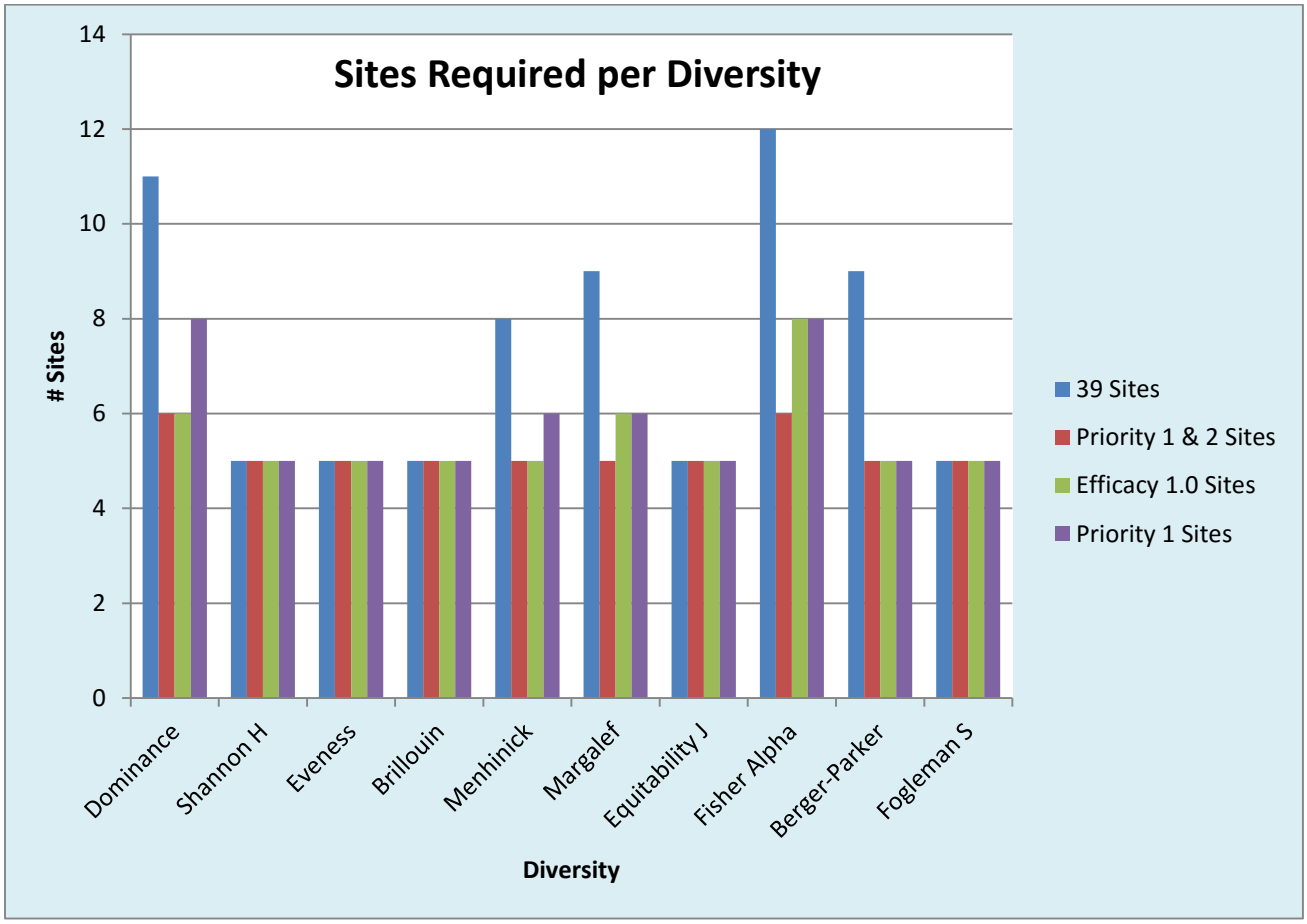
Arcsine transformed data for absolute percent cover of taxa were used to calculate efficacious sampling effort per species per site. Confidence interval estimates were used to estimate the number of transects required to detect a minimum 40% change per species (using 500 points per transect; 2500 points per site). Transect values > 6 were omitted; species where < 8 sites were identified were omitted; excepting cottonwood. GJ=Grand Junction sites; MO = Moab sites; UC = Uncompahgre sites; DL = Dolores sites. Green = priority level one; purple = priority level two.

Figure 12: Number of Sites Required for Efficacious Sampling *per* Priority Site/ Sabaj Efficacy Group (A); Mean Percent Cover *per* Cover Type *per* Study Site Grouping (B).



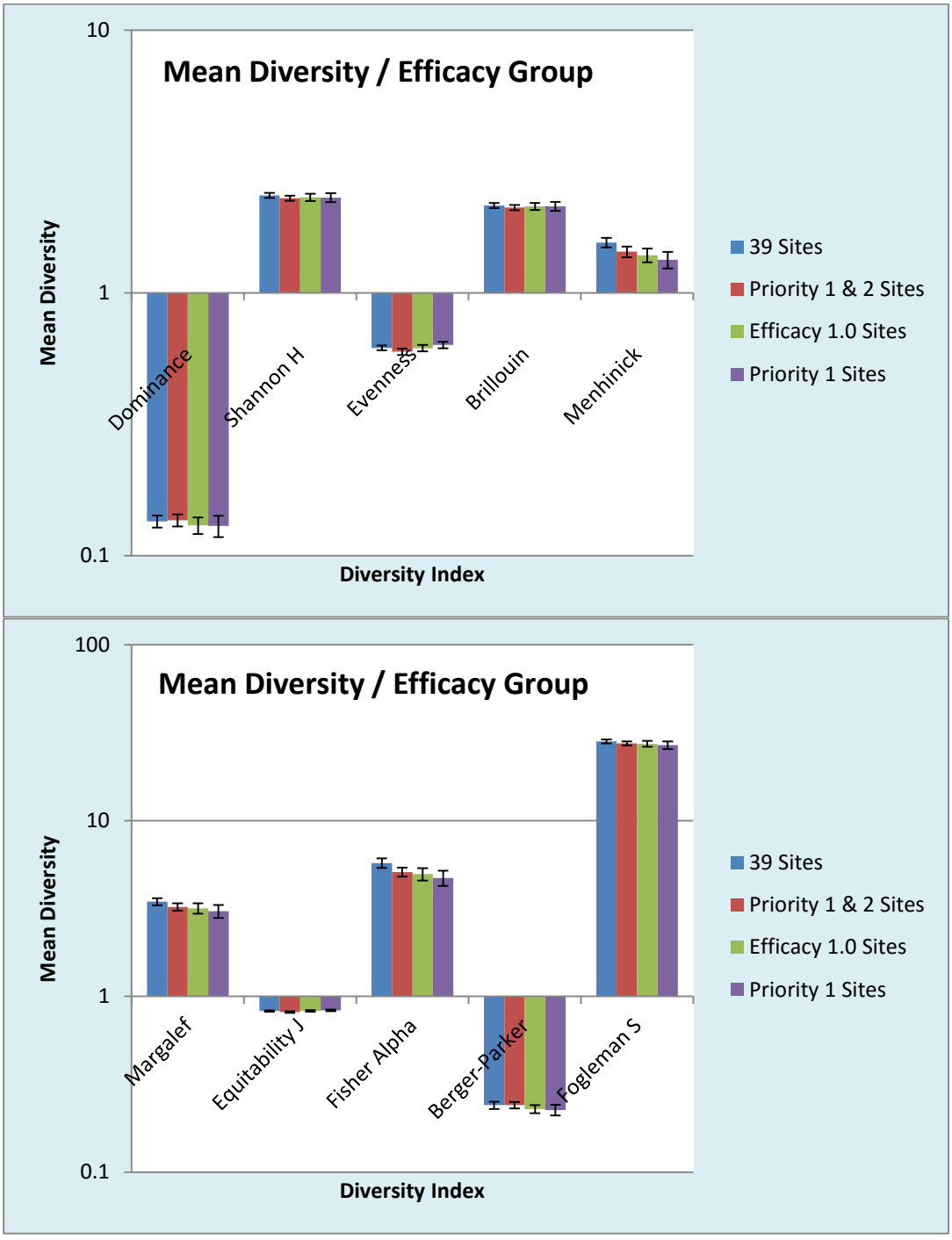
Arcsine transformed data for absolute percent cover estimates of taxa were used to calculate efficacious sampling effort per community type or species. Confidence interval estimates were used to estimate number of sites required to detect a minimum 25% change per community type or 40% change per species (using 500 points per transect; 2500 points per site). Priority 1 sites = GJ1, GJ3, MO4, MO10, UC2, UC4 and UC10. Priority 2 sites = GJ7, MO8, UC1, UC3, DL5 and DL6. Efficacy 1.0 sites required 5 transects for efficacious sampling of all four community types. Efficacy 0.75 sites required 5 transects for efficacious sampling of ¾ of community types. Efficacy 0.05 sites required 5 transects for efficacious sampling of ½ of community types. Efficacy 0.25 sites required 5 transects for efficacious sampling of ¼ of community types. Efficacy 0.00 sites are where 5 transects were insufficient for efficacious sampling of none of the four community types. Arcsine transformed, absolute mean percent cover per community type or species are shown with standard error bars.

Figure 13: Sites Required to Measure Biodiversity *per* Priority Site/ Sabaj Efficacy.



Arcsine transformed data for absolute percent cover estimates of taxa were used to calculate all diversity indices. Dominance (first grouping) was defined as Simpson's Dominance. Evenness (third grouping) was defined Buzas and Gibson's evenness (e^H/ S). Confidence interval estimates were used to estimate number of sites required to detect a minimum 25% change per diversity index. Priority 1 sites = GJ1, GJ3, MO4, MO10, UC2, UC4 and UC10. Priority 2 sites = GJ7, MO8, UC1, UC3, DL5 and DL6. Efficacy 1.0 sites are sites where 5 transects are required for efficacious sampling of all four community types (i.e., native, exotic, woody and herbaceous).

Figure 14: Mean Diversity *per* Priority Site/ Sabaj Efficacy Group.



Arcsine transformed data for absolute percent cover estimates of taxa were used to calculate all diversity indices. Dominance (first grouping) was defined as Simpson's Dominance. Evenness (third grouping) was defined as Buzas & Gibson's evenness (e^H/ S). Priority 1 sites = GJ1, GJ3, MO4, MO10, UC2, UC4 and UC10. Priority 2 sites = GJ7, MO8, UC1, UC3, DL5 and DL6. Efficacy 1.0 sites are sites where 5 transects are required for efficacious sampling of all four community types (i.e., native, exotic, woody and herbaceous).Standard error bars are displayed.

The Priority Site Determination, Detection of Change, & Efficacy v. Diversity

Table 5: The Gehrt-Mueller Priority Site Determination.

	Number of Transects Required for Efficacious Sampling					
Site	Native	Exotic	Woody	Herb	Tamarisk	Cottonwood
GJ1	5	5	5	5	5	
GJ3	5	5	5	5	5	
GJ7	8	5	5	5	5	
MO4	5	5	5	5		5
MO8	5	5	5	5		
MO10	5	5	5	5	5	5
UC1	9	5	5	5	5	
UC2	5	5	5	5	5	
UC3	5	6	5	5	5	
UC4	5	5	5	5	5	
UC10	5	5	5	5	5	
DL5	5	5	5	5		
DL6	5	5	6	5	5	

Arcsine transformed data for absolute percent cover estimates of taxa were used to calculate sampling effort per community type or species. Confidence intervals estimated number of transects required to detect a 25% change per community type or 40% change per species. Priority 1 sites = green; Priority 2 sites = purple. Priority 1 sites required 5 transects to sample four community types, and tamarisk or cottonwood. Priority 2 sites either required 5 transects to sample the four community types, or 5 transects to sample 3 of 4 community types and tamarisk.

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Table 6: Percent Cover of Priority Sites & Detection Levels of Change.

Site		GJ1		GJ3		GJ7		MO4		MO8	
Community/ Species		**% Cover**	**Change**	**% Cover**	**Change**	**% Cover**	**Change**	**% Cover**	**Change**	**% Cover**	**Change**
Native	**B=25%**	35.63	8.91	48.39	12.10	33.55	8.39	56.89	14.22	32.68	8.17
Exotic	**B=25%**	29.15	7.29	40.76	10.19	55.19	13.80	22.70	5.67	41.47	10.37
Woody	**B=25%**	30.98	7.74	59.55	14.89	50.82	12.71	43.92	10.98	36.75	9.19
Herbaceous	**B=25%**	33.65	8.41	29.90	7.48	37.95	9.49	37.42	9.35	37.35	9.34
Tamarisk	**B=40%**	15.54	6.22	30.47	12.19	39.67	15.87	0.00	0.00	22.97	9.19
Cottonwood	**B=40%**	0.00	0.00	8.03	3.21	0.00	0.00	28.49	11.40	0.00	0.00
Site		**MO10**		**UC1**		**UC2**		**UC3**			
Community/ Species		**% Cover**	**Change**	**% Cover**	**Change**	**% Cover**	**Change**	**% Cover**	**Change**		
Native	**B=25%**	34.82	8.70	17.08	4.27	32.32	8.08	49.92	12.48		
Exotic	**B=25%**	46.07	11.52	41.18	10.29	56.76	14.19	52.49	13.12		
Woody	**B=25%**	39.69	9.92	30.09	7.52	50.46	12.61	82.10	20.52		
Herbaceous	**B=25%**	41.32	10.33	31.46	7.86	38.44	9.61	24.59	6.15		
Tamarisk	**B=40%**	20.11	8.04	27.05	10.82	41.03	16.41	44.52	17.81		
Cottonwood	**B=40%**	9.07	3.63	2.25	0.90	0.00	0.00	0.00	0.00		
Site		**UC4**		**UC10**		**DL5**		**DL6**			
Community/ Species		**% Cover**	**Change**	**% Cover**	**Change**	**% Cover**	**Change**	**% Cover**	**Change**		
Native	**B=25%**	31.73	7.93	64.12	16.03	43.59	10.90	19.11	4.78		
Exotic	**B=25%**	40.73	10.18	41.86	10.47	34.36	8.59	40.19	10.05		
Woody	**B=25%**	40.46	10.11	83.35	20.84	31.81	7.95	29.86	7.46		
Herbaceous	**B=25%**	32.10	8.02	26.36	6.59	45.91	11.48	31.63	7.91		
Tamarisk	**B=40%**	32.57	13.03	37.83	15.13	1.86	0.74	28.86	11.54		
Cottonwood	**B=40%**	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		

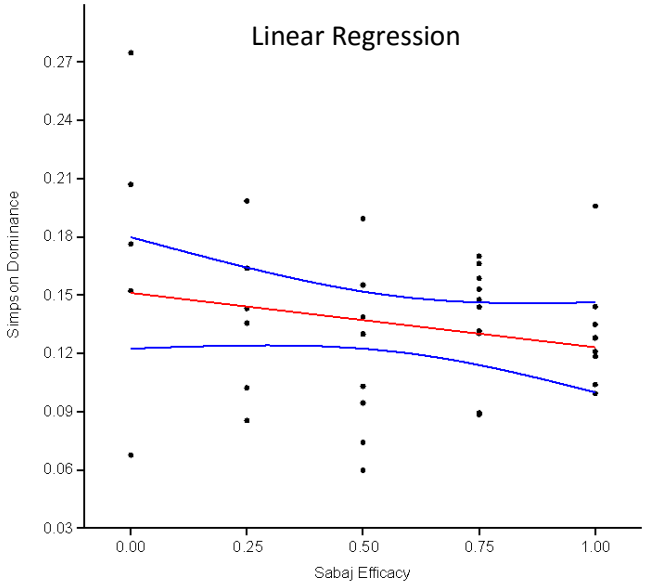
Arcsine transformed data for absolute percent cover estimates of community types and taxa were used to calculate percent cover. Also shown are the minimum detection levels of percent change (+/-)

Table 7: Diversity Indices of Priority Sites & Detection Levels of Change.

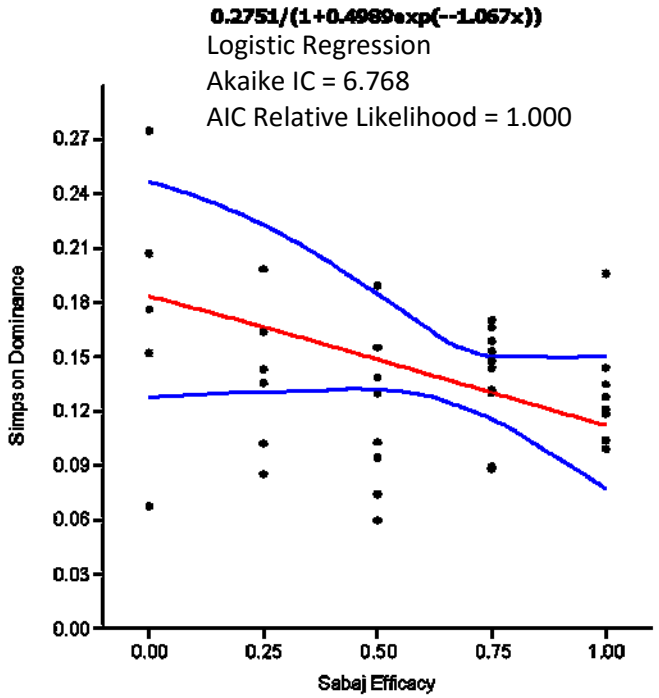
Site	GJ1		GJ3		GJ7		MO4		MO8	
Diversity Index	**Index**	**Change**	**Index**	**Change**	**Index**	**Change**	**Index**	**Change**	**Index**	**Change**
Simpson Dominance	0.118	0.03	0.104	0.03	0.130	0.03	0.099	0.02	0.121	0.03
Shannon H	2.325	0.58	2.492	0.62	2.365	0.59	2.510	0.63	2.438	0.61
Evenness e^2/H	0.640	0.16	0.604	0.15	0.626	0.16	0.684	0.17	0.572	0.14
Brillouin	2.131	0.53	2.310	0.58	2.191	0.55	2.333	0.58	2.227	0.56
Menhinick	1.471	0.37	1.549	0.39	1.367	0.34	1.405	0.35	1.712	0.43
Margalef	3.142	0.79	3.714	0.93	3.174	0.79	3.333	0.83	3.865	0.97
Equitability J	0.839	0.21	0.832	0.21	0.835	0.21	0.869	0.22	0.814	0.20
Fisher Alpha	4.988	1.25	5.933	1.48	4.874	1.22	5.156	1.29	6.458	1.61
Berger-Parker	0.202	0.05	0.183	0.05	0.257	0.06	0.174	0.04	0.226	0.06
Fogleman S	26.746	6.69	30.209	7.55	27.638	6.91	28.511	7.13	30.209	7.55
Site	MO10		UC1		UC2		UC3			
Diversity Index	**Index**	**Change**	**Index**	**Change**	**Index**	**Change**	**Index**	**Change**		
Simpson Dominance	0.196	0.05	0.166	0.04	0.128	0.03	0.148	0.04		
Shannon H	1.779	0.44	2.233	0.56	2.311	0.58	2.216	0.55		
Evenness e^2/H	0.658	0.16	0.518	0.13	0.672	0.17	0.510	0.13		
Brillouin	1.666	0.42	1.994	0.50	2.154	0.54	2.061	0.52		
Menhinick	0.812	0.20	1.806	0.45	1.198	0.30	1.387	0.35		
Margalef	1.663	0.42	3.696	0.92	2.769	0.69	3.316	0.83		
Equitability J	0.810	0.20	0.772	0.19	0.853	0.21	0.767	0.19		
Fisher Alpha	2.237	0.56	6.425	1.61	4.083	1.02	5.105	1.28		
Berger-Parker	0.283	0.07	0.272	0.07	0.262	0.07	0.265	0.07		
Fogleman S	19.726	4.93	28.511	7.13	25.833	6.46	28.511	7.13		
Site	UC4		UC10		DL5		DL6			
Diversity Index	**Index**	**Change**	**Index**	**Change**	**Index**	**Change**	**Index**	**Change**		
Simpson Dominance	0.128	0.03	0.135	0.03	0.144	0.04	0.153	0.04		
Shannon H	2.360	0.59	2.349	0.59	2.213	0.55	2.199	0.55		
Evenness e^2/H	0.623	0.16	0.551	0.14	0.538	0.13	0.563	0.14		
Brillouin	2.164	0.54	2.182	0.55	2.036	0.51	1.987	0.50		
Menhinick	1.483	0.37	1.427	0.36	1.458	0.36	1.570	0.39		
Margalef	3.280	0.82	3.476	0.87	3.257	0.81	3.231	0.81		
Equitability J	0.833	0.21	0.798	0.20	0.781	0.20	0.793	0.20		
Fisher Alpha	5.202	1.30	5.394	1.35	5.130	1.28	5.285	1.32		
Berger-Parker	0.248	0.06	0.229	0.06	0.250	0.06	0.278	0.07		
Fogleman S	27.638	6.91	29.368	7.34	27.638	6.91	26.746	6.69		

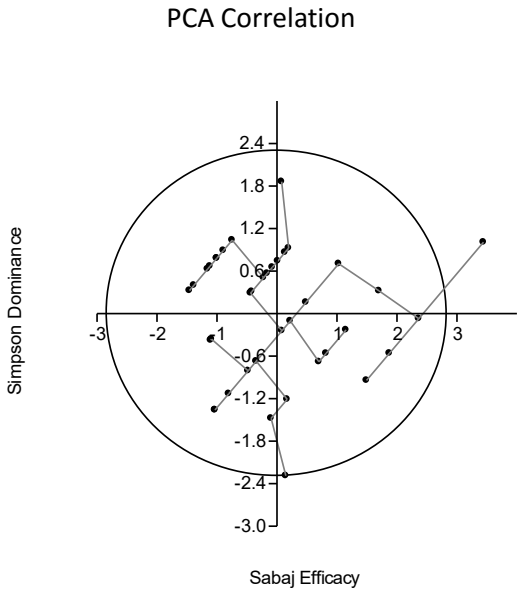
Arcsine transformed data for absolute percent cover estimates of taxa were used to calculate all diversity indices. Also shown are the minimum detection levels of percent change (+/-). These detection levels were set at +/- 25%, as were used in establishing confidence intervals for diversity (figure 13).

Figure 15: Linear Regression, Logistic Regression & PCA Correlation of Sabaj Efficacy v. Simpson's Dominance.



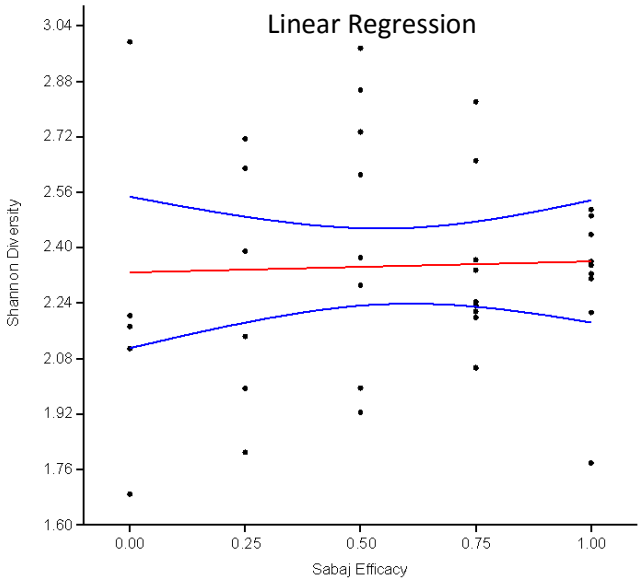
Y intercept: 0.151
Chi square: 0.072
r: -0.211
r^2: 0.045
p (a=1): 0.000



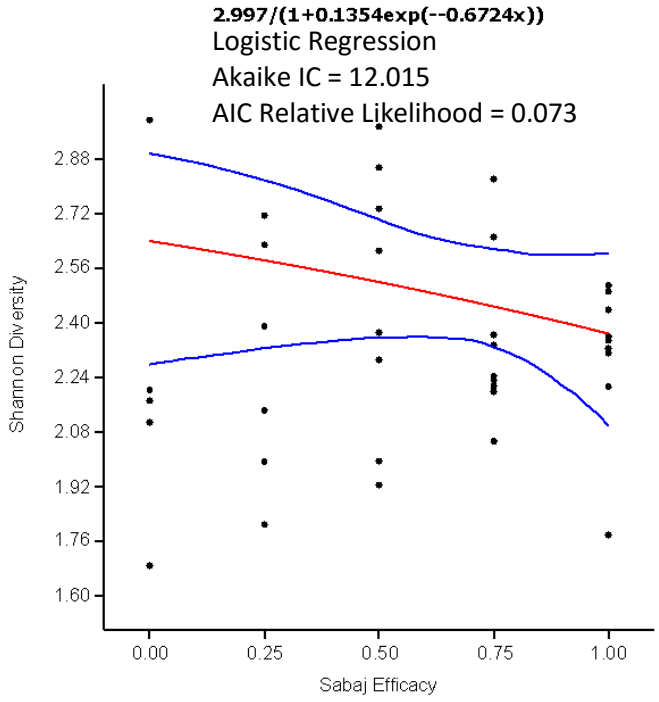


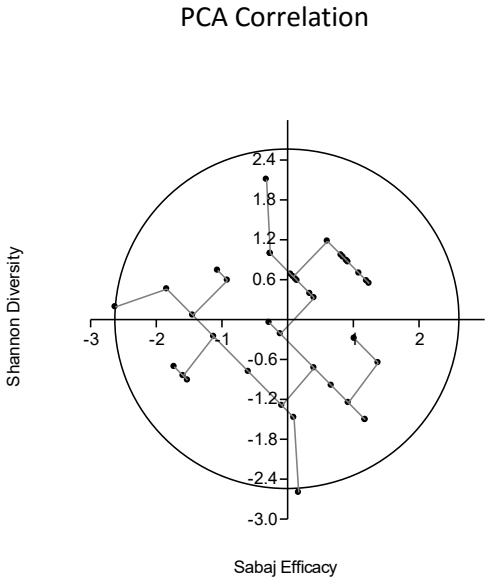
Arcsine transformed data of mean percent cover per species were used to derive Sabaj efficacy and Simpson's dominance per study site. Sabaj efficacy and Simpson's dominance values were uniformly distributed. Sabaj efficacy was defined as the proportion of community types (native, exotic, woody & herbaceous) requiring 5 transects; 500 points per transect & 2500 points per site to detect a minimum 25% in community structure at 90% confidence (i.e.,10% error).

Figure 16: Linear Regression, Logistic Regression & PCA Correlation of Sabaj Efficacy v. Shannon's Diversity.



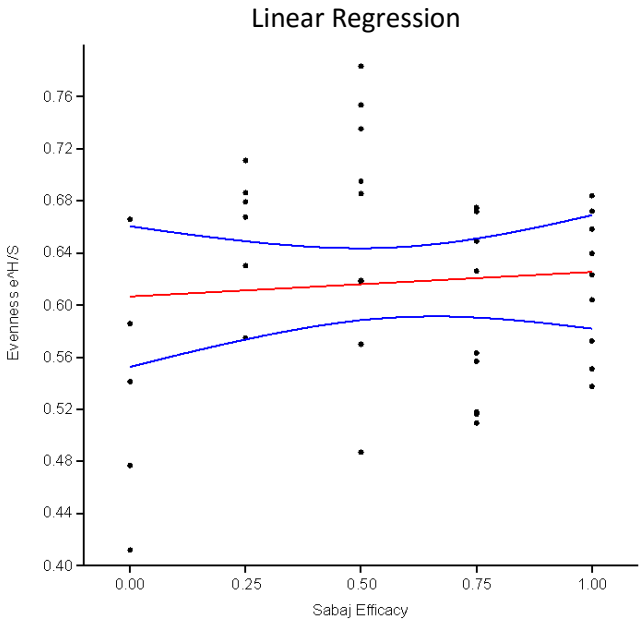
Y intercept: 2.329
Chi square: 4.148
r: 0.032
r^2: 0.001
p (a=1): 6.78E-07



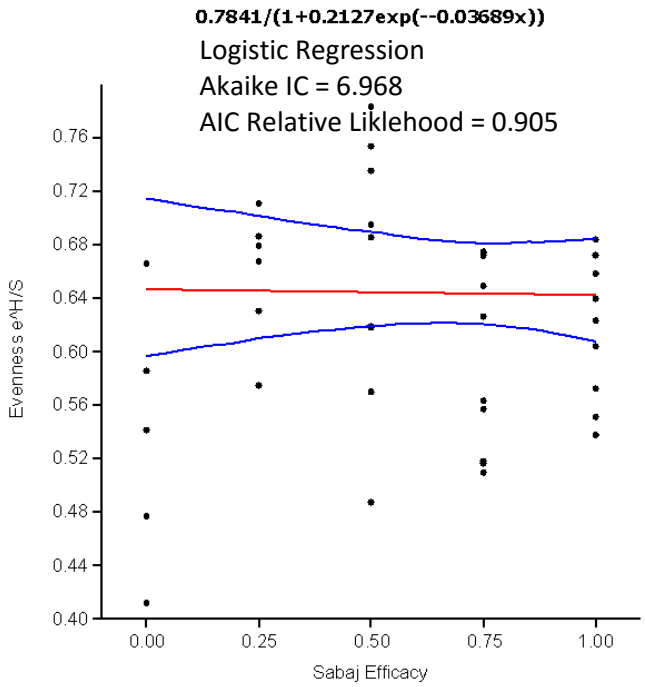


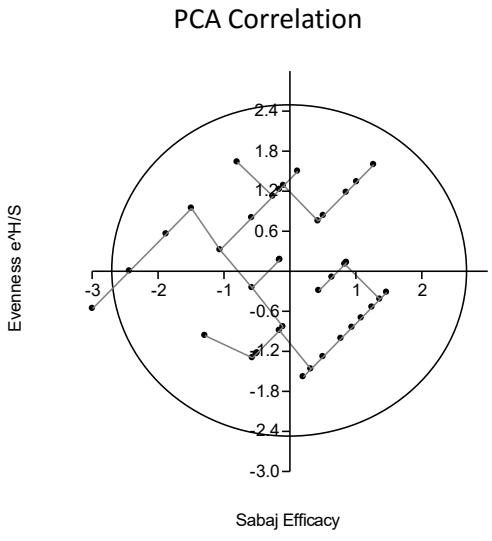
Arcsine transformed data of mean percent cover per species were used to derive Sabaj efficacy and Shannon's diversity per study site. Sabaj efficacy and Shannon's diversity values were uniformly distributed. Sabaj efficacy was defined as the proportion of community types (native, exotic, woody & herbaceous) requiring 5 transects; 500 points per transect & 2500 points per site to detect a minimum 25% in community structure at 90% confidence (i.e.,10% error).

Figure 17: Linear Regression, Logistic Regression & PCA Correlation of Sabaj Efficacy v. Buzas & Gibson's Evenness.



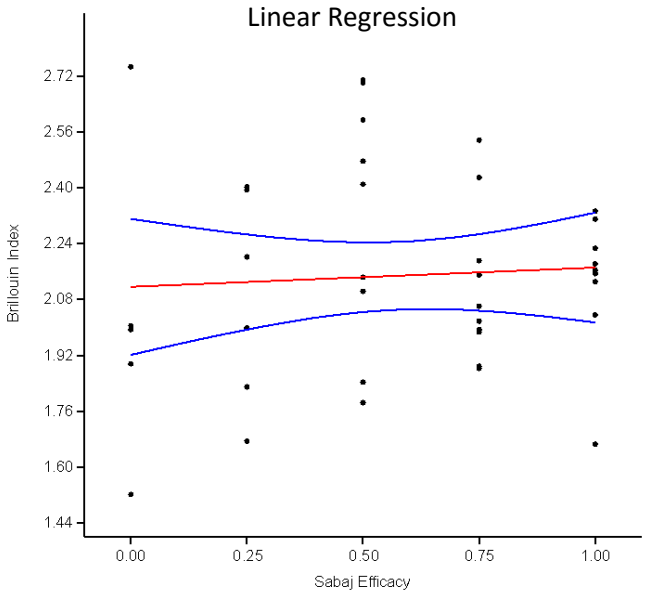
Y intercept: 0.607
Chi square: 0.253
r: 0.077
r^2: 0.006
p (a=1): 1.73E-24



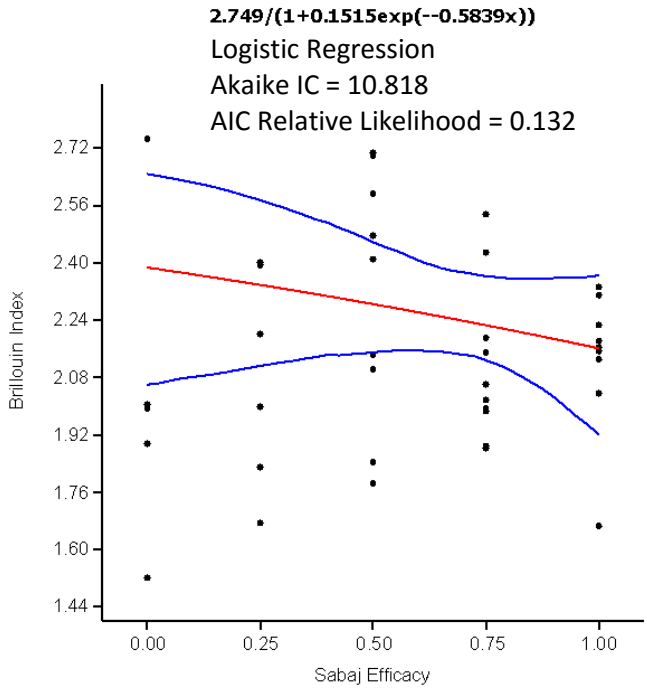


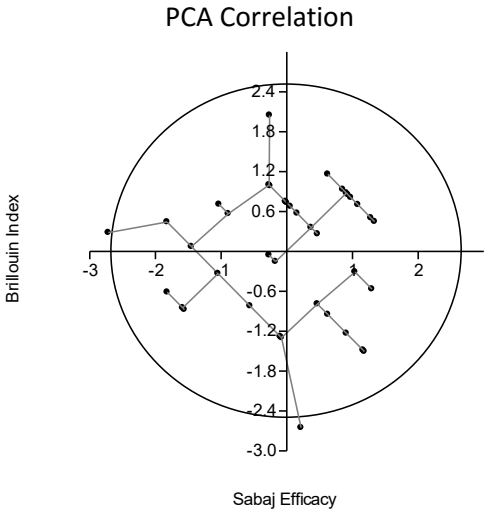
Arcsine transformed data of mean percent cover per species were used to derive Sabaj efficacy and Buzas & Gibson's evenness per study site. Sabaj efficacy and evenness values were uniformly distributed. Sabaj efficacy was defined as the proportion of community types (native, exotic, woody & herbaceous) requiring 5 transects; 500 points per transect & 2500 points per site to detect a minimum 25% in community structure at 90% confidence (i.e.,10% error).

Figure 18: Linear Regression, Logistic Regression & PCA Correlation of Sabaj Efficacy v. Brillouin's Index.



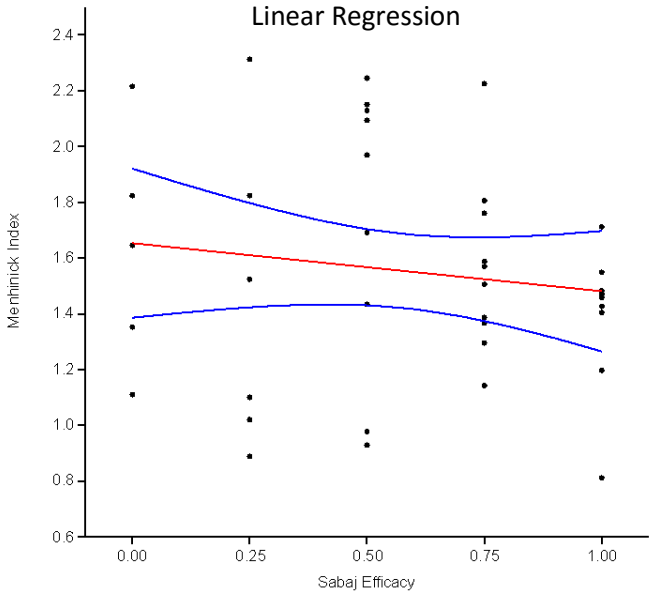
Y intercept: 2.116
Chi square: 3.295
r: 0.063
r^2: 0.004
p (a=1): 1.16E-07



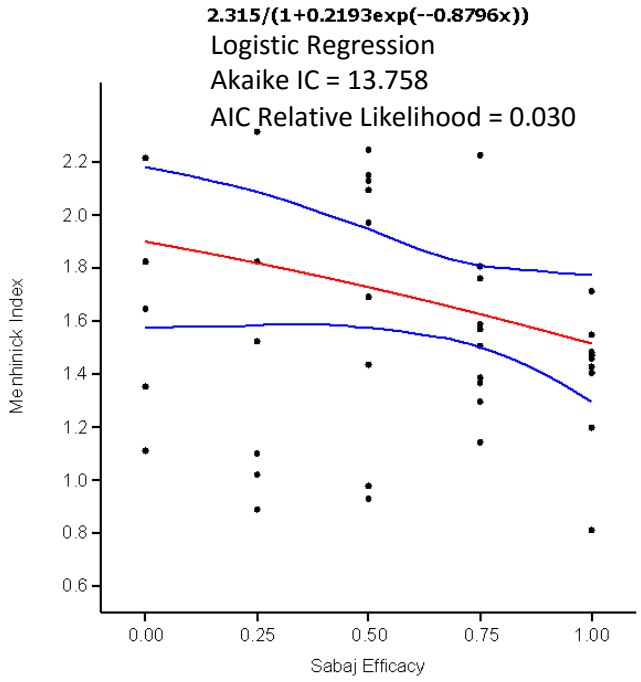


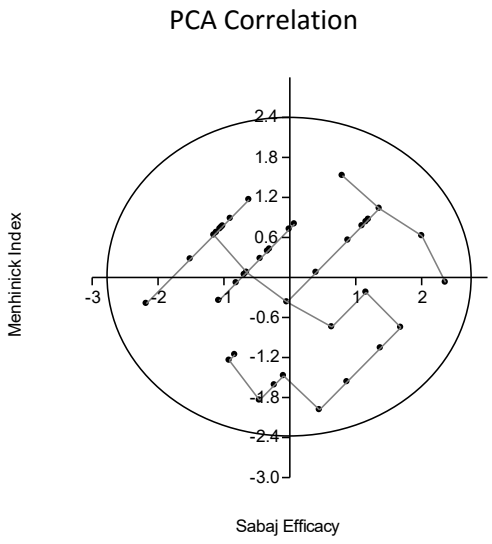
Arcsine transformed data of mean percent cover per species were used to derive Sabaj efficacy and Brillouin's diversity per study site. Sabaj efficacy and Brillouin's diversity values were uniformly distributed. Sabaj efficacy was defined as the proportion of community types (native, exotic, woody & herbaceous) requiring 5 transects; 500 points per transect & 2500 points per site to detect a minimum 25% in community structure at 90% confidence (i.e.,10% error).

Figure 19: Linear Regression, Logistic Regression & PCA Correlation of Sabaj Efficacy v. Menhinick's Index.



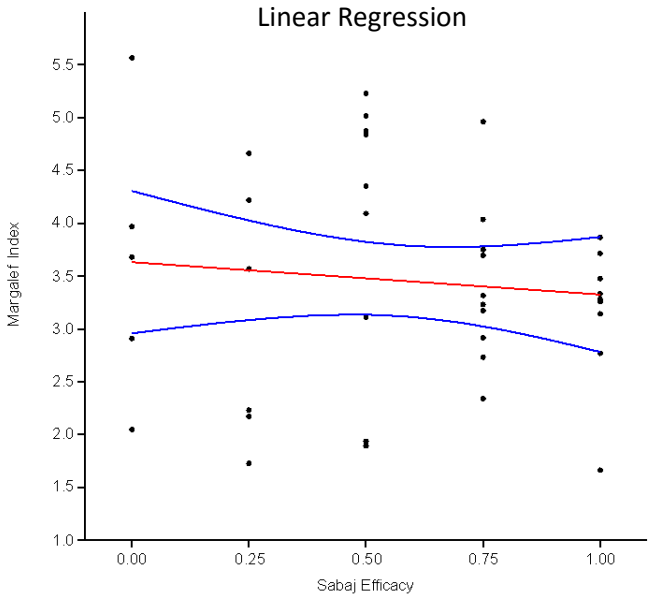
Y intercept: 1.653
Chi square: 6.211
r: -0.141
r^2: 0.020
p (a=1): 8.28E-07



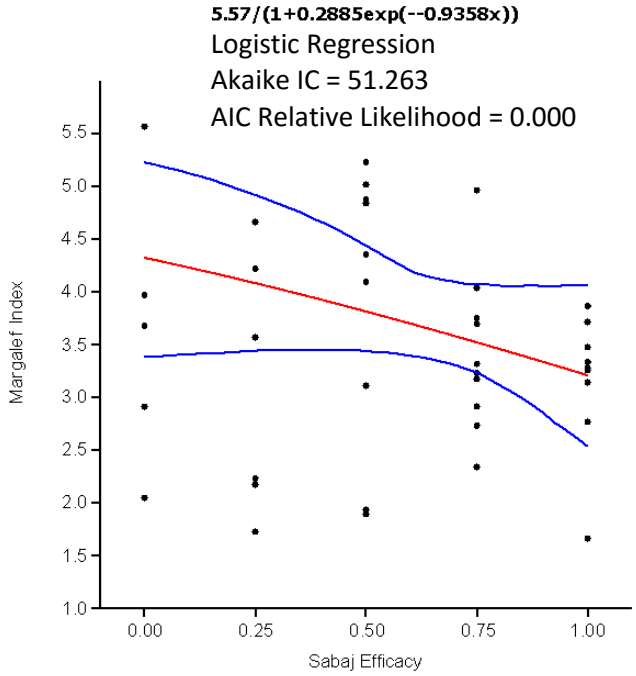


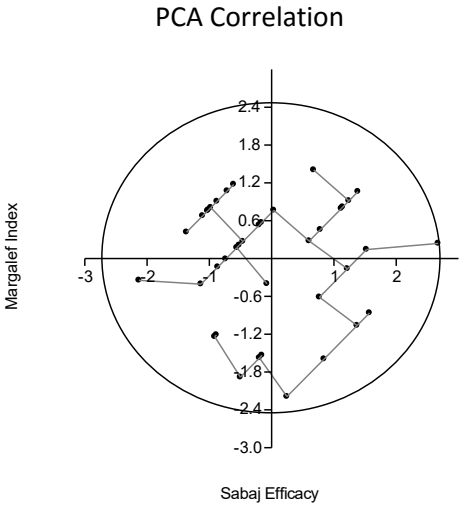
Arcsine transformed data of mean percent cover per species were used to derive Sabaj efficacy and Menhinick's diversity per study site. Sabaj efficacy and Menhinick's diversity values were uniformly distributed. Sabaj efficacy was defined as the proportion of community types (native, exotic, woody & herbaceous) requiring 5 transects; 500 points per transect & 2500 points per site to detect a minimum 25% in community structure at 90% confidence (i.e.,10% error).

Figure 20: Linear Regression, Logistic Regression & PCA Correlation of Sabaj Efficacy v. Margalef's Index.



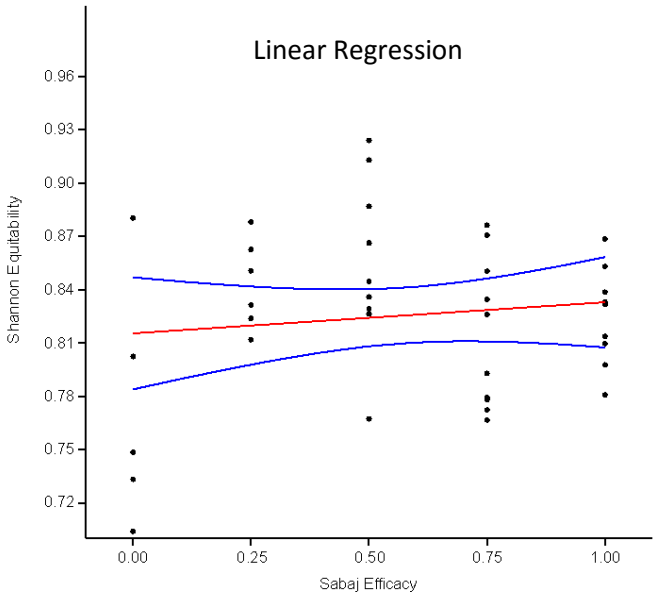
Y intercept: 3.361
Chi square: 39.430
r: -0.100
r^2: 0.010
p (a=1): 0.013



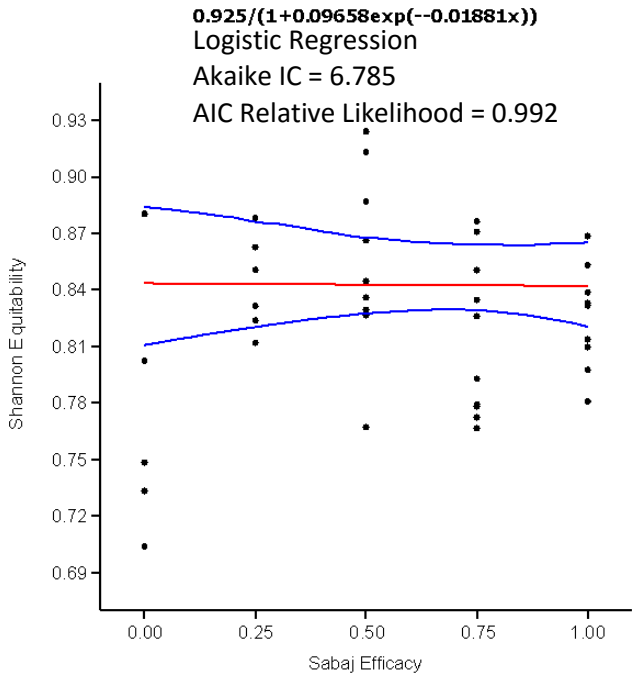


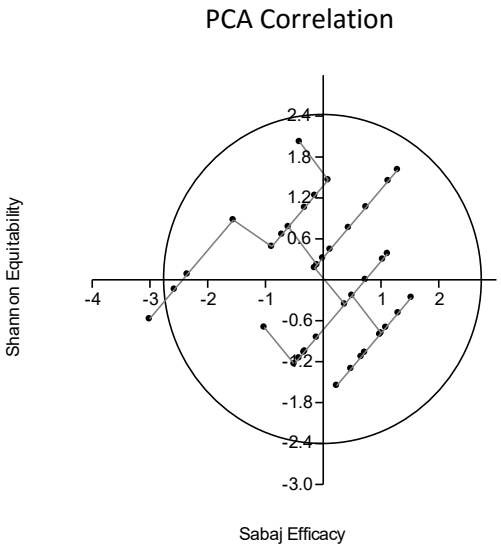
Arcsine transformed data of mean percent cover per species were used to derive Sabaj efficacy and Margalef's diversity per study site. Sabaj efficacy and Margalef's diversity values were uniformly distributed. Sabaj efficacy was defined as the proportion of community types (native, exotic, woody & herbaceous) requiring 5 transects; 500 points per transect & 2500 points per site to detect a minimum 25% in community structure at 90% confidence (i.e.,10% error).

Figure 21: Linear Regression, Logistic Regression & PCA Correlation of Sabaj Efficacy v. Shannon's Equitability (J).



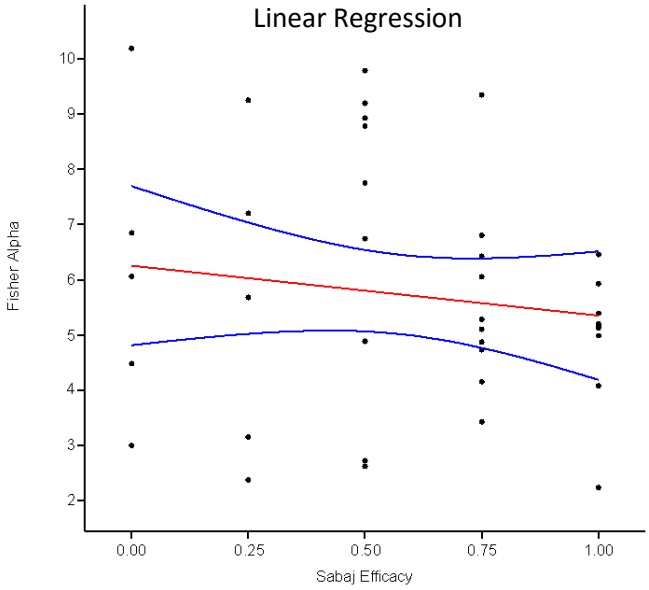
Y intercept: 0.815
Chi square: 0.086
r: 0.122
r^2: 0.015
p (a=1): 7.73E-33



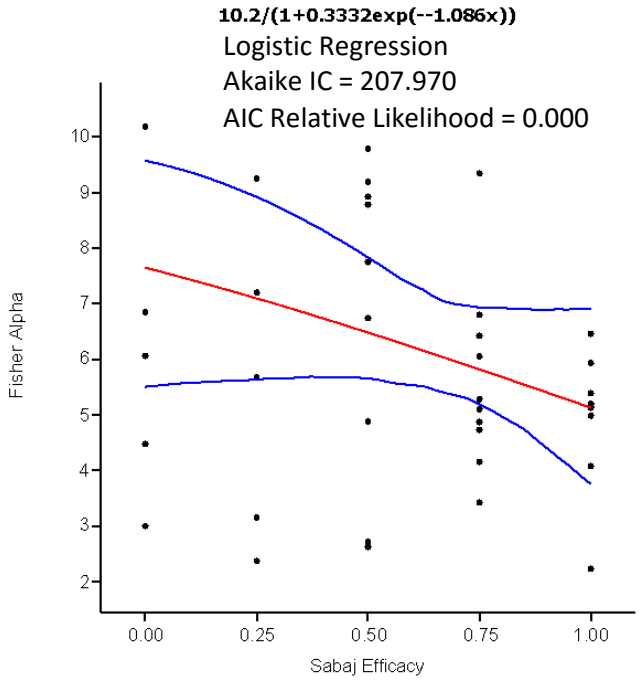


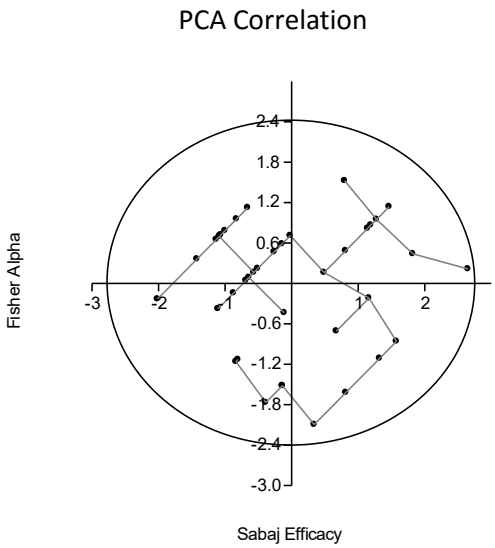
Arcsine transformed data of mean percent cover per species were used to derive Sabaj efficacy and Shannon's equitability per study site. Sabaj efficacy and Shannon's equitability values were uniformly distributed. Sabaj efficacy was defined as the proportion of community types (native, exotic, woody & herbaceous) requiring 5 transects; 500 points per transect & 2500 points per site to detect a minimum 25% in community structure at 90% confidence (i.e.,10% error).

Figure 22: Linear Regression, Logistic Regression & PCA Correlation of Sabaj Efficacy v. Fisher's Alpha.



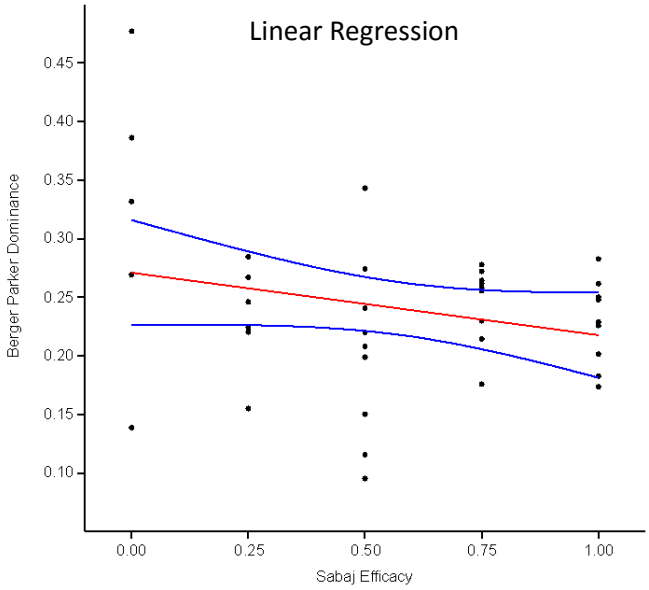
Y intercept: 6.255
Chi square: 180.420
r: -0.138
r^2: 0.019
p (a=1): 0.083



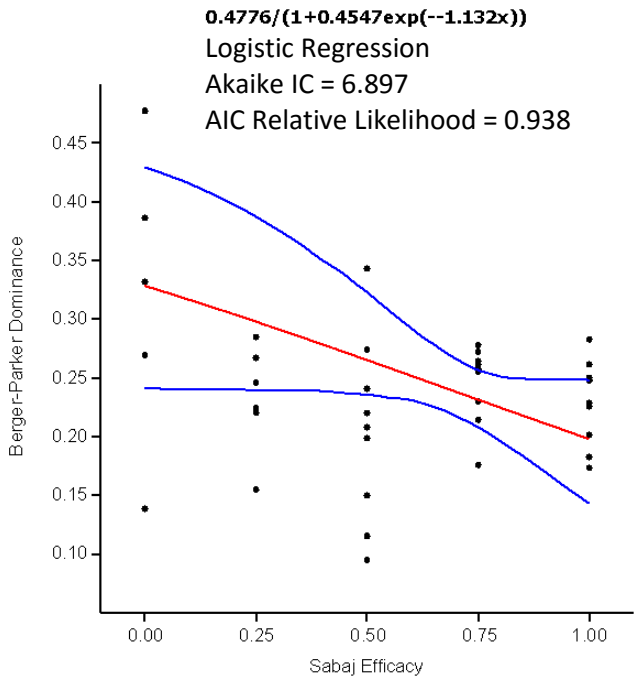


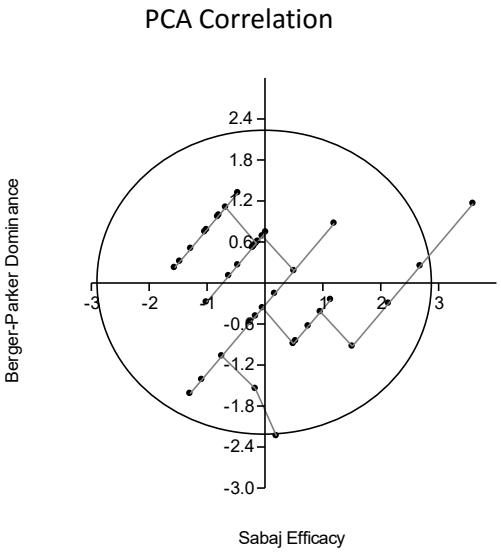
Arcsine transformed data of mean percent cover per species were used to derive Sabaj efficacy and Fisher's alpha per study site. Sabaj efficacy and Fisher's alpha values were uniformly distributed. Sabaj efficacy was defined as the proportion of community types (native, exotic, woody & herbaceous) requiring 5 transects; 500 points per transect & 2500 points per site to detect a minimum 25% in community structure at 90% confidence (i.e.,10% error).

Figure 23: Linear Regression, Logistic Regression & PCA Correlation of Sabaj Efficacy v. Berger-Parker's Dominance.



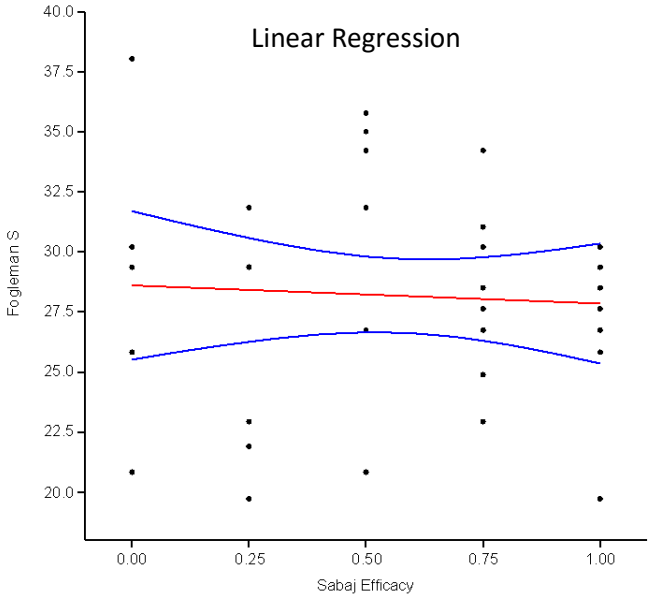
Y intercept: 0.271
Chi square: 0.176
r: -0.254
r^2: 0.064
p (a=1): 2.40E-28



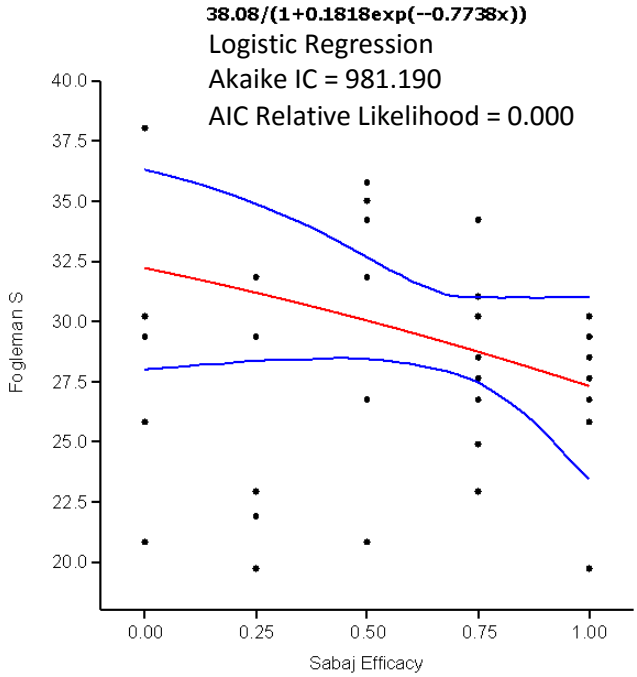


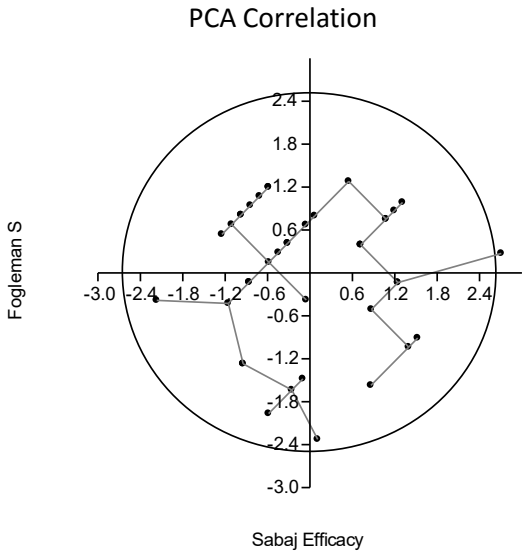
Arcsine transformed data of mean percent cover per species were used to derive Sabaj efficacy and Berger-Parker's dominance per study site. Sabaj efficacy and Berger-Parker's dominance values were uniformly distributed. Sabaj efficacy was defined as the proportion of community types (native, exotic, woody & herbaceous) requiring 5 transects; 500 points per transect & 2500 points per site to detect a minimum 25% in community structure at 90% confidence (i.e.,10% error).

Figure 24: Linear Regression, Logistic Regression & PCA Correlation of Sabaj Efficacy v. Fogleman's Richness (S).



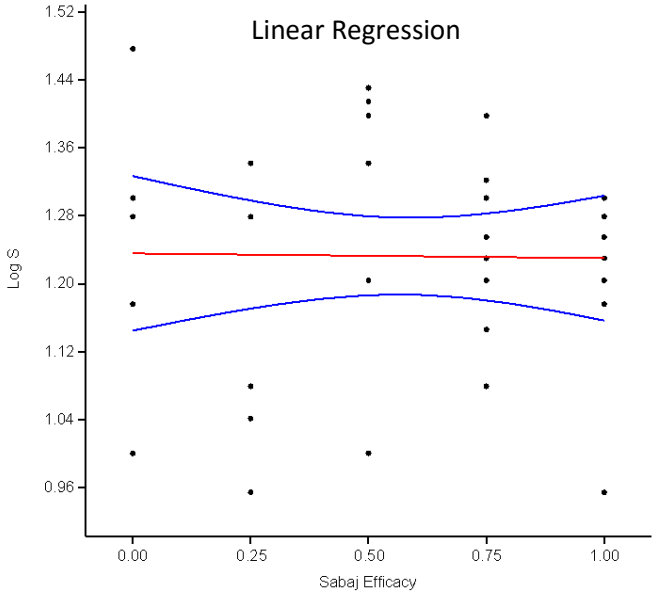
Y intercept: 28.612
Chi square: 830.330
r: -0.054
r^2: 0.003
p (a=1): 0.448



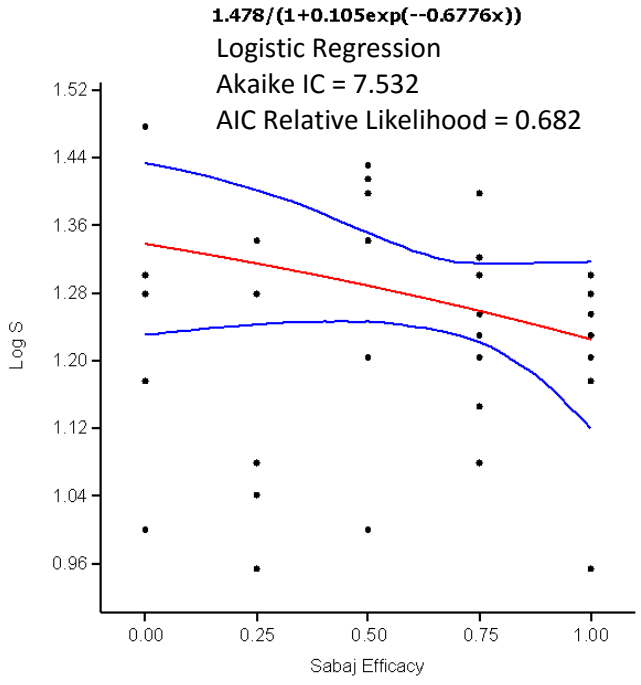


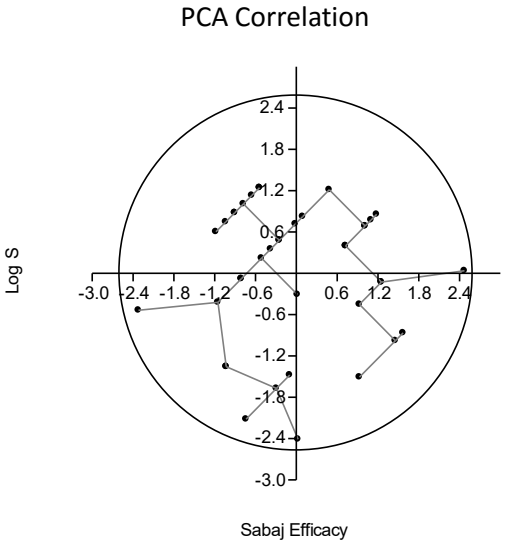
Arcsine transformed data of mean percent cover per species were used to derive Sabaj efficacy and Fogleman's richness per study site. Sabaj efficacy and Fogleman's richness values were uniformly distributed. Sabaj efficacy was defined as the proportion of community types (native, exotic, woody & herbaceous) requiring 5 transects; 500 points per transect & 2500 points per site to detect a minimum 25% in community structure at 90% confidence (i.e.,10% error).

Figure 25: Linear Regression, Logistic Regression & PCA Correlation of Sabaj Efficacy v. Log Richness (S).



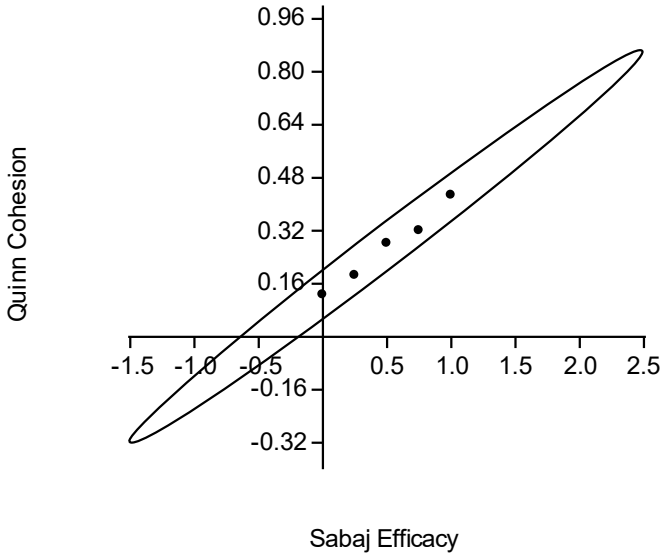
Y intercept: 1.236
Chi square: 0.722
r: -0.014
r^2: 0.000
p (a=1): 3.44E-17





Arcsine transformed data of mean percent cover per species were used to derive Sabaj efficacy and log richness per study site. Sabaj efficacy and log richness values were uniformly distributed. Sabaj efficacy was defined as the proportion of community types (native, exotic, woody & herbaceous) requiring 5 transects; 500 points per transect & 2500 points per site to detect a minimum 25% in community structure at 90% confidence (i.e.,10% error).

Figure 26: The Quinn Cohesion Index.



The Quinn Cohesion Index (QCI) was derived from the PCA correlation matrices in figures 15 through 25, excluding Fisher's alpha and Fogleman's S. Fisher's alpha and Fogleman's S were independent ($p > 0.05$) of Sabaj efficacy per simple regression. QCI is an approximation of the cohesion between the variables used in the PCA (i.e., Sabaj efficacy and 9 diversity indices). The index ranges from zero (no cohesion) to one (maximum cohesion). QCI is defined as the proportion of diversity indices with zero line breaks per Sabaj efficacy group/ sum of diversity indices used per Sabaj efficacy group in the PCA correlation matrices (i.e., 9); divided by the proportion of the number of line breaks per Sabaj efficacy/ diversity index pairing to the sum of all line breaks in all PCA correlation matrices, plus unity (one) (table 8). Data points were plotted as three-point moving averages.

Table 8: Calculating the Quinn Cohesion Index:

Summary Line Breaks per Efficacy Group:

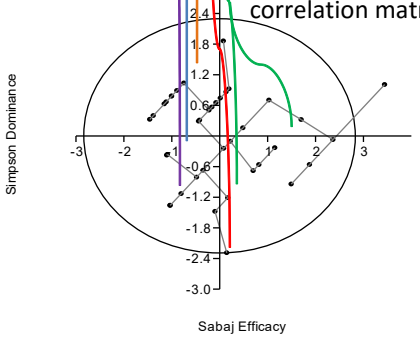
S.E.	S.D.	S.H.	Ev	Br	Mn	Mr	S.J.	B.P.	L.S.	Sum	Den	Den + 1	Num	QQ
1		1	1	0	1	0	1	0	0	1	5	0.12	1.12	0.56	0.495
0.75		1	1	1	1	1	1	0	0	0	6	0.15	1.15	0.33	0.291
0.5		0	1	2	2	1	2	1	0	2	11	0.27	1.27	0.22	0.175
0.25		2	0	0	0	2	1	0	1	1	7	0.17	1.17	0.44	0.380
0		1	2	1	2	1	1	1	1	2	12	0.29	1.29	0.00	0.000
											41				

5 over 9 (# indices)

5 over 41

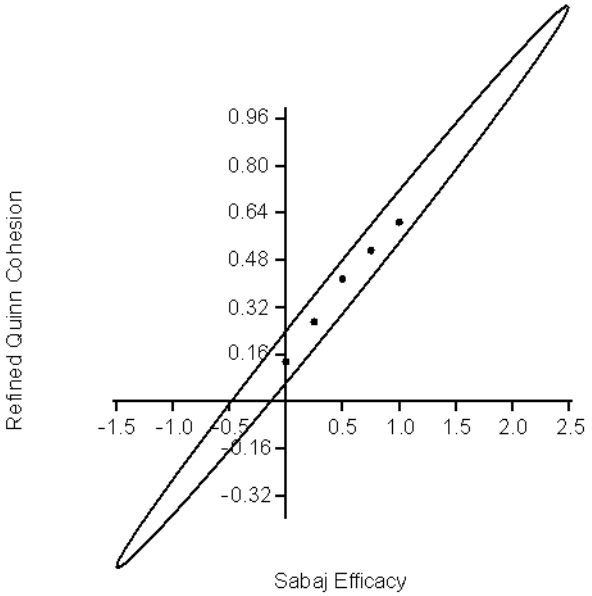
0.56 over 1.12

Arrows (left) indicate line breaks per Sabaj Efficacy/ diversity pairing in the PCA correlation matrix.



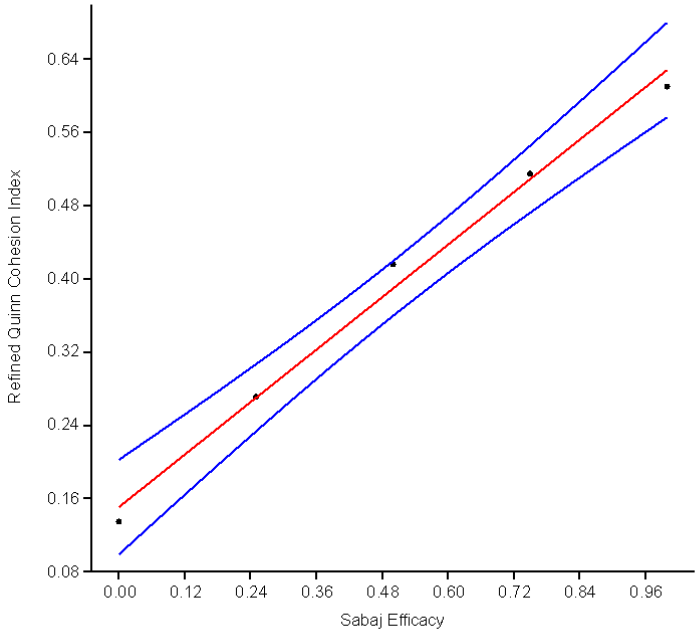
The Quinn Cohesion Index (QCI) was derived by plotting the Quinn Quotient (y-axis) to Sabaj efficacy (x-axis) as a three-point moving average (see figure 26). S.E. = Sabaj efficacy; S.D. = Simpson's dominance; S.H. = Shannon's H; Ev = Evenness (e^H/S); Br = Brillouin's index; Mn = Menhinick's index; Mr = Margalef's index; S.J. = Shannon's J; B.P. = Berger-Parker's dominance; L.S. = Log richness; Den = Denominator; Num = Numerator; QQ = Quinn Quotient.

Figure 27: The Refined Quinn Cohesion Index.



The Refined Quinn Cohesion Index (r-QCI) was derived from the PCA correlation matrices, using only those indices shown to a) have linear relationships with efficacy per linear regression and b) contribute significant information per Akaike Relative Likelihood, shown in figures 15 through 25. Simpson's dominance, Berger-Parker's dominance, Buzas & Gibson's evenness, and Pielou's J were used, as shown in table 8, to derive the r-QCI. The index is an approximation of the cohesion between the variables used in the PCA. The index ranges from zero (no cohesion) to one (maximum cohesion). Data points were plotted as three-point, moving averages.

Figure 28: The r-QCI Simple Regression.



Y intercept: 0.151
Chi square: 0.001
r: 0.995
r^2: 0.991
p (a=1): 0.0003

The r-QCI simple regression was defined as the linear regression resulting from the three-point moving averages plotted in figure 27, where Sabaj efficacy was the x-axis variable & R-QCI the y-axis variable.

Discussion

The foray into The Theory of Quantum Microbiogeography begins with assessments of distributions. The theory predicts a parsimonious quantum of highly efficacious study sites with regard to sampling of ecologically relevant community types and species of interest approximate beta diversity. The various distributions identified among taxa, community types (native, exotic, woody and herbaceous), barren ground, Sabaj efficacy, and eleven diversity indices are given in figures 2 through 8, and tables 1 and 2. These analyses were conducted to determine whether or not various data constructs obeyed assumptions of parametric statistics. Briefly, parametric statistics assume a normal distribution, with the mean and standard deviation adherent to the central limit theorem. Nonparametric procedures are often employed when distributions are not normal, or do not obey key assumptions of normality. However, these procedures are less powerful in so much as they tend to increase the probability of committing a type II error, require larger sample size to have the same power as parametric tests, and require use of ranked values rather than actual data (Rosner 2010).

As a primary goal of the research was to identify and implement a quantitative approach for selection of long term monitoring priority sites based upon efficacious sampling of ecologically relevant community types and species of interest, the acquisition of normal data or other distributions adherent to the central limit theorem were of importance. Often, investigators assume frequency distributions obey assumptions of normalcy, but do not test for it, because even when distributions are not normal, residuals are, given adequate sample size. Application of parametric statistics to non-normal data can result in erroneous conclusions. The following details the novel approaches and reasoning employed for use of parametric procedures in formulation of the Gehrt-Mueller Priority Site Determination (GM-PSD).

Arcsine-square root transformed data were used for all distribution tests, excepting log S (richness). Absolute percent cover data for taxa were summed and averaged across all 39 sites for assessment of the species distribution. The species distribution conformed to log normal (figure 3). The log normal distribution is a continuous probability distribution of a random variable whereby the logarithm is normally distributed (Aitchison & Brown 1957). Log normal species distributions are common and exhibit positive skew when a few species are relatively dominant. Skewness can adversely affect some parametric statistical approaches. For log normal distributions, the most precise and efficient method for estimating μ and σ relies on the log transformation (Limpert et al. 2001). Thus, the log transformation of arcsine transformed data would likely yield a species distribution adherent to assumptions of the central limit theorem.

However, these data were not log transformed for several reasons. The log normal distribution obeys the multiplicative version of the central limit theorem in probability theory (Limpert et al. 2001). Limpert et al. (2001) applied a proposed characterization, using the geometric mean and multiplicative standard deviation, yielding standard deviation intervals representative of the normal distribution. The additive effects of the normal distribution parallel the multiplicative effects of the log normal distribution (Limpert

et al. 2001). Of potential importance concerning species distributions, arithmetic means of normal distributions assume independence between all estimates, which seems problematic. As the occurrence of one species often influences occurrences of others, independence of observations among the species frequency distribution is unlikely. Thus, there exist advantages in use of the multiplicative, geometric average of the log normal distribution. The geometric average can be derived from a variety of distributions using specified formulae. Further complicating the issue rests upon outcomes of using the arithmetic or geometric mean of the geometric distribution.

The geometric mean is the arithmetic mean of the logs of the viable under consideration. The geometric mean is equal to or less than the arithmetic mean (Jacquier et al. 2003). Use of the geometric mean in percentage growth forecasts results in downward bias, whereas use of the arithmetic mean can result in upward bias (Jacquier et al. 2003). While the work of Jacquier et al. (2003) is based upon the compounding of interest related to financial investments, the general trends revealed also apply to species distributions. That is, it takes longer to recover from substantial investment losses, even when future returns are high, while relatively less time is needed to earn capital when reserves are high, even if interest rates are comparably lower. The same concepts apply to the reproductive potentials of natural populations. To illustrate the difference between these two averages, the arithmetic mean of means (v. the geometric mean of means) for native, exotic, woody and herbaceous community types were 36.20 (v. 33.97), 37.68 (v. 33.42), 42.63 (v. 40.10), and 32.39 (v. 31.34); respectively, illustrating the geometric mean was consistently less than the arithmetic mean of the geometrically distributed community types.

As with the log normal species distribution, geometric distributions exhibit positive skew, and for large values of *k*, approach a symmetric distribution. That is, small *k* values represent over-dispersion, with the negative binomial approaching the Poisson distribution as parameter *k* approaches infinity (Nåsell 1982). As such, skewness in of itself does not preclude application of parametric tests, especially when the distribution approaches symmetry and variances become homogeneous. The arcsine-square root transformation of absolute proportions of species cover imparted greater symmetry to the species distribution and the derived community distributions by stretching the ends of the distribution. Thus the truncation caused when the mean of the binomial distribution approaching zero or one becomes less severe (Wilson & Hardy 2002).

Ultimately, arithmetic means of geometrically distributed community types were used in formulation of the GM-PSD, as this seemed reasonable in constructing confidence intervals used for predicting change in percent cover of community types over time. In so doing, the requirement that confidence interval estimates use the arithmetic mean and standard deviation for their derivation was achieved, and seemed appropriate given negative binomial distributions of community types approached the Poisson distribution upon arcsine transformation. As such, sequential combining of arcsine transformed, absolute percent cover estimates of taxa into community types, yielding geometric distributions of community types, were used with the arithmetic mean and standard deviations to construct exact sets of confidence intervals for the purpose of defining Sabaj efficacy.

While the species distribution for raw data was also log normal (data not shown), arcsine transformed percent cover estimates resulted in improved Sabaj efficacy across a spectrum of individual study sites. That is, many of the 39 study sites exhibited increased efficacy for community types using arcsine transformed data. These improvements resulted from increased homoscedasticity. As it was necessary to a) establish confidence intervals about the means of community types, b) utilize community types for determination of Sabaj efficacy and c) regress Sabaj efficacy with an array of diversity indices; log transformation of the already arcsine transformed, log normal species distribution was unnecessary. Furthermore, use of simple and multiple logistic regression is appropriate when negative binomial distributions display symmetry (Wilson & Hardy 2002).

Also impacting the decision making process were ubiquitous occurrences of barren ground throughout the lower Dolores watershed. As *relative* species abundances are used for log transformation, impacts of barren ground (which were significant along the lower Dolores) become obscured. Alternatively, ordinal (class) scale data can be used for species distributions, but such data limit application of an array of higher order statistical analyses (Adler et al. 2010). In preserving the barren ground element among community assemblages, land managers are afforded the opportunity to assess potential changes in barren ground percent cover as alterations occur within the watershed. However, understand for those diversity indices assessing abundance, relative (not absolute) species abundance was used.

The arcsine transformation is applied to data expressed as percentages, and is restricted to data obtained from counts. Proportions are used for the transformation. The distribution of percentages is often binomial, and arcsine transformation of count data tends to make these distributions normal (Rasmussen & Dunlap 1991). It is also recommended to use a modification prior to arcsine transformation for proportions of zero and one. The transformation for these proportions is improved by replacing zero with (1/4n), and one with [1-(1/4n)], where n is the number of observations based on which p is estimated for each group (Rasmussen & Dunlap 1991). However, these modifications were not applied in order to preserve the elements of non-occurrence (i.e., zero p) and saturation (i.e., one p) as it pertained to absolute percent cover estimates.

Initially, the arcsine-square root transformation was applied to all proportions for all taxa per transect. As such, the only instances in which zero proportions were encountered was when a given species did not occur along a given transect, but did occur along other transect(s) within a given study site. Then, arcsine transformed, absolute percent cover estimates for each taxon were averaged across five transects per site. Thus, there were not any zero proportions (p) of taxa used in any subsequent analyses. Absent these modifications, zero p remained zero p and one p transformed to 0.90 p upon arcsine transformation. As no species exhibited 1.00 p across all five transects for any given site, all transformed species averages per site were less than 0.90 p. By not implementing these modifications, homoscedasticity was improved while the original, log normal species distribution was retained. As noted, there are several advantages to using log normal, rather than normal species distributions for statistical analyses.

The arcsine transformation yields proportions in radians. The resulting angle ranges from –π/2 to π/2. Results can be expressed in degrees by multiplying values by 180/π (Rasmussen & Dunlap 1991). Sequential combining of arcsine transformed, absolute percent cover estimates of species into ecologically relevant community types resulted in geometric distributions for three of four community types (with the exotic community deviating somewhat from this assumption). The geometric distribution is especially useful in ecology, as it is a niche apportionment model, assessing resource allocation in a linear fashion (Motomura 1932). The geometric series is closely related to the dominance pre-emption model, having the least evenness of existing niche apportionment models (Tokeshi 1990).

Establishment of confidence intervals about the means of geometric distributions has long been problematic. Historically, many have employed the approach based upon inverting an equal-tailed test, giving standard and exact confidence interval estimates in distributions including binomial, Poisson, negative binomial, geometric and hypergeometric (Blaker 2000). Blyth & Still (1983) report an exact confidence set has coverage probability larger than or equal to the nominal level for all possible parameter values. That is, the exact confidence interval set for a geometric distribution is more, not less, conservative than the set derived from existing, modified approaches. Thus, exact confidence interval sets were utilized to ensure assessment of change in community dynamics utilized the most conservative and reliable of approaches.

Sabaj efficacy and eleven diversity indices represent the final component of distribution analyses (table 2). The Sabaj Efficacy Index was calculated as the proportion of community types requiring five transects, with 500 points per transect and 2500 points per study site, to assess 25% or greater change in community composition, using single point in time parameter estimates for confidence interval estimates (Elzinga et al. 2001). Standard formulae were used to calculate ten diversity indices, with the eleventh (Fogleman's richness) described in the methods. For those indices requiring counts of species, arcsine transformed percent cover estimates of taxa were used. Sabaj efficacy and all diversity indices, excepting log S and Fogleman's S, were calculated using arcsine transformed, absolute percent cover estimates of taxa, averaged across five transects *per* study site. Counts of the number of species *per* site were used to calculate log S and Fogleman's S.

Sabaj Efficacy and all diversity indices assessed conformed to uniform distributions (table 2). The uniform distribution is a family of probability distributions where for each member of the family, all intervals of the same length are equally probable (Kuipers & Niederreiter 2006). Uniform distributions can be transformed to normal, using a variety of approaches, such as the Ziggurat algorithm or Box-Muller transform (Box & Cox 1964). Uniform distributions were not transformed to normal in the interest of conservatism. Regression analysis is highly sensitive to deviations from normal as it pertains to mean and variance. However, the uniform distribution adheres to these assumptions, as the mean and variance of the uniform do not deviate from normal when sample size is sufficient (Wilcox 2010). Furthermore, standard deviation and variance estimates from the uniform distribution are more, not less, conservative than those from the normal. That is, the standard deviation and variance from the uniform are larger than those from the normal

equivalent (Kuipers & Niederreiter 2006).

As it was important relating to theoretical implications to obtain the most conservative estimates from linear regressions of Sabaj efficacy with diversity for hypothesis testing, uniform distributions appeared to provide an added element of security. Specifically, it was necessary to determine a) the potential independence of efficacy from elements of alpha diversity and/ or b) the degree of potential interaction of efficacy with elements of alpha diversity. While small probability (p) values (usually < 0.05) are indicative of predictive, linear relationships between *X* and *Y* variables, they make no predictions concerning the proportion of total variation explained by the model. To clarify, p values assess the null hypothesis of the slope of the regression line equaling zero. However, it is not uncommon for extremely small p values to result from large datasets even when no linear relationships exist (Johnson 1999). It will become apparent, at least in some cases, that the effects of a large dataset obscured determinations of linearity.

The p values from simple regressions were also assessed to determine potential relationships between efficacy and diversity for the purpose of calculating Quinn Cohesion (figure 26). Those diversity indices regressed with efficacy where $p < 0.05$ were used to calculate QCI (table 8). As the lower Dolores 2010 dataset encompassed 97,500 data points assessed across 39 sites, it may have been preferable to use r values (rather than p values) to assess the potential for linear relationships. The correlation coefficient (r) ranges from -1.00 to 1.00, and measures the strength of the direction of a linear relationship between two variables (Sheskin 2004). When r approaches zero, no linear relationship exists given distributional assumptions were obeyed. However, a quandary presented itself in attempting to use r values for determination of potential linearity.

The r values from simple regression (figures 15 through 25) ranged from -0.014 (log S v. Sabaj Efficacy) to -0.254 (Berger-Parker dominance v. Sabaj Efficacy). Note the sign of r indicates the direction of the relationship, thus the range was defined independent of sign. In general, r values were indicative of weak linear relationships at best. The r^2 values for linear regressions were universally small, with 10 of 11 indices having $r^2 < 0.05$ (Berger-Parker dominance v. Sabaj Efficacy, $r^2 = 0.064$). The coefficient of determination (r^2) indicates the proportion of total variation explained by the model (Sheskin 2004). That is, r^2 represents the fraction of variation in the y-axis variable explained by its relationship with the x-axis variable, which was generally less than five percent. As such, it was painfully apparent, regardless of any potential linearity, that relatively little variation in *Y* was explained by *X*. Thus, p values were used for determinations of linearity in simple regressions.

Individual rarefaction, sample rarefaction and SHE analyses were used to assess the ability of the sampling protocol to capture elements of ecosystem diversity. Individual rarefaction (figure 9) was calculated using arcsine transformed, absolute percent cover for all taxa across all sites. The method estimates how the number of species in a sample changes with the number of individuals. That is, individual rarefaction computes how many taxa would be expected in a sample given a smaller number of individuals (Hammer et al. 2001). The chart presents changes in richness with increasing number of individuals *per* study site. Generally, sites with relatively low richness experienced a lower rate of

increase in richness compared to those sites with relatively higher richness. Sites with relatively lower richness appeared to approach the asymptote for richness before those sites exhibiting relatively higher richness. In general, individual rarefaction indicated all sites were under-sampled for the entire range of richness. That is, the point-intercept method failed to capture a variety of rare species.

Sample rarefaction (Mao tau) (figure 10) was calculated using arcsine transformed, absolute percent cover for all taxa across all sites. Sample rarefaction calculates species accumulation curves as a function of the number of samples, and estimates number of species observed for different numbers of samples (Hammer et al. 2001). The sample range was from zero to 39 (the maximum number of samples in the dataset). Note sample rarefaction indicates sampling under-estimated the range of taxa, and it does not appear the species accumulation curve approached the horizontal asymptote. Richness was therefore under-estimated for the ecosystem, largely a consequence of missing rare species.

SHE analysis (figure 11) was conducted using arcsine transformed data for absolute, mean percent cover of all taxa across all sites. SHE analysis examines the relationship between richness (S), Shannon-Wiener diversity (H), and evenness (Pielou J; E). SHE assesses the contributions of S and E to changes in diversity with increasing sampling effort (Hammer et al. 2001). Note the pattern exhibited in the chart was indicative of a log normal species distribution (Hayek & Buzas 1997). Especially revealing were trends exhibited in S, H and E. Concerning evenness, it appeared to plateau after 12 study sites, an especially important observation as it pertains to mean ecosystem diversity and the Gehrt-Mueller Priority Site Determination. The chart also indicates the plateau for contributions of richness to Shannon-Wiener diversity was not attained, but the rate of increase substantially lessened after 28 sites. As such the approach of using 10-cm sampling intervals, resulting in 500 points per transect and 2500 points per site appeared an effective means of characterizing evenness of the lower Dolores watershed. As was the case with individual and sample rarefaction, SHE analysis suggested the complete range of ecosystem richness was not captured.

Individual rarefaction, sample interpolation and SHE analyses indicated ecosystem richness was under estimated relative to sampling effort. The under estimate of richness was primarily due to a failure to detect rare species. While these missing species would contribute to increases in richness and overall diversity, their potential effects on alpha and beta diversity would be negligible. Of greater importance pertaining to the novel concepts presented, the impacts of rare species on standard errors surrounding the means of ecosystem diversity would likely be negligible due to extremely low absolute, arcsine transformed average percent covers within a given study site or group of sites. As the GM-PSD and Theory of Quantum Microbiogeography rest upon the cornerstones of alpha and beta diversity, these missing rare species would likely be of minimal consequence. Evenness has greater impact upon biodiversity than do isolated occurrences of rare species, and so it is notable evenness was captured after the sampling of just 12 study sites. However, it should be noted species existed within the watershed that the sampling protocol failed to identify.

Efficacy of sampling effort was also evaluated as it pertained to species of interest, community types and diversity. These assessments paved the way for development of the novel concepts of Sabaj efficacy, the Gehrt-Mueller Priority Site Determination and The Theory of Quantum Microbiogeography. Table 3 presents arcsine transformed, absolute percent cover estimates and sampling effort required for efficacious sampling of community types. Confidence intervals were used to estimate the number of transects required to detect a minimum 25% change per community type, using 500 points per transect and 2500 points per site. In general, as it pertained to native, exotic, woody and herbaceous communities; sampling effort was deemed sufficient for purposes of the GM-PSD.

The "barren community" is an abiotic feature of the ecosystem, and as such was not included in any additional analyses pertaining to the GM-PSD or Theory of Quantum Microbiogeography. However, land managers wanting to measure changes in mean barren ground cover as tamarisk and knapweed are removed and replaced by other species may use these original, derived values for this purpose. Correlations of changes in percent barren ground cover with potential changes in hydrology and salinity might reveal key ecosystem recovery processes in future years of study. Percent barren ground cover was derived by summing the arcsine transformed covers of native and exotic communities and subtracting those values from 100. A dilemma presented itself insomuch as the arcsine transformation of 1.00 is 0.90 (or 90 percent). Thus, while it might have been preferable to derive barren ground percent cover using 0.90, rather than 1.00, as the subtractive value, table 3 reveals study sites GJ5, GJ10, UC3, UC9, and UC10 would have produced negative barren ground percent covers. Thus, 1.00 was used instead of 0.90. Alternatively, 0.90 could have been used, with those five study sites yielding negative values considered "saturated" for biotic cover, with corresponding barren ground covers of zero percent. Either approach seems useful from a management perspective.

For nine of 39 sites (23%), all four biotic communities required five transects, utilizing 500 points per transect and 2500 points per site, to detect a minimum 25% change per community, as assessed via confidence interval estimates. Ten of 39 sites (26%) met these criteria for three of four biotic community types. Nine of 39 sites (23%) adhered to these requirements for two of four biotic community types. Lastly, just 11 of 39 sites (28%) had one or none of four biotic community types meeting these criteria. For purposes of both long- and short-term monitoring, it is suggested this group of 11 sites, where just one or none of the four community types can be efficaciously sampled, be abandoned from the current study protocol. These low efficacy study sites provide little return in terms of assessing ecosystem recovery on a community level compared to the effort and funding expended for monitoring in future years of study.

Table 4 presents sampling effort required *per* species *per* site, using arcsine transformed data for absolute percent cover of taxa. Confidence interval estimates were used to estimate the number of transects required to detect a minimum 40% change per species, using 500 points per transect and 2500 points per site. Transect values greater than six were omitted, and species where fewer than eight sites were identified for six or fewer transects *per* site were also omitted (excepting cottonwood). While these cut-offs were somewhat arbitrary in nature, it seemed unlikely land managers would invest additional

monitoring funds for the purpose of adding more than one (i.e., more than six total) transect *per* site for purposes of assessing species.

The eight site cut-off for inclusion was also somewhat arbitrary. However, eight sites represented 40 transects and 20,000 data points. Thus it was assumed sufficient data were amassed to evaluate these species in future years of study. Cottonwood did not meet these criteria, but was included because a) it experiences high niche overlap with tamarisk and b) it would be useful going forward to assess the tamarisk/ cottonwood competitive interaction as tamarisk is removed from the lower Dolores, if and when historic hydrologic regimes are restored. Bear in mind, however, that the focus of the current work is on a community, rather than individual species, scale. Thus, far greater emphasis was given to community level analyses.

Tamarisk and knapweed required five or six transects *per* site to assess 40% or greater change in their respective covers among 21 sites, representing 105 transects and 52,500 data points. Analyses presented in figure 12A revealed 21 study sites for assessment of tamarisk were more than sufficient among a variety of study site groupings. Of key importance, the 39 site prediction for efficacious monitoring of tamarisk was 13 sites, and 11 sites for the priority one and priority one/ priority two site groupings. As such, use of 13 sites for the Gehrt-Mueller Priority Site Determination was deemed sufficient for long term monitoring of tamarisk.

Land managers can be confident sampling efforts were sufficient for quantitative assessments of these species. Given tamarisk and knapweed eradication are among key management objectives for lower Dolores riparian corridors, intensive monitoring of these sites relative to these invasive species seems prudent. Thus, even though it was recommended land managers eliminate monitoring of eleven sites for purposes of community level study, eight of these sites (GJ2, GJ6, GJ9, MO1, MO5, MO6, UC9 and DL9) required 5 or 6 transects to efficaciously monitor tamarisk and/ or knapweed. As tamarisk and knapweed are removed from these areas, it would be useful to monitor these sites for potential reestablishment of tamarisk and knapweed or shifts in community structure.

Monitoring of these two invasive species, exclusive of all other species or community constructs within these eight sites, using the point intercept method as described, would represent nominal increases in effort and funding, allowing for expanded study of these invasive species. However, because sampling efficacy of community types within these eight sites was nominal at best, it is recommended funds not be expended for monitoring of other species or communities. This approach would enable land managers to evaluate the effectiveness of various treatment protocols for removal of these invasive species within these sites. Once those species have been eradicated future comprehensive studies can be performed to ascertain if community types have become efficacious with regard to sampling effort. If and when these community efficacy standards are attained, land managers can revisit the possibility of comprehensive monitoring of these eight study sites.

Figure 12A presents the number of sites required for efficacious sampling of communities and tamarisk, *per* all 39 sites and *per* priority site/ Sabaj efficacy group. Figure 12B displays mean percent cover *per* community and species of interest, *per* efficacy/ priority site group. Arcsine transformed data for absolute percent cover estimates of taxa were used to calculate efficacious sampling effort *per* community type or species. Confidence interval estimates were used to estimate the number of sites required to detect a minimum 25% change per community type or 40% change per species, using 500 points per transect and 2500 points per site. Confidence intervals can be used to estimate the mean of any system variable, given assumptions of normality are satisfied pertaining to means and variances. Thus, confidence interval estimates were applied to assess a variety of ecosystem variables from the lower Dolores watershed. Assessment of these variables allowed for determination of 13 study sites required to efficaciously monitor all ecosystem variables of interest.

The 13 site determination was made using point in time parameter estimates (Elzinga et al. 2001). Thus, assessment of parameter change over time requires sites are monitored on or very near the initial dates of monitoring for each site (in this instance, the first week of August). Monitoring during other seasons, relative to the initial year of study, would produce erroneous outcomes especially with regard to native and exotic herbaceous annuals. It is also crucial monitoring data are acquired over many successive years (preferably several decades) in order to exclude episodic year-to-year fluctuations in precipitation, hydrology, salinity, temperature, grazing, and so on from obscuring long term ecosystem trends. Attempts to interpret ecosystem recovery over minimal annual cycles are strongly discouraged.

The 13 long term monitoring sites were selected on the basis of Sabaj efficacy *and* associated species criteria pertaining to the four community types, and tamarisk and/ or cottonwood. As such, it is important to understand selection of long term priority sites was based upon *intentionally biased* criteria. That is, these sites were not selected randomly, as is often the standard for ecologic studies. Of particular importance in figure 12 and subsequent figures are the priority 1/ priority 2 site grouping. This group of sites contains the 13 long term study sites as determined by the Gehrt-Mueller Priority Site Determination (table 5).

Priority one sites are represented by seven Sabaj efficacy 1.0 sites. These sites required five transects to detect 25% or greater change in community structure of all community types, and also detect 40% or greater change in percent cover of tamarisk and/ or cottonwood. Priority two sites are represented by two Sabaj efficacy 1.0 sites, absent tamarisk/ cottonwood selection criteria (MO8 and DL5). The remaining four priority two sites had Sabaj efficacy standards of 0.75. This subset of four priority two sites were where three of four community types required five transects to detect 25% or greater change in community structure, and also detect 40% or greater change in percent cover of tamarisk and/ or cottonwood.

Data from all 39 sites (figure 12A) indicate a range from eight (herbaceous community) to thirteen (tamarisk) sites were required to efficaciously sample the four community types and tamarisk. The 13 study site estimate for efficacious sampling of tamarisk was the

maximum site estimate for any of the ecosystem variables assessed. Hence, the 13 study site estimate for efficacious sampling of all ecosystem variables of interest was used for the Gehrt-Mueller Priority Site Determination (table 5), resulting in the priority one plus priority two site grouping displayed throughout the results. Please note priority one, priority one plus two, and efficacy 1.0 groupings in figure 12A do not exceed the 13 study site estimate of the 39 site grouping for efficacious sampling. However for efficacy groupings of 0.75 or less, estimates often exceeded the 13 site estimate of the 39 site group. These results indicate that as sampling efficacy of community types decreases, more sites must be sampled in order to adequately estimate percent covers of community types or species of interest within the ecosystem.

Figure 12B compares mean percent covers of the four community types, tamarisk and cottonwood among the 39 site, priority one plus two, Sabaj Efficacy 1.0, and priority one site groupings. Of particular importance was the comparison of the priority one plus two group to the 39 site group. Standard errors for percent covers of the four community types, tamarisk, cottonwood and barren ground overlap with one another. Thus, selection of the 13 study sites from the priority one plus two site group for long term monitoring appeared to adequately estimate mean percent covers of all four community types, barren ground and species of interest *per* the 39 site estimates. Please note confidence interval estimates for cottonwood were qualitative, as insufficient replication occurred primarily due to its scarcity throughout the impounded watershed. These 13 sites represented the *parsimonious quantum* of highly efficacious study sites. Parsimony was assessed using minimum tree distances among the PCA correlation matrices (figures 15 through 25). These outcomes supported the assertion that it was appropriate to reduce by two thirds (from 39 sites to 13 priority sites) the number of study sites required for long term, efficacious monitoring of ecosystem variables.

Figure 13 presents the number of study sites required to measure beta diversity, richness, evenness, and dominance *per* the 39, priority 1 + priority 2, Sabaj Efficacy 1.0, and priority 1 site groupings. Arcsine transformed data for absolute percent cover estimates of taxa were used to calculate all diversity indices. Those indices calculating abundance transformed those estimates to relative abundance. Confidence interval estimates were used to establish these parameters. Of specific interest was the ability to measure biodiversity as it pertained to selection of long term study sites. As selection of priority sites was solely based upon sampling efficacy of community types, cottonwood and/ or tamarisk, (i.e., a *biased* selection process), it was important to determine whether or not measurements of biodiversity remained unbiased among these 13 sites. Specifically, it was crucial to illustrate if the novel system developed to maximize sampling efficacy of community types and species of interest among a parsimonious quantum of study sites was largely independent of site level and ecosystem level biodiversity.

Eleven diversity indices were evaluated to test the general hypothesis that sampling efficacy was independent of ecosystem diversity. Specific hypotheses are given below. Where indices required use of total number of individuals *per* sample, the value was determined as the average of the arcsine transformed percent covers of each species across five transects. Two dominance indices (Simpson's and Berger-Parker's), two sample size-dependent richness indices (log S and Fogleman's S), two sample size-

independent richness indices (Menhinick's and Margalef's), two evenness indices (Buzas & Gibson's and Pielou's J), and three total diversity indices (Shannon's H, Brillouin's and Fisher's alpha) were assessed. Note for purposes of figures 13 and 14, log S was omitted as arcsine transformed data were not used to calculate log S (see figures 25 and 26 for more information pertaining to log S).

Dominance (the compliment of evenness) is often treated separately from diversity, or not included in diversity assessments, dependent upon study objectives. For purposes of the current work, dominance was assessed as a third component of biodiversity. While this approach might seem redundant and unnecessary given the complimentary nature of dominance to evenness, both were assessed for purposes of potential dependencies upon efficacy, and pattern analyses derived from the principal components matrices in figures 15 through 25. Additional information concerning diversity indices is available from several excellent sources (Chaneton & Facelli 1991; Hammer et al. 2001; Heip & Engels 1974; Jost 2010; Whittaker 1965; Williams 2009).

Figure 13 demonstrates a maximum of 12 sites (i.e., Fisher's alpha) were required to estimate all diversity measures assessed, thus adhering to the limit of 13 long term monitoring sites identified using the GM-PSD (table 5). While the 13 site group (i.e., priority one plus two sites) in some cases under-estimated the total number of sites required to estimate specific diversity indices *per* the 39 site group, more often than not the 13 site group estimates were in agreement with the 39 site group estimates. Also encouraging were that five of ten diversity indices required five sites to estimate diversity across all efficacy groups tested. These outcomes indicated the sampling protocol was also efficacious with regard to estimating beta diversity.

Figure 14 presents biodiversity *per* the 39, priority one plus two, Sabaj efficacy 1.0, and priority one site groups. These are perhaps among the most important of analyses revealed. The initial hypothesis, based upon a singular test of sampling efficacy with diversity (El waer et al. 2010), alleged sampling efficacy was independent of biodiversity. In general, standard errors of the 13 site group (i.e., priority one plus two) overlapped with standard errors of the 39 site group. In many cases, standard errors of the 13 site group encompassed the mean of the 39 site group. Thus it appears selection of sites based upon sampling efficacy of communities and species of interest was largely independent of biodiversity. Various estimates of these indices by several efficacy/ priority groups remain very close or within the standard errors of the 39 site group, providing additional support for independence of sampling efficacy from biodiversity. It should be noted the lower Dolores riparian zone was dominated by a few species, with most others occurring relatively sparsely. Thus, total diversity was relatively low compared to ecosystems where species display greater evenness. The general suppression of diversity likely impacted the degree to which diversity estimates of different site groupings agreed with one another.

Table 5 presents the first-ever derivation of the Gehrt-Mueller Priority Site Determination (GM-PSD). The GM-PSD provides the platform upon which the far reaching practical applications of The Theory of Quantum Microbiogeography are revealed. It is important to understand criteria used for the GM-PSD were established *a priori*. That is, sampling

efficacy standards for both community types and species were identified before derivation of the GM-PSD; as were criteria used to identify priority one and two sites. Lower levels of priority; i.e., three, four and so on were also established, but not presented. These *a priori* approaches to the GM-PSD were necessary in order to obviate bias as it pertains to identification of long term priority sites. It would be highly inappropriate to "fit" these criteria using *a posteriori* determinations.

The GM-PSD criteria were established by determining the number of sites required to estimate a) mean absolute percent cover of community types (table 3) and b) mean absolute percent cover of species of interest (i.e., tamarisk and cottonwood) (table 4). Mean ecosystem diversity (figure 13) among priority sites was evaluated following their selection. Estimates ranged from a minimum of five, to a maximum of 13 study sites required for quantitative assessment of these ecosystem variables. Arcsine transformed data for absolute percent cover estimates of taxa were used to calculate sampling effort *per* community type, species or diversity index. Confidence intervals estimated the number of transects required to detect a 25% change *per* community type, 40% change *per* species, and 25% change *per* diversity index. Priority one sites required five transects to sample four community types, tamarisk and/ or cottonwood. Priority two sites either required five transects to sample the four community types or five transects to sample three of four community types and tamarisk.

By way of analogy, the GM-PSD is compared to a rudimentary college admissions process. Priority one sites required "five fives" (i.e., five transects to sample four community types and tamarisk/ cottonwood,) while priority two sites required "four fives" (i.e., either five transects to sample the four community types or five transects to sample three of four community types and tamarisk/ cottonwood). Hypothetically evaluating grade point averages (GPAs) from high schools of college applicants, a university could rate priority one students as those with GPAs rounded to 4.0 (based upon a five-tier system of grade A, B, C, D and F), and priority two students as those with GPAs rounded to 3.0. The university, presumably, would have determined *a priori* the number of students (equivalent to number of sites) to be admitted for any given academic year. Then, offers of admission would be extended to a predetermined number of students based upon admissions criteria. If those criteria were solely high school GPAs, the university would make selections in a top-down fashion, first taking those students with 4.0 GPAs, then 3.0 GPAs, and so on, until all available student slots were filled.

Seven sites (GJ1, GJ3, MO4, MO10, UC2, UC4 and UC10) achieved criteria established for priority one sites. These sites were also defined as Sabaj efficacy 1.0 sites, satisfying the admission criterion of "five fives," with an equivalent GPA of 4.0. Consequently, six sites remained for selection in order to fulfill the *a priori* "admission number" of 13 for "academic year" 2010. Two sites (MO8 and DL5) adhered to criteria for all four community types, but not tamarisk or cottonwood. Four sites (GJ7, UC1, UC3, and DL6) met criteria for three of four community types, and tamarisk or cottonwood. Thus, these remaining six sites earned "four fives," having an equivalent GPA of 3.0. In short, the 13 most efficacious sites with regard to sampling efficacy of community types and/ or species of interest were selected, with an average GPA of 3.54.

Tables 6 and 7 communicate information pertaining to detection limits of minimum change for community types (25% minimum detection level), individual species (40% minimum detection level), and diversity (25% minimum detection level). These data were included to illustrate established detection levels of change were within reasonable expectations of change for the lower Dolores riparian ecosystem. Specifically, large-scale removal of the two most dominant species (tamarisk and knapweed) via active management is anticipated to induce changes in percent covers of community types and species, and biodiversity index values, within established parameters. Additional potential modifications to the ecosystem including altered hydrologic regimes below the McPhee dam, changes in cattle grazing patterns, active planting of cottonwood, and so on could also impact the degree of observed changes among riparian flora.

While detection limits of 25% and 40% might appear somewhat liberal, it is important to acknowledge alpha levels for community types, individual species and diversity were set at 0.90, providing an error limit of 0.10. Adherence to an alpha of 0.90 is somewhat remarkable, given observer error can (and often does) exceed 50% relative to percent cover estimates (Sabaj-Stahl, unpublished data). Adherence to this low error limit relative to percent cover and diversity estimates was possible because of a) sampling methodology and b) sampling effort. Assessment of change in percent cover and diversity were calculated relative to the various site groupings and not on an individual site basis. Thus, it is crucial these parameters are assessed using averages from the 13 long term monitoring priority sites. Levels of change were presented on a site-by-site basis in tables 6 and 7 to communicate the magnitude of change required within the 13 site group.

Implementation of the point intercept method vastly reduced error comparable to ocular estimation methods (Sabaj-Stahl, unpublished data). Sampling at 10 cm intervals, with 500 points per transect and 2500 points per site appeared sufficient for mean estimates of percent cover of community types and species of interest. Diversity estimates of priority sites also appeared representative of ecosystem values. As such, relatively high confidence is afforded among mean estimates of percent cover and diversity. Investigators may opt for higher error limits, with correspondingly lower detection levels of change in the derivation of the GM-PSD. However, error limits and percent levels of detection of change ought to be established *a priori*, thus it might be preferable to conduct pilot studies for this purpose. Pilot studies may reveal increased sampling efforts, rather than increased error limits, are appropriate.

The works herein quantitatively elucidate many key principles of alpha and beta diversity as originally defined by Whittaker (1960) and MacArthur (1965). The classic ecological concepts underlying diversity were verified and expanded upon to reveal a novel concept underpinning relationships between sampling effort, sampling efficacy, biogeography and biodiversity: *The Theory of Quantum Microbiogeography*. Inspection of SHE analysis (figure 11) revealed evenness (i.e., relative species abundance) of the ecosystem was captured after just 12 sites (i.e., 30,000 data points assessed), whereas richness and total diversity continued to increase (albeit slowly) after 39 sites were sampled. Based upon myriad analyses, it appeared mean diversity of the ecosystem was captured (figure 14 and table 7) absent total richness and total diversity. The contributions of missing rare species to mean percent cover and mean total diversity estimates appeared negligible

relative to sampling effort. The Theory of Quantum Microbiogeography rests upon these fundamental biogeographical concepts, wherein mean absolute percent cover of community types and species of interest (figure 12B), and beta diversity (figure 14) were captured among a parsimonious quantum of priority sites (table 5).

The *prima facie* practical applications of the GM-PSD were manifest as it pertains to identification of efficacious, long term ecosystem-level monitoring sites. Having the ability to quantitatively assess changes in ecologically relevant community types, species of interest and beta diversity among a *parsimonious quantum* of highly efficacious study sites enables a transition from qualitative to exacting approaches. Transitioning toward more quantitative approaches in the assessment of biodiversity might allow for identification of universal mechanisms driving ecosystem processes. Evidence for quantitative methods driving mechanistic discoveries in ecology is provided, in part, by *The Theory of Quantum Microbiogeography*.

Initially, a portion of this mechanism appeared to be revealed using a singular linear regression of sampling efficacy to Simpson's diversity (using a modified equation) (El waer et al. 2010). Since this initial simple regression, analyses investigating the mechanism of The Theory of Quantum Microbiogeography were vastly expanded (figures 15 through 28; tables 8 & 9). In figures 15 through 25, simple regressions, logistic regressions and principal components correlation matrices are displayed for eleven diversity indices regressed with efficacy. These analyses were performed in an attempt to reveal the potential independence/ dependence of Sabaj efficacy in relation to alpha diversity for the purpose of exposing the mechanism driving The Theory of Quantum Microbiogeography.

Simple regression is perhaps among the most elegant of statistical approaches. The hypothesis concerning dependency could not be any "simpler," or more powerful in nature. The null hypothesis predicts the slope of the regression line equals zero (Stanton 2001). A rejection of the null (slope does not equal zero) concludes some portion of the variation in *Y* is explained by *X*. Moreover, *Y* is predicted given *X*, with the regression line representing the change in the mean of *Y per* unit increase in *X*. However, it is important to obey the assumptions of regression analysis, as it is very sensitive to deviations from normal, and specifically homoscedasticity of errors for the dependent variable (Stanton 2001). Other types of distributions can be used with simple regression, given the assumptions of normalcy and homoscedasticity are obeyed. It remains crucial, therefore, to confirm all assumptions, especially with small sample size.

Because the slope of the regression line equals the correlation between *Y* and *X*, corrected by the ratio of standard deviations of these variables, homoscedasticity is required (Stanton 2001). Failure to verify the assumptions of normality, especially concerning homogeneity of variances for small samples, can lead to erroneous conclusions. Large samples often adhere to assumptions of normality because even when distributions are not normal, residuals display normality and homogeneity of variance (Berry 1993). Large samples can introduce other problems, as highlighted below. Application of the arcsine transformation to absolute percent cover estimates appeared to improve homogeneity of variances among community types. Combined with

large sample size, use of linear regression seemed potentially appropriate.

Use of regression for parametric inference assumes the errors of the dependent variable are a) independent of one another, b) normally distributed with c) the same variance for each level of the independent variable (i.e., homoscedasticity of errors) (Berry 1993). Usually, the dependent variable is continuous, although adjustments can be applied to discrete dependent variables for use in linear regression (Berry 1993). Regression also assumes the relationship of the variables is linear (i.e., slope ≠ 0.00) (Berry 1993; Stanton 2001). However, the fourth assumption applies to predicting *Y* given *X*. For purposes of *The Theory of Quantum Microbiogeography*, the absence of a linear relationship (i.e., slope = 0; $p > 0.05$) between efficacy and alpha diversity could reveal the mechanism driving the theory, while dependence of alpha diversity to efficacy might as well.

Because the theory in part predicts independence of sampling efficacy from alpha diversity, simple regression was not exclusively used to predict alpha diversity given efficacy. Thus, violation of the fourth assumption could support the theory. It is also appropriate to use discrete (i.e., categorical) predictors as independent variables in simple regression, so long as those variables are properly "coded" (Berry 1993). For example, if sex were plotted along the *X*-axis of a linear regression, zero would represent one gender, and one the other. In the current study, efficacy was coded from zero (no efficacy) to one (maximal efficacy), with three intermediate and evenly spaced intervals (i.e., 0.25. 0.50 and 0.75).

The residuals of a given distribution become "more perfectly" distributed than the parent distribution from which they were derived (Quesenberry & Quesenberry 1982). As such, residuals derived from uniform distributions of Sabaj efficacy and eleven diversity indices used in simple regressions were more, not less uniformly distributed than the parent distributions. As the mean and variance of the uniform distribution are the same as the normal, given sufficient sampling (Wilcox 2010), these assumptions were obeyed for the dependent variables.

The four assumptions of simple regression can be tested by a) examining the degree to which the variables adhere to criteria of normality, homoscedasticity and linearity beforehand or b) studying plots of residuals and performing diagnostic statistics after regression (Wilcox 2010). All distributions used were uniform (table 2). In 9 of 11 cases, the fourth assumption (i.e., linearity between variables) was supported ($p < 0.05$, two-tailed test), presenting a potential dilemma concerning *The Theory of Quantum Microbiogeography*. That is, the independence of diversity from efficacy, at least in part, was predicted to explain why the most efficacious study sites approximated beta diversity.

The null hypothesis concerning the mechanism driving the observed phenomenon of beta diversity occurring among a biased selection of priority sites is that sampling efficacy independent of diversity. The alternative hypothesis asserts cohesion (i.e., dependency) of sampling efficacy with diversity. Put another way, the null hypothesis suggests sampling efficacy does not predict biodiversity and thus, the slopes of the regression lines for these variables equal zero. Failure to reject the null when the alternative is supported is a type II error, but generally has fewer potential adverse outcomes than type I errors

(Johnson 1999). That is, incorrectly concluding no relationship exists between two variables tends to be safer (i.e., incorrectly recommending against the use of a therapeutic drug) than incorrectly rejecting the null (i.e., recommending land managers adopt a defective monitoring protocol related to weed management). While study objectives often hinge upon rejection of the null, a failure to reject it here would support the primary hypothesis of independence between sampling efficacy and diversity, potentially revealing the mechanism driving *The Theory of Quantum Microbiogeography*.

The alternative hypothesis predicts the cohesion of diversity to sampling efficacy explains the consistent occurrence of beta diversity among the most efficacious of study sites. That is, dependence of diversity upon sampling efficacy would be evidenced in a rejection of the null, concluding variation in alpha diversity is explained, at least in part, by sampling efficacy. As such, the alternative hypothesis also has potential of explaining the mechanism driving the theory.

These hypotheses were developed for exploration of the mechanism driving *The Theory of Quantum Microbiogeography*. Simply stated, the theory predicts a parsimonious quantum of highly efficacious study sites with regard to sampling of ecologically relevant community types and species of interest approximate beta diversity. These hypotheses reflect the notions of either a complete independence of the variables, resulting in random diversity outcomes explain the occurrence of beta diversity among priority sites; or a dependence of the variables, resulting in biased diversity outcomes, explaining the occurrence of beta diversity among priority sites. As discussed above, the ambiguities presented by small p values, weak r values, and small r^2 values among linear regressions complicated determinations of dependence. Thus, other approaches (logistic regression and PCA correlation) were employed as potential means for elucidating the mechanism driving the theory.

Biodiversity measurements were derived from the original, arcsine transformed, absolute percent cover estimates of individual taxa, except for sample size-dependent estimates of richness. Understand those indices using abundance transformed absolute percent cover estimates of taxa to relative percent cover. For log S, raw counts of the number of species *per* site were log transformed. Fogleman's S made use of a specialized adaptation to arcsine transform richness (see methods). For Fogleman's S, discrete values were used as dependent variables in simple regressions. While use of discrete variables on the *Y*-axis of simple regression is not ideal, it was unavoidable in this situation. In all, 79 taxa were identified for these calculations (appendix I). While regression variables were derived from the arcsine transformed, log normal distribution of taxa (figure 3), Sabaj efficacy and the eleven diversity indices regressed conformed to uniform distributions (table 2).

Uniform outcomes were not entirely unexpected, as distributions of diversity variables can be independent of the type of species distributions from which they were derived (Giavelli et al. 1986). Nor was it unexpected Sabaj Efficacy obeyed a uniform distribution, as five (ranging from zero to one) discrete, evenly spaced classes composed the index in its current but highly plastic form. Nonetheless, these were fortuitous outcomes, as uniform distributions obey assumptions of the central limit theorem. Because variables in a

uniform distribution are equidistant from one another, and the likelihood of one variable being selected is equal to that of all others, the mean and variance of the uniform distribution are the same as the normal, given adequate sample size (Wilcox 2010). Thus, these data appeared to have conformed to the assumptions of simple regression, absent linearity between 2 of 11 variables and absent continuous measurements for arcsine transformed, sample size-dependent, arcsine transformed richness.

Linear regressions (figures 15 through 25) revealed just one instance where $r^2 > 0.05$ (Berger-Parker's dominance v. Sabaj efficacy; $r^2 = 0.064$). Thus, regardless of linearity, less than 5% of total variation was generally explained by the models. Associated p values were less than 0.05 for 9 of 11 diversity indices regressed with efficacy, suggesting linearity. Fisher's alpha ($p = 0.083$) and Fogleman's S ($p = 0.448$) were nonlinear with efficacy. By and large, r values indicated universally weak linear relationships. Taken together with the occurrences of exceptionally small p values among six of eleven regressions, it was not entirely clear to what extent linear regression revealed any mechanistic trends concerning the theory. As such, the nine indices which appeared linear with Sabaj efficacy were used to calculate Quinn cohesion (figure 26, table 8). Quinn cohesion provides an estimate of the potential relationship between alpha diversity and sampling efficacy.

Potential independence of efficacy from diversity does not, in of itself, explain why the most efficacious sites (i.e., Sabaj efficacy = 1.00) approximated mean ecosystem (i.e., beta) diversity. Selection of priority sites (table 5) was based solely upon sampling efficacy of four community types and two species of interest (tamarisk and cottonwood). While sampling efficacy of community types and diversity were uniformly distributed, it was not immediately apparent how a biased selection of study sites based upon efficacy would consistently yield mean beta diversity among those sites. Simple inspection of figures 15 through 25 for linear regression revealed, on average, that a higher proportion of the most efficacious sites occur within 95% confidence intervals of regression when compared to other efficacy groups. In fact, for the eleven diversity indices, 75% of the most efficacious sites were constrained within these confidence intervals, representing a proportion higher than the four remaining lower levels of efficacy.

It is of importance to understand part of this relationship was due to confidence intervals of linear regression expanding as they travel further from the mean of efficacy. However, visual inspection of regressions revealed confidence interval expansion was not the sole reason for the observed phenomenon. In fact, confidence intervals of zero efficacy groups were consistently larger than those of the most efficacious groups, yet encompassed only 38% of the total sites for that group among the eleven regressions. These outcomes indicated something beyond the proposed simple independence of Sabaj efficacy from biodiversity explained the most efficacious sites approximating beta diversity. Thus, a paradox of sorts presents itself, as the 95% confidence intervals predict the mean value of *Y* in the population for a particular value of *X*. Observations reveal, however, that these predictions were more reliable for the most efficacious group (Sabaj efficacy = 1.00), so the expectation of equal dispersion of *Y* upon independent categories of *X* did not occur. Violation of this key assumption of linear regression renders interpretation of these analyses suspect. However, unequal dispersion could provide clues concerning the

mechanism.

Ambiguities presented by simple regressions obscured, rather than resolved the mechanism driving *The Theory of Quantum Microbiogeography*. Thus, logistic regressions (figures 15 through 25) were utilized as an alternative approach. Logistic regression allows for prediction of discrete variables by either continuous or discrete predictors (Peng et al. 2002). Continuous response variables can be used so long as they are expressed as proportions, ranging from zero to one. When discrete variables are used on the *Y*-axis, they must be expressed as a dichotomy. Polytomous, categorical variables can also be used, so long as a dummy variable scheme converts them to a dichotomy (Peng et al. 2002).

This convention was reversed by placing the discrete variable (efficacy) on the *X*-axis and the continuous variable (for 10 of 11 diversity indices) on the *Y*-axis of logistic regressions. Fogleman's S (a sample size-dependent richness index) was also discrete. As none of the indices used for the response variable were expressed as proportions ranging from zero to one, criteria for the *Y*-axis were violated. The reasons for not adhering to these requirements were a) to display data and confidence intervals in a manner consistent with linear regression and b) zero values (i.e., zero efficacy) cannot be logit transformed as required for the y axis. While a dummy variable scheme could have eliminated the issue caused by zero efficacy and a polytomous variable regressed on the *Y*-axis, it was considered better to preserve the element of zero efficacy throughout the analyses. Logistic regression was utilized to reveal trends potentially consistent with linear regression, within 95% confidence intervals of the logistic regression line, and assessment of regression coefficients. While the approach was obviously lacking in elegance, it was hoped these "brute-force" tactics would help explain the patterns observed in simple regression.

Logistic regression addresses the same questions as simple regression, but with no distributional assumptions on predictors. Logistic regression is often used when the relationship between a discrete variable and a predictor is non-linear (Peng et al. 2002). Use of the discrete variable as the predictor in linear regression was more, not less, conservative as it related to the primary hypothesis of *The Theory of Quantum Microbiogeography*. That is, use of discrete predictors in simple regression tends to overestimate any potential associations (Stanton 2001). As 9 of 11 diversity indices were apparently dependent upon Sabaj efficacy using the discrete variable as the predictor, greater confidence was imparted in the independence of the remaining two indices (Fisher's alpha and Fogleman's S) from efficacy, compared to using the discrete variable as the response. As noted, unequal dispersion of *Y* upon *X* in linear regressions complicated determinations of linearity and dependence.

Use of discrete variables in logistic regression also requires sufficient responses in each category to ensure standard errors do not become excessive. Specifically, categories with no data artificially inflate standard error estimates in logistic regression (Peng et al. 2002). This assumption was not applicable, as continuous variables were used on the *Y*-axis. Despite these obvious flaws, logistic regression as applied might be useful for purposes of comparing it to linear regression concerning 95% confidence interval trends. Because

use of a discrete variable resulted in discrete outcomes, thus violating a key assumption of linear regression, logistic regression was used as a means to validate 95% confidence interval trends observed in linear regressions and to judge if any of the dependencies inferred by linear regression were, in fact, over-estimates resulting from use of the discrete variable as the predictor.

Concerning the most efficacious sites (Sabaj efficacy = 1.00), 77% fell within 95% confidence intervals for logistic regressions, compared to 75% for linear. The least efficacious sites (Sabaj efficacy = 0.00) evidenced 33% occurred within 95% confidence intervals for logistic regressions, compared to 38% for linear. Thus, while requirements for the response variable were violated in logistic regression, the patterns were consistent with simple regression. As such, confidence interval trends of logistic regressions essentially provided the same outcomes related to the *McIsaac Paradox* as did linear regressions. The McIsaac Paradox is so named for Hugh McIsaac PhD, who very astutely pointed out the apparent paradox concerning the efficacious outcomes of the GM-PSD. The McIsaac Paradox inquires: *Why do so many more sites proportionally fall within 95% confidence intervals for the most efficacious sites, compared to the least efficacious sites, when equal dispersion of the Y-variable (diversity) upon independent categories of X (efficacy) is expected?*

The central concept underlying logistic regression is the logit. The logit is the natural logarithm of an odds ratio, described by the equation in figures 15 through 25 for logistic regression (Peng et al. 2002). Logistic regression applies the logit transformation to the dependent variable, overcoming limitations presented by heteroscedasticity and non-normal data (Peng et al. 2001). The model predicts the logit of *Y* from *X*. Odds predicted by the logit are ratios of probabilities (π) of *Y* happening, to probabilities (1 – π) of *Y* not happening, based upon the binomial distribution. Logistic regression can accommodate categorical outcomes that are dichotomous or polytomous (Peng et al. 2002). Simple logistic models adopt the form Logit $y = \alpha + \beta X$ (equation (a)). The antilog of the equation predicts the probability of the occurrence of the outcome of interest as follows: π = Probability (*Y* = outcome of interest; *X* = x, a specific value of *X*) = $e^{\alpha+\beta x} / 1 + e^{\alpha+\beta x}$ (equation (b)), where π is the probability of the outcome of interest, α the Y intercept, β the regression coefficient, and *e* the base of the system of natural logarithms (Peng et al. 2002). The equations presented in figures 15 through 25 for logistic regression provide the odds ratio of obtaining the logit of *Y* given *X*.

The relationship between logit (*Y*) and *X* is linear per equation (a), but nonlinear according to equation (b). The natural log transformation of the odds ratio in equation (a) causes the relationship between a categorical outcome variable and its predictor to become linear, allowing assessment of the regression coefficient (i.e., beta) relative to linearity (Peng et al. 2002). The value of coefficient β determines the direction of the relationship between *X* and the logit of *Y*. The null hypothesis predicts β equals zero, meaning no linear relationship exists between the variables (Peng et al. 2002). If logistic models hold, a Chi-squared distribution goodness of fit test is often suggested to confirm it, with small p values indicative of data not fitting the model (Peng et al. 2002). However, a litany of statisticians assert p values and their related goodness of fit tests, used to confirm linearity in least squares regression, quite often are not appropriate for logistic regression (Peng

& So 2002; Kuss 2002; Archer et al. 2007; Mair et al. 2008).

Upon evaluating the magnitude of β coefficients and comparing them to outcomes from simple regression, few trends seemed apparent. There seemed to be little agreement between the relative magnitude of β coefficients and linearity v. non-linearity as determined *per* simple regression using p values. Shannon's and Brillouin's diversity were linear *per* simple regression p values, with relatively intermediate logistic regression β coefficients. Alternatively, Fisher's alpha was non-linear *per* linear regression with a relatively robust β coefficient. Buzas and Gibson's evenness and Pielou's J were linear *per* simple regression p values, but with correspondingly minimal logistic regression β coefficients. Sample size-dependent and sample size-independent richness indices were linear *per* simple regression, excepting Fogleman's S. All richness indices produced relatively large β coefficients in logistic regressions with efficacy. Linear regression r values also appeared to have little overall agreement with logistic regression β coefficients.

Dominance presented some agreement concerning linear and logistic models. Simpson's dominance and Berger-Parker's dominance (figures 15 and 23, respectively) exhibited small p values and relatively high r- and r^2 values *per* linear regression with efficacy. Dominance indices also had relatively robust β coefficients *per* logistic regression with efficacy. Thus, linear and logistic models, despite deficiencies already noted (i.e., unequal dispersion of *Y* upon *X*; use of continuous response variables for logistic models) were suggestive of a potential relationship between dominance and efficacy. Conversely, evenness outcomes were ambiguous, with relatively intermediate r values *per* linear regression further complicating determinations of linearity with efficacy.

As outcomes of linear and logistic models generally clouded determinations of linearity and dependence, they failed to resolve the McIsaac Paradox, or explain the mechanism of *The Theory of Quantum Microbiogeography*. As discussed, p values from various goodness of fit tests for logistic regression require strict adherence to all logistic assumptions for proper interpretation relative to the global null hypothesis (i.e., $\beta = 0$). Violations of assumptions pertaining to the response variable rendered goodness of fit tests essentially useless. Thus, information theory was hoped to resolve the paradox, revealing the underlying mechanism. As such, likelihood estimates of logistic regression were investigated as a potential means to identify the mechanism driving the theory. These methods seek to reveal information content from logistic models regressing efficacy with diversity in figures 15 through 25.

The Akaike Information Criterion (AIC) was used to estimate information lost in logistic regressions of efficacy with diversity. Generally, $AIC = 2k - 2\ln(L)$, where k = number of parameters in the model, and L = the maximal value of the likelihood function for the estimated model (Akaike 1974). When a set of logistic models are considered (as with the 11 models presented in figures 15 through 25), the "preferred" model is the one with the minimum AIC value (in this case, Simpson's dominance, figure 15, AIC = 6.768). AIC estimates *relative* goodness of fit and *relative* amount of information lost in a model, but does not test a null hypothesis related to model fit. Thus, AIC provides no clues as to how well data fit the logistic model in an absolute manner (Akaike 1974). In the application of

AIC, a model in which all relative information is lost (i.e., the logistic regression of Fogleman's S to Sabaj efficacy; figure 24; AIC Relative Likelihood = 0.000) indicates poor relative goodness of fit and poor relative information content. However it does not confirm or reject anything pertaining to absolute goodness of fit. These qualities seemed ideal for testing the assumptions of *The Theory of Quantum Microbiogeography*, as linear models did not provide clarity concerning why the most efficacious sites approximated beta diversity. As AIC Relative Likelihood does not test linearity, it might provide a useful alternative.

AIC Relative Likelihood was calculated as $\exp((AIC_{min} - AIC_i)/ 2)$, where AIC_{min} = Simpson's dominance regressed with Sabaj efficacy (figure 15) = 6.768; $AIC_i = AIC_1$ through AIC_{11} (figures 15 through 25). Notice there is not a means by which to calculate the amount of information lost in AIC_{min}. Thus, an unknown amount of information lost from this model is not accounted for (Akaike 1974). Some compelling trends were observed concerning AIC Relative Likelihood (AIC-RL) estimates. An *a priori* cut-off of 0.50 or more for AIC-RL values was established for models communicating relevant information. That is, models where 50% or more relative information was lost were excluded from considerations pertaining to information theory.

For evenness measurements, defined as Buzas & Gibson's evenness (figure 17) and Pielou's J (figure 21), AIC-RL = 0.905 and 0.992, respectively. However, logistic regression coefficients (β) were -0.037 and -0.019, respectively, with slopes of the regression lines apparently approaching zero. As such, these regressions appear to communicate relatively high information content and exhibit relatively high goodness of fit, but with marginal β coefficients, perhaps suggesting independence of diversity from efficacy.

Concerning the compliments of evenness, measured as Simpson's dominance (figure 15) and Berger-Parker's dominance (figure 23), AIC-RL = 1.00 and 0.938, respectively; with β = -1.067 and -1.132, respectively. These logistic regressions exhibited relatively high information content and relative goodness of fit, with relatively robust β coefficients, suggesting potential dependence of dominance upon efficacy. At first glance, the McIsaac Paradox does not appear resolved as it pertains to potential non-linearity of efficacy with evenness, and approximation of beta diversity among the most efficacious sites. Thus a dichotomy exists between evenness and dominance in the logistic regressions. Both evenness and dominance exhibit relatively high information content, yet evenness appears independent of efficacy while dominance is not, *per* β coefficients of logistic regression and line slopes of linear and logistic regressions; p values not withstanding. (Please note the lower the index values for Simpson's and Berger-Parker's indices, the greater the dominance, hence the negative slopes.)

It is here the final layers of the onion are peeled away, exposing the apparent mechanism driving *The Theory of Quantum Microbiogeography*. Logistic regression plots revealed a) dominance tended to increase with increased efficacy and b) evenness tended to remain constant with increased efficacy. It was not intuitively apparent how evenness could be independent of efficacy and evidence relatively high information content with efficacy *per* the AIC Relative Likelihood method. Further analysis of linear and logistic regression

plots, and PCA correlation matrices revealed while mean evenness remained constant as efficacy increased, the range of evenness was curtailed from both ends of the distribution as efficacy increased. The most efficacious group for evenness was more narrowly distributed compared to all sites, with sites uniformly clustered about the mean of ecosystem evenness. Thus, while mean evenness was independent of efficacy, the range of evenness was not, and was inversely dependent upon efficacy in a two-tailed fashion. It is believed the dichotomy presented by the mean and range of evenness was, at least in part, responsible for the unequal dispersion of *Y* upon *X* in the linear regression models.

Dominance was dependent upon efficacy *per* the mean and range. The mean of dominance increased as efficacy increased, with the range inversely dependent upon efficacy. Given these outcomes, the alternative hypothesis predicting the cohesion of biodiversity to sampling efficacy was supported upon rejection of the null. Specifically, the dependence of dominance and evenness upon efficacy in part explains the consistent occurrence of beta diversity among the most efficacious of study sites. However, the null hypothesis was not rejected concerning the mean of evenness, concluding mean evenness was independent of efficacy. Next, an attempt is made to model this information such that an intellectual construct appears representative of the mechanism driving *The Theory of Quantum Microbiogeography*.

The hypotheses tested the potential dependence of diversity upon efficacy. It is suggested part of the mechanism involved establishment of confidence intervals about the means of ecologically relevant community types. Having applied 25% confidence intervals with an error of 0.10 restricted the range of individual community types from both ends of the distribution while preserving the means of those community types as efficacy increased. These community distributional effects were imparted to species, causing mean ecosystem evenness to be independent of Sabaj efficacy. Thus it is suggested mean evenness occurs "upstream" of efficacy, as selection of long term monitoring sites on the basis of sampling efficacy did not alter mean evenness outcomes.

Community types represented two levels of independence (native v. exotic and woody v. herbaceous) and four levels of overlap (native-woody v. native-herbaceous v. exotic-woody v. exotic-herbaceous). These symmetrical associations, formed by a quartet at the primary community level (native, exotic, woody and herbaceous) and a quartet at the secondary community level (nw, nh, ew and eh), are believed to play a substantial role in the preservation of mean ecosystem evenness across a spectrum of community efficacy standards.

Dependence of dominance upon efficacy is suggested to result from species-community constructs. Riparian corridors were highly stratified in occurrence of species and communities. The exotic-woody community was dominated by tamarisk (species rank of 1; appendix 1); the exotic-herbaceous community by knapweed and cheatgrass (species ranks of 2 and 5, respectively, appendix 1); the native-woody by sandbar willow and stretchberry (species ranks of 3 and 4, respectively; appendix 1), and the native-herbaceous by scratchgrass (species rank of 6; appendix 1). Species dominating these communities tended to occur as highly monocultural, banded swaths of vegetation

perpendicular to transect lines. Efficacious sampling of these communities translated into selecting sites wherein there was good agreement of percent cover among all transects of a given study site, and consequently the dominant species among those community types, causing dominance to increase as efficacy increased. The dependence of the mean and range of dominance upon efficacy implies dominance outcomes occur "downstream" of efficacy.

Thus, a proposed mechanism is revealed for *The Theory of Quantum Microbiogeography*: A parsimonious quantum of highly efficacious study sites with regard to sampling of ecologically relevant community types and species of interest approximates beta diversity because efficacy creates a bottleneck for a) the range of evenness and b) the mean and range of dominance; with mean evenness independent of the bottleneck. The bottleneck curtails the range of evenness in a two-tailed fashion while independence of mean evenness from efficacy constrains the remaining range to the 95% confidence intervals of evenness. These effects cause the most efficacious of sites to uniformly cluster about the mean of evenness. Preservation of mean evenness across efficacy standards causes the most efficacious sites to approximate beta diversity. The effects observed upon dominance were primarily a consequence of the priority site selection process.

For logistic regression of log S to Sabaj Efficacy (figure 25), AIC-RL was 0.682, indicating relative goodness of fit and relatively high information content concerning richness and efficacy. The significant AIC-RL value suggests richness might have direct involvement concerning the mechanism. However, in logistic regressions of Fogleman's S (AIC-RL = 0.00), Margalef's S (AIC-RL = 0.00), and Menhinick's S (AIC-RL = 0.030); to efficacy, relatively low information content and relatively low goodness of fit were observed. Fogleman's S represents the arcsine transformed equivalent of log S, and both are sample size-dependent estimates of richness. Margalef's and Menhinick's indices are sample size-independent estimates of richness, with arcsine transformed, absolute percent cover estimates of individual taxa used to derive them. Thus, regression of a log transformed variable with arcsine transformed efficacy was judged to yield an artifactual AIC-RL value. As such, it was excluded from further consideration as a direct component of the mechanism. To clarify, SHE analysis (figure 11) revealed contributions of richness to total diversity continued after sampling of 26 sites, but those contributions were the result of rarer species with correspondingly low absolute percent covers. As such, potential impacts of additional rare species on alpha or beta diversity would be negligible, and unlikely to significantly alter outcomes related to standard error estimates of biodiversity across efficacy standards.

The McIsaac Paradox is explained by the independence of mean evenness from efficacy, and the inverse cohesion of the range of evenness to efficacy, as efficacy increases. The dichotomous association of evenness with efficacy produces highly discrete diversity outcomes for the most efficacious sites. In short, the McIsaac Paradox results from the *uneven association of evenness with efficacy*. Simple inspection of PCA correlation matrices in figures 15 through 25 revealed unequal dispersion of *Y* upon *X* produced these highly discrete diversity outcomes for the most efficacious of sites, thereby violating a key assumption of linear regression. The matrices display minimum tree distances between study sites on the basis of efficacy and diversity. For purposes of clarification

pertaining to the Quinn Cohesion Index and Refined Quinn Cohesion Index (figures 26 & 27; table 8), Principle Components Analysis (PCA) assumes multivariate normality and continuous variables only when used for hypothesis testing relative to p values (Jolliffe 2002). As PCA was not used for this purpose, these distributional assumptions can be ignored (Jolliffe 2002).

While prior analyses provided support for the notion of variable cohesion (i.e., increased levels of dependence of diversity upon efficacy as efficacy increased), PCA correlation matrices were uniquely applied to further assess cohesion. The novel procedure takes advantage of a discrete, categorical variable (Sabaj Efficacy) regressed with a litany of continuous variables (diversity). Casual observation of PCA correlation matrices (figures 15 through 25) revealed outcomes became more discrete with increasing efficacy. Thus, Sabaj efficacy appeared cohesive with diversity. The initial attempt to approximate the force of cohesion of efficacy with diversity is represented by the Quinn Cohesion Index (QCI) (figure 26). QCI was derived from PCA correlations in figures 15 through 25, excluding Fisher's alpha (figure 22) and Fogleman's S (figure 24). Fisher alpha's and Fogleman's S were independent ($p > 0.05$) of Sabaj efficacy *per* simple regression, and were not included in the QCI because as devised, linear regressions over-estimated dependence.

The QCI is an approximation of cohesion between variables used in the PCA (i.e., Sabaj efficacy and 9 diversity indices). The index was calculated utilizing minimum tree distances (an indication of study site relatedness) plotted in the PCA correlation matrices. Casual observation of minimum tree distances suggested in general, that as efficacy increased so too did the cohesion of diversity to efficacy. Tree distances between study sites generally shortened as efficacy increased, and linkages appeared more discrete among the most efficacious of sites. The index ranges from zero (no cohesion) to one (maximum cohesion). The QCI is defined as the proportion of diversity indices with zero line breaks per Sabaj efficacy group to the sum of diversity indices used *per* Sabaj efficacy group in the PCA correlation matrices (i.e., 9); divided by the proportion of the number of line breaks *per* Sabaj Efficacy/ diversity index pairing to the sum of all line breaks in all PCA correlation matrices, plus unity (one) (table 8). Data points were plotted as three-point moving averages. Three-point moving averages tend to reveal trends occurring between variables.

The initial attempt to estimate cohesion appeared suggestive of a linear relationship between diversity and efficacy. As efficacy increased, cohesion of efficacy to alpha diversity also appeared to increase. If this relationship held then it would, at least in part, explain why the most efficacious sites approximated beta diversity. However, inspection of the 95% confidence ellipse in figure 26 revealed the errors of some data points overlapped, perhaps confounding any potential determinations of linearity. As discussed, linear regression relative to p values becomes problematic for large datasets and complicates decisions related to potential linearity between variables. The overlap of errors evidenced in QCI (figure 26) were suggestive of ambiguities presented by large datasets (i.e., 39 sites; 97,500 data points assessed) relative to p values. Thus, some diversity indices used in the calculation of QCI may have been independent of efficacy.

The Akaike Relative Likelihood method (figures 15 through 25) was utilized to select those indices contributing significant information to the logistic model between efficacy and diversity. The Refined Quinn Cohesion Index (r-QCI) (figure 27) was derived from the PCA correlation matrices as described, using only those indices shown to a) have potential relationships with efficacy per linear regression ($p < 0.05$) and b) contribute significant information per Akaike Relative Likelihood via logistic regression, in figures 15 through 25. Simpson's dominance, Berger-Parker's dominance, Buzas & Gibson's evenness, and Pielou's J were used to calculate r-QCI, as shown in table 8. The index is an approximation of cohesion between variables used in the PCA. The index ranges from zero (no cohesion) to one (maximum cohesion). Data points were plotted as three-point moving averages.

The slope of the line from r-QCI (figure 27) was steeper than that of the QCI (figure 26); with the 95% confidence ellipse narrowed compared to the QCI (figure 26). Overlap of errors was reduced between data points in r-QCI compared to QCI. As such, it appeared a significant positive relationship occurred between efficacy and the cohesion of diversity to efficacy. In order to further test the alternative mechanistic hypothesis of dependence, a simple regression was performed using Sabaj efficacy on the *X*-axis and r-QCI on the *Y*-axis. (figure 28). The least squares regression outcomes were compelling, with $r = 0.995$, $r^2 = 0.991$ and $p < 0.001$. The null hypothesis (i.e., slope = 0.00) was rejected, concluding *X* predicted *Y* with high fidelity. In fact, the linear relationship was nearly perfect, with 99% of the variation in *Y* explained by its relationship with *X*. The strength of the linear relationship suggests the cohesion of diversity (specifically, evenness and dominance) to efficacy plays a significant role in the mechanism driving *The Theory of Quantum Microbiogeography*.

The simple regression provided additional support for the alternative hypothesis of the cohesion of diversity with efficacy driving the mechanism of The Theory of Quantum Microbiogeography. As discussed, cohesion of the mean and range of dominance to efficacy, and the range of evenness to efficacy were observed with increased efficacy. Independence of mean evenness from efficacy also provided mechanistic clues. Thus, the null hypothesis was supported with regard to mean evenness, and the alternative concerning the range and mean of dominance, and the range of evenness.

To reiterate, the mechanism proposed to operate the theory is a consequence of selection of priority sites on the basis of efficacious sampling of ecologically relevant community types and species of interest. Confidence interval constructs about the means of these caused the range of evenness to become truncated from both ends of the distribution. Independence of mean evenness from efficacy caused the most efficacious sites to uniformly cluster about the mean of evenness, and within the 95% confidence intervals of linear and logistic regressions of efficacy with diversity. These attributes were imparted to total diversity, causing the most efficacious sites to approximate beta diversity. The mean and range of dominance were cohesive with efficacy in large part because as community types became more efficacious, dominant species become more prevalent. Modest decreases in richness were observed among the most efficacious sites, but richness was not identified as a primary element driving the mechanism. Thus it is believed decreases in richness were secondary to increases in dominance.

The application of an array of statistical procedures appears to have revealed the mechanism driving *The Theory of Quantum Microbiogeography*. The theory predicts a parsimonious quantum of highly efficacious study sites with regard to sampling of ecologically relevant community types and species of interest approximate beta diversity. It is believed the novel approaches presented for selection of long term monitoring sites provide a highly quantitative means for assessment of change in a) ecologically relevant community types, b) species of interest and c) biodiversity. The system appears highly effective concerning habitats represented by uniform bands of vegetation and dominant invasive species. Ecosystems wherein botanical communities are primarily represented by patched species occurrences and/ or greater evenness would likely require fine tuning of the protocols described herein. Specifically, it would be crucial to adjust sampling area, transect spacing and/ or sampling frequency along transects in order to adequately capture true evenness of the ecosystem. Using the protocols described, evenness was captured after the sampling of 12, one-acre using five transects randomly placed within 16-meter intervals. Transects were sampled at 10 cm intervals, resulting in 500 points per transect and 2500 points per site. Adjustments to one or more of these sampling attributes should permit application of the system to varied landscapes. There might also exist advantages in attempting to transform species distributions to normal from other habitats for subsequent analyses.

Some discussion seems warranted concerning potential experimental manipulations of priority sites. The approaches presented served to identify the minimum number (i.e., parsimonious quantum) of sites required for efficacious monitoring of key ecosystem variables. Results indicate use of a smaller number of sites for quantitative assessments would be ill-advised as it would curtail application of parametric statistics. Thus, subdivision of priority sites into subsets for application of varied experimental manipulations is discouraged. Currently, the lower Dolores watershed is ubiquitously colonized by an introduced biocontrol, *Diorhabda carinulata* (unpublished data, Sabaj Stahl). The beetle has defoliated vast swaths of tamarisk throughout the watershed, and may serve as a long term means by which to reduce tamarisk cover and/ or prevent its reestablishment. Currently, absent other experimental manipulations, priority sites are deemed sufficient for evaluating impacts of tamarisk defoliation upon community assemblages, species of interest, and diversity.

Alternatively, multiple manipulations could be used, so long as they were equally applied to all priority sites. For example, cattle grazing exclosures could be implemented if they were installed for all priority sites. Multivariate approaches could be used to assess the independent and interactive effects of multiple experimental manipulations. As a last resort, or for future studies endeavoring to implement multiple approaches independently, additional quanta could be identified within an ecosystem through expansion of the initial pool of study sites. Concerning the lower Dolores watershed, it was revealed 39 sites were required to derive the parsimonious quantum of 13, and so an additional 39 sites would likely require assessment to derive a second quantum. It would be fascinating, given sufficient resources, to compare outcomes for multiple manipulations applied across one quantum to individual manipulations applied across multiple quanta. In so doing, the young science of restoration ecology might achieve a quantum leap toward becoming a more quantitative discipline.

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References

Adler S., Hübener T., Dreßler M., Lotter A.F. & Anderson N.J. 2010. A Comparison of Relative Abundance versus Class Data in Diatom-based Quantitative Reconstructions. *Journal of Environmental Management.* 91: 1380-1388.

Akaike H. 1974. A New Look at the Statistical Model Identification. *IEEE Transactions on Automatic Control.* 19(6): 716–723.

Aitchison J. & Brown J.A.C. 1957. The lognormal distribution. Cambridge University Press, Cambridge, UK.

Archer K.J., Lemeshow S. & Hosmer D. W. 2007. Goodness-of-fit Tests for Logistic Regression Models when Data are Collected using a Complex Sampling Design. *Computational Statistics & Data Analysis.* 51: 4450 – 4464.

Berry W.D. 1993. Understanding regression assumptions. Sage, Thousand Oaks, CA.

Blaker H. 2000. Confidence Curves and Improved Exact Confidence Intervals for Discrete Distributions. *The Canadian Journal of Statistics.* 28(4): 1-16.

Blyth C.R. & Still H.A. 1983. Binomial Confidence Intervals. *Journal of the American Statistical Association.* 78: 108-116.

Box G.E.P. & Cox D.R. 1964. An Analysis of Transformations. *Journal of the Royal Statistical Society B* 26: 211-252.

Chaneton E.J. & Facelli J.M. 1991. Disturbance Effects on Plant Community Diversity: Spatial Scales and Dominance Hierarchies. *Plant Ecology.* 93(2): 143-155.

Cole D.N. & Bayfield N.G. 1993. Recreational Trampling of Vegetation: Standard Experimental Procedures. *Biological Conservation.* 63: 209-215.

El waer H., Anderson R., Whitney R. & Sabaj-Stahl D. 2010. Baseline Monitoring Relative to Tamarisk Invasion of Riparian Corridors of the Lower Dolores. *Technical Bulletin 11-2010*, Stahl Publishing, Denver, 18 p.

Elzinga C.L., Salzer D.W., Willoughby J.W. & Gibbs J.P. 2001. Monitoring plant and animal populations. Blackwell Science, Malden, MA, 360 p.

Giavelli G., Rossi O. & Sartore F. 1986. Comparative Evaluation of Four Species Diversity Indices Related to Two Specific Ecological Situations. *Field Studies.* 6: 429-438.

Gibson K.D., Dirks R., Medlin C.R. & Johnston l. 2004. Detection of Weed Species in Soybean using Multispectral Digital Images. *Weed Technology.* 18: 742-749.

Hammer Ø., Harper D.A.T. & Ryan P.D. 2001. PAST: Paleontological Statistics Software Package for Education and Data Analysis. *Palaeontologia Electronica.* 4(1): 9p. http://palaeo-electronica.org/2001_1/past/issue1_01.htm

Heip C. & Engels P. 1974. Comparing Species Diversity and Evenness Indices. *Journal of the*

Marine Biological Association UK. 54: 559-563.

Hayek L.C. & Buzas M.A. 1997. Surveying natural populations. Columbia University Press, New York, 592 p.

Hoffman L., Ries R.E. & Gilley J.E. 1983. Relationship of Runoff and Soil Loss to Ground Cover of Native and Reclaimed Grazing Land. *Agronomy Journal.* 75(4): 599-602.

Jacquier E., Kane A. & Marcus A.J. 2003. Geometric or Arithmetic Mean: A Reconsideration. *Analysts Journal.* 59(6): 46-53.

Johnson D.H. 1999. The Insignificance of Statistical Significance Testing. *Journal of Wildlife Management.* 63(3): 763-772.

Jolliffe I.T. 2002. Principle component analysis. (2nd ed). Springer, USA. 487 p.

Jost L. 2010. The Relation between Evenness and Diversity. *Diversity* 2: 207-232.

Kuipers L. & Niederreiter H. 2006. Uniform distribution of sequences. Dover Publications, Mineola, NY, 391 p.

Kupper L.L. & Hafner K.B. 1989. On Assessing Interrater Agreement for Multiple Attribute Responses. *Biometrics.* 45(3):957–967.

Kuss O. 2002. Global Goodness-of-fit Tests in Logistic Regression with Sparse Data. *Statistics in Medicine.* 21: 3789–3801.

Limpert E., Stahel W.A. & Abbt M. 2001. Log-normal Distributions across the Sciences: Keys and Clues. *Bioscience.* 51(5): 341-352.

MacArthur R.H. 1965. Patterns of Species Diversity. *Biological Review.* 40: 510-533.

Mair P., Reise S.P. & Bentler P.M. 2008. IRT Goodness-of-Fit Using Approaches from Logistic Regression. UCLA Press, Los Angeles, 13 pages.

Motomura I. 1932. A Statistical Treatment of Associations. *Japanese Journal of Zoology.* 44: 379–383.

Nåsell I. 1982. The Role of the Breakpoint in Schistosomiasis Eradication. Proceedings of the Seventh Conference on Probability Theory (Brasov, Romania). VNU Science Press, The Netherlands.

Peng J.C.Y., Manz B.D. & Keck J. 2001. Modeling Categorical Variables by Logistic Regression. *American Journal of Health Behavior.* 25(3): 278-84.

Peng J.C.Y., Lee K.C. & Ingersoll G.M. 2002. An Introduction to Logistic Regression Analysis and Reporting. *The Journal of Educational Research.* 96(1): 3-14.

Peng J.C.Y. & So H.T.S. 2002. Logistic Regression Analysis and Reporting: A primer. *Understanding Statistics.* 1(1): 31-70.

Porensky L., Riginos C., Balachowski J. & Belnap J. 2011. Guide to Monitoring Boma Sites: Version 3. Laikipia Wildlife Forum and USAID-Kenya, 24 p.

Quesenberry C. P. & Quesenberry C. Jr. 1982. On the Distribution of Residuals in Fitted Parametric Models. *Journal of Statistical Computation and Simulation.* 15: 129-140.

Rasmussen J. & Dunlap W. 1991. Dealing with Nonnormal Data: Parametric Analysis of Transformed Data vs. Nonparametric Analysis. *Educational and Psychological Measurement.* 51(4): 809-820.

Richards R.J. & Leib K.J. 2011. Characterization of Hydrology and Salinity in the Dolores Project Area, McElmo Creek Region, Southwest Colorado, 1978—2006. *U.S. Geological Survey Scientific Investigations Report 2010–5218*, 38 p.

Rosner B. 2000. Fundamentals of biostatistics. California: Duxbury Press, 876 p.

Sheskin D. 2004. Handbook of parametric and non-parametric statistical procedures. (3rd ed.) Florida: Chapman & Hall/ CRC, 1195 p.

Stanton J. M. 2001. Galton, Pearson, and the Peas: A Brief History of Linear Regression for Statistics Instructors. *Journal of Statistics Education.* 9(3): 1-10.

Tokeshi M. 1990. Niche Apportionment or Random Assortment: Species Abundance Patterns Revisited. *Journal of Animal Ecology.* 59: 1129-1146.

Whittaker R.H. 1960. Vegetation of the Siskiyou Mountains, Oregon and California. *Ecological Monographs.* 30: 279-338.

Whittaker R. H. 1965. Dominance and Diversity in Land Plant Communities. *Science.* 15(147): 250-260.

Wilcox R.R. 2010. Fundamentals of modern statistical methods: Substantially improving power and accuracy. (2nd ed.) Springer, New York, 249 p.

Williams K. 2009. Evaluating Community Evenness as a Function of Environmental Gradients: Do Trends in Evenness Occur? Thesis, Montana State University Press, Bozeman, MT, 25 p.

Wilson K. & Hardy I.C.W. 2002. Statistical analysis of sex ratios: An introduction. In: Sex ratios: concepts and research methods, ed. I. A. C. Hardy. Cambridge University Press.

Appendix 1: Species List & Rank Cover.

Species	Common Name	Rank
Abronia elliptica (n)	sand verbena	25
Acer negundo (n)	boxelder	55
Achnatherum hymenoides (n)	Indian ricegrass	54
Acroptilon repens (e)	knapweed	2
Agrostis gigantea (e)	redtop	28
Alyssum alyssoides (e)	pale madwort	74
Apocynum cannabinum (n)	Indianhemp	57
Artemisia ludoviciana (n)	white sagebrush	51
Artemisia tridentata (n)	big sagebrush	9
Astragalus sp. *(u)*	milkvetch	68
Atriplex canescens (n)	fourwing saltbush	17
Atriplex confertifolia (n)	shadscale saltbush	41
Atriplex hortensis (e)	garden orache	63
Bromus tectorum (e)	cheatgrass	5
Bromus ciliatus (n)	fringed brome	40
Castilleja chromosa (n)	desert paintbrush	31
Cardaria chalepensis (e)	lenspod whitetop	72
Carex sp. *(n)*	sedge	46
Carex aquatilis (n)	water sedge	66
Carex utriculata (n)	Northwest Territory sedge	36
Carex vulpinoidea (n)	fox sedge	33
Chenopodium atrovirens (n)	pinyon goosefoot	29
Chrysomanthus Nutt. *(n)*	rabbitbrush	15
Cirsium vulgare (e)	bull thistle	61
Clematis ligusticifolia (n)	western white clematis	44
Cryptantha mensana (n)	southwestern cryptantha	59
Cymopterus lemmonii (n)	alpine false springparsley	70
Distichlis spicata (n)	saltgrass	11
Elymus lanceolatus (n)	thickspike wheatgrass	78
Elymus repens (e)	quack/ couch grass	62
Elymus trachycaulus (n)	slender wheatgrass	34
Ephedra cutleri (n)	Cutler's jointfir	64
Equisetum arvense (n)	field horsetail	21
Ericameria nauseosa (n)	rubber rabbitbrush	7
Erodium cicutarium (e)	redstem stork's bill	77
Euphorbia brachycera (n)	horned spurge	48
Forestiera pubescens (n)	stretchberry	4
Fraxinus anomala (n)	singleleaf ash	71
Glycyrrhiza lepidota (n)	American licorice	19

Species	Common Name	Rank
Gutierrezia sarothrae (n)	broom snakeweed	20
Halogeton glomeratus (e)	saltlover	50
Helianthus praetermissus (n)	New Mexico sunflower	60
Hesperostipa comata (n)	needle and thread	39
Hesperostipa neomexicana (n)	New Mexico feathergrass	35
Heterotheca villosa (n)	hairy false goldenaster	58
Hordeum jubatum (n)	foxtail barley	52
Juniperus osteosperma (n)	Utah juniper	47
Kochia scoparia (e)	burningbush/ knapweed	16
Lepidium perfoliatum (e)	clasping pepperweed	79
Machaeranthera coloradoensis (n)	Colorado tansyaster	67
Melilotus officinalis (e)	sweetclover	27
Muhlenbergia asperifolia (n)	scratchgrass	6
Opuntia phaeacantha (n)	tulip pricklypear	32
Parthenocissus vitacea (n)	woodbine	65
Pascopyrum smithii (n)	western wheatgrass	38
Phalaris arundinacea (n)	reed canarygrass	30
Phragmites australis (n)	common reed	14
Plantago lanceolata (e)	narrowleaf plantain	45
Pleuraphis jamesii (n)	James' galleta	53
Populus deltoides wislizeni (n)	Rio Grande cottonwood	13
Rosa woodsii (n)	Woods' rose	37
Rhus trilobata (n)	skunkbush sumac	8
Salix exigua (n)	narrowleaf (sandbar) willow	3
Salsola kali (e)	Russian thistle	24
Sarcobatus vermiculatus (n)	greasewood	10
Senecio triangularis (n)	arrowleaf ragwort	12
Sisymbrium altissimum (e)	tall tumblemustard	76
Solidago canadensis (n)	Canada goldenrod	22
Sphaeralcea coccinea (n)	scarlet globemallow	75
Stanleya pinnata (n)	desert princesplume	73
Suaeda moquinii (n)	Mojave seablite	18
Tamarix chinensis (e)	tamarisk	1
Fragaria vesca (n)	woodland strawberry	69
Typha latifolia (n)	broadleaf cattail	56
Ulmus pumila (e)	Siberian elm	42
Xanthium strumarium (n)	rough coklebur	49
Grazed Native Forb *(n)*	forb	43
Grazed Native Grass *(n)*	grass	23
Grazed Native Shrub *(n)*	shrub	26

Species ranks were determined using absolute, arcsine-transformed percent covers of taxa averaged across all 39 study sites. (n) = native; (e) = exotic; (u) = unknown.