Flagging Aberrant Sites and Assemblages in Restoration Projects

Theo D. Wassenaar,1,2 Sam M. Ferreira,1,3 and Rudi J. van Aarde1,4

Abstract

The recovery of an ecosystem in response to a restoration program that relies on natural processes may be characterized by heterogeneous changes in species composition and structure. In most cases, such variability is natural and should even be welcomed. However, variability that arises from a specific restoration site, as opposed to randomly from all sites, may indicate problems with the restoration process and may jeopardize the outcome of a project. Here, we describe a technique to flag those sites and assemblages that tend to develop aberrantly. We use data on plant and animal assemblages, collected during routine monitoring operations over several surveys on a chronosequence of rehabilitating dune forests. Using this technique, we show that a bird assemblage on one of the sites at our study area on the coast of southern Africa tends to develop slower than expected. This site is situated farther than others from potential source areas (intact forests) and closer to human habitation. In essence, the technique uses a permutation test to identify ecological variables and assemblages that tend to be more variable than expected. It then focuses on these to identify specific aberrant sites. The technique allows management to concentrate scarce resources to determine the causes of aberrant changes, as well as possible mitigating actions, for specific sites instead of across the board. This cost-efficient rapid assessment technique will lead to improved chances of restoration success. It may be applied in all projects where a chronosequence of sites can be sampled repeatedly, as is often the case in post-mining restoration.

Key words: aberrant changes, dune forest, early detection, mining.

Introduction

The recovery of species composition and structure is the most fundamental of all restoration goals (Cairns 2000; Anand & Desrochers 2004). There are several ways to achieve this goal (Lockwood 1997). Some managers actively introduce species to a degraded site (e.g., Martínez-Garza & Howe 2003) and achieve varying degrees of success (e.g., Holl 2002). However, when a project aims to restore a native ecosystem (e.g., Thompson & Thompson 2000; Wassenaar et al. 2005), most methods rely on succession (Bradshaw 2000; Prach et al. 2001). This approach is also closest in spirit and letter to the Society for Ecological Restoration’s definition of restoration (SER 2004). Natural succession arguably has a greater chance of success than attempts to reconstruct a habitat manually.

In many cases, succession leads to predictable pathways along which an ecosystem may develop. If so, theory and inference from space-for-time studies can predict changes over time at a degraded site (Pickett 1989). For instance, Wassenaar et al. (2005) showed that the patterns of change in coastal dune forest sites that are recovering from mining remained remarkably constant for most groups of species across years. They used space-for-time substitution studies and showed that both plant and animal assemblages converged onto those of undisturbed dune forest, notwithstanding high variability in some cases. They could also predict a time to convergence for several assemblages and identified those that were diverging from the reference site.

It is likely that assemblages will vary naturally across sites during the recovery process (Klötzli & Grootjans 2001; Wiegleb & Felinks 2001; Choi 2004). However, such variation may hide aberrant trends on some sites and/or assemblages amid many others. Although the overall pattern of change across sites may thus reassure the restoration manager, it is often the more local or site-specific issues that can derail a project (Parker 1997). Clearly, such unwanted changes can put a restoration project at risk, especially if those in charge identify the problem sites too late. Restoration projects will thus benefit from a reliable “early-warning” protocol to help identify problem sites and assemblages.

In this article, we present such a protocol and apply it to our data on dune forest plant and animal assemblages (Wassenaar et al. 2005). The protocol uses an analysis of community development on sites of sequential age since mining (a “chronosequence”). In short, it defines aberrant sites and assemblages as those that consistently deviate
from a common trajectory across the chronosequence. We show here how we identified a site and an assemblage that are developing comparatively slowly over time and are thus deviating from the expected trajectory toward a coastal dune forest. By identifying specific sites, we may help to make management more cost-efficient because mitigating actions can now be focused on areas where they will make the largest difference.

Methods

Conceptual Approach

Ecological changes are slow relative to the life span of a human. As a result, few research projects can afford to collect data over long enough periods to detect meaningful changes in the abundance of animal and plant species and hence changes in community composition. Space-for-time substitution is the most common way to circumvent this problem (Gratzer et al. 2004). Substituting space for time means that the spatial pattern of differences sampled at the same time on sites that range from 1 to 100 years old should represent the temporal changes that would have been recorded on any one of them over 100 years.

Space-for-time studies are constrained by the assumption that sites have to be the same in all aspects except their postdisturbance age (Pickett 1989; Gratzer et al. 2004). This condition seldom occurs because sites often differ in size, are adjoined by diverse landscapes, experience continuous disturbance, and so on. The value of an ecological variable may thus be very different between sites, and these differences might be unrelated to predictable temporal changes.

Although natural variation is the rule rather than the exception, a similar direction and rate of development on all sites are an implicit objective for the restoration of a particular ecosystem. An ideal restoration of the same type of ecosystem on several sites over a number of years should therefore form a chronosequence. In such a case, each site in the chronosequence should develop at the same rate over time as what the spatial rate (the development rate as calculated between a site and its next older neighbor) suggests (Fig. 1). In other words, $d_{\text{time}}$ (rate of change over time) = $d_{\text{space}}$ (rate of change over age), where $d_{\text{time}} = \left(\frac{\text{var}_{t2} - \text{var}_{t1}}{t2 - t1}\right)$ and $d_{\text{space}} = \left(\frac{\text{var}_{a2} - \text{var}_{a1}}{a2 - a1}\right)$, where var = the value for any ecological variable, $t$ = time, and $a$ = site age.

A simple test of this prediction is whether the regression between $d_{\text{time}}$ and $d_{\text{space}}$ has a slope that does not exclude 1. With $d_{\text{space}}$ as the independent variable, a slope less than 1 would imply that changes generally occur slower over time than what the age-related chronosequence suggests, and vice versa.

Furthermore, a chronosequence should not vary excessively around this regression line. For us “not excessive” means that for each value of $X$, $Y$ should not vary with more than an ecologically reasonable 20%. We acknowledge that this is an arbitrary cutoff and that other more stringent values may be valid.

With variability greater than 20%, the variable chosen may simply be unsuitable for the test. For instance, the chronosequence assumption should be robust for most structural variables like species composition, but it may not be so for measures such as evenness, which would thus be unsuitable. More to the point, however, too much variability could also come from one or a few outlier sites that have a tendency to develop slower (or faster) over

![Figure 1. A line diagram illustrating the concept that each of a set of sequentially aged sites (the chronosequence) should develop over time (represented by the solid arrows that connect each site over time and denoted by $d_{\text{time}}$) at the same rate as the difference between it and the next older site suggests (represented here by the dotted arrows that connect next older sites and denoted by $d_{\text{space}}$). Each time the chronosequence is surveyed, all sites will have grown older by the number of years that separate the two surveys, and a new site (for instance site c) is added. Across all sites, $d_{\text{time}}$ should always equal $d_{\text{space}}$.](image-url)
of the assemblages, surveyed on seven rehabilitating sites that range in age from 1 to 27 years at the time of sampling. Here, we summarize only the most salient aspects of the sampling designs. We name the sampled sites stand 1 (the oldest at about 27 years after mining in 2005) through stand 7 (about 5 years old in 2005).

In brief, the four assemblages and their sampling methods are as follows: (1) trees, all woody vegetation taller than 20 cm, surveyed in 16 × 16-m quadrates per site. (2) Herbaceous vegetation, surveyed in an “exploded plot”: a set of 10 1-m² grids arranged along the sides of a 7 × 30-m transect, with each 1-m² grid separated from its neighbors by 5 m. The 1-m² grids consisted of 10 cells each, and the abundance for a species was the number of grid cells it occupied per plot. (3) Birds, surveyed by one surveyor at a time on approximately 300-m long line transects per site, with only perching birds recorded. (4) Millipedes, surveyed in 6 × 35-m strip transects, with all individuals up to 3 m above the ground being recorded. In all groups except birds, where the length of the line transects prevented it, the sampling units were located randomly within a site each time it was surveyed and sampling stopped only when no more new species were recorded. Herbaceous vegetation was surveyed five times (1994, 1995, 1999, 2003, and 2004), trees were surveyed four times (1992, 1997, 1999, and 2001), millipedes were surveyed six times (1993 and every year from 1998 to 2002), and birds were surveyed eight times (1993, every year from 1997 to 1999 and 2001 to 2004).

The number of times we surveyed a taxon may have influenced the probability of obtaining the true value of a variable. (A further potential cause of data-related error, the length of the monitoring period, was similar for all taxa in our study.) However, we are not interested in the true value of a variable here but only whether a specific site tends to cause irregular patterns. We therefore included all these taxa in our tests, reasoning that an inclusive dataset will give us a better chance to identify problem sites.

We measured species composition and structure in the four focal assemblages, using five different variables (Table 1). The first variable is Bray–Curtis distance, which measures the multivariate distance between the species composition at a sample site and that of an undisturbed forest site used as a reference (Table 1) (Legendre & Legendre 1998). As an index of community structure, we used four diversity measures, all related to the richness and abundances of species (Table 1).

Numerical Analysis

For all assemblages, we calculated $d_{time}$ and $d_{space}$ as the rate of change between successive surveys in each variable on a particular site and the rate of suggested change between the same site and a next older one, respectively. Assemblages with more successive surveys had more such time versus space comparisons. For instance, birds,
surveyed eight times in total, had 35 comparisons, whereas trees, surveyed four times, had only seven comparisons.

We used a Monte Carlo permutation test (Gentle 1943), first to test the expectation of \( d_\text{time} = d_\text{space} \) and second the expectation of reasonable variability. The first is a test of whether the slope of the regression \( d_\text{time}(Y) \) against \( d_\text{space}(X) \) differs from 1. If the slope were equal to 1, one would expect each \( Y \) value to be equal to its corresponding \( X \), within reasonable limits. For each \( X \), we thus randomly drew \( Y \) values from a normal distribution with a mean equal to each \( X \) and standard deviation equal to a coefficient of variation of 20%. We did this 1,000 times, each time calculating a slope and its 99% confidence interval (99% CI). An observed slope was significantly different from 1 if it was larger or smaller than 95% of the randomly generated slopes. For the second test, we counted the number of observed and random values that fell outside the 99% CI of each randomly generated slope. The variability was excessive if the distribution of the observed values outside the 99% CI was different from that of the random values outside that same interval. Here, we used a \( G \) test for goodness of fit (Sokal & Rohlf 1995).

The test for outliers (the aberrant sites) is a simple extension of the test for variability—we defined a value as aberrant if it always fell outside the 99% CI of the 1,000 random slopes. Still, being flagged as aberrant once does not by itself qualify a site as worthy of further attention, because even natural variability will sometimes produce an outlier. But if many of these outlier values originate from the same site, there is probably something wrong on that site. A site will thus only be aberrant if, across all

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Structure</td>
<td>The number of species per sampling unit, an estimate of the total number of species per site in a particular group. Richness should increase with site age, although this pattern is dependent on total taxon richness.</td>
</tr>
<tr>
<td>Margalef’s richness (Magurran 2004)</td>
<td>((S-1)/\ln(n)), where (S) = number of taxa and (n) = number of individuals. This is the number of species per unit area as a function of their total numbers.</td>
</tr>
<tr>
<td>Proportion of forest species</td>
<td>The proportion of species from the total number of species in the reference sites (i.e., the source pool) present on a particular sampling unit in the rehabilitating sites. Proportion of forest species should increase with site age.</td>
</tr>
<tr>
<td>Rare forest species</td>
<td>The number of forest specialist species (species usually associated with forests or thickets) from the 75% least abundant group of species in the reference sites, per sampling unit. This is essentially the rarest and most habitat-specialized subset of “proportion of forest species” above.</td>
</tr>
<tr>
<td>Composition</td>
<td></td>
</tr>
<tr>
<td>BCD</td>
<td>D is calculated as (1 - S), where (S) is the Bray–Curtis measure of similarity. BCD is a one-dimensional measure of how dissimilar a rehabilitating site and the reference site are in terms of the species present and their abundances. The smaller the value of (D), the more similar the two sites are. BCD should decrease with site age.</td>
</tr>
</tbody>
</table>

With two exceptions, these variables were calculated per sampling unit (line transects, quadrates, or plots) for four groups: herbaceous species, trees, millipedes, and birds. The exceptions were the herbaceous species, where number of rare forest species could not be calculated because of a lack of reliable data on the habitat associations of all the herbaceous species, and trees, where Margalef’s richness could not be calculated because our earliest data on tree distribution and abundance consist of relative abundance values only. BCD, Bray–Curtis distance.

Table 2. The slope ± SE of the relationship between the rate of change over space (the difference between two sites of successive age per unit of time) and the rate of change over time (the difference between two successive surveys on the younger of the two sites, per unit of time).

<table>
<thead>
<tr>
<th>Group</th>
<th>Species Richness</th>
<th>n Rare Forest Species</th>
<th>Margalef’s Richness</th>
<th>Forest Species</th>
<th>Bray–Curtis Distance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Herbs (n = 17)</td>
<td>0.98 ± 0.62 (0.48)</td>
<td>—</td>
<td>0.27 ± 0.71 (0.00*)</td>
<td>1.19 ± 0.63 (0.23)</td>
<td>−2.34 ± 0.47 (0.00*)</td>
</tr>
<tr>
<td>Trees (n = 7)</td>
<td>0.38 ± 0.62 (0.06)</td>
<td>0.71 ± 0.69 (0.26)</td>
<td>—</td>
<td>0.36 ± 0.54 (0.08)</td>
<td>0.52 ± 0.40 (0.13)</td>
</tr>
<tr>
<td>Millipedes (n = 20)</td>
<td>0.41 ± 0.39 (0.003*)</td>
<td>0.30 ± 0.36 (0.00*)</td>
<td>0.71 ± 0.47 (0.08)</td>
<td>0.42 ± 0.39 (0.01*)</td>
<td>0.90 ± 0.71 (0.33)</td>
</tr>
<tr>
<td>Birds (n = 35)</td>
<td>2.03 ± 0.51 (0.00*)</td>
<td>0.90 ± 0.53 (0.28)</td>
<td>2.38 ± 0.57 (0.00*)</td>
<td>2.02 ± 0.50 (0.00*)</td>
<td>0.96 ± 0.72 (0.42)</td>
</tr>
</tbody>
</table>

A slope close to 1 implies that the rate of change on a particular site over time is the same as that suggested by the rate of change across regeneration age. Values in parentheses are the probability that the slope is different from 1, as tested using a Monte Carlo permutation test. Neither Margalef’s richness in trees nor the number of rare forest herb species could be calculated (see text for reasons).

* Significantly different from slope = 1 at \(p = 0.05\).
assemblage–variable combinations, it tends to fall outside the confidence interval all the time. If these outlier values further tend to fall on one side of the regression line, it may indicate a systematic problem on that site. In the same way, a particular survey year that crops up as an outlier more often than others may for instance indicate a seasonal or specific sample effect.

We thus calculated indexes of the tendency to produce aberrant changes overall, per assemblage and per ecological variable. In each case the index was the number of outliers for each site. To correct for differences in sample sizes, we divided each variable or assemblage by the number of surveys as well as the number of assemblages and variables, respectively.

If the number of observations per site becomes large enough, it is possible to test statistically whether the number of times a site or year is an outlier is significant or not. However, we do not yet have enough data points for all sites; hence, this part of the test depends on a somewhat subjective visual assessment of the frequency of outlier sites, years, assemblages, and variables relative to others.

Results

Slopes of the relationships varied from −2.34 (Bray–Curtis distance in herbs) to 2.38 (Margalef’s richness in birds) (Table 2), but most values ranged from 0.3 to 1.2 (Fig. 2). The high standard errors for these slopes reflect on the high variability in the observed changes (Table 2). Almost half of the slopes (eight out of 18) differed significantly from 1, this being especially common for millipedes and birds (three of five slopes each) (Table 2).

All the assemblage–variable combinations were more variable than could be expected by chance (G tests; Table 3). Of all the variables, the proportion of forest species showed the least variability and Bray–Curtis distance the most, driven largely by excessive variability in birds (Table 3).

Over all assemblages and variables, stands 2 (the second oldest stand) and 5 were the most prone to change either slower or faster than expected (Fig. 3). Stand 2 in particular tended to change slower than expected, but the other sites were equally likely to change slower or faster than expected (Fig. 3).

An assemblage-specific analysis showed that different stands were most affected for different assemblages (Table 4). For instance, stand 5 was the worst for herbs and stand 4 for millipedes (Table 4). Birds showed a much larger tendency for aberrant changes (most of them slower than expected) than the next assemblage (millipedes) and trees had the fewest (Table 4). None of the variables were more or less prone to aberrant changes than others, but

Table 3. The frequency distribution of proportions of data points inside the confidence limits was tested with a G test for goodness of fit.

<table>
<thead>
<tr>
<th>Group</th>
<th>Species Richness</th>
<th>n Rare Forest Species</th>
<th>Margalef’s Richness</th>
<th>Forest Species</th>
<th>Bray–Curtis Distance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Herbs</td>
<td>2,699.79</td>
<td>—</td>
<td>953.62</td>
<td>2,421.30</td>
<td>1,680.24</td>
</tr>
<tr>
<td>Trees</td>
<td>889.97</td>
<td>1,931.90</td>
<td>—</td>
<td>694.55</td>
<td>1,392.60</td>
</tr>
<tr>
<td>Millipedes</td>
<td>850.38</td>
<td>3,953.30</td>
<td>2,084.82</td>
<td>344.17</td>
<td>4,393.15</td>
</tr>
<tr>
<td>Birds</td>
<td>2,211.08</td>
<td>1,560.59</td>
<td>2,994.93</td>
<td>1,528.71</td>
<td>9,099.16</td>
</tr>
</tbody>
</table>

Here, we report the value of G. All G values were significant, meaning that all group–variable combinations varied more than could be expected by chance alone. Critical G was 67.5 (p = 0.05) for all tests. Neither Margalef’s richness (trees) nor the number of rare forest species (herbs) could be calculated for this report (see text for reasons).
the analysis here did confirm stand 2’s overall higher tendency for aberrant changes (Table 5).

The most recent two survey years, in particular 2002, produced many sites that appeared to change slower than expected (Fig. 4). In general, with the exception of 1998, there was an apparent trend for later years to produce more aberrant sites than earlier ones (Fig. 4).

Discussion

One of the biggest challenges in a restoration project is to know when it is failing and why (Ormerod 2003). Data on how recovering assemblages deviate from their expected trends may thus help the design of adaptive restoration plans (Cooke & Johnson 2002). Data on restoration failures may advance ecological theory (Ormerod 2003) because ecological restoration is an “acid test” for theoretical understanding (Bradshaw 2002). Several authors have pointed out that monitoring and assessment of restoration success are as much part of the project as the actual landscaping or introduction of species is (see, e.g., Holl & Cairns 2002; SER 2004; Thompson & Thompson 2004). However, development of general assessment methods has perhaps lagged behind the development of restoration techniques themselves, due inter alia to a lack of publication of such studies (Hackney 2000). Still, because it is so central to the success of any restoration project, the subject has been receiving more and more attention in the literature (e.g., Anand & Desrochers 2004; Martin et al. 2005; Rayfield et al. 2005; Ruiz-Jaen & Aide 2005a, 2005b).

To have any relevance, assessment needs to evaluate changes over ecologically meaningful time and spatial scales (Storch & Gaston 2004). However, in most cases it is prohibitively expensive to monitor an ecosystem for a long enough period to detect changes in populations of long-lived trees for instance. Many assessment methods therefore rely on once-off comparisons of the restored ecosystem to that on a neighboring reference system (Zedler & Callaway 2000; Martin et al. 2005; see also the references in Ruiz-Jaen & Aide 2005a). When the emphasis is on rates and trajectories of community recovery, however, space is often substituted for time, especially in those cases where the evaluation needs to be rapid (Kindscher & Tieszen 1998; Baer et al. 2002; Holl 2002; Sluis 2002; Nakamura et al. 2003; Parkes et al. 2003).

We used such a space-for-time analysis before to show the recovery of a number of key forest species assemblages after mining (Davis et al. 2002; Wassenaar et al. 2005). A typical pattern is the one for the bird assemblage where the rate of decay in compositional distance from that of a reference site suggests that it will be restored within 32 years (see Fig. 4 and Table 3 in Wassenaar et al. 2005). Different to Wassenaar et al. (2005), our present approach takes into account year-to-year variability on specific sites and in specific assemblages. This approach showed that all the assemblages (and in particular the birds) were more variable than we would have predicted given our previous analyses of the same groups. Of course, variability is to be expected, and indeed even welcomed, given that we aim to restore an ecosystem with all its inherent heterogeneity (Palmer et al. 1997).

Table 4. An index of how often a group tended to change either slower or faster than expected in each of the seven rehabilitation stands, excluding stand 1, which is the oldest site and hence has no older reference point.

<table>
<thead>
<tr>
<th>Group</th>
<th>Stand 1</th>
<th>Stand 2</th>
<th>Stand 3</th>
<th>Stand 4</th>
<th>Stand 5</th>
<th>Stand 6</th>
<th>Stand 7</th>
<th>Overall</th>
</tr>
</thead>
<tbody>
<tr>
<td>Herbs</td>
<td>—</td>
<td>0.50</td>
<td>0.35</td>
<td>0.38</td>
<td>0.56</td>
<td>0.00</td>
<td>0.38</td>
<td>2.16</td>
</tr>
<tr>
<td>Trees</td>
<td>—</td>
<td>0.13</td>
<td>0.06</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.19</td>
</tr>
<tr>
<td>Millipedes</td>
<td>—</td>
<td>0.33</td>
<td>0.24</td>
<td>0.60</td>
<td>0.32</td>
<td>0.33</td>
<td>0.40</td>
<td>2.23</td>
</tr>
<tr>
<td>Birds</td>
<td>—</td>
<td>0.80</td>
<td>0.73</td>
<td>0.55</td>
<td>0.60</td>
<td>0.57</td>
<td>0.50</td>
<td>3.75</td>
</tr>
<tr>
<td>Average</td>
<td>—</td>
<td>0.44</td>
<td>0.34</td>
<td>0.38</td>
<td>0.37</td>
<td>0.23</td>
<td>0.41</td>
<td></td>
</tr>
</tbody>
</table>

The index gives the probability that change in a group will be aberrant per site. It was calculated as the number of times that a group was an outlier, divided by the number of variables that was measured (Margalef’s richness and rare forest species were not calculated for trees and herbs, respectively—see text for explanation), divided by the number of surveys per stand. The overall index is the sum of indexes across all stands.
results were thus surprising in light of our previous work (Wassenaar et al. 2005). However, variability becomes much more important when it consistently originates from a specific site.

Our approach allowed us to identify such a site, stand 2, where both assemblage structure and composition tend to develop slower than normal. It was particularly the bird assemblage of stand 2 that was affected, but even herbs were changing slower here than on other sites. Even the tree assemblage, although its index was comparatively low, changed relatively slow. The method seems to be sensitive enough to detect specific sites for specific assemblages. For instance, the millipede assemblage on stand 4 changed atypically, as did the herb assemblage on stand 5.

In this analysis, we have not dealt with the causes of irregular changes. Likely candidates include continued disturbances due to some sites (in our study, stand 2) being located closer to human habitation and being exposed to grazing by cattle. Stand 2 is also situated further away from the primary intact forest source areas, so that colonization might be lagging behind here. Apparent aberrant changes on the youngest sites may be the result of larger fluctuations in the microclimate because vegetation structure has not developed sufficiently to buffer these.

Several factors may slow down the development of a specific assemblage, ranging from human-induced disturbances to priority effects. But the important thing is that we now have a method to identify sites and assemblages that develop atypically or not in accordance with the expected trajectories. Consequently, we can focus scarce resources on detecting factors that are specific to a site or assemblage and manage these. Flagging such sites is certainly the first step in identifying potential causes for unwanted changes. It may be possible, for instance, to improve a site’s performance by creating habitat for specific groups, e.g., birds, or simply through paying more attention to the control of human-induced disturbances there.

Our method is not a total solution or the ultimate tool for restoration monitoring. It merely identifies aberrant sites and taxa. As with many other issues in natural resource management, it requires multiple approaches and techniques to identify problem sites and assemblages in restoration. The technique is conceptually sound and simple to apply, in that it needs only a few repeated surveys of the same chronosequence (although these will have to be conducted at least a season or two apart). This situation often arises in post-mining projects, where rehabilitation commences soon after mining does and continues for the life of the mine. Because many mines have a life span of 20 years or more, quite lengthy chronosequences are possible.

It is unlikely that the method would be applicable across widely separated sites because it assumes similar restoration management and the same species source pool for all sites. Moreover, there may be statistical data limitations, in the sense that too few surveys, or too few sites, may give unreliable results. Still, even preliminary investigations at relatively early stages may qualitatively flag obviously aberrant sites or groups. This is because the central concept, the identification of specific aberrant sites through comparison with its peers, is relatively simple. By mitigating against specific disruptions on particular sites, a program’s cost-efficiency improves and with it the chance of successful restoration. Our approach could thus

### Table 5

<table>
<thead>
<tr>
<th>Variables</th>
<th>Stand 1</th>
<th>Stand 2</th>
<th>Stand 3</th>
<th>Stand 4</th>
<th>Stand 5</th>
<th>Stand 6</th>
<th>Stand 7</th>
<th>Overall</th>
</tr>
</thead>
<tbody>
<tr>
<td>Species richness</td>
<td>—</td>
<td>2.75</td>
<td>2.25</td>
<td>2.25</td>
<td>2.50</td>
<td>1.50</td>
<td>1.00</td>
<td>12.25</td>
</tr>
<tr>
<td>Bray–Curtis distance</td>
<td>—</td>
<td>3.00</td>
<td>2.25</td>
<td>3.00</td>
<td>2.50</td>
<td>1.00</td>
<td>0.50</td>
<td>12.25</td>
</tr>
<tr>
<td>Forest species</td>
<td>—</td>
<td>2.75</td>
<td>2.25</td>
<td>1.75</td>
<td>2.25</td>
<td>1.75</td>
<td>0.75</td>
<td>11.50</td>
</tr>
<tr>
<td>Margalef’s richness</td>
<td>—</td>
<td>3.33</td>
<td>2.33</td>
<td>2.67</td>
<td>2.67</td>
<td>2.00</td>
<td>1.33</td>
<td>14.33</td>
</tr>
<tr>
<td>n Rare forest species</td>
<td>—</td>
<td>3.33</td>
<td>3.00</td>
<td>2.33</td>
<td>1.33</td>
<td>0.67</td>
<td>0.33</td>
<td>11.00</td>
</tr>
<tr>
<td>Average</td>
<td>—</td>
<td>3.03</td>
<td>2.42</td>
<td>2.40</td>
<td>2.25</td>
<td>1.38</td>
<td>0.78</td>
<td></td>
</tr>
</tbody>
</table>

The index is the sum of all aberrant changes per variable, standardized by the number of groups per variable (Margalef’s richness and rare forest species were not calculated for trees and herbs, respectively—see text for explanation). The overall index is the sum of the indexes across all stands.
prove useful for many projects, other than our own, that use repeated surveys of chronosequences as part of their evaluation of restoration success.

**Implications for Practice**
- Specific aberrant sites may put a whole restoration project in jeopardy but is usually time-consuming and costly to identify.
- By repeatedly sampling assemblages on a chronosequence of restored sites, one can identify specific sites where community structure and/or composition tend to change aberrantly.
- This allows management to focus scarce resources where it matters most and where mitigating actions will have the largest effect.
- Such intervention is thus more cost-effective and will thus have a greater effect on the chances of successful restoration.

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**LITERATURE CITED**


