Flagging Aberrant Sites and Assemblages in Restoration Projects

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

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 2004; 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

[1] Conservation Ecology Research Unit, University of Pretoria, Pretoria, 0002, Gauteng, South Africa.
[2] Present address: African Wilderness Restoration, PO Box 11997, Klein Windhoek, Khomas, Namibia, 9000.
[3] Present address: Department of Statistics, University of Auckland, Auckland, New Zealand.
[4] Address correspondence to R. J. van Aarde, rjvaarde@zoology.up.ac.za

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_{time} (rate of change over time) $= d_{\text{space}}$ (rate of change over age), where $d_{\text{time}} = (\text{var}_{t_2} - \text{var}_{t_1})/(t_2 - t_1)$ and $d_{\text{space}} = (\text{var}_{a_2} - \text{var}_{a_1})/(a_2 - a_1)$, 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_{time} and d_{space} has a slope that does not exclude 1. With d_{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
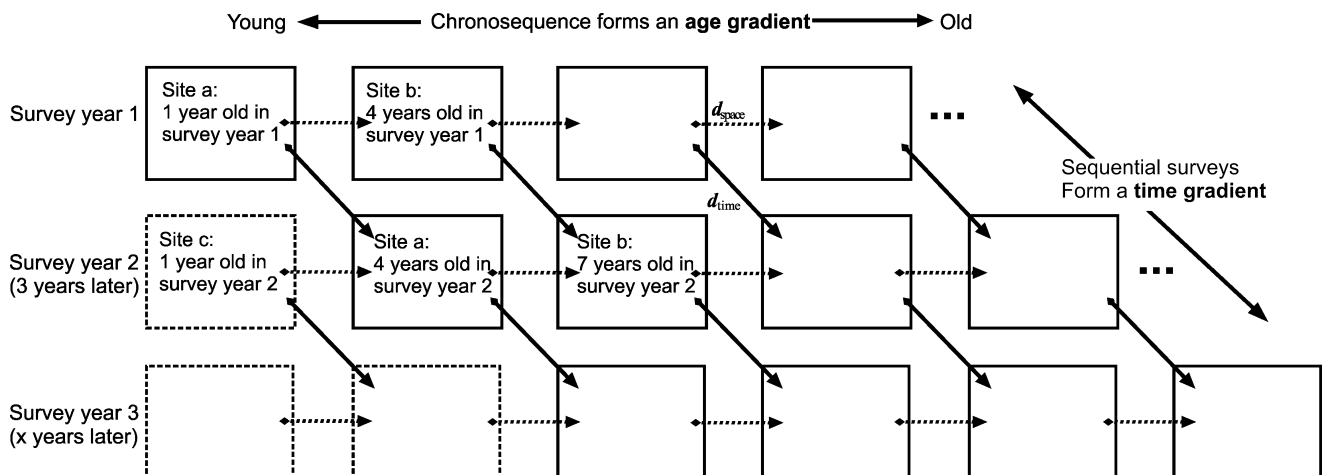

Figure 1. A line diagram illustrating the concept that each of a set of sequentially aged sites (the chronosequence) should develop over time (represented by the solid arrows that connect each site over time and denoted by d_{time}) at the same rate as the difference between it and the next older site suggests (represented here by the dotted arrows that connect next older sites and denoted by d_{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_{time} should always equal d_{space}.

time than across space. These are the aberrant sites. Our challenge is to reliably identify such sites in a large database, given natural variability in almost all structural community measures.

Study Site

The humid subtropical forests on coastal dunes on the northeast coast of South Africa are floristically linked to the Maputaland centre of plant endemism (van Wyk & Smith 2001). Wassenaar et al. (2005) provide a description and a map of the study area. The region has conservation value, and the company that mine these dunes (Richards Bay Minerals) is committed to restore a native dune forest on part of the mined area (van Aarde et al. 1996).

The mining process and the rehabilitation techniques have been the same since their inception in 1976 and 1977, respectively. The company dredges the dunes, separates the heavier minerals from the sand, and then deposits the tailings (approximately 95% of the original volume) behind the dredging pond. These tailings, shaped to approximate the pre-mining topography and covered with topsoil, form the basis on which rehabilitation of the dune forest takes place. Topsoil is collected after clearing the vegetation in front of the dredge ponds and is subsequently spread on the tailings to initiate the recovery process.

The rehabilitation program aims to mimic the successional pathway from grassland to dune forest that Weisser and Muller (1983) described before. The seed of the pioneer tree (*Acacia kosiensis*) is present in the topsoil of most sandy soils in the region. *A. kosiensis* germinates prodigiously in the first few years, first forming dense thorny thickets and later stands of closed woodland. As a site increases in age, naturally dispersing forest plant species from neighboring unmined areas replace the dominant *A. kosiensis* (van Aarde et al. 1996; Wassenaar et al. 2005). As a result, the site's plant species composition and their relative abundances become more similar with age to those of a nearby but unmined dune forest (Wassenaar et al. 2005). In general, this convergent pattern also occurs in soil measures, birds, and millipedes but not in rodents or dung beetles (van Aarde et al. 1996; Wassenaar et al. 2005).

The region's climate is subtropical with most rain falling from January to March (peak in February). Extended droughts are uncommon, and about 70% of the annual rainfall of approximately 1,292 mm occurs in the summer (Wassenaar & van Aarde 2001). Mean annual temperature is 21.5°C (Wassenaar & van Aarde 2001).

Data

Our database was compiled from information on structural changes in several assemblages collected over a period of 12 years by our research group (described by Wassenaar et al. 2005). The present article focuses on four

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-m^2 grids arranged along the sides of a 7×30–m transect, with each 1-m^2 grid separated from its neighbors by 5 m. The 1-m^2 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 to1999 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,

Table 1. Variables used for the monitoring of ecological development of post-mining rehabilitating coastal dune forests.

Variable	Description
Structure	
Richness (Magurran 2004)	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.
Margalef's richness (Magurran 2004)	$(S - 1)/\ln(n)$, 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.
Proportion of forest species	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.
n Rare forest species	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.
Composition	
BCD D (Legendre & Legendre 1998)	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.

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.

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 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).

Group	Species Richness	n Rare Forest Species	Margalef's Richness	Forest Species	Bray–Curtis Distance
Herbs ($n = 17$)	0.98 ± 0.62 (0.48)	—	0.27 ± 0.71 (0*)	1.19 ± 0.63 (0.23)	−2.34 ± 0.47 (0.00*)
Trees ($n = 7$)	0.38 ± 0.62 (0.06)	0.71 ± 0.69 (0.26)	—	0.36 ± 0.54 (0.08)	0.52 ± 0.40 (0.13)
Millipedes ($n = 20$)	0.41 ± 0.39 (0.003*)	0.30 ± 0.36 (0.00*)	0.71 ± 0.47 (0.08)	0.42 ± 0.39 (0.01*)	0.90 ± 0.71 (0.33)
Birds ($n = 35$)	2.03 ± 0.51 (0.00*)	0.90 ± 0.53 (0.28)	2.38 ± 0.57 (0.00*)	2.02 ± 0.50 (0.00*)	0.96 ± 0.72 (0.42)

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).
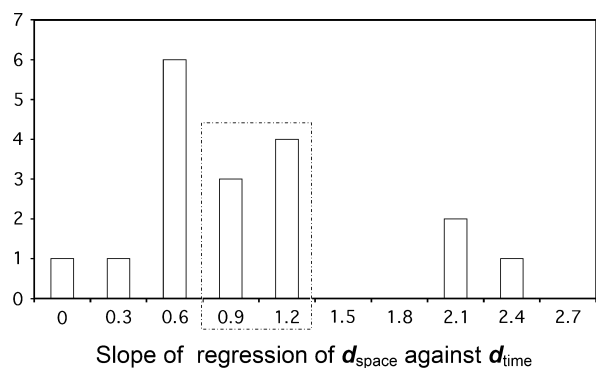* Significantly different from slope = 1 at $p = 0.05$.

Figure 2. The number of times that a slope of a specific value was found in the regressions of d_{space} against d_{time}, for all group–variable combinations. Ideally, the slopes should be close to 1 (in other words, fall within the rectangle). Most slopes ranged from 0.3 to 1.2 but many ranged from 0.3 to 0.6. Birds produced three very high slopes (between 2.1 and 2.4), meaning that in those variables, the bird community tends to change almost twice as fast over time as what the chronosequence suggests. One slope for herbs (Bray–Curtis distance) was −2.34 (shown here in the 0–0.3 class).

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.

In essence, the technique uses two criteria—a slope's difference from 1 and the amount of variability. It identifies assemblage–variable combinations for which a large number of sites develop either in the wrong direction, or too slow, or too fast. It then focuses on these to determine whether the excessive values originate from a particular site. If so, we flag such a site as aberrant for a specific assemblage–variable combination. This approach does not exclude the potential for aberrant changes in other assemblage–variable combinations and other sites. However, it allows us to focus on those combinations and sites where there is a tendency for this to happen.

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.

Group	Species Richness	n Rare Forest Species	Margalef's Richness	Forest Species	Bray–Curtis Distance
Herbs	2,699.79	—	953.62	2,421.30	1,680.24
Trees	889.97	1,931.90	—	694.55	1,392.60
Millipedes	850.38	3,953.30	2,084.82	344.17	4,393.15
Birds	2,211.08	1,560.59	2,994.93	1,528.71	9,099.16

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).
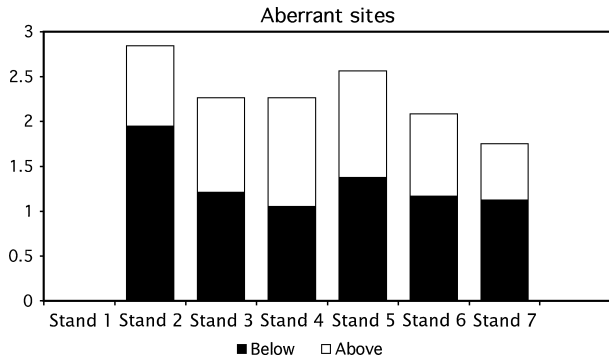
Aberrant sites

Figure 3. The number of times that a particular site (on the X-axis, numbered from 1, the oldest stand, to 7, the youngest) was changing either faster (above) or slower (below) than what the pattern across the chronosequence would suggest. The values were standardized by the number of surveys conducted in each, so the stands are directly comparable. Stand 2, the second oldest site, was clearly the most aberrant, largely because changes over time were slower than what would have been predicted. Stand 5, however, is a close second, with not much difference between the rest of the sites. Stand 1 is not included because it is the oldest site and hence has no older reference point.

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). Our current

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.

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

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.

Table 5. An index of the number of times each variable tended to change either slower or faster than expected for each of the seven rehabilitation stands, excluding stand 1, which is the oldest site and hence has no older reference point.

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

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.
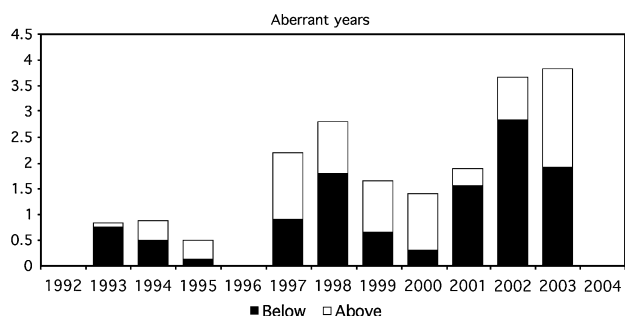

Figure 4. The number of times that any of the sites sampled in a particular year turned out to be changing either faster (above) or slower (below) than what the pattern across the chronosequence would suggest, across all group–variable combinations. The values were standardized by the number of sites and groups that were sampled in each year, so the years are directly comparable. The latest survey (2004) is not included because it is the time reference point for the analysis.

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

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.

LITERATURE CITED

Anand, M., and R. E. Desrochers. 2004. Quantification of restoration success using complex systems and models. Restoration Ecology **12:**117–123.

Baer, S. G., D. J. Kitchen, J. M. Blair, and C. W. Rice. 2002. Changes in ecosystem structure and function along a chronosequence of restored grasslands. Ecological Applications **12:**1688–1701.

Bradshaw, A. D. 2000. The use of natural processes in reclamation—advantages and difficulties. Landscape and Urban Planning **51:**89–100.

Bradshaw, A. D. 2002. Introduction and philosophy. Pages 3–9 in M. R. Perrow and A. J. Davy, editors. Handbook of ecological restoration, vol. 1: Principles of restoration. Cambridge University Press, Cambridge, United Kingdom.

Cairns, J. 2000. Setting ecological restoration goals for technical feasibility and scientific validity. Ecological Engineering **15:**171–180.

Choi, Y. D. 2004. Theories for ecological restoration in changing environment: towards 'futuristic' restoration. Ecological Research **19:**75–81.

Cooke, J. A., and M. S. Johnson. 2002. Ecological restoration of land with particular reference to the mining of metals and industrial minerals: a review of theory and practice. Environmental Review **10:**41–71.

Davis, A. L. V., R. J. van Aarde, C. H. Scholtz, and J. H. Delport. 2002. Increasing representation of localized dung beetles across a chronosequence of regenerating vegetation and natural dune forest in South Africa. Global Ecology & Biogeography **11:**191–209.

Gentle, J. E. 1943. Random number generation and Monte Carlo methods. Springer-Verlag, New York.

Gratzer, G., C. Canham, U. Dieckmann, A. Fischer, Y. Iwasa, R. Law, et al. 2004. Spatio-temporal development of forests—current trends in field methods and models. Oikos **107:**3–15.

Hackney, C. T. 2000. Restoration of coastal habitats: expectation and reality. Ecological Engineering **15:**165–170.

Holl, K. D. 2002. Long-term vegetation recovery on reclaimed coal surface mines in the eastern USA. Journal of Applied Ecology **39:**960–970.

Holl, K. D., and J. Cairns Jr. 2002. Monitoring and appraisal. Pages 411–432 in M. R. Perrow and A. J. Davy, editors. Handbook of ecological restoration, vol. 1: Principles of restoration. Cambridge University Press, Cambridge, United Kingdom.

Kindscher, K., and L. L. Tieszen. 1998. Floristic and soil organic matter changes after five and thirty-five years of native tallgrass prairie restoration. Restoration Ecology **6:**181–196.

Klötzli, F., and A. P. Grootjans. 2001. Restoration of natural and semi-natural wetland systems in Central Europe: progress and predictability of developments. Restoration Ecology **9:**209–219.

Legendre, P., and L. Legendre. 1998. Numerical ecology. Elsevier, Amsterdam, The Netherlands.

Lockwood, J. L. 1997. An alternative to succession—assembly rules offer guide to restoration efforts. Restoration & Management Notes **15:**45–50.

Magurran, A. E. 2004. Measuring biological diversity. Blackwell Science Publishers, Oxford, United Kingdom.

Martin, L. M., K. A. Moloney, and B. J. Wilsey. 2005. An assessment of grassland restoration success using species diversity components. Journal of Applied Ecology **42:**327–336.

Martínez-Garza, C., and H. F. Howe. 2003. Restoring tropical diversity: beating the time tax on species loss. Journal of Applied Ecology **40:**423–429.

Nakamura, A., H. Proctor, and C. P. Catterall. 2003. Using soil and litter arthropods to assess the state of rainforest restoration. Ecological Management and Restoration **4:**S20–S28.

Ormerod, S. J. 2003. Restoration in applied ecology: editor's introduction. Journal of Applied Ecology **40:**44–50.

Palmer, M. A., R. F. Ambrose, and N. L. Poff. 1997. Ecological theory and community restoration ecology. Restoration Ecology **5:**291–300.

Parker, V. T. 1997. The scale of successional models and restoration objectives. Restoration Ecology **5:**301–306.

Parkes, D., G. Newell, and D. Cheal. 2003. Assessing the quality of native vegetation: the 'habitat hectares' approach. Ecological Management and Restoration **4:**S29–S38.

Pickett, S. T. A. 1989. Space-for-time substitution as an alternative to long-term studies. Pages 110–135 in G. E. Likens, editor. Long-term studies in ecology. Approaches and alternatives. Springer-Verlag, New York.

Prach, K., S. Bartha, C. B. Joyce, P. Pyšek, R. van Diggelen, and G. Wiegleb. 2001. The role of spontaneous vegetation succession in ecosystem restoration: a perspective. Applied Vegetation Science **4:**111–114.

Rayfield, B., M. Anand, and S. Laurence. 2005. Assessing simple versus complex restoration strategies for industrially disturbed forests. Restoration Ecology **13:**639–650.

Ruiz-Jaen, M. C., and T. M. Aide. 2005a. Restoration success: how is it being measured? Restoration Ecology **13:**569–577.

Ruiz-Jaen, M. C., and T. M. Aide. 2005b. Vegetation structure, species diversity, and ecosystem processes as measures of restoration success. Forest Ecology and Management **218:**159–173.

SER (Society for Ecological Restoration Science & Policy Working Group). 2004. The SER primer on ecological restoration (available from www.ser.org) accessed 3 January 2006.

Sluis, W. J. 2002. Patterns of species richness and composition in recreated grassland. Restoration Ecology **10:**677–684.

Sokal, R. R., and F. J. Rohlf. 1995. Biometry. The principles and practice of statistics in biological research. 3rd edition. W.H. Freeman and Company, New York.

Storch, D., and K. J. Gaston. 2004. Untangling ecological complexity on different scales of space and time. Basic and Applied Ecology **5:**389–400.

Thompson, S. A., and G. G. Thompson. 2004. Adequacy of rehabilitation monitoring practices in the Western Australian mining industry. Ecological Management and Restoration **5:**30–33.

van Aarde, R. J., S. M. Ferreira, J. J. Kritzinger, P. J. van Dyk, M. Vogt, and T. D. Wassenaar. 1996. An evaluation of habitat rehabilitation on coastal dune forests in northern KwaZulu-Natal, South Africa. Restoration Ecology **4:**334–345.

van Wyk, A. E., and G. F. Smith. 2001. Regions of floristic endemism in Southern Africa. Umdaus Press, Pretoria, South Africa.

Wassenaar, T. D., and R. J. van Aarde. 2001. Short-term responses of rehabilitating coastal dune forest ground vegetation to livestock grazing. African Journal of Ecology **39:**329–339.

Wassenaar, T. D., R. J. van Aarde, S. L. Pimm, and S. M. Ferreira. 2005. Community convergence in disturbed sub-tropical dune forests. Ecology **86:**655–666.

Weisser, P. J., and R. Muller. 1983. Dune vegetation dynamics from 1937 to 1976 in the Mlalazi-Richards Bay area, Natal, South Africa. Bothalia **14:**661–667.

Wiegleb, G., and B. Felinks. 2001. Predictability of early stages of primary succession in post-mining landscapes of Lower Lusatia, Germany. Applied Vegetation Science **4:**5–18.

Zedler, J. B., and J. C. Callaway. 2000. Evaluating the progress of engineered tidal wetlands. Ecological Engineering **15:** 211–225.