Use of biomass predicted by regression from cover estimates to compare vegetational similarity of sagebrush-grass sites

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USE OF BIOMASS PREDICTED BY REGRESSION FROM COVER ESTIMATES TO COMPARE VEGETATIONAL SIMILARITY OF SAGEBRUSH-GRASS SITES

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Abstract.— Regressions between vegetational cover, estimated with a two-tiered, gridded sampling frame, and biomass were used to obtain predicted biomass values from cover values. Comparisons of eight sites based on pre dicted biomass data and comparisons of the sites based on cover data indicate that predicted biomass data may better identify differences among sites. Also, some suggestions are made regarding the methods of using cover-bio mass regressions to obtain predicted biomass values.

Biomass data are generally considered to most precisely represent the relative impor tance of species in a community (Whittaker 1975). However, biomass sampling is often time consuming, especially when sampling a large number of plots is required. As an alter native, many methods of cover estimation have been used. Methods of weight estima tion (Pechanec and Pickford 1937, Wilm et al. 1944, Tadmore et al. 1975) and relative weight estimation (Hutchings and Schmautz 1969) have also been used. However, weight estimation methods are inherently dependent on the skill of the observer and results may vary. Cook et al. (1948) estimated units of cover, determined biomass per unit, and ob tained biomass estimates by multiplying mass per unit of cover by number of units of cover for a species. Payne (1974) presented linear regressions between cover and biomass for many herbaceous species. Anderson and Kothmann (1982) presented a method of cal culating mass from estimated cover based on linear regression between cover and mass. Such methods can give data that approximate biomass data but require much less time than extensive biomass sampling.

Following methods similar to those of An derson and Kothmann (1982), I used regres sions between biomass and cover to obtain predicted biomass values from cover values for species on eight sagebrush (*Artemisia tri dentata*) -grass sites. Cover estimates used in the regressions were obtained by a method that is more consistent and depends less on

the skill of the observer than does weight es timation or many other cover estimation methods. The use of a more precise and con sistent cover estimation method should result in better cover-biomass regressions. The methods by which regressions were calcu lated differed most notably from those of An derson and Kothmann (1982) in that sizes of biomass samples used in my regressions were representative of the range of sizes of cover values commonly encountered in cover sam pling. Also, some suggestions are made re garding the methods of using cover-biomass regressions to obtain predicted biomass val ues. Using the predicted biomass values for these eight sites, I present an assessment of advantages of predicted biomass data over cover in comparing vegetation among sites. I compared vegetational similarity among the eight sites based on predicted biomass values to vegetational similarity among the same sites based on cover values. This comparison indicated that predicted biomass values may often better identify differences among sites than can cover data.

METHODS

The results presented here are based on data collected on eight sites in southeastern Idaho for a study of postfire succession in sagebrush-grass areas (Humphrey in press). Each sample site consisted of a 100- x 50-m plot. On each site, ten 50-m lines were estab lished parallel to the 50-m axis of the site.

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These lines were chosen at random from a population of 100 lines that were at 1-m intervals along the 100-m axis. On each 50-m line, there were five sample points at 10-m intervals for a total of 50 sample plots on each site.

A 1.0- x 0.5-m sampling frame consisting of two tiers, superimposed 10 cm apart and gridded off in 1-dm² divisions, was used for cover estimation. The superimposed grids made it possible to sight vertically for esti-mating cover in each 1 dm². The frame was placed at each sample plot and leveled by use of adjustable legs and level bulbs on the frame. Cover for each species was estimated to the nearest 1/4 dm² (or 1/8 dm² in the case of very small plants). This method is more precise and less dependent on skill or bias of the observer than estimation by cover class (e.g., Daubenmire 1959) or other esti-mation methods that use single-tiered sam-pling frames because the superimposed grids make it possible to more accurately sight each dm². Floyd and Anderson (1982) de-scribed the use of a similar frame for cover estimation by point sighting. The point sight-ing method should also give reliable data and is less time consuming than the cover estima-tion method used in this study.

On one of every 10 cover plots on each site, the current year's growth of each species was clipped, oven dried, and weighed to de-termine aboveground biomass. In this way, biomass samples of several sizes representa-tive of the range of sizes of cover samples commonly encountered was obtained. Thus, the regressions could be assumed to be valid for the entire range of cover values encoun-tered. (Alternatively, representative biomass samples for each species could be taken (An-derson and Kothmann 1982), but these sam-ples should encompass the range of sizes of cover samples commonly encountered.) Lin-ear regressions between cover and oven dry biomass were calculated from biomass values and corresponding cover values for the clipped plots, with biomass as the indepen-dent variable. (Biomass was chosen as the in-dependent variable because cover was con-sidered to be an estimated value that is dependent on the more precisely determined biomass.) Individual regressions were calcu-lated for single species or for groups of mor-

phologically similar species using pooled data for the eight sites. An equation for inverse prediction from regression equations (Zar 1974) was used to obtain a predicted biomass value from each cover value for each species. If the Y intercept was significantly different from zero, a regression forced through the origin was done (Snedecor and Cochran 1980), and this regression was used to obtain predicted biomass values.

Similarity index values for each site paired with each of the other sites (Bray and Curtis 1957) were calculated with both cover values and predicted biomass values. These sim-ilarity index values were used to compare the way these two data sets described differences among the eight sites. The sign test (Snedecor and Cochran 1980) was used to determine if the two sets of similarity index values were significantly different, and the nature of dif-ferences between the two sets of similarity index values was examined.

Results and Discussion

Good cover-biomass regressions were ob-tained for several individual species and for several groups of two or more species that were judged to be morphologically similar (Table 1). Some of these groups are obviously morphologically similar, such as the group *Chrysothamnus viscidiflorus* (green rabbit-brush), *C. nauseosus* (gray rabbitbrush), and *Gutierreza sarothrae* (broom snakeweed), the group *Artemisia tridentata* (big sagebrush), *A. tripartita* (threetip sagebrush), and the group *Balsamorhiza sagittata* (arrowleaf balsam-root), *B. macrophylla* (bigleaf balsamroot), and *Wyethia amplexicaulis* (mule's ear). Other groups are perhaps less obviously sim-ilar, although they are similar enough to pro-vide good cover-biomass regressions. The an-nual species in group 8 in Table 1 are morphologically similar in that they are all small, slender annuals. *Agropyron dasysta-chyum* (thickspiked wheatgrass) and *A. spica-tum* (blue-bunch wheatgrass) were grouped together because, on these sites, *A. dasysta-chyum* usually grew in quite dense stands, making its growth habit similar to that of *A. spicatum*. If desired to reduce the number of regressions calculated, or the number of bio-mass samples taken, it appears that single

regressions can often be done for groups of species similar in morphological characteristics such as height, leaf size, and leaf density.

Relationships between cover and biomass for the same species may vary with differences in site characteristics such as productivity, mesicness, and other species present. But a regression should be consistent for the same species on other sites in addition to those sites where biomass samples were obtained, if the data used to calculate the regression cover the range of differences in site characteristics of those other sites, and if the regression explains much of the variance in Y (has a high r^2). Thus, if these conditions are met, the same regressions could be used for different sites and different studies, if the species are in roughly the same seasonal stage of development (for example, peak biomass)

and the same cover estimation method is used. In this way, the amount of time-consuming biomass sampling needed to obtain predicted biomass values can be reduced even further. Regressions have been used in a similar manner to obtain biomass estimates for trees (Whittaker 1966, Dabel and Day 1977).

The percent similarity values among sites based on predicted biomass data were significantly different (at the 1% level) from those based on cover data by sign test comparison. Predicted biomass data indicated lower similarity among sites, i.e., greater distinctions among sites over all. The difference between the medians of the two sets of similarity index values was rather small, but the maximum and minimum values of the two sets show that predicted biomass data also indicated greater extremes of high and low sim-

TABLE 1. Results of cover-biomass regressions for species or groups of morphologically similar species. Cover data was in cm²; biomass data was in g. For species or species groups where the Y intercept of the regression was significantly different from zero, the results of the regression forced through the origin are presented. Slopes of all regressions listed are significant ($P < 0.05$). Y is cover; X is biomass (independent variable). (Nomenclature of all plants follows Hitchcock and Cronquist 1973.)

Group	Species	Regression	r^2	n
1	*Phlox longifolia*	$Y = 0.30\ X$ (forced through origin)	0.80	9
2	*Lithospermum ruderale, Helianthella uniflora*	$Y = 0.339 + 0.197\ X$	0.94	14
3	*Crepis acuminata, Achillea millefolium*	$Y = -0.158 + 0.632\ X$	0.91	11
4	*Balsamorhiza sagittata, B. macrophylla, Wyethia amplexicaulis*	$Y = 0.083 + 0.357\ X$	0.99	10
5	*Penstemon spp.*	$Y = 0.844 + 0.325\ X$	0.78	13
6	*Tragopogon dubius*	$Y = 0.184 + 0.517\ X$	0.84	8
7	*Lupinus spp.*	$Y = 0.272 + 0.286\ X$	0.92	7
8	*Polygonum douglasii, Gayophytum diffusum, Collomia linearis, Lappula redowskii*	$Y = 1.34\ X$ (forced through origin)	0.94	14
9	*Cirsium arvense*	$Y = 0.789 + 0.114\ X$	0.95	8
10	*Bromus tectorum*	$Y = 1.024\ X$ (forced through origin)	0.86	13
11	*Agropyron dasystachyum, A. spicatum*	$Y = 0.114 + 0.488\ X$	0.80	23
12	*Poa nevadensis, P. sandbergii*	$Y = 0.188 + 0.186\ X$	0.77	14
13	*Poa pratensis*	$Y = 0.597 + 0.439\ X$	0.95	7
14	*Artemisia tridentata, A. tripartita*	$Y = 2.744 + 0.185\ X$	0.77	17
15	*Chrysothamnus viscidiflorus, C. nauseosus, Gutierreza sarothrae*	$Y = 0.294 + 0.366\ X$	0.92	16
16	*Amelanchier alnifolia, Symphoricarpos oreophilus*	$Y = 0.968 + 0.235\ X$	0.80	10
17	*Purshia tridentata*	$Y = 0.275 + 0.235\ X$	0.99	8

Table 2. The median and the maximum and minimum values of the set of similarity index values based on cover and based on predicted biomass.

	Cover	Predicted biomass
Median:	34.1	32.1
Maximum:	56.4	58.8
Minimum:	13.5	10.8

ilarity among sites (Table 2). In other words, similar sites appeared more similar, and dissimilar sites appeared less similar. The difference between each similarity index value based on predicted biomass and the corresponding value based on cover (Fig. 1) illustrates more clearly that predicted biomass data indicated less similarity among sites over all and a greater range of similarities among sites. At low similarities, predicted biomass data indicated lower similarity between sites than did cover; at moderate similarities, it indicated lower similarity than did cover in most cases; while at relatively high similarities it tended to indicate greater similarity between sites than did cover.

This study suggests that predicted biomass data may often describe distinctions among sites better than cover data. For differences to exist between comparisons of sites based on the two types of data, differences in the relationship of biomass to cover must exist among species, and the species with different ratios of biomass to cover must be unevenly distributed among sites. In this study, predicted biomass data tended to indicate greater differences among sites because predicted biomass data emphasized species with higher ratios of biomass to cover, and many species that varied more in abundance among sites had higher ratios of biomass to cover. These were tall herbaceous species (groups 2, 9 in Table 1) and shrubs (groups 14, 16, 17 in Table 1). Similarly, predicted biomass data indicated higher similarity than did cover between some pairs of sites that were both dominated by the same species (of shrubs) that had higher ratios of biomass to cover. Predicted biomass data can provide more accurate information on the relative importance of species in a community than can cover data alone, and it appears that this greater accuracy may often result in greater ability to identify differences among sites.
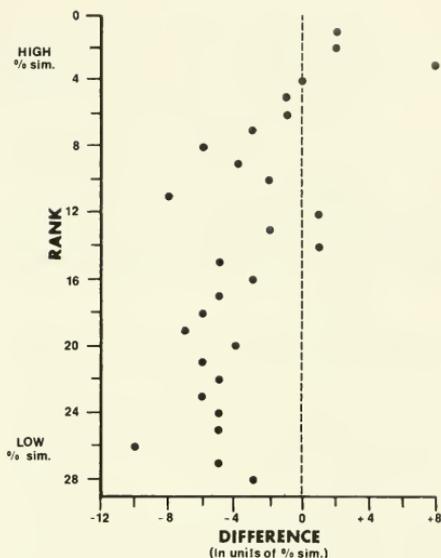

Fig. 1. Differences between similarity index values based on cover and based on predicted biomass. Differences between paired similarity index values (biomass - cover) arranged in order of decreasing percent similarity based on biomass data.

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