AN ABSTRACT OF THE THESIS OF

Patrick J. Kennelly for the degree of Doctor of Philosophy in Geography presented on October 25, 1997. Title: Effects of Scale Properties on Biodiversity Mapping in Oregon.

Abstract approved: A. Jon Kimerling
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The effect of scale is an important concern in mapping of biodiversity. Scale issues include the grid cell size used for analysis and the effect of the extent and internal boundaries. Because biodiversity analysis involves combinatorial processes, determining the proper scale is data dependent and cannot be predicted from the initial data values and their distribution.

Biodiversity analysis often samples combinations of species within geopolitical boundaries. The effects of ecoregion boundaries on prioritization analysis was analyzed in two ways. This study determined that prioritization hexagons for Oregon do not fall preferentially on ecoregion boundaries. This research also concluded that results of prioritization analysis are geographically stable with the elimination of hexagons on ecoregion boundaries from analysis.

Species maps based on the Environmental Protection Agency's Environmental Monitoring and Assessment Program (EMAP) grid were analyzed. Grid cells 7 times as large result in species richness maps statistically similar to maps made with the EMAP grid. Patterns of localized variation between grid cells indicate no one area is contributing to the overall variation. Prioritization maps, however, show different patterns of selected

hexagons. Grid cells 49 times as large show a loss of species richness variation and a different pattern of prioritization hexagons.

Richness maps based on wildlife habitat relations were used to map species richness at seven different three-fold compositions and decompositions of the EMAP grid. Analysis of statistics indicates that no scale shows a small relative decrease in coefficient of variation(CV), indicating no scale is relatively superior for richness mapping.

Prioritization analysis was performed on the new combinations of species lists for five grid cell sizes ranging from 1/9 to 9X's the size of the EMAP grid. Efficiency of prioritization and map patterns of prioritization areas indicate that grid cells 1/3 the size of the EMAP hexagons are optimal.

Comparisons can be made between the two biodiversity analyses at the EMAP scale for wildlife habitat vs. EMAP grid based species range maps. CV values have increased and the efficiency of prioritization is enhanced. This can be attributed to finer resolution sampling capturing additional information.

Effects of Scale Properties on Biodiversity Mapping in Oregon

by

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I understand that my thesis will become part of the permanent collection of Oregon State University libraries. My signature below authorizes release of my thesis to any reader upon request.

Patrick J. Kennelly

Patrick J. Kennelly, Author

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CHAPTER 1. INTRODUCTION

INTRODUCTION

Biodiversity analysis in the state of Oregon identifies areas in which species and ecosystem biodiversity are represented completely or as completely as possible. Inherent in this analysis is the need to sample distributions of species throughout an appropriate area using a proper grid cell.

To measure the biodiversity of Oregon, it is necessary to "divide the state into sample areas and use an algorithm to select the subset of areas in which all types will be represented" (Csuti, 1994). Although much effort has been focused on the algorithm to select these sample areas (Csuti et al., 1997), no work has been done to determine the proper scale (grid cell size) into which sample areas should be divided, or whether the state boundary is the proper extent on which to map these samples.

Other research has related grid cell size used for mapping to statistical measures over the entire study area. Stoms (1992) related rank correlation coefficient to minimum mapping unit (MMU) west of the Sierra Nevada crest in California for species richness mapping. This method was refined by Stoms (1994) to relate coefficient of variation (CV) to sampling unit area. Stoms recognized here that agglomerating sampling units and species contained within is not a classical spatial statistics problem that can be addressed by such methods as calculating semivariance; "aggregation is not a simple numerical averaging over different sampling sizes, but is a logical union of sets (species lists)" (p. 347).

Biodiversity analysis has traditionally used political boundaries as the extent of mapping, and effects of natural boundaries have not been extensively studied. Species distributions within an ecoregion and along its boundaries are important to understand in selecting prioritization areas for potential reserves. The effect of ecoregions as natural extents has never been addressed in the conservation literature.

OBJECTIVES

The purpose of this research is to determine scales of sampling and extent boundaries best suited for biodiversity mapping, which involves three objectives. The first two objectives are to determine the proper grid cell size for minimizing species richness variance and to determine how this variance effects prioritization analysis for the state of Oregon. The third objective is to determine if political boundaries (i.e. the state of Oregon) should be used as the extent for prioritization analysis although natural, internal boundaries in the form of ecoregion boundaries exist.

METHODOLOGIES

Objectives 1 and 2

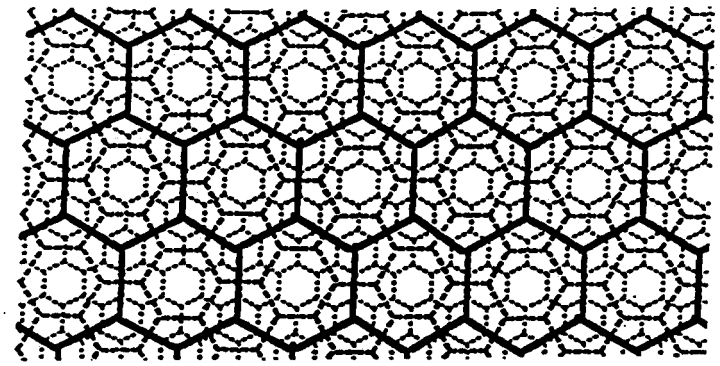
The first two objectives are to determine the proper grid cell size for minimizing species richness variation and then to determine how this variance affects prioritization analysis for the state of Oregon. Because species richness is a logical union of sets and not a numerical average, variance at different scales can only be determined by performing logical unions at all scales of interest and calculating variance directly (Stoms, 1994, p. 347).

The three most useful geometries for composition and decomposition of hexagonal grids are resented in **Figure 1.1.** Hexagonal grids can be composed or decomposed to new hexagonal grids by either a factor of three or four. Composing a hexagonal grid by a factor of three involves taking a central hexagon and one third of all six neighboring hexagons. The resulting hexagon will be rotated by 30 degrees with respect to the original. Composing a hexagonal grid by a factor of four involves taking a central hexagon and one half of all neighboring hexagons. The resulting hexagons will show no rotation. Three and four-fold decompositions can be performed in a similar manner.

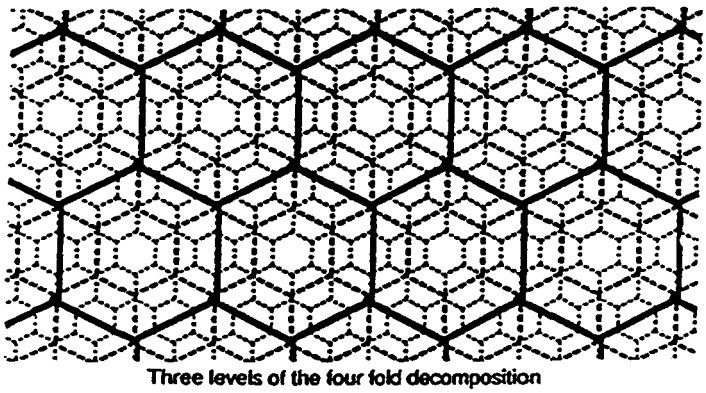
A seven-fold composition of a hexagonal grid is also possible by taking a central hexagon and all six neighboring hexagons. Although the resulting polygon is not a hexagon, further iterations of composition can be performed on this polygon in a similar manner. Seven-fold decompositions are not possible on a hexagonal grid. All compositions and decompositions described continue to produce a grid without gaps and with all polygons equidistant from all neighboring polygon.

The fold of the composition or decomposition determines the number of unique grids capable of being iterated. For example, each of the seven hexagons in a seven-fold composition can serve as the central hexagon. Each grid results in a unique union of species richness (**Figure 1.2**).

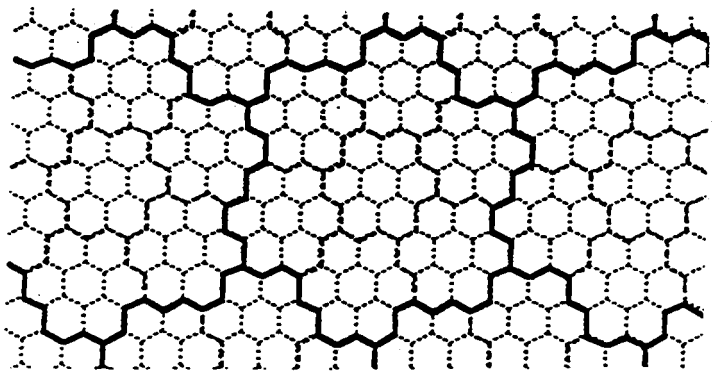
This study will look at the coefficient of variation of two sets of species richness maps of terrestrial vertebrates at different scales. Terrestrial vertebrates include more than 420 species of amphibians, reptiles, summer birds, and mammals (ARSM) identified in the state of Oregon. The first set of range maps is based on probable or confirmed occurrence of each species in grid cells of the Environmental Protection Agency's Environmen-



Three levels of the three fold decomposition



Three levels of the four fold decomposition



Three levels of the seven fold decomposition

Figure 1.1: Three compositions of a hexagonal grid.
(Courtesy of Denis White)

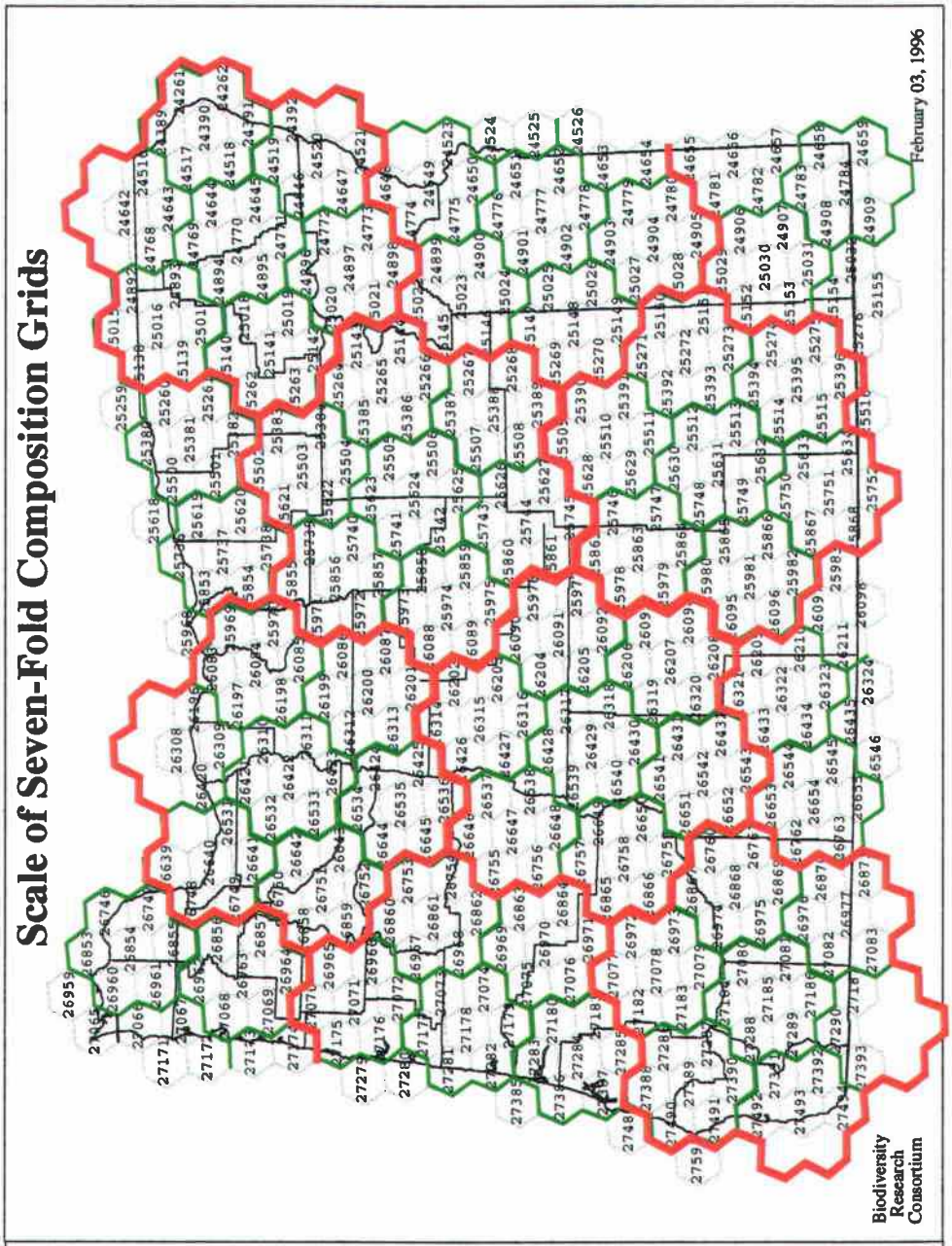


Figure 1.2: Two successive seven-fold compositions of the Oregon EMAP grid.

tal Monitoring and Assessment Program (EMAP) 640 km^2 grid (White et al., 1992). The second set of range maps are more detailed maps determined from wildlife habitats. Seven-fold compositions only are possible on range maps based on the EMAP hexagonal grid without making further assumptions. These composite grids simply combine existing hexagons and allow for logical unions of species data in their present form. Three-fold analysis will use habitat range maps based on actual vegetation maps for the state of Oregon cut by the smallest hexagonal grid to be used in the analysis.

Seven-Fold Composition

Object oriented (C++) programming was used to perform two seven-fold compositions, one iteration of which is presented as **Figure 1.2**. The program draws the boundary of the new polygons and performs a logical union on lists of ARSM species present. The first composition (1X's 7-fold composition) requires seven grid cells and associated datasets and the second composition (2X's 7-fold composition) requires 49. The resulting dataset allows the creation of a richness map using existing programs and the calculation of the coefficient of variation(CV) for the map using Splus software.

The EMAP grid has a single iteration. The 1X's 7-fold composition has seven unique combinations of EMAP hexagons for its grid cell size. The 2X's 7-fold composition has 49 unique combinations of hexagons for the same grid cell size.

The statistics for these ranges are determined after combining all grid cell richness values at a given scale. Coefficient of variation (CV) values will be compared for pronounced breaks in slope representing rapid increases in variance. As this analysis represent only three grid cell sizes, analysis will be limited. Also, since both new compositions

will be larger, this analysis cannot address the question of whether richness should be mapped with finer resolution.

Three-Fold Composition

The three-fold analysis begins with the smallest hexagonal grid to be used in this study, a four times (4X's) 3-fold decomposition having grid cells of approximately 8 km^2. A three-fold composition has been chosen for this study over a four-fold composition to obtain finer resolution between scales.

More detailed habitat-based range maps are used for this analysis. Habitat range maps are input as Arc/Info coverages. This coverage is then united with a coverage containing all of the triangles that make up a 4X's 3-fold decomposition, resulting in a matrix of triangular building blocks for all compositions.

Variance data from the three-fold analysis can then be compared to data from the seven-fold analysis. Seven-fold data would be expected to correspond with three-fold data where analysis overlaps. Lack of correspondence may be due to differences inherent in the species range and habitat range mapping techniques.

Prioritization analysis at these scales demonstrates if variance of species richness has any influence on the location of hexagons chosen. Results indicate not only the grid cell size at which species richness should be mapped in the state of Oregon, but also whether grid cell sizes associated with similar species richness variance result in any variations in prioritization analysis.

Statistics associated with species accumulation can also be analyzed for prioritization maps created at multiple scales. As well as statistical analysis, a more qualitative analysis of the appearance of the maps at different scales is also attempted.

Objective 3

The third objective is to determine if political boundaries (i.e. the state of Oregon) should be used as the extent for prioritization analysis although natural, internal boundaries in the form of ecoregion boundaries exist.Three ecoregion maps covering the state of Oregon compiled by Bailey (1980), Omernik (1987) and Kagan(1996) of the Oregon Natural Heritage Program are used in this study. Also used are "data driven" ecoregion boundaries, based on a Jaccard analysis. Neighboring hexagons showing the maximum amount of normalized difference in species lists are used as Jaccard ecoregion boundaries.

A potential species range boundary sampling problem can be evaluated by comparison of hexagons located along ecoregion boundaries with prioritization hexagons. Some species ranges terminate abruptly, possibly due to ecoregion boundaries. Hexagons that straddle ecoregion boundaries may include many edges of species ranges and not represent some species in the manner intended. The importance of the effect of hexagons straddling range boundaries can be evaluated in the following manner for each ecoregion map.

First, a list of hexagons selected by current prioritization analysis at all cardinalities for ARSM is compiled. All hexagons that fall on a ecoregion boundary are then listed. The ratio of hexagons that fall on ecoregion boundaries vs. within ecoregions are calculated. The two lists of hexagons can then be compared to see which prioritization hexagons fall upon ecoregion boundaries. The ratio of prioritization hexagons on ecoregion boundaries

vs. within ecoregions are calculated and compared. Any significant difference between these ratios imply that hexagons on ecoregion boundaries may be sampling edges of many species range values associated with those ecoregion boundaries.

Prioritization analysis using buffered ecoregions would require the elimination of all hexagons on ecoregion boundaries. If boundary hexagons are statistically significant, prioritization analysis within ecoregions would be expected to yield significantly different prioritization hexagon locations.

Prioritization analysis using buffered ecoregions can be used to evaluate the contribution to complementarity of differences inherent in ecoregions. Complementarity explains how new hexagons can be chosen that do not correspond to hexagons at a lower cardinality of prioritization(i.e. number of hexagons chosen to maximize species diversity); "a site may be relatively species poor, but if it adds the most species not already represented, then it has maximum complementarity" (Csuti and Kiester, 1996). Locations of two prioritization hexagons with high complementarity can occupy significantly different locations than any hexagon at the previous prioritization cardinality. Some or all complementarity currently observed may be caused in part by more homogenous species distributions at an ecoregion level and more heterogeneous species distributions between ecoregions (e.g. at a state level).

The contribution of ecoregion heterogeneity to prioritization analysis can be evaluated by comparing the prioritization analyses after elimination of hexagons on ecoregion boundaries. If different hexagons are eliminated but prioritization hexagons are still chosen in a proximal geographic location, the implication is that complementarity is more a

function of a species assemblage in an area, as opposed to a unique species list for an isolated hexagon.

SIGNIFICANCE OF RESEARCH

Some research has been done on the effects of scale properties on combinatorial mapping methods. These include investigating the coefficient of variation of species richness with grid cell size (Stoms, 1994). No studies, however, had related variability inherent in the sampling scale of the analysis to effects on prioritization analysis. Results will be applicable to all future prioritization mapping efforts in the state of Oregon, and similar techniques can be applied to other geographic locations.

This study is the first to perform several spatial analyses. It is the first to analyze variance in species richness on a hexagonal grid and compare results of multiple hexagonal fold compositions. It is the first to see if species richness variance can be related to changes in hexagons selected for prioritization analysis. It is the first study to do prioritization mapping after removing grid cells associated with ecoregion boundaries.

Finally, future research in the state of Oregon will begin to evaluate biodiversity on a landscape scale. The importance of understanding the effects of scale on all statewide mapping could be quite significant, especially if the state scale mapping has been used in part to determine the location or size of the landscape planning area.

CHAPTER 2

Effects of Ecoregion Boundaries on Prioritization Analysis

Patrick J. Kennelly

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ABSTRACT

Biodiversity analysis is typically done by sampling combinations of species within a geopolitical boundary. This study addresses issues associated with sampling along ecoregion boundaries within the prioritization study area. Studying the effects of ecoregion boundaries on prioritization analysis resulted in two major conclusions. This study determined that prioritization hexagons for the state of Oregon do not fall preferentially on ecoregion boundaries. This research also concluded that results of prioritization analysis are geographically stable with the elimination of hexagons on ecoregion boundaries from analysis. Both of these results have implications concerning the scale of species distribution being evaluated in prioritization mapping.

INTRODUCTION

Prioritization analysis is used in studying biodiversity. Prioritization analysis of species first requires sampling a region's species on a regular grid. Analysis begins by selecting the one grid cell which contains the highest diversity of known species. Subsequent steps add one grid cell at a time to the analysis, which finds the combination of grid cells with the highest diversity of species. Each step represents an increase of one in the cardinality of the analysis. This process continues until all species are represented in the selected grid cells. Inherent in this analysis is the idea of complementarity. The grid cell richest in species may never again be chosen at subsequent cardinalities, as "a site may be relatively species poor, but if it adds the most species not already represented, then it has maximum complementarity" (Csuti and Kiester, 1996). An example of different hexagons

being chosen by prioritization analysis at cardinalities one and two is evident for summer birds in the state of Oregon (**Figure 2.1**).

Several assumptions are inherent in the way in which most prioritization analysis is performed. One is that geopolitical boundaries are appropriate extents for such analysis, such as the use of the state boundary of Oregon in the example given above. This assumption is necessitated by the geopolitical organization of biodiversity analysis.A related assumption is that internal boundaries such as ecoregions will not have a significant effect on the analysis. An assumption about the utility of results from prioritization analysis is also key to the way in which the analysis is done. Prioritization analysis selects grid cells able to be used in reserve design. If grid cells selected straddle two or more very different habitat assemblages (as may be found in different ecoregions) it is possible that no one reserve within a selected grid cell could preserve all species selected in the analysis. Although valid, the prioritization analysis would be giving a misleading picture to subsequent efforts in an area's reserve design.

The purpose of this study is to address the above issues in two ways. First, it will be determined if prioritization grid cell hexagons in the state of Oregon preferentially fall on ecoregion boundaries. This will be done by comparing percentages of total hexagons with prioritization hexagons on ecoregion boundaries. Second, it will be determined if ecoregion boundaries have a significant effect on the geographic location of prioritization hexagons. This will be done by comparing results of prioritization analyses before and after removing hexagons on ecoregion boundaries.

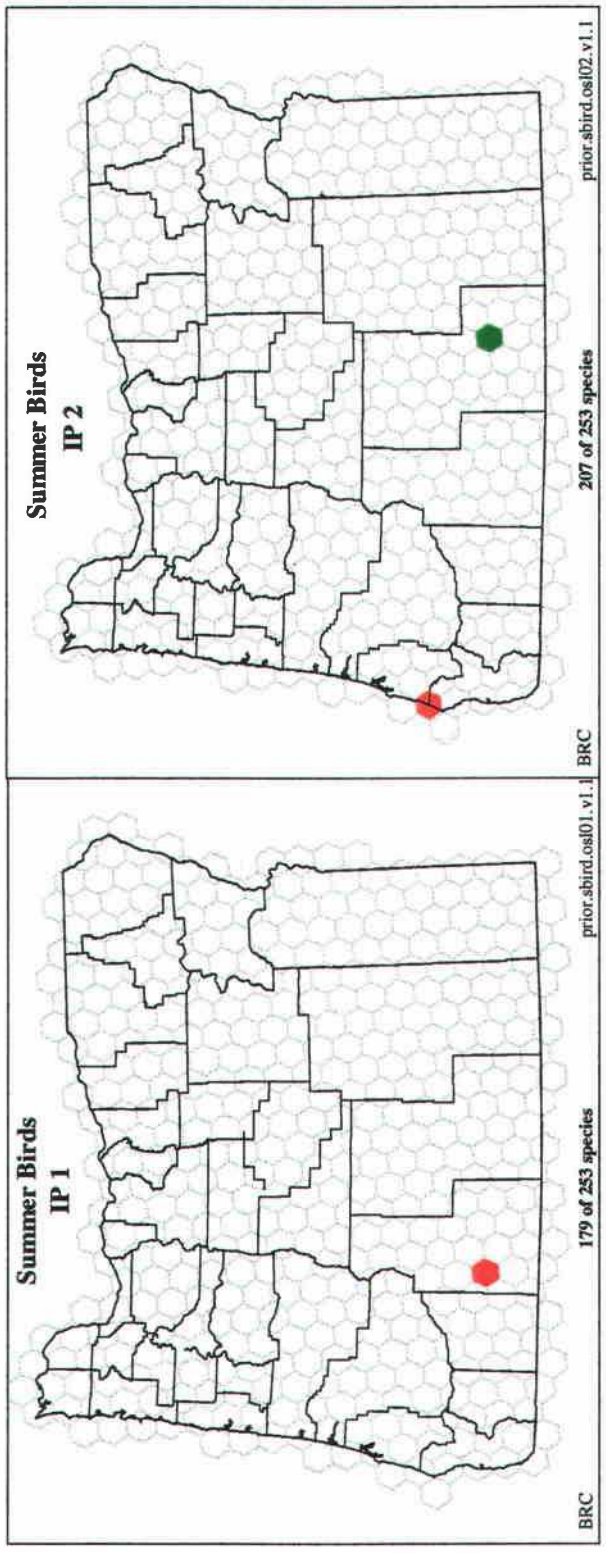

Figure 2.1: Complementarity at the second cardinality of prioritization of Oregon summer birds.

ECOREGION BOUNDARIES

Five ecoregion maps in the state of Oregon will be evaluated. These will include the Omernik ecoregions, the Bailey ecoregions, a compilation ecoregion map put together by the Oregon Natural Heritage Program, and two "data driven" ecoregion maps, developed by calculating differences in the species lists between adjacent hexagons.

Bailey Ecoregions

The Bailey ecoregion boundaries are based on the 1994 revised ecoregion map of the United States (Bailey, 1994) and presented as **Figure 2.2**. The ecoregion classification scheme is hierarchical; "the two broadest, domains and divisions, are based on the ... large ecological climate zones" (Bailey, 1980, p. 1). Climate is emphasized at this level because of "its overriding effect on the composition and productivity of ecosystems from region to region" (Bailey, 1980, p. 1). Further divisions are provinces based on vegetational macrofeatures, believed to "express more refined climatic differences than the domain and divisions" (p. 2). Finally, altitudinal climate changes are also taken into account. Ecoregion boundaries on this map are the most generalized (i.e. least detailed) of the three non-data driven boundaries.

Omernik Ecoregions

Omernik ecoregion boundaries are based on the 1987 ecoregions of the United States map (Omernik, 1987) with recent revisions made in the northwestern United States (Thiele et al., 1996). These revised boundaries are presented as **Figure 2.3**. Omernik ecoregion boundaries are based on "perceived patterns of a combination of causal and

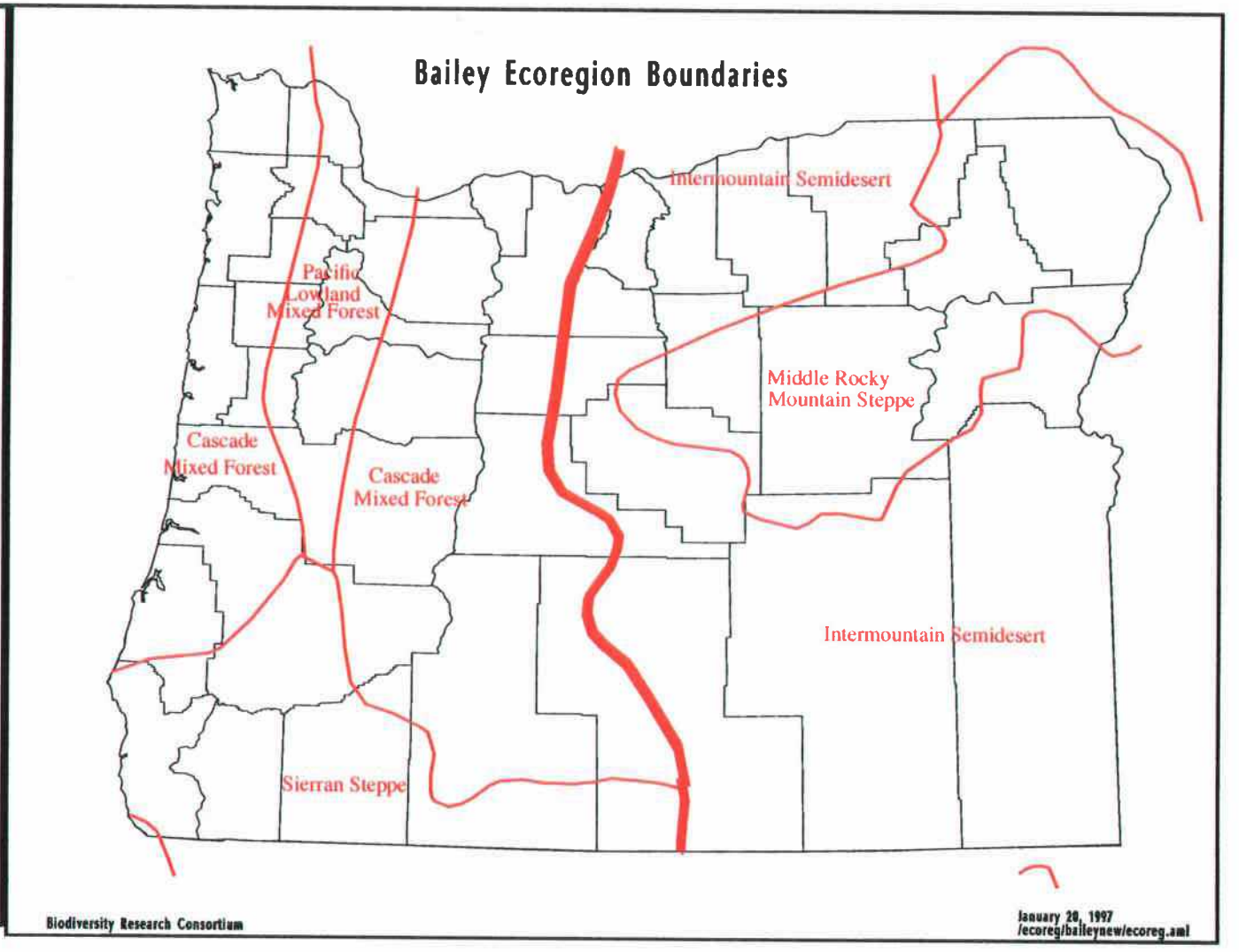

Figure 2.2: Bailey ecoregion boundaries of Oregon.

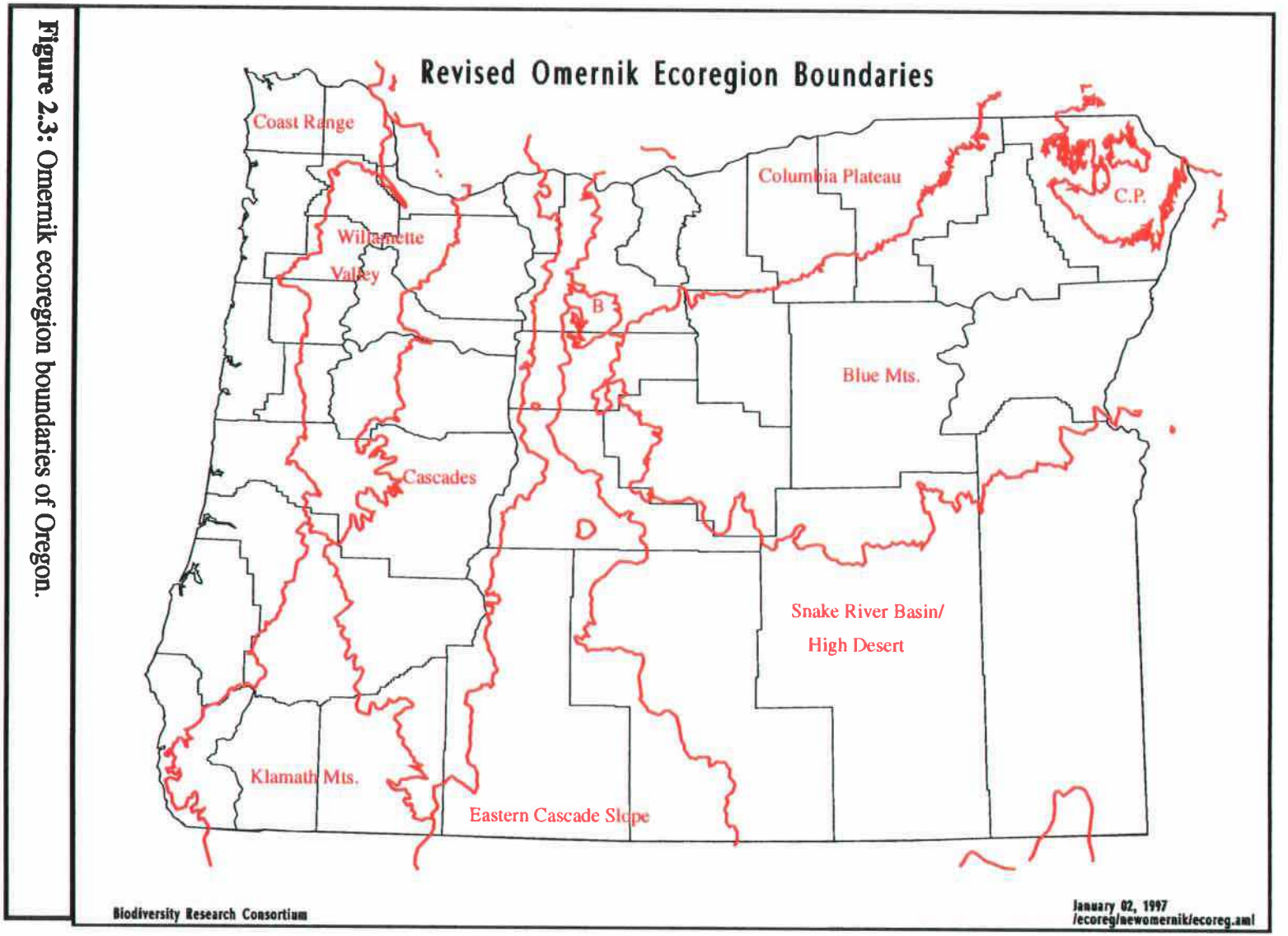

Figure 2.3: Omernik ecoregion boundaries of Oregon.

integrative factors including land use, land surface form, potential natural vegetation, and soils" (Omernik, 1987, p. 118). Ecoregion boundaries on this map are the least generalized (i.e. most detailed) of the three non-data driven boundaries.

ONHP Ecoregions

The Oregon Natural Heritage Program(ONHP) ecoregion map is a compilation of the Bailey and revised Omernik ecoregion boundaries (Kagan, 1996, personal communication). ONHP ecoregion boundaries are presented as **Figure 2.4**. Ecoregion boundaries on this map are of a level of generalization intermediate to the Bailey revised Omernik ecoregion maps.

Jaccard "Data Driven" Ecoregions

Jaccard analysis calculates numbers of species that are unique between all adjacent hexagons in the state of Oregon. This is done by looking at the assemblage of species in a list associated with each hexagon, and then accounting for all species unique when compared to neighboring hexagons (See Magurran, 1988). A hexagon with six neighboring hexagons, therefore, will have six unique Jaccard indices. Unpublished results of Jaccard analysis by Kiester and Sahr(1996) are presented as **Figure 2.5**. Each triangle will have the same Jaccard index as the adjacent triangle in the neighboring hexagon. Areas of large differences in species between neighboring hexagons are assigned warmer colors.

Visual analysis allows areas of higher contrast to be readily identified. To make the Jaccard index more quantitatively meaningful, however, it is necessary to normalize these numbers to the background. To do this, the Jaccard index was recalculated normalizing

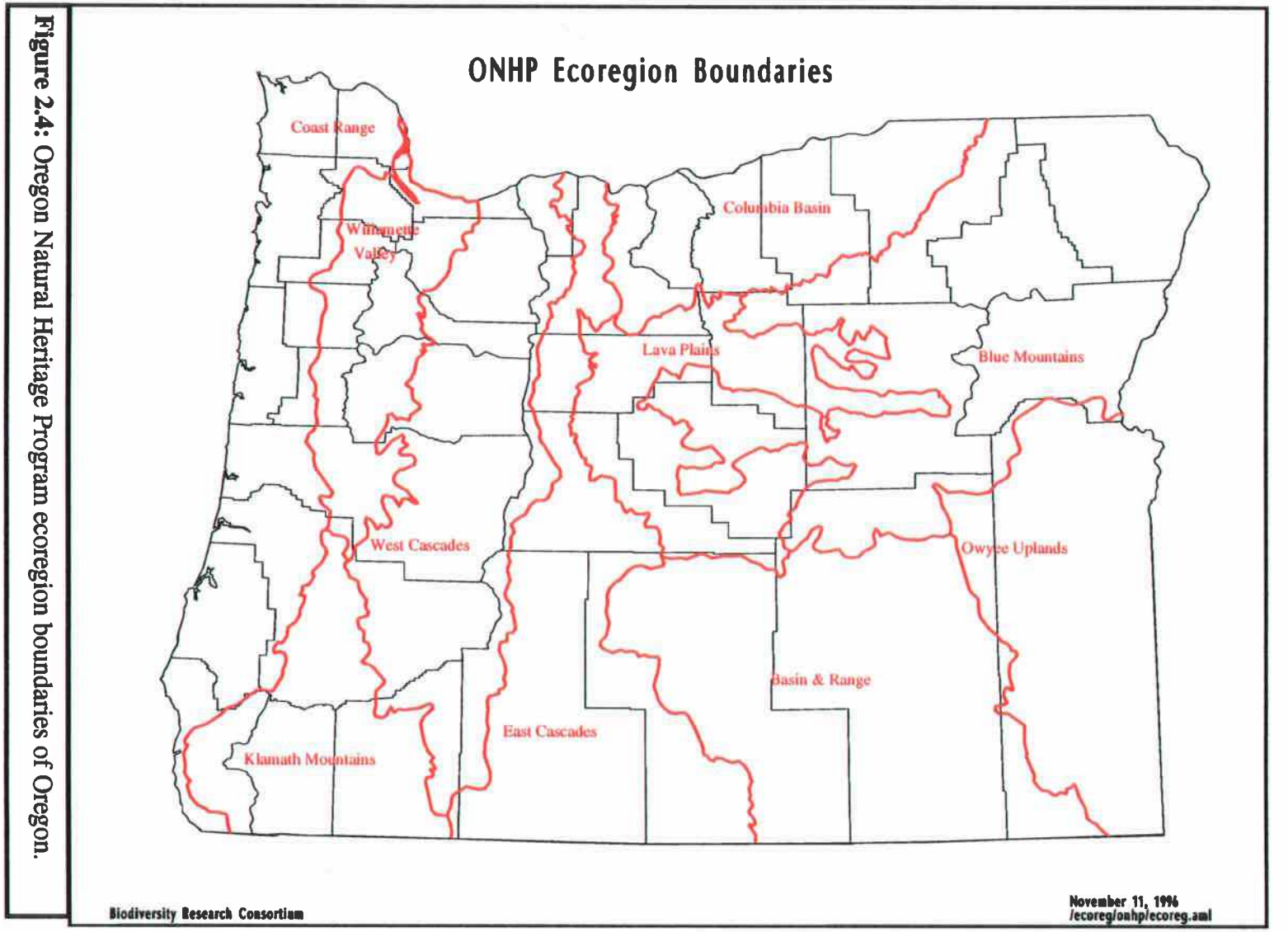

Figure 2.4: Oregon Natural Heritage Program ecoregion boundaries of Oregon.

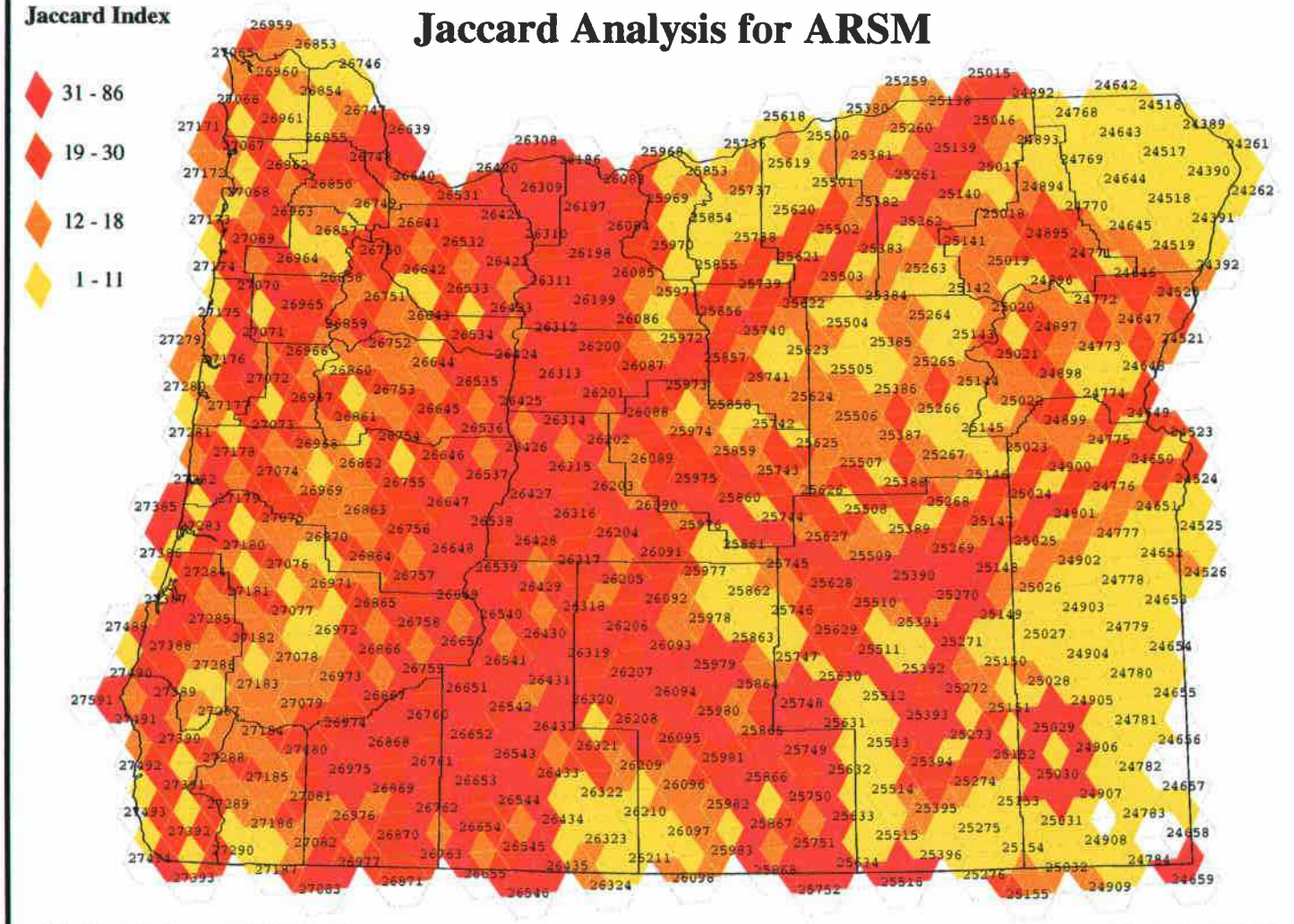

Figure 2.5: Magnitude of Jaccard index between all neighboring EMAP hexagons. **(Map by Ross Kiester and Kevin Sahr)**

differences to the species richness of the hexagon. The normalized Jaccard index is thus a percentage between 0% (i.e. no difference in species list between hexagons) and 100% (i.e. no species the same between hexagons). The hexagons which contain at least one triangle with a" high" Jaccard index, therefore, can be thought of as part of "data driven" ecoregion buffers.

In order to eliminate Jaccard ecoregion boundary hexagons, a threshold normalized Jaccard index must be selected. This study used two thresholds, a high cut which eliminated 42.4% of the hexagons, defined by all neighboring hexagons with a normalized Jaccard index over 19%, and a low cut which eliminated 25.4% of the hexagons defined by all neighboring hexagons with a normalized Jaccard index over 25%. These cutoffs were established after analysis of the three ecoregions discussed above, and are designed to bracket the high and low number of hexagons eliminated. Hexagons remaining after buffering are presented as **Figure 2.6**. Black hexagons were eliminated as part of low-cut Jaccard ecoregion boundary. Gray hexagons were additionally eliminated as part of high-cut Jaccard ecoregion boundary.

INITIAL PRIORITIZATION ANALYSIS

The initial prioritization analysis was conducted on 422 species of terrestrial vertebrates whose range maps were defined on the Environmental Protection Agency's Environmental Monitoring and Assessment Program (EMAP) grid (White et al., 1992). This includes 253 birds, 114 mammals, 27 amphibians, and 28 reptiles. The EMAP grid was also used for sampling species lists. This hexagonal grid is a Lambert azimuthal equal area projection composed of grid cells approximately 640 km^2 in size.

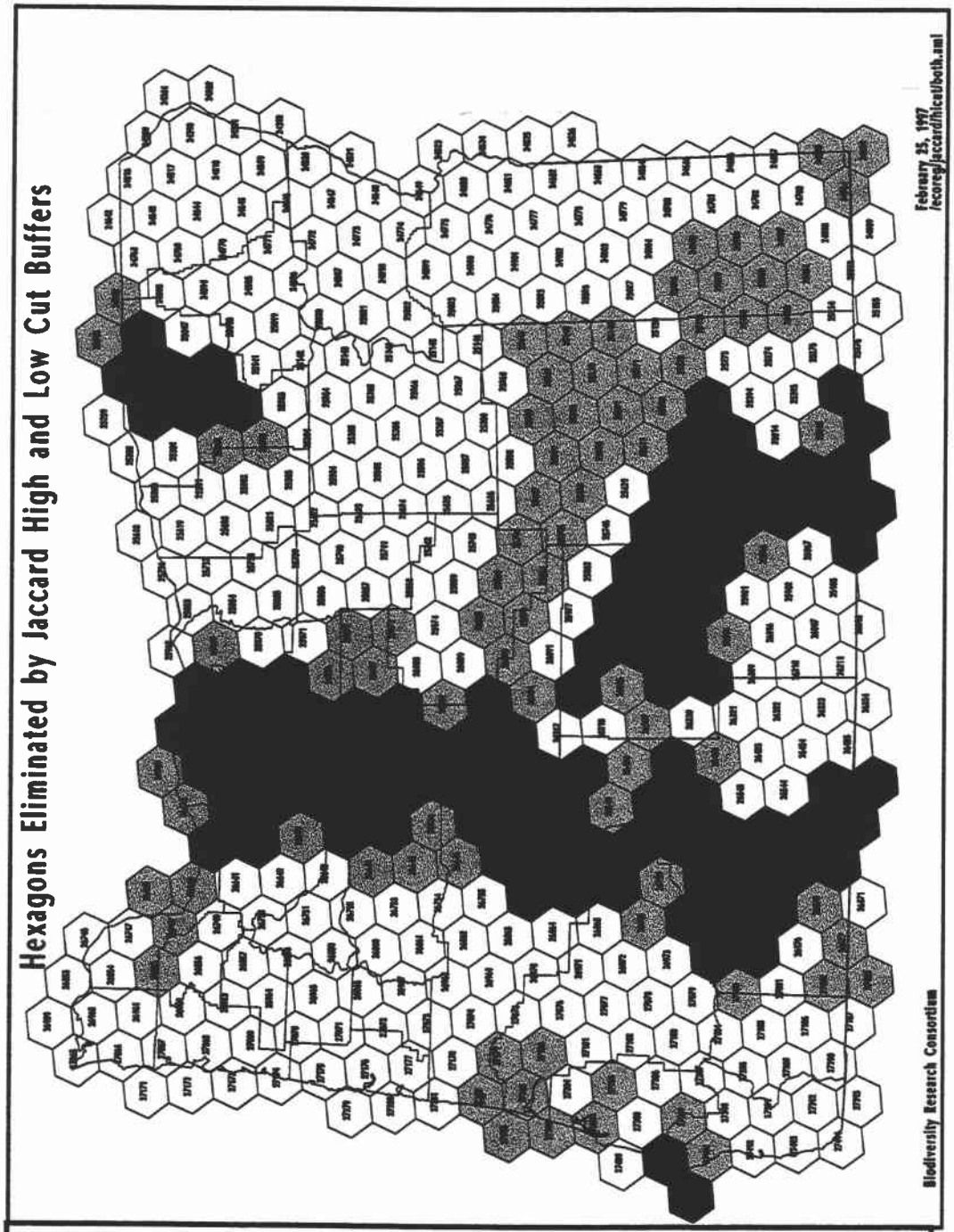

Figure 2.6: Hexagons defining two Jaccard "data driven" ecoregion boundaries.

Analysis was necessary at 23 cardinalities to achieve full coverage of the 422 terrestrial vertebrates for the state of Oregon. At any given cardinality, many different combination of hexagons can achieve an optimal prioritization solution, with each of these solutions referred to as a path. An arbitrary limit of 1,000 paths was set in the prioritization program. Thus, after finding 1,000 unique paths at any given cardinality, the program discontinues its search. In all 23 cardinalities and all paths at these cardinalities, 110 of the possible 441 hexagons were chosen at least once. Prioritization hexagons for terrestrial vertebrates therefore account for one fourth of all Oregon hexagons. All of these hexagons were selected at least once, and any of these hexagons could have been chosen at each of the 23 cardinalities.

If the number of cardinalities for which each of the 110 prioritization hexagons is selected is taken into account, 995 hexagons were selected in the 23 cardinalities. A map showing the location of all 110 prioritization hexagons and the number of times each of these hexagons was used at all cardinalities is included as **Figure 2.7.** It may be noted that the locations of hexagons used most and least frequently are not located in one particular geographic area.

Each of these cardinalities, moreover, can have up to 1,000 unique paths. When the number of paths for each of the 995 prioritization hexagons at all cardinalities is taken into account, 218,636 total hexagons were selected in the prioritization analysis. A map showing the number of times each hexagon was used on different paths at different cardinalities is included as **Figure 2.8**. Once again, the locations of hexagons used most and least frequently do not appear clustered.

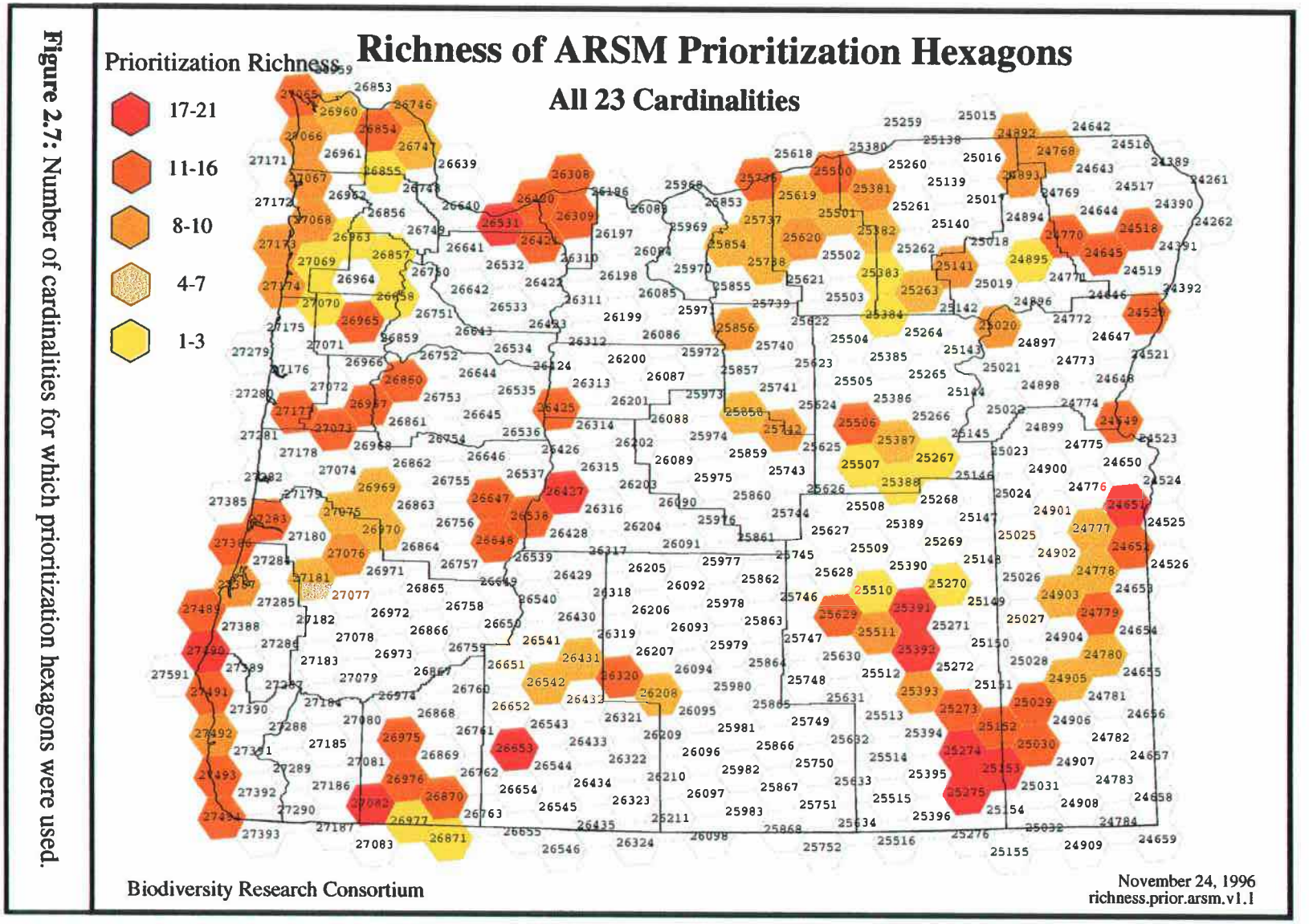

Figure 2.7: Number of cardinalities for which prioritization hexagons were used.

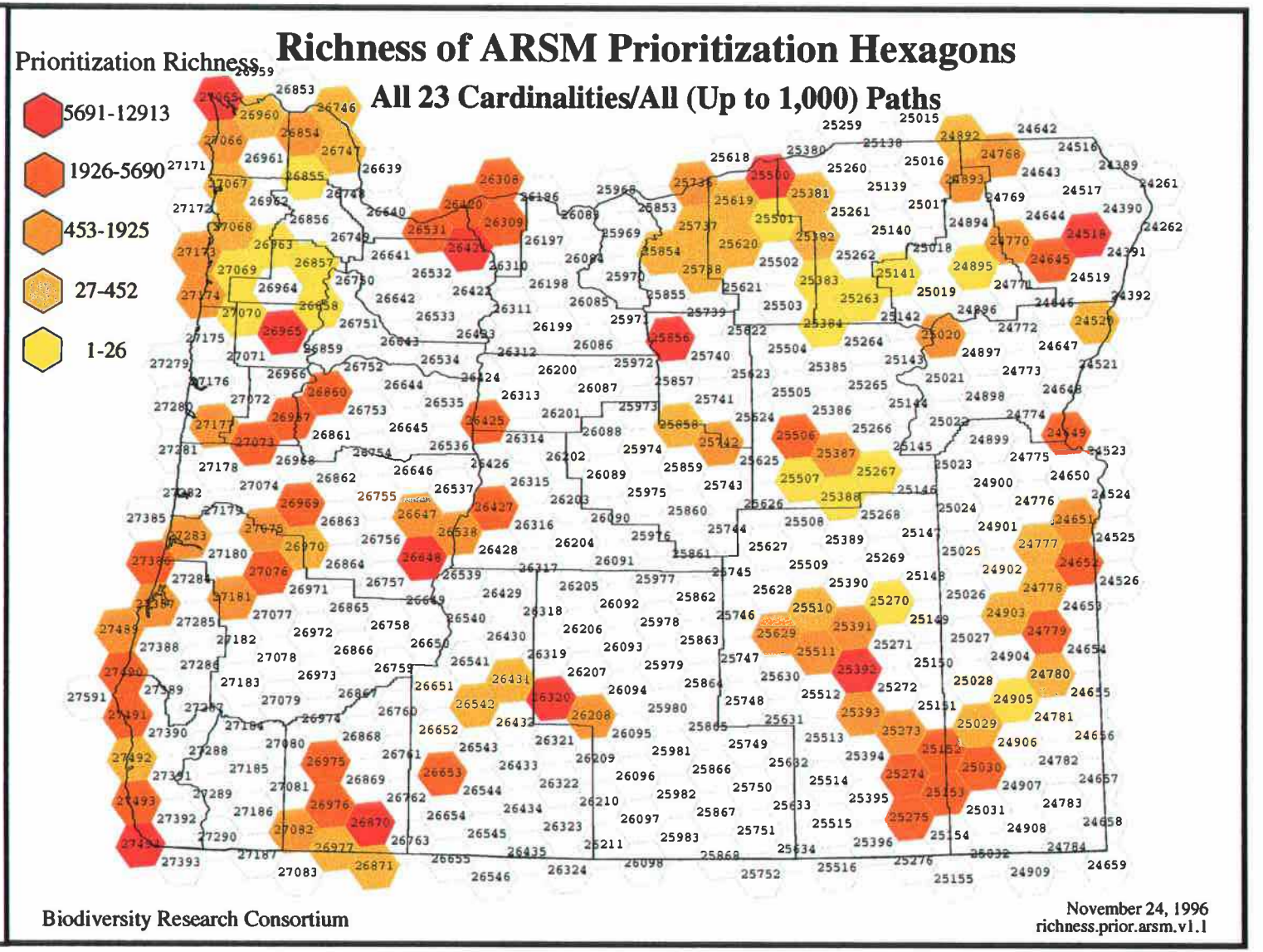

Figure 2.8: Number of paths (all cardinalities) for which prioritization hexagons were used.

It should be noted that this is not an exhaustive solution to the prioritization analysis. If the arbitrary number of paths entered into the program were increased, hexagons at new locations may be selected (i.e. 110 may not be the maximum number of hexagon locations). This study assumes, therefore, that the 1,000 paths account for a statistically representative sampling of solutions.

ECOREGION BOUNDARY STATISTICS

Results of comparing percentages of total hexagons and prioritization hexagons on ecoregion boundaries is presented as **Table 2.1**. The Bailey ecoregion boundaries are included in 113 of the 441, or 25.6%of the total hexagons. If prioritization hexagons were selected preferentially on these boundaries, more than 25.6%, or more than 28 of the 110 prioritization hexagon sites would have been cut by the Bailey ecoregion boundaries. Instead, only 21 of the 110 prioritization hexagons, or 19.1%, are cut. If the total number of prioritization hexagons at all cardinalities are included, 176 of the 995 prioritization hexagons, or 17.7% are cut by the Bailey ecoregion boundaries. If the total number of prioritization hexagons at all cardinalities and on all paths are included, 42,258 of the 218,636, or 19.3% are cut by Bailey ecoregion boundaries. In each case, the statistical implication is that prioritization hexagons are preferentially chosen within, not upon, the Bailey ecoregion boundaries. The same trend is true with the ONHP ecoregion boundaries. 40.6% of total hexagons include the ONHP ecoregion boundaries. As for prioritization hexagons, only 35.5% of the prioritization hexagon locations are cut. This number changes to32.8% if prioritization hexagons selected at all cardinalities are included, and

Table 2.1: Percentage of Hexagons vs. Prioritization Hexagons on Ecoregion Boundaries

	Bailey Ecoreg Buffer	Omernik Ecoreg Buffer	ONHP Ecoreg Buffer	Jaccard Low Cut Buffer	Jaccard High Cut Buffer
Total Hexagons	441	441	441	441	441
Hexagons on Ecoregion Boundary	113	175	179	112	187
% Hexagons on Ecoregion Boundary	**25.6%**	**39.7%**	**40.6%**	**25.4%**	**42.4%**
Total Prioritization Hexes **All Locations**	110	110	110	110	110
Prioritization Hexagons on Ecoregion Boundary	21	36	39	19	31
% Prioritization Hexagons on Ecoregion Boundary	**19.1%**	**32.7%**	**35.5%**	**17.3%**	**28.2%**
Total Prioritization Hexes **All Cardinalities (23)**	995	995	995	995	995
Prioritization Hexagons on Ecoregion Boundary	176	332	326	216	434
% Prioritization Hexagons on Ecoregion Boundary	**17.7%**	**33.4%**	**32.8%**	**21.7%**	**43.6%**
Total Prioritization Hexes **All Cardinalities (23) & All Paths (<= 1,000)**	218,636	218,636	218,636	218,636	218,636
Prioritization Hexagons on Ecoregion Boundary	42,258	96,825	83,144	53,106	104,899
% Prioritization Hexagons on Ecoregion Boundary	**19.3%**	**44.3%**	**38.0%**	**24.3%**	**48.0%**

38.0% if all paths at all cardinalities are included. Once again, prioritization hexagons are preferentially chosen within OHNP ecoregions.

This trend is not as evident for the Omernik ecoregion boundaries. 39.7% of total hexagons are cut by the Omernik ecoregion boundaries. As for prioritization hexagons, only 32.7% are cut. This number changes to 33.4% if prioritization hexagons selected at all cardinalities are included. If, however, all prioritization hexagons on all paths are included, the percentage cut increases to 44.3%, a ratio greater than that for total hexagons of 39.7%. This increase may be due to the much greater range of values for prioritization hexagons at all cardinalities and on all paths and will be discussed later in this paper.

The Jaccard low-cut filter eliminated 25.4% of total hexagons. Of the hexagons eliminated, 17.3% were prioritization hexagon locations, 21.7% were prioritization hexagons at all cardinalities, and 24.3% were prioritization hexagons at all cardinalities on all paths. This follows the general trend observed in the Bailey and ONHP ecoregion analysis. The Jaccard high-cut filter eliminated 42.4% of total hexagons. Of the hexagons eliminated, 28.2% were prioritization hexagon locations, which follows the general trend. The percentage, however, increased to 43.6% for prioritization hexagons at all cardinalities, and to 48.0% at all cardinalities on all paths. This difference from the norm will also be discussed below.

DISCUSSION OF ECOREGION BOUNDARY STATISTICS

The general trend of the Bailey, ONHP and Omernik ecoregion analysis is that prioritization hexagons were selected that preferentially fall within ecoregions. This is true in all examples for both prioritization hexagon locations and prioritization hexagons at all

cardinalities. It is also true for all but the Omernik data with respect to prioritization hexagons at all cardinalities and on all paths.

This difference may be due in part to greater variation in number of occurrences. For prioritization hexagons at all cardinalities, the range of values is between 1 and 21, with the top 10% ranging between 17 and 21 (See key in **Figure 2.7**). Any of the 11 red hexagons could thus change the percentages reported by 1.7% to 2.1%. For prioritization hexagons at all cardinalities and on all paths, however, the range of values is from 1 to 12,913, with the top 10% ranging between 5,691 and 12,913 (See key in **Figure 2.8**). Any of these 11 red hexagons, therefore, could change the percentages reported by 2.6% to 5.9%. In fact, the Bailey, Omernik, and ONHP ecoregion boundaries all cut the hexagon chosen the most times (12,913) for all cardinalities on all paths. Excluding this one hexagon from this analysis could actually decrease all three percentages in the bottom row of **Table 2.1** by nearly 6%.

It is also unclear which of the three measures of hexagon use in prioritization analysis highlights the most important hexagons. Because a hexagon is part of a larger group that can be recombined in a thousand ways to give an optimal prioritization solution at one cardinality does not necessarily mean it is hundreds of times more important than a hexagon used on only one path at all 23 cardinalities.

Also, hexagons appearing in red (top 10%) in **Figure 2.8** are generally not selected until higher cardinalities. Of the 11 red hexagons in **Figure 2.8,** only one is selected below a cardinality of 8. Prioritization analysis shows that the first seven cardinalities cover 94.3% of the terrestrial vertebrate species, and only include one hexagon that will go on to

be chosen most frequently. Most hexagons chosen on the numerous paths, therefore, seem to be contributing combinations of two or three key species to the analysis.

The fact that the low cut Jaccard analysis showed the same trend of preferential selection of hexagons within "data driven" ecoregions is significant. In essence, the Jaccard analysis eliminates hexagons that show a very localized difference in species lists, which are on the scale of adjacent hexagons. Even if the two hexagons with the most different species list were separated by a single hexagon with an intermediate species list, it is possible that none of these three hexagons would be eliminated as part of a Jaccard ecoregion boundary. Alternatively, one hexagon with a very different species list than its more homogenous neighbors can be responsible for eliminating all seven hexagons. Areas remaining after Jaccard buffering, therefore, would have heterogeneities on a scale larger than the grid cells used in analysis. The implication, therefore, is that prioritization analysis is driven by heterogeneity at a scale larger than the grid cell size used in this analysis.

In the case of the high-cut Jaccard analysis, much larger areas are being eliminated from analysis. Unlike the Omernik ecoregion buffer, which also eliminated over 40% of total hexagons, the Jaccard high-cut buffer eliminated large areas on the scale of entire ecoregions. These areas are much more amalgamated, not nearly as linear as the other ecoregions. This ecoregion-scale clustering of eliminated hexagons may explain why more prioritization hexagons are eliminated percentage-wise on ecoregion boundaries for all cardinalities and all paths of all cardinalities than total hexagons.

PRIORITIZATION ANALYSIS WITH ECOREGION BUFFERS

This study also performed prioritization analysis for five new datasets after eliminating hexagons on ecoregion boundaries. To eliminate these hexagons from analysis, appropriate data were eliminated from the species and hexagon matrix. In removing the rows associated with some hexagons, all occurrences of a few, narrowly endemic species were also eliminated. This decreased the total number of species from the original 422 to 420 for the Bailey analysis, 418 for the ONHP analysis, 417 for the Omernik analysis, 419 for the Jaccard low-cut, and 411 for the Jaccard high-cut. Different levels of prioritization, therefore, result in different percentages of species covered in all of these analyses. Results of these analyses as well as the original analysis for Oregon are reported as **Table 2.2 - Table 2.7** in this chapter's **Appendix.**

The Jaccard low-cut still required 23 cardinalities for total coverage, although it covers three less species than the original analysis. The Jaccard high-cut and the Bailey analysis required 22 cardinalities, and the Omernik and ONHP analyses required 21 cardinalities. In all analyses, well over 90% of the species are covered by the fifth cardinality (see this chapter's **Appendix**).

DISCUSSION OF BUFFERED PRIORITIZATION ANALYSIS

Prioritization analysis on buffered ecoregion maps demonstrates that prioritization hexagons are geographically stable, even with the exclusion of hexagons on ecoregion boundaries from analysis. To illustrate this stability, examples of prioritization analysis for the fifth cardinality will be compared for the different analyses. This cardinality ensures

that well over 90% of all terrestrial vertebrates in the state of Oregon will be covered in each analysis.

The original prioritization analysis for the state of Oregon is presented as **Figure 2.9**. Although two hexagons appear in the southwest corner of the state, the remaining hexagons are well dispersed. This can be compared with the Bailey ecoregion analysis, presented as **Figure 2.10**. In this analysis, two of the cardinality five hexagons are eliminated, 27490 and 26531. In both cases, the new prioritization analysis selects adjacent hexagons, 27489 and 26421. It is also worth noting that all five of the prioritization hexagons fall in different Bailey ecoregions. Similar results apply to the ONHP analysis.

The original analysis is also quite similar to the cardinality five Omernik ecoregion analysis, presented as **Figure 2.11.** In this example, two of the original prioritization hexagons are eliminated, 26531 and 24645. The same adjacent hexagon was once again chosen in place of 26531, hexagon 26521. Instead of hexagon 24645, hexagon 24895 was selected. This hexagon is not adjacent, but only two hexagon steps away. The presence of two green and two yellow hexagons means that multiple paths exist for finding an optimal solution. The green hexagons are adjacent and the yellow hexagons are two hexagon steps separate. All five different colored hexagons occur exclusively within five different Omernik ecoregions.

The low-cut Jaccard analysis has similar results. Once again, both original prioritization hexagons 27490 and 26531 were eliminated. The adjacent hexagon 26640 and the hexagon two hexagon steps away, 27492, were used instead. It is more difficult to comment on the distribution of prioritization hexagons throughout ecoregions, as Jaccard "data driven" ecoregions are not divided into several disjoint areas.

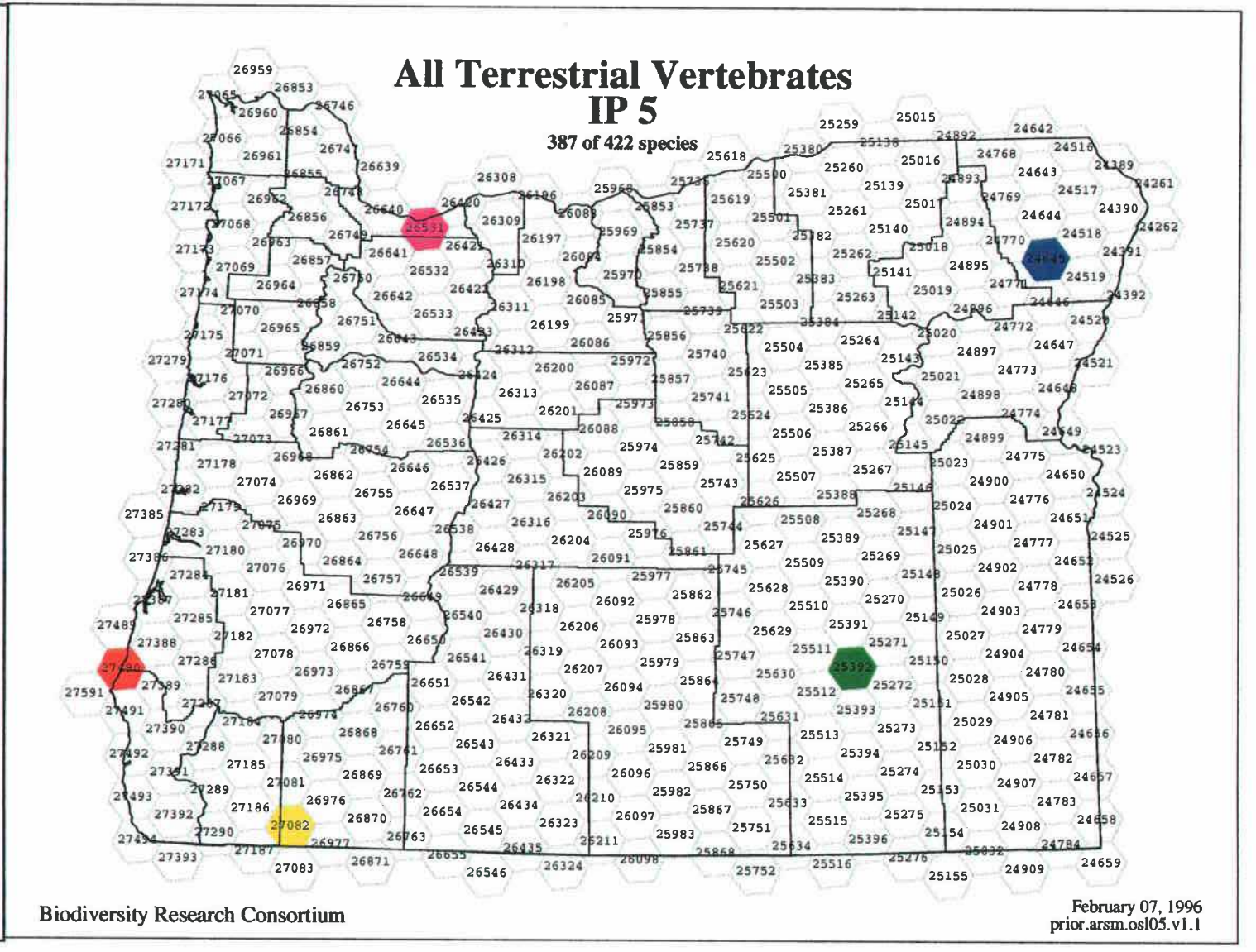

Figure 2.9: Prioritization hexagons at cardinality 5.

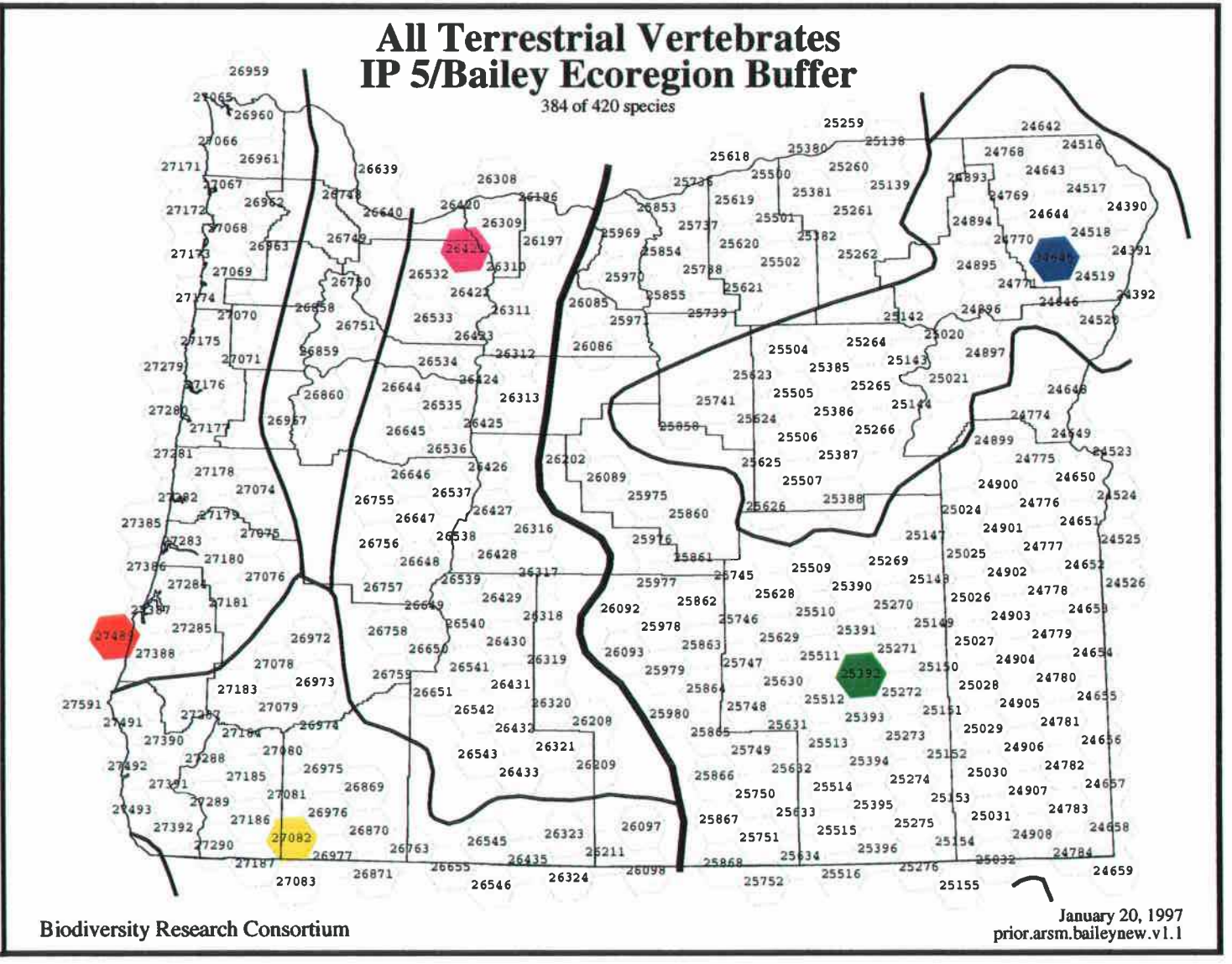

Figure 2.10: Prioritization hexagons after removing hexagons on Bailey ecoregion boundary.

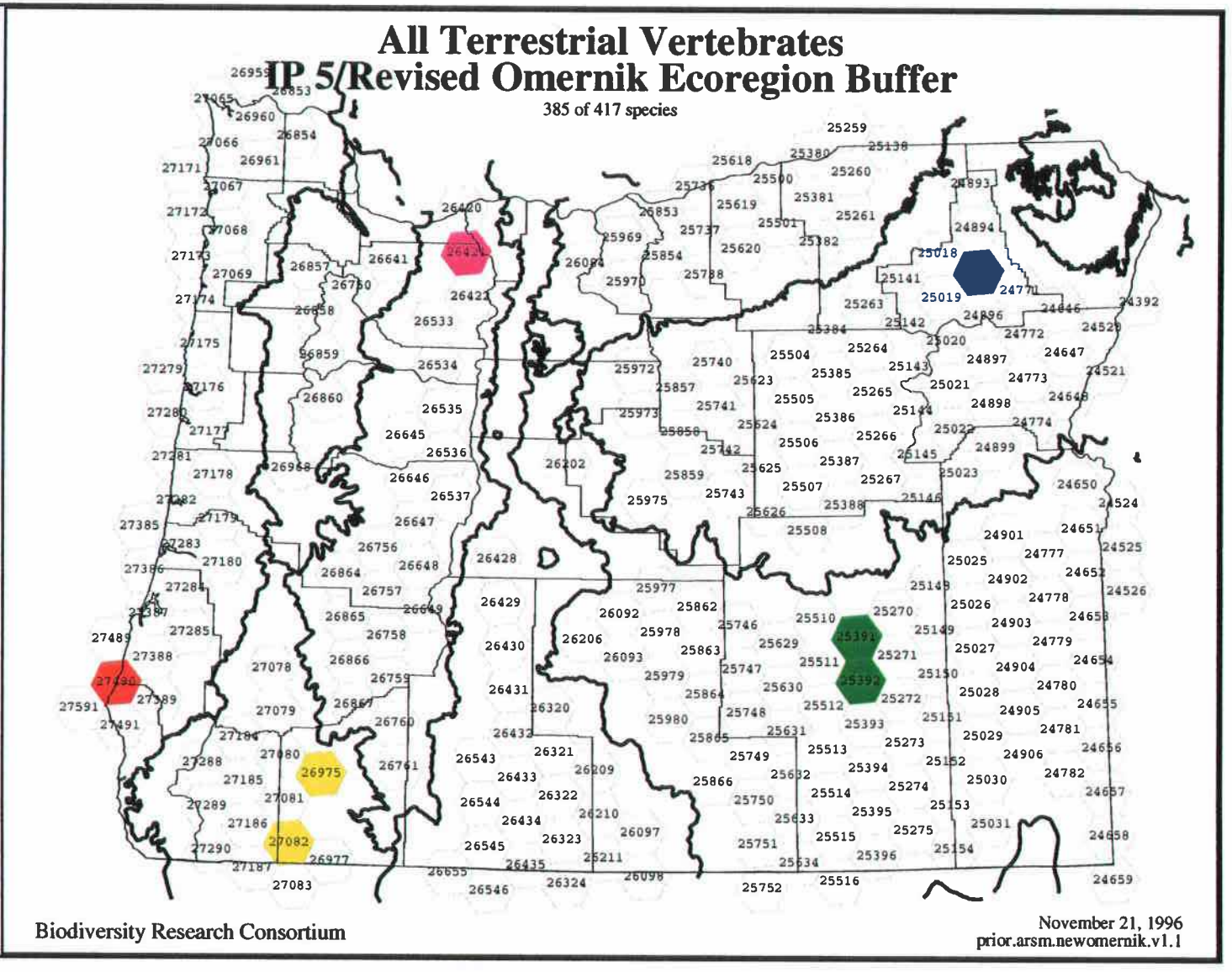

Figure 2.11: Prioritization hexagons after removing hexagons on Omernik ecoregion boundary.

The elimination of large, continuous areas with the high cut Jaccard analysis provides the most dramatic change at cardinality five (**Figure 2.12**). Four of the five original prioritization hexagons have been eliminated. The blue hexagon not eliminated in the northeast part of the state has moved two hexagons steps. Two of the eliminated hexagons have been replaced with adjacent hexagons. The other two original hexagons and all of their adjacent hexagons save one have been eliminated in the Jaccard high cut buffer. This has caused one location to move from the northwestern part of the state to the southeastern part, near the other displaced hexagon. Once again, discussion of presence in different ecoregions is made difficult by the lack of well defined disjoint areas.

CONCLUSIONS AND DISCUSSION

Results from this study lead to two major conclusions. The first is that prioritization hexagons do no fall preferentially on most ecoregion boundaries. The second is that prioritization analysis results remain geographically stable after eliminating hexagons along ecoregion boundaries.

These results have interesting implications concerning the scale of biodiversity processes affecting prioritization analysis. First, hexagons straddling ecoregion boundaries and sampling different biotic assemblages are not a driving factor in prioritization analysis. If this were true, percentages of prioritization hexagons on ecoregion boundaries would be higher than the percentage of total hexagons that are prioritization hexagons. The Jaccard buffer analysis also indicates that localized changes in species lists on the order of adjacent hexagons are also not a scale which drives prioritization analysis.

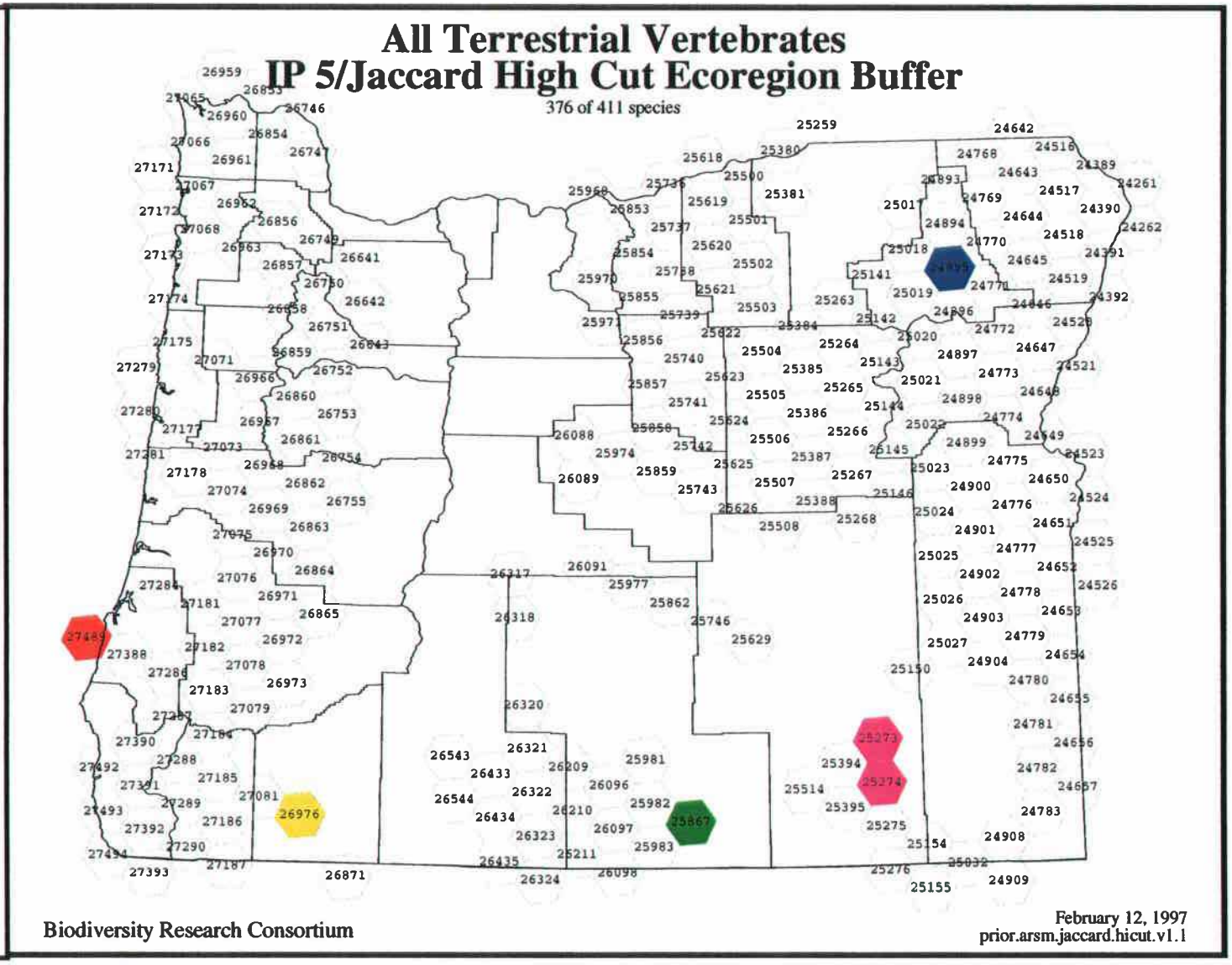

Figure 2.12: Prioritization hexagons after removing hexagons on Jaccard high-cut data driven ecoregion boundary.

Inferences can also be drawn from the geographic stability of results. This implies that geographic areas on the scale of ecoregions may be an important factor in prioritization analysis. Also, when multiple paths are selected, hexagons are often proximal and within the same ecoregion. This may imply that the most important heterogeneity for prioritization analysis may be differences found at a scale similar to the sizes of ecoregions in Oregon.

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Appendix

Results of Ecoregion Buffered Prioritization Analysis

Table 2.2: Oregon Prioritization Analysis

Oregon All Vertebrates Prioritization v1.1
441 hexes and 422 total species

# of hexes/path	# of paths	# of hexes	# species covered	% species covered
1	1	1	259	61.38
2	2	3	319	75.60
3	3	5	357	84.60
4	4	6	376	89.10
5	1	5	387	91.71
6	2	7	393	93.13
7	10	12	398	94.32
8	109	26	401	95.03
9	64	23	404	95.74
10	877	47	406	96.21
11	>1000	51	408	96.69
12	>1000	53	410	97.16
13	112	32	412	97.64
14	>1000	73	413	97.87
15	>1000	84	414	98.11
16	>1000	86	415	98.35
17	>1000	82	416	98.58
18	>1000	57	417	98.82
19	>1000	57	418	99.06
20	>1000	55	419	99.29
21	945	70	420	99.53
22	>1000	80	421	99.77
23	>1000	80	422	100.00

Biodiversity Resource Consortium February 9, 1996

Table 2.3: Bailey Ecoregion Buffer Prioritization

Oregon All Vertebrates Prioritization v1.1
328 hexagons and 420 total species

# of hexes/path	# of paths	# of hexagons	# species covered	% species covered
1	1	1	255	60.71
2	2	3	319	75.95
3	1	3	357	85.00
4	1	4	374	89.05
5	1	5	384	91.43
6	8	13	390	92.86
7	50	18	395	94.05
8	64	23	399	95.00
9	50	28	402	95.71
10	51	34	404	96.19
11	20	17	407	96.90
12	61	22	409	97.38
13	51	35	410	97.62
14	55	28	412	98.10
15	50	42	413	98.33
16	50	57	414	98.57
17	51	67	415	98.81
18	50	64	416	99.05
19	50	67	417	99.29
20	51	68	418	99.52
21	50	66	419	99.76
22	50	72	420	100.00

Biodiversity Resource Consortium January 20, 1997

Table 2.4: Revised Omernik Ecoregion Buffer Prioritization

Oregon All Vertebrates Prioritization v1.1
265 hexagons and 417 total species

# of hexes/path	# of paths	# of hexagons	# species covered	% species covered
1	1	1	255	61.15
2	2	3	319	76.50
3	1	3	357	85.61
4	1	4	376	90.17
5	3	7	385	92.33
6	25	16	390	93.53
7	8	14	395	94.72
8	50	23	399	95.68
9	52	29	402	96.40
10	50	24	404	96.88
11	51	25	406	97.36
12	50	30	408	97.84
13	50	37	409	98.08
14	50	42	410	98.32
15	50	48	411	98.56
16	50	44	412	98.80
17	50	54	413	99.04
18	50	51	414	99.28
19	50	46	415	99.52
20	50	51	416	99.76
21	50	51	417	100.00

Biodiversity Resource Consortium November 21, 1996

Table 2.5: ONHP Ecoregion Buffer Prioritization

Oregon All Vertebrates Prioritization v1.1
239 hexagons and 418 total species

# of hexes/path	# of paths	# of hexagons	# species covered	% species covered
1	1	1	255	61.00
2	2	3	319	76.32
3	2	4	357	85.41
4	4	6	376	89.95
5	1	5	386	92.34
6	12	18	391	93.54
7	17	13	396	94.74
8	10	13	401	95.93
9	51	25	403	96.41
10	55	27	405	96.89
11	55	26	407	97.37
12	76	21	409	97.85
13	53	38	410	98.09
14	50	33	411	98.33
15	50	31	412	98.56
16	50	32	413	98.80
17	51	37	414	99.04
18	50	40	415	99.28
19	50	42	416	99.52
20	50	44	417	99.76
21	50	42	418	100.00

Biodiversity Resource Consortium November 3, 1996

Table 2.6: Jaccard Low-Cut Ecoregion Buffer Prioritization

Oregon All Vertebrates Prioritization v1.1
329 hexagons and 419 total species

# of hexes/path	# of paths	# of hexagons	# species covered	% species covered
1	2	2	245	58.47
2	1	2	319	76.13
3	1	3	357	85.20
4	17	13	373	89.02
5	1	5	383	91.41
6	16	21	388	92.60
7	2	10	394	94.03
8	2	11	398	94.99
9	2	11	401	95.70
10	16	19	403	96.18
11	49	25	405	96.66
12	64	22	407	97.14
13	50	34	408	97.37
14	32	20	410	97.85
15	54	43	411	98.09
16	51	38	412	98.33
17	50	36	413	98.57
18	50	36	414	98.81
19	50	36	415	99.05
20	50	37	416	99.28
21	52	40	417	99.52
22	50	40	418	99.76
23	50	41	419	100.00

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Table 2.7: Jaccard High-Cut Ecoregion Buffer Prioritization

Oregon All Vertebrates Prioritization v1.1
254 hexagons and 411 total species

# of hexes/path	# of paths	# of hexagons	# species covered	% species covered
1	2	2	245	59.61
2	1	2	316	76.89
3	1	3	347	84.43
4	1	4	364	88.57
5	2	6	376	91.48
6	1	6	384	93.43
7	4	9	389	94.65
8	2	9	393	95.62
9	2	10	396	96.35
10	11	16	398	96.84
11	9	15	400	97.32
12	53	33	401	97.57
13	60	40	402	97.81
14	50	40	403	98.05
15	50	40	404	98.30
16	50	36	405	98.54
17	50	43	406	98.78
18	50	44	407	99.03
19	50	47	408	99.27
20	50	44	409	99.51
21	50	49	410	99.76
22	50	49	411	100.00

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CHAPTER 3

Scale Analysis Using Seven-Fold Compositions of the EMAP Grid

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ABSTRACT

The effect of scale on combinatorial mapping has received little attention to date. This study looks at the effect of increasing grid cell size on biodiversity mapping in Oregon. The data being analyzed are species range maps, whose extents are based on the Environmental Protection Agency's Environmental Monitoring and Assessment Program (EMAP) grid. Species richness and prioritization maps are made with grid cells seven and 49 times as large as the original grid. Grid cells seven times as large result in species richness maps statistically similar to maps made with the EMAP grid. Patterns of localized variation between grid cells at this scale can be mapped, indicating there is not just one area contributing to the overall variation. Prioritization maps, however, show different patterns of selected hexagons. Grid cells 49 times as large show a loss of species richness variation and a different pattern of prioritization hexagons.

INTRODUCTION

The purpose of this study is to determine the effect of increasing grid cell size by two factors of seven on biodiversity mapping of terrestrial vertebrates in the state of Oregon. This research will look at the effect of scale on both richness mapping and prioritization mapping. Effects of scale on richness mapping will be examined at both a regional and a localized level. All analysis will be based on species range maps delineated by the Environmental Protection Agency's EMAP hexagonal grid discussed below.

Constructing richness maps at different scales is a combinatorial procedure. Each hexagonal EMAP grid cell has a unique species list associated with it. As these hexagons are combined into larger grid cells, a new data dependent species list will result. These

results cannot be predicted by traditional geostatistical techniques. Issues associated with such procedures are addressed by Stoms (1994).

The effect of changes in grid cell size on prioritization mapping will also be examined. Prioritization mapping selects a given number of grid cells which maximize the number of different species present. This analysis involves comparing species lists of multiple grid cells. As grid cells and their associated species list change with scale, new combinations may give geographically dissimilar results.

DATA

The grid currently used for mapping biodiversity in Oregon is the Environmental Protection Agency EMAP hexagonal grid, which provides complete coverage for the contiguous United States. This Lambert azimuthal equal area map projection surface is composed of hexagonal grid cells approximately 640 km^2. This size was selected as a "suitable compromise between the desired spatial resolution of sampling and the projected available financial resources" (White et al., 1992, p. 18).

Biodiversity analysis in Oregon has used this grid in mapping species ranges and in sampling the data for richness and prioritization analysis. The first version of range maps for 422 terrestrial vertebrates was compiled by The Nature Conservancy. These range maps are based on several criteria. Documented species sitings from such resources as museum specimens serve as the basis. Expert opinions are then used to augment these maps, assigning hexagons a confirmed, probable, or possible status. All confirmed and probable species are assigned to appropriate grid cells. The resulting list of hexagons and associated species are used for all analysis in this study.

The EMAP grid acts both as the minimum mapping unit (MMU) for the input data and the sampling unit for the output data. Analysis at a grid cell size smaller than 640km^2, therefore, is impossible with these data without making further assumptions.

METHODOLOGY

Species richness maps are created by summing the total number of species in each grid cell. Although these maps provide spatial information on what areas are rich or poor in number of species, they are not suited to answer other important questions in conservation biology (Williams et al., 1996, Prendergast et al., 1993). Prioritization maps look to maximize the number of unique species in a given number of grid cells, an example of a maximum covering location problem (MCLP) (Church et al., 1994). Analysis in Oregon uses a linear programming algorithm, which ensures "optimal solutions to the reserve selection algorithm" (Csuti et al., 1997, p. 83).

A change in the size of the grid cell will result in a new list of species associated with each new grid cell sample. Stoms (1994) recognizes that agglomerating sampling units and species contained within is not a classical spatial statistics problem that can be addressed by such methods as calculating semivariance; "aggregation is not a simple numerical averaging over different sampling sizes, but is a logical union of sets (species lists)" (p. 347).

Figure 3.1 illustrates this principle of Stoms (1994) for a simple example. Grid cell size 1 has eight cells with no variations in species richness between cells. All four grid cells left of center contain the same 100 species. The logical union of these four would still represent 100 species, as illustrated in the left cell of grid cell size 2. The right four

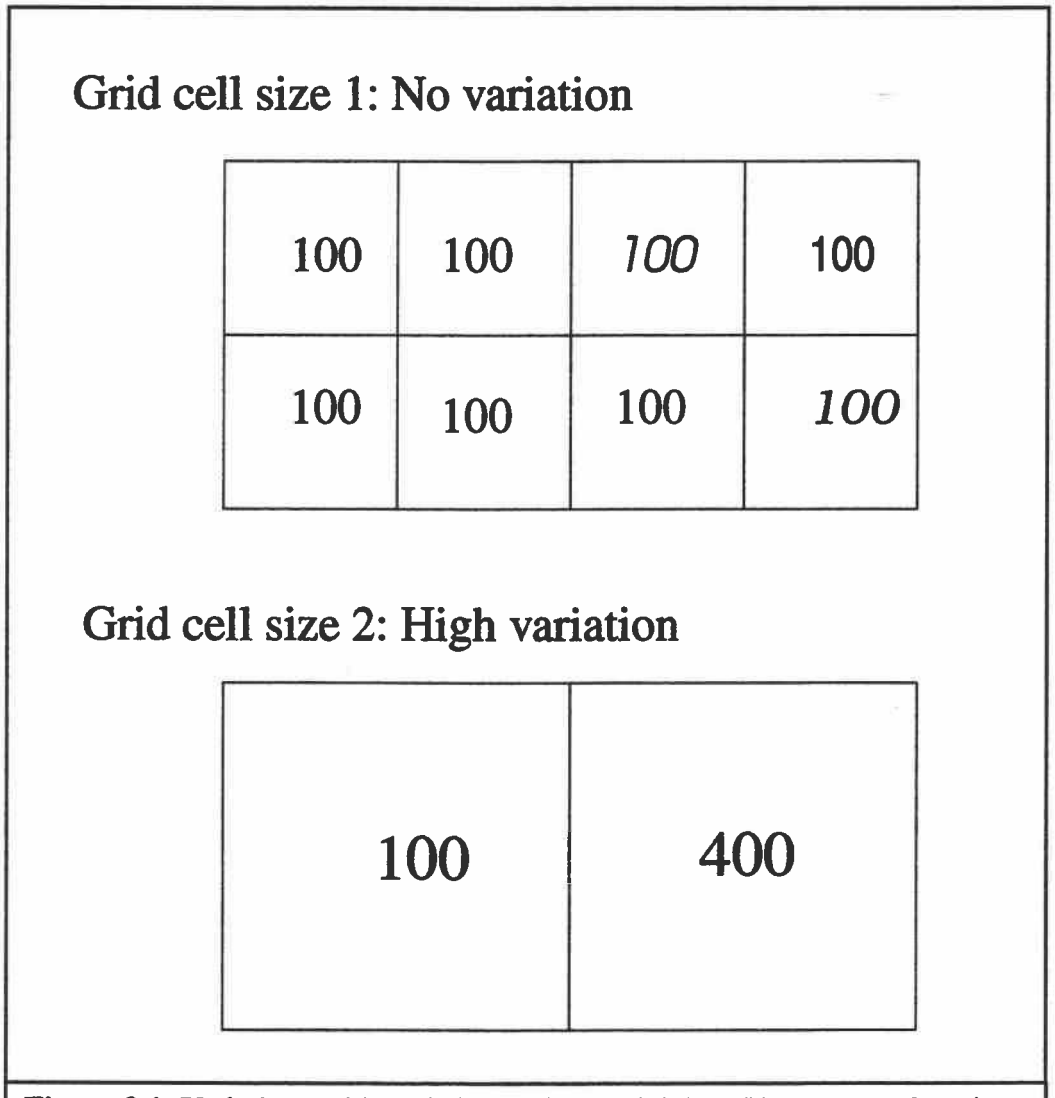

Figure 3.1: Variations with scale in combinatorial data (From an explanation in Stoms, 1994).

grid cells for grid cell size 1, however, contain four sets of 100 mutually exclusive species. Their logical union would contain 400 species, as illustrated in the right cell of grid cell size 2. Stoms found that coefficient of variation(CV) decreased with increased sampling area. No current research has attempted to relate changes in grid cell size to potential differences in locations of samples selected by biodiversity prioritization analysis.

This study looks at biodiversity mapping on the EMAP hexagonal grid. Three geometries for the composition and decomposition of these grid cells are presented as **Figure 1.1**. All three of these geometries will preserve the important attributes found in a hexagonal grid, such as grid cells filling 2-D space and all adjacent grid cells being equidistant.

Two of these methods of composition require the hexagonal grid to be subdivided into triangles for resampling. The three fold composition takes a central hexagon and one third of all six neighboring hexagons. The four fold uses a central hexagon and one half of all six neighboring hexagons. As the species range maps used in this study are based on absence or presence in each hexagonal grid cell, three and four fold compositions are inappropriate without additional assumptions.

A seven fold composition of a hexagon takes a central hexagon and the six adjacent hexagons. The resulting polygon is not a hexagon. This polygonal grid, nevertheless, can undergo further compositions to larger polygons and preserves all important properties of hexagonal grid cells. A seven fold decompositon is not possible from range maps based on the original EMAP hexagon.

Two compositions of the EMAP grid cell are appropriate for analysis in Oregon. A third iteration would create a grid cell nearly as large as the state. The two compositions are illustrated in **Figure 1.2**. 441 EMAP grid cells of approximately 640 km^2 cover the state of Oregon. After one composition, the grid will contain approximately 50 polygonal cells, each 7 times as large (approximately 4,480 km^2). The 50 polygonal cells do not include fractional grid cells produced, as biodiversity mapping requires all grid cells to be equal in area. Fractional grid cells were thus eliminated from analysis. Two levels of com-

position results in a grid of approximately three polygonal cells, each 49 times as large (approximately 31,360 km^2). Once again, fractional grid cells were eliminated from analysis.

Seven unique grid cells can be constructed at the first composition. **Figure 1.2** illustrates one example. Other seven fold compositions could be created by shifting the first composition grid one EMAP hexagon to the north, northeast, southeast, south, southwest, or northwest with respect to the grid shown. Seven unique grids and unique combinations of species lists would result. This is not a sampling of the data in the statistical sense. Each of the seven maps will be an exhaustive sample of the data captured at the EMAP scale (except for edge effects). Unique, exhaustive combinations will help to better define combinatorial changes in the data with scale. The above is also true for the second composition, where 49 unique combinations of the EMAP grid are possible.

Species diversity maps in this study divide the range of species richness values into classes for color map displays. Five classes are defined based on the statistical distribution of species richness values. The class divisions are 0% to 15%, 15% to 40%, 40% to 65%, 65% to 90% and 90% to 100% of the species richness values, and represent suitable class ranges for such distributions. This study combines richness values from all datasets at the same composition level before dividing the distribution into classes. The first composition will therefore have seven unique maps, but the classes on each map will be the same and based on the entire distribution of values. Five of the maps have 50 grid cells and two of the maps have 51, thus giving 352 unique richness values for defining quantiles of the distribution.

This method for determining a statistical distribution is necessary with the classes for the composition 2 maps, as none of the 49 maps have more than five grid cells. Combining richness values from all maps allows 167 richness values to define the distribution. This number includes five maps with 2 grid cells, 23 maps with 3, 17 maps with 4, and four maps with 5.

Prioritization analysis uses a matrix of grid cells and species to determine which grid cells in combination will represent the most species for a given number of grid cells. This study uses species lists combined from all maps at a given composition. The matrix files for the first and second composition thus contain 352 and 167 lists of species present, respectively.

This method of combining all data at a scale permits one comprehensive prioritization analysis to be done for each composition. Combining all species lists at one scale also allows for the overlap of higher order grid cells in prioritization analysis. The implications of overlapping grid cells to families of hexagons in prioritization areas will be discussed later in this paper.

Regional Variations in Biodiversity Mapping

Statistical measures associated with the resulting biodiversity maps have rarely been assessed. No obvious metric measures dissimilarity of locations of prioritization hexagons on two different maps. This study will use observations of larger prioritization hexagons overlapping, not overlapping or being adjacent to prioritization hexagons selected at a smaller scale as a measure of spatial stability.

Several statistical measures, however, are possible for richness mapping at different scales. These include both measures made at a local level and ones made for the entire range of values. Previous work in comparing statistics from maps based on the same datasets includes Stoms (1992) relating of rank correlation coefficient to minimum mapping unit for richness mapping west of the Sierra Nevada crest in California. In more recent work, Stoms (1994) relates coefficient of variation(CV) to sampling unit area.

CV is defined as the sample standard deviation expressed as a percentage of the sample mean (Steel and Torrie, p. 27). In combining species lists at larger scales, values for average and standard deviation can be highly volatile. An example of the simplicity of behavior for numerically averaged data as opposed to combinatorial data is presented as **Figures 3.2 and 3.3**.

Figure 3.2 shows an example of a numerically averaged dataset sampled at four different scales, each scale represented in a different graph. The length of the solid line segments in each graph represents the grid cell size. The values on the y axis represent the values associated with each grid cell. Average values as well as maximum minus minimum (max-min) are calculated at each scale. The dashed line displays the average value at each scale. Although max-min is not a true measure of variance, it is similar in that it helps define the range of values. As grid cell size increases, the max-min values decrease and the average stays the same. In this example, calculating a value (max-min / average) as a pseudo coefficient of variation ("CV") is not instructive, as average is a constant and thus "CV" relates directly to max-min.

Figure 3.3 shows a similar example with combinatorial data. An addition is made to this display from **Figure 3.2** as a "Total" value of 360 is given. This number represents

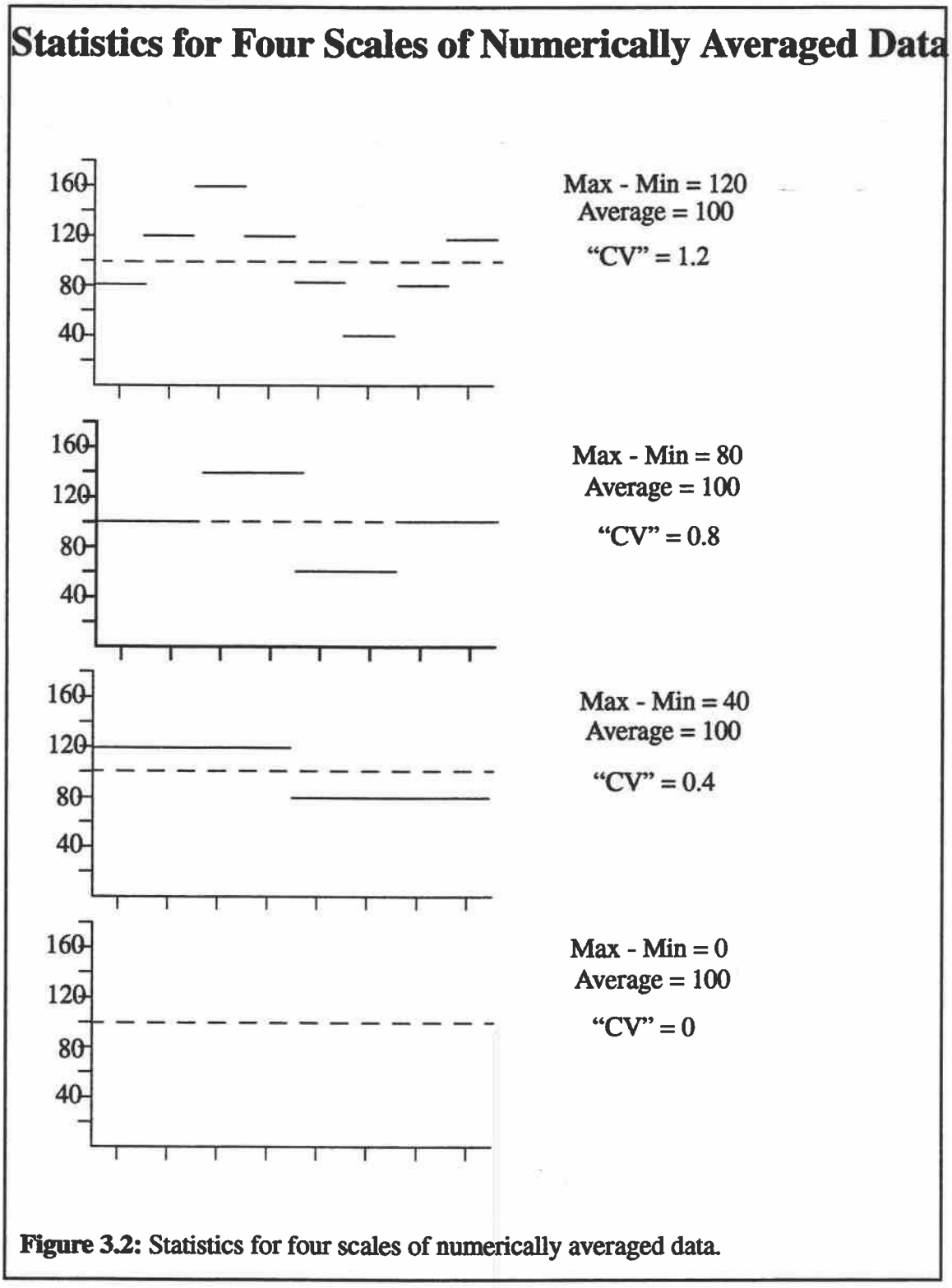

Figure 3.2: Statistics for four scales of numerically averaged data.

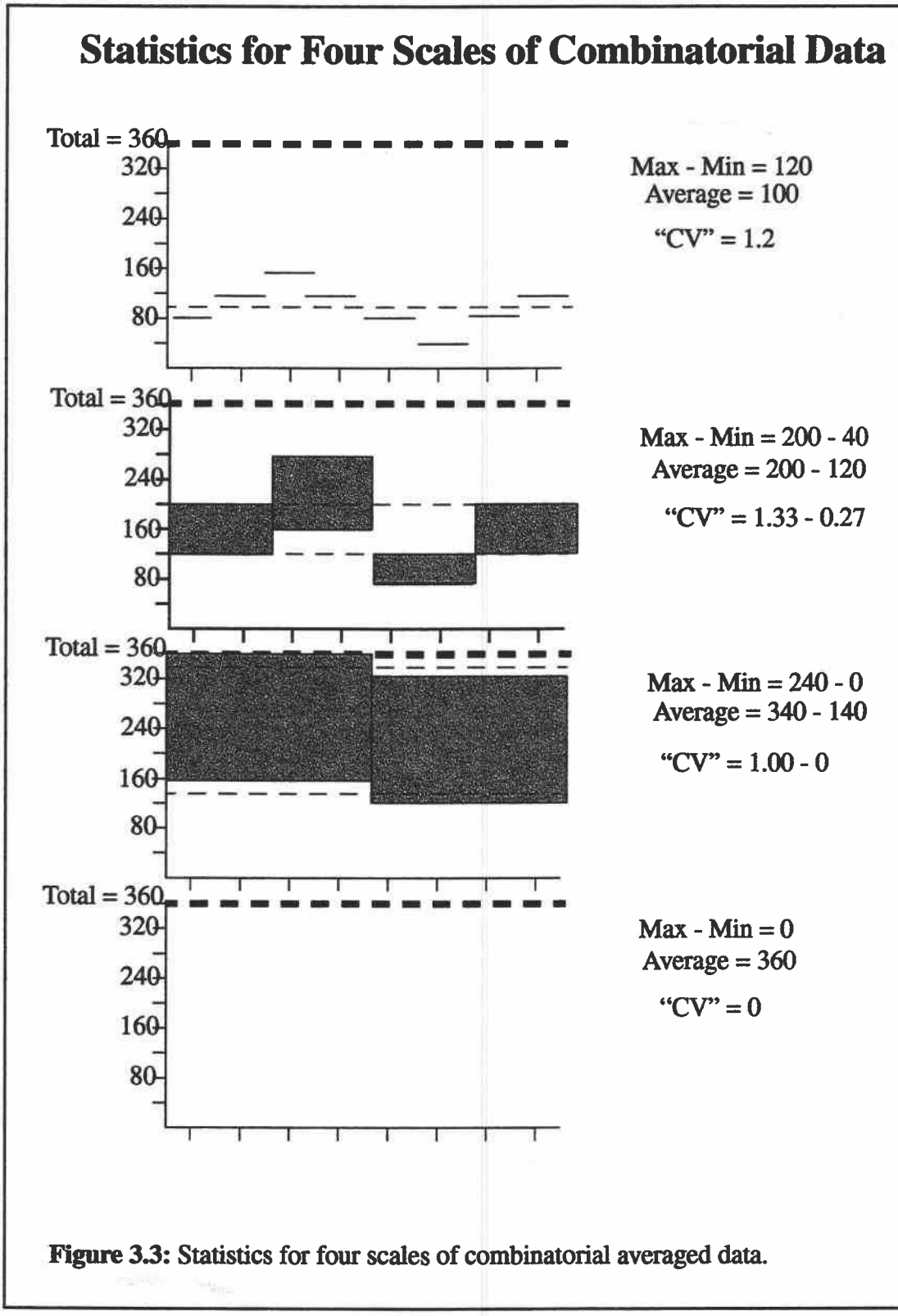

Figure 3.3: Statistics for four scales of combinatorial averaged data.

the total number of possible types of samples in an extent (e.g. total species in a state). As grid cells are combined, the new grid cell could have a range of values based on the number of unique elements in each smaller grid cell. For example, the two smallest grid cells to the left contain 80 and 120 elements. As they are combined into a larger grid cell in the second graph, the new grid cell may have as few as 120 elements (i.e. all 80 elements in the first grid cell also appear in second grid cell) or up to 200 elements(i.e. all 80 elements in the first grid cell are different from all 120 elements present in the second grid cell). Ranges of possible values are highlighted on appropriate graphs using shaded areas.

Because values span a range at the second and third scale, the average will also have a range of values. The smallest and largest possible averages are displayed on appropriate graphs with two dashed lines. The fourth scale shows one grid cell equal to the extent. In this example, all types are represented in the extent, thus the grid cell will have a value and an average equal to the total of 360.

One important observation from this example is that for a smooth distribution of high and low numbers, the top of high ranges can increase much faster than the base of the low numbers. While the second grid cell at scale two takes an additive value (160 + 120 = 280) as the top of its range of values, the third grid cell at scale two takes a maximum of two values value (the maximum of 40 and 80 is 80) as its minimum value. It is therefore possible for max-min variation to increase with increasing grid cell size. Note that max-min at scale two can be as much as 200, well over the max-min value of 120 at the first scale.

In this example, the average value will increase in moving from the first to the second scale. If the max-min increases proportionately, the "CV" will remain the same

(where "CV" = max-min / ave). It is also possible, however, for the "CV" to decrease or increase with increased grid cell size. Results are dependent on individual datasets.

Another important observation of this example is that the total number of types is important to how ranges of values will change. At the third scale, the top of the range for the left grid cell is not an additive value (200 + 280 = 480), but rather the maximum number of types in the extent (total = 360). This helps to limit the range of possible values, and ultimately decrease the range of values as the average value continues to increase. The resulting effect on "CV" will be a number destined to decrease and finally reach zero as the grid cell size equals the extent. It should also be noted that CV could also decrease at any step if average increases proportionately faster than max-min.

Although changes in variance and average will be data dependent with changes in scale, CV seems to be an appropriate statistic for measuring these changes. Although CV may increase, decrease, or stay the same at smaller scales, we should be able to detect breaks due to reaching regional limits to the number of types present in an area. This may also be true when using this procedure for detecting subregional limits at smaller scales, where more species will not be added within a range of scales because areas with complementary species are too geographically distant to be included in grid cells.

Localized Variations in Biodiversity Mapping

Measuring changes in coefficient of variation provides a richness mapping statistic for comparison of all data within the extent of the study area. Each set of maps at a different scale will have one coefficient of variation associated with all of the richness values. Each map in the set, however, will show some localized variations. The geometry of the 7

fold composition allows a unique opportunity to measure and geographically display local variations.

The method used for looking at localized variations is illustrated in **Figure 3.4**. Most hexagons at the EMAP grid cell size (cyan hexagon) will contribute richness information to seven larger polygons (red outlines) at the first seven fold composition. Each of these larger red polygons will have a richness value, contributed in part by the cyan hexagon. By looking at the maximum minus the minimum value (max-min), a measure of localized variations in richness can be determined. By measuring this value at every EMAP hexagon using the seven appropriate first composition polygonal grid cells, a map of localized variation can be constructed.

EMAP hexagons in areas of greater richness would be expected to have a larger difference in max-min simply because their values are larger. It is appropriate, therefore, to calculate a localized "coefficient of variation" by dividing the max-min value for each grid cell by its average richness value for all surrounding polygons. Maps of average richness, max-min richness, and normalized max-min richness can all be constructed for comparison.

The normalized max-min map will show the distribution of localized variation. A random pattern of richness would indicate that no areas the size of all 19 EMAP hexagons in **Figure 3.4** contributes more to total variation than any other. A clustered richness map pattern would highlight areas with greater and lesser amounts of variation. A pattern similar to the average richness pattern would indicate that areas of greater average richness are also areas of greater normalized variation in richness. These map patterns will be discussed with the results of this study.

Example of maximum - minimum number of species

Central polygon richness	250
North polygon richness	244
Northeast polygon richness	**275 = Maximum**
Southeast polygon richness	266
South polygon richness	240
Southwest polygon richness	**233 = Minimum**
Northwest polygon richness	252
Maximum - minimum	**42**
Average	**251.43**
(Max-Min)/Average	**0.17**

Figure 3.4: Example of maximum minus minimum number of species.

RESULTS

The results of richness mapping at three different scales is presented as **Table 3.1.** 0X's 7-fold composition is the EMAP grid, with the first and second compositions labeled 1X's 7-fold and 2X's 7-fold. The minimum, maximum and mean values increase at each composition in accordance to the general pattern from **Figure 3.3**. The variance increases for the first composition before decreasing from the first to the second. This increase and decrease in variation is part of the data dependent volatility of these numbers, as illustrated in the range of max-min in **Figure 3.3.**

The coefficient of variation (CV) stays virtually the same from the EMAP grid to the first composition, changing from 10.45% to 10.66%. This implies that no statistical variations in richness values are present between the two scales. The EMAP scale richness map and two of the seven richness maps at the first composition are included as **Figures 3.5, 3.6, and 3.7**.

The CV decreases at 2X's 7-fold composition. This implies that some of the variations seen at smaller scales have been lost at this scale. Seven of the 49 richness maps at this scale are included as **Figure 3.8** for comparison. Maps at 2X's 7-fold composition contain only two to five grid cells. It is not surprising that variations seen at the two previous scales would be lost at this scale, as the grid cell size approaches the extent of the study area. This same pattern of decreasing values of CV with increased grid cell size were documented by Stoms (1994).

Table 3.1: Richness Map Statistics for 7-Fold EMAP Compositions

	0X's 7-Fold (EMAP)	1X's 7-Fold Comp	2X's 7-Fold Comp
Number of Polygons	441	352	167
Min	143	178	266
Max	259	307	357
Mean	197.11	232.08	308.89
Variance	424.28	612.52	528.29
St Dev	20.60	24.75	22.98
Coeff of Variance	**10.45%**	**10.66%**	**7.44%**

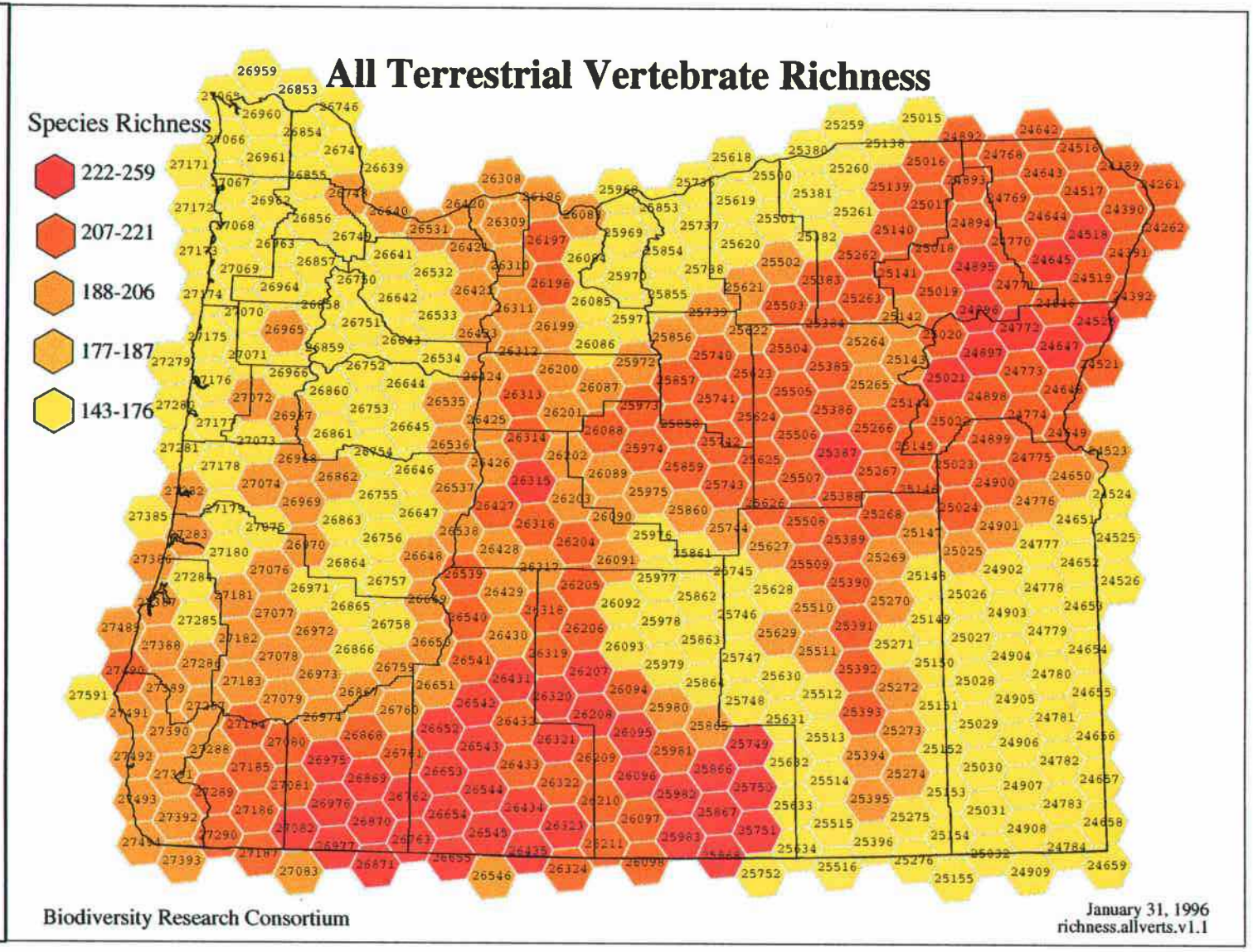

Figure 3.5: Richness map at EMAP scale.

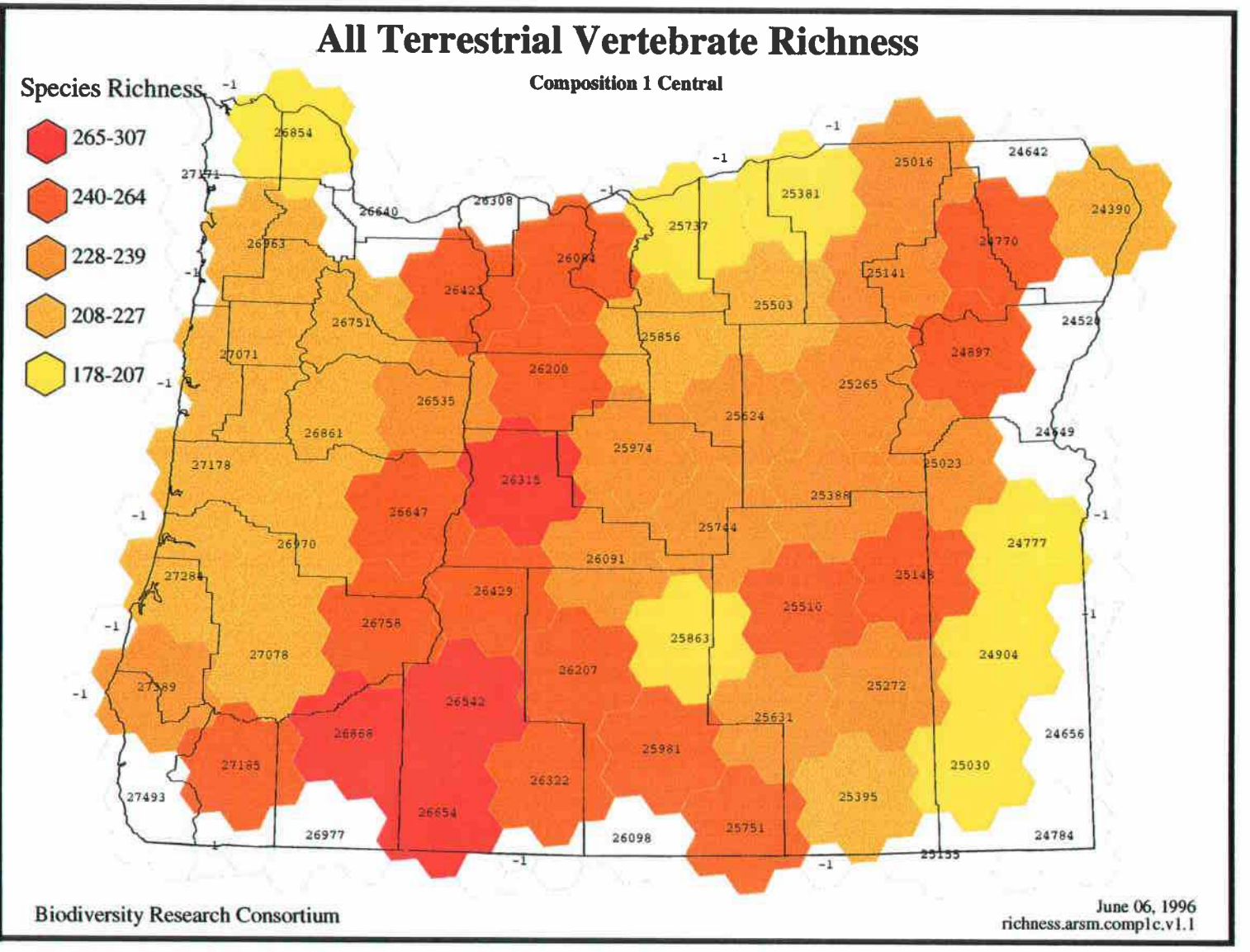

Figure 3.6: Richness map using grid cells seven times EMAP scale (Example 1).

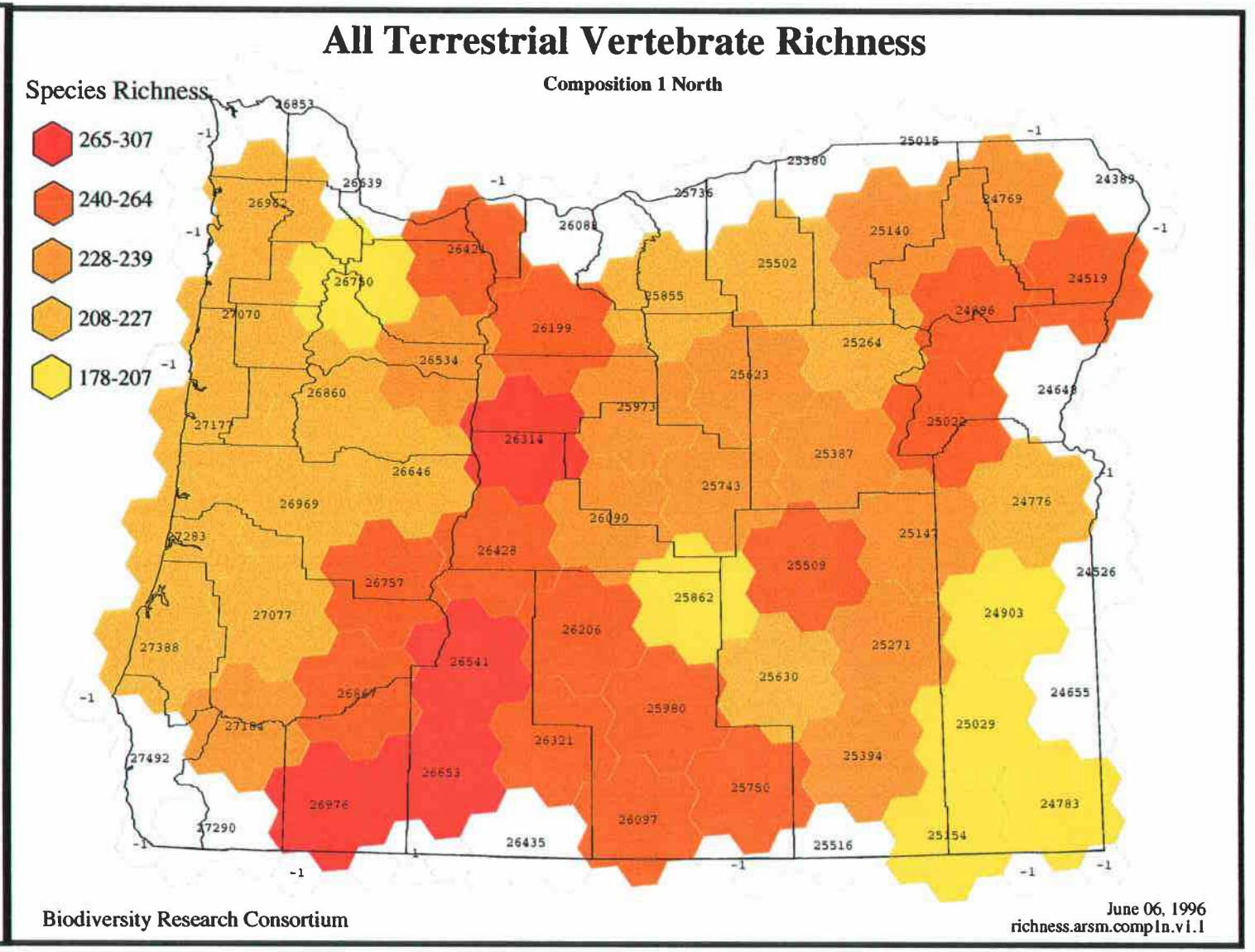

Figure 3.7: Richness map using grid cells seven times EMAP scale (Example 2).

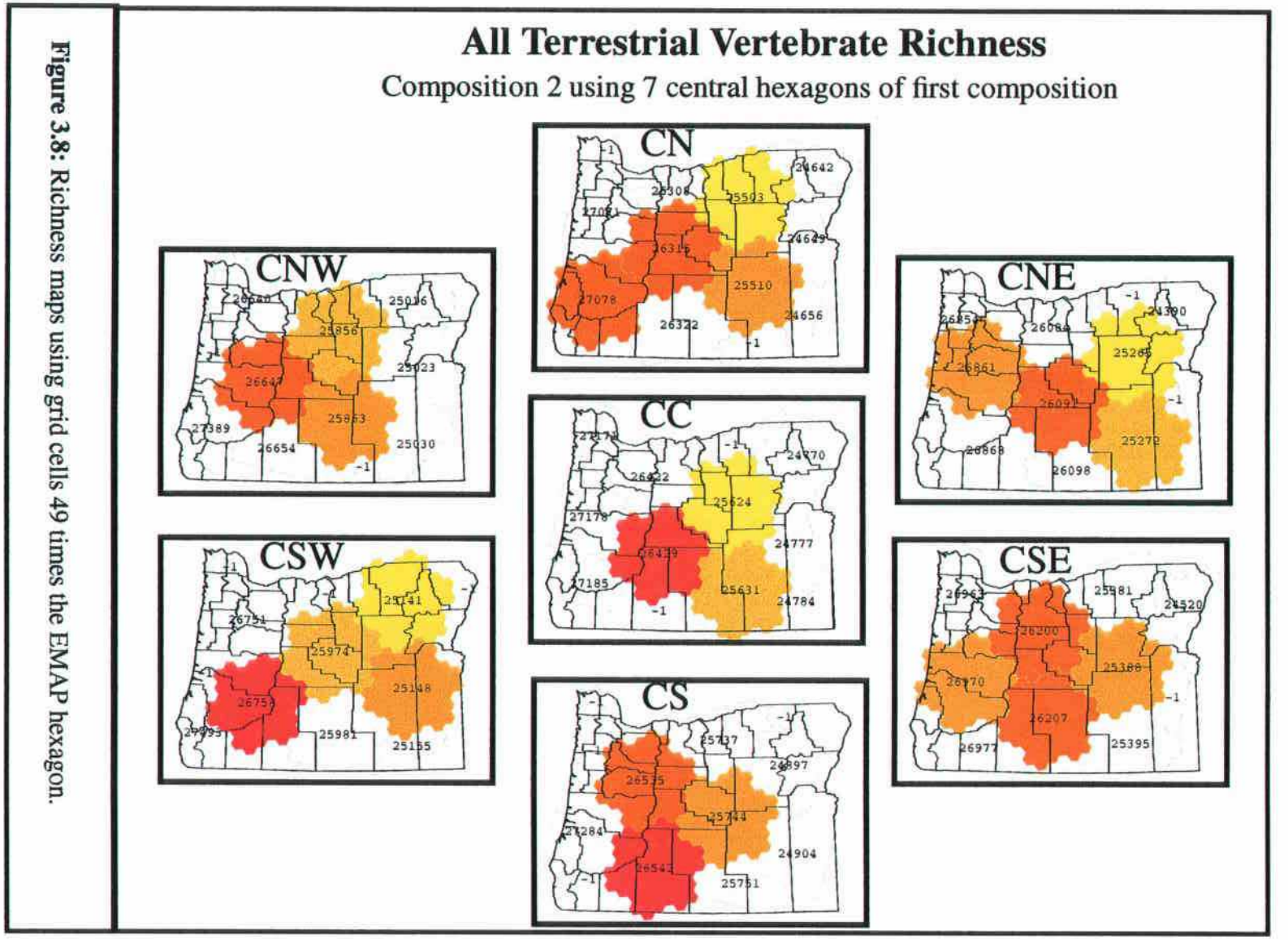

Figure 3.8: Richness maps using grid cells 49 times the EMAP hexagon.

Differences in map patterns can be detected by comparing the two maps from the first composition(See **Figures 3.6 &3. 7**). To quantify the differences between all seven maps at this scale and display results in a geographical format, a normalized max-min map was constructed at this scale. **Figure 3.9** shows a map of max-min number of species. This map is normalized by average values for each grid cell as presented in **Figure 3.10**. Although the average map looks somewhat like a smoothed version of the EMAP richness map (**Figure 3.5**), it was constructed by averaging richness values from all 7 overlapping 1X's 7-fold composition polygons for each EMAP grid cell (except EMAP edge hexagons with insufficient hexagons to construct complete 1X's 7-fold composition grid cells).

The final normalized max-min map is presented as **Figure 3.11**. Although grid cells of different richness are distributed throughout the state, some clustering of values seems to occur. This implies that different areas of the state are contributing variations to the summary CV for the scale of mapping referenced in **Table 3.1**. The change in scale results in no overall change in variation, although localized changes in variation occur throughout the entire state.

The richness map results allow us to gain insight into factors that may affect prioritization mapping. There is no significant change in CV from the EMAP scale to composition 1. It is possible, therefore, to perform prioritization analysis on two species lists resulting from a change in scale with no statistical differences in CV of richness maps. Results of prioritization of the 1X's 7-fold and 2X's 7-fold composition are presented in this chapter's **Appendix** as **Table 3.2 and 3.3**. These results can be compared with the original prioritization analysis for the EMAP grid presented as **Table 2.2** in the **Appendix** of **Chapter 2**.

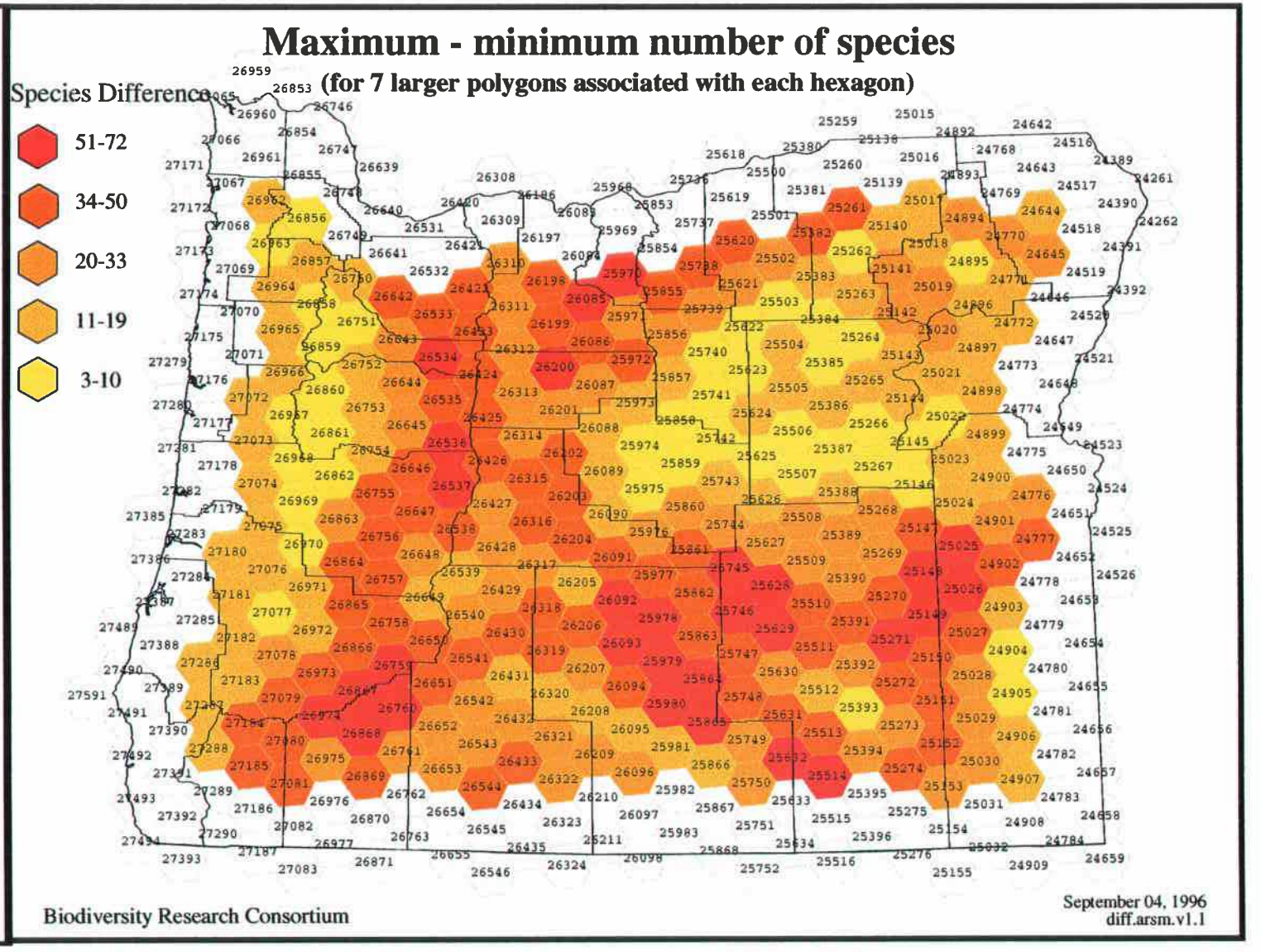

Figure 3.9: Maximum minus minimum richness values (See **Figure 3.4**).

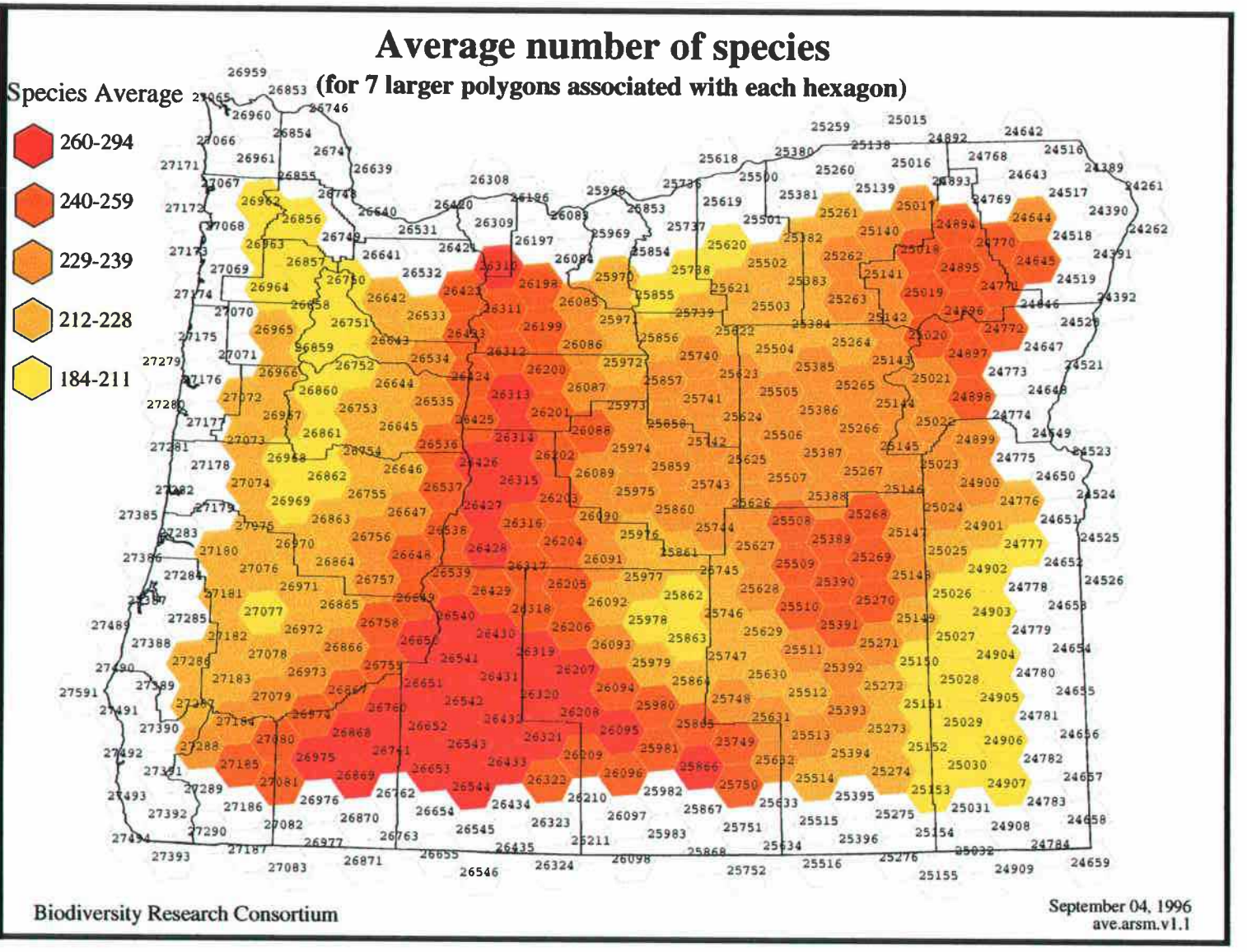

Figure 3.10: Average richness values (See **Figure 3.4**).

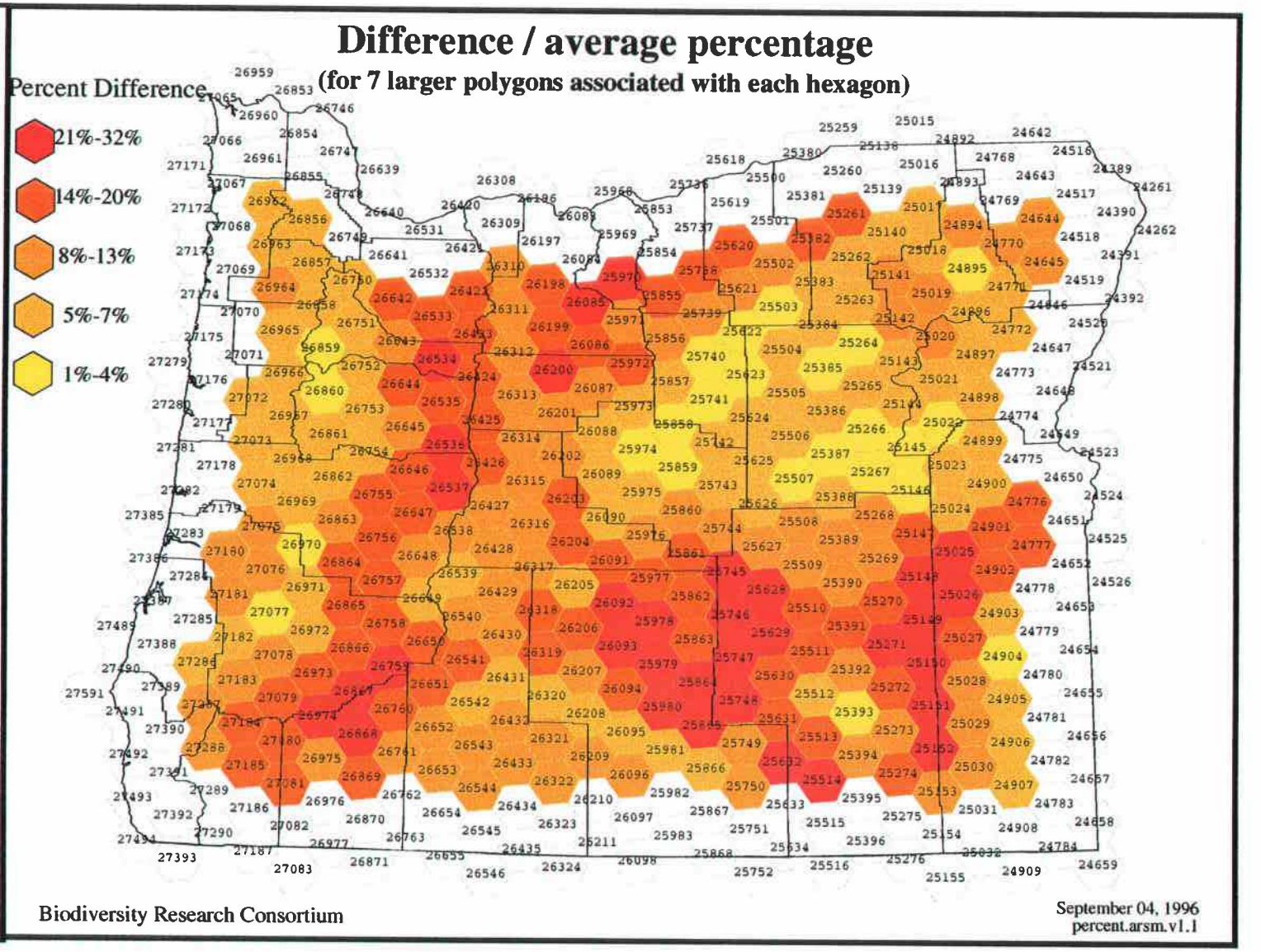

Figure 3.11: Normalized max-min richness values [(Max-Min)/Ave.](See **Figure 3.4**).

Prioritization based on the EMAP grid uses 441 non-overlapping hexagons and 422 total species of terrestrial vertebrates. Five hexagons are able to cover 387 species (91.71%). **Figure 2.9** shows the results of this prioritization. A total of 23 hexagons would be necessary to cover all 422 species (100%).

Prioritization based on the first composition grids uses 352 overlapping polygons for the same 422 species. This method allows two or more prioritization polygons at the same scale to overlap. Five polygons are now able to cover 396 species (93.84%). 13 total polygons are now needed for full coverage. Such changes are not surprising as now each grid cell has seven times the area of an EMAP grid cell. **Figure 3.12** shows the prioritization with five polygons. Two prioritization polygons selected on this map overlap the two magenta polygonal grid cells in the west-central portion of the state. Although the idea of a family of geographically aggregated grid cells has previously been recognized (see Csuti and Kiester, 1996), this analysis allows for overlapping aggregations.

Location of prioritization hexagons can also be compared between the two scales. Most prioritization polygons chosen at a larger scale do not overlap EMAP prioritization hexagons. Of the five grid cells selected in each map, only the yellow polygon in northeastern Oregon selected at a larger scale in **Figure 3.12** overlaps a selected EMAP prioritization hexagon in **Figure 2.9**. In addition, the green polygon is one hexagon away from a EMAP prioritization hexagon, and the red polygon two hexagons away.

Prioritization based on the second composition grids uses 167 overlapping polygons for the same 422 species. Five polygons cover 421 species, with one more polygon necessary for 100% coverage. Prioritization using five hexagons now overlaps three of the hexagons from the EMAP scale and portions of all five of the polygons from the fifth pri-

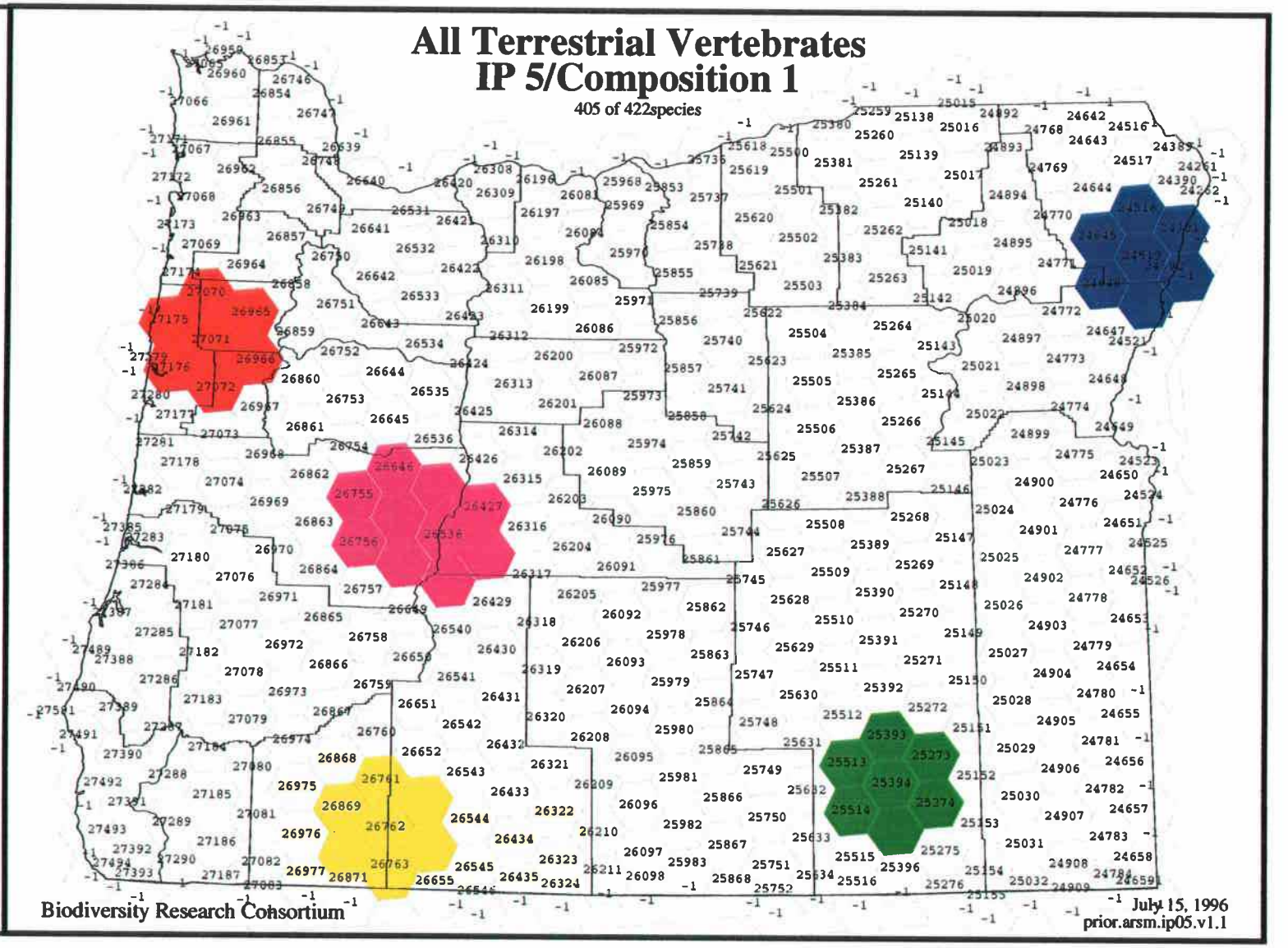

Figure 3.12: Fifth cardinality of prioritization at seven times EMAP scale.

oritization at 1X's 7-fold composition. This increase in overlapping prioritization hexagons is probably not significant, as a majority of the state's area is covered by prioritization grid cells using the 2X's 7-fold composition. (i. e. of the original 441 EMAP hexagons, approximately 245 hexagons [49 EMAP hexagons x five 2X's seven-fold composition prioritization polygons] will be used at this scale).

DISCUSSION

The relationship of prioritization to richness mapping is not straightforward. In the above example, analysis at the EMAP and 1X's seven-fold composition scale is compared. Both scales result in richness maps with statistically similar measures of CV. Localized differences in the new composition 1 richness maps are not the result of localized variations in one particular geographic area. The statistical inference is that there is little difference between the amount of information on richness variation contained in richness maps at these two scales.

Significant differences, however, exist in the location of prioritization grid cells at the two scales. Two key factors could be influencing the difference in these maps. The most important factor is undoubtedly the difference in the type of value being mapped. Species richness maps sum species present in each grid cell, but do not account for differences in the actual species lists between grid cells. Mapping richness at different scales and mapping prioritization at a single scale are both set theoretical processes. Prioritization analysis is data dependent, and can only be mapped by looking at many combinations of species lists at a single scale.

Another factor may be the extent used to study changes in grid cell size. Although this study varies grid cell size, the mapping extent is always the state of Oregon. This extent could contain areas in which the species list is more homogeneous than that for the entire state. One example of this may be ecoregions. Identifying mapping scales which minimize variation within sub-areas and maximize variation between sub-areas could help to relate richness and prioritization mapping.

CONCLUSIONS

Multi-scale biodiversity analysis identifies proper scales for mapping species richness. An optimal scale would maximize variation and grid cell size while minimizing the number of grid cells required for mapping. It cannot, however, be used to determine proper scales for prioritization analysis.

The grid cell size for mapping richness of terrestrial vertebrates in Oregon could be increased by a factor of seven over the EMAP grid cell without losing any statistically significant information on species variation. Local changes in variation from the EMAP grid to one seven times as large are not influenced by any single area within the mapping extent. If the grid cell size is increased again by a factor of seven, variations previously present in the map would be lost, as measured by the coefficient of variation.

The proper scale for prioritization analysis cannot be determined with this method. It may be necessary to look at results of prioritization mapping at smaller scales, or mapping with less change in grid cell size between scales, to find geographically consistent prioritization results. Richness maps based on more homogenous extents may also help to relate proper scale and extent of species richness mapping to prioritization mapping.

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Appendix

Results of Multi-Scale Seven-Fold Prioritization Analysis

Table 3.2: 1X's 7-Fold Composition Prioritization Statistics

Oregon All Vertebrates Prioritization v1.1
352 overlapping polygons and 422 total species

# of hexes/path	# of paths	# of hexes	# species covered	% species covered
1	1	1	307	72.75
2	4	5	356	84.36
3	2	4	381	90.28
4	1	4	396	93.84
5	2	6	405	95.97
6	8	13	410	97.16
7	42	27	413	97.87
8	22	24	416	98.58
9	51	32	418	99.05
10	50	32	419	99.29
11	50	55	420	99.53
12	50	72	421	99.76
13	50	66	422	100.00

Biodiversity Resource Consortium July 19, 1996

Table 3.3: 2X's 7-Fold Composition Prioritization Statistics

Oregon All Vertebrates Prioritization v1.1
167 overlapping polygons and 422 total species

# of hexes/path	# of paths	# of polygons	# species covered	% species covered
1	1	1	357	84.60
2	2	3	401	95.02
3	5	7	413	97.87
4	54	21	418	99.05
5	2	6	421	99.76
6	53	25	422	100.00

Biodiversity Resource Consortium October 24, 1996

CHAPTER 4

Scale Analysis Using Three-Fold Compositions and Decompositions of the EMAP Grid

Patrick J. Kennelly

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ABSTRACT

The effect of scale is an important concern in mapping of biodiversity. Because biodiversity analysis involves combinatorial processes, determining the proper scale is data dependent and cannot be predicted from the initial data values and their distribution.

This study maps species richness at seven different compositions and decompositions of the Environmental Protection Agency's EMAP grid, from a scale 1/81 to nine times (9X's) the size of the EMAP grid. Analysis of statistics indicates no relatively small decrease in coefficient of variation (CV), indicating no optimal scale for richness mapping.

Prioritization analysis was performed on the new combinations of species lists for five grid cell sizes ranging from a scale of 1/9 to 9X's the size of the EMAP grid. Efficiency of prioritization and map patterns of prioritization areas indicates that of these five scales, the grid cells 1/3 the size of the EMAP hexagons are relatively the best for this analysis.

This study uses a second generation of species range maps as the basis for analysis. New species range maps are based on habitat maps interpreted from Landsat MSS imagery. This differs from previous studies which used species range maps, where species were assigned to EMAP grid cells based on sitings, samples and expert opinions. Comparisons can be made between the two biodiversity analyses at the EMAP scale. CV values have increased from 10.45% from earlier richness maps to 13.93% for the new richness maps.This change of nearly 3.5 percentage points represents an increase in variations in richness values of nearly 33%. The efficiency of prioritization is also enhanced. Prioritization analysis based on the new data allows coverage of the same number of total spe-

cies with less than 60% of the grid cells required initially. Both of these improvements indicate that new species range maps allow for the preservation of more information based on an increase in overall variability of species richness values and presence of unique species in species grid cell lists. This can be attributed to finer resolution sampling capturing additional information.

INTRODUCTION

The purpose of this study is to determine the proper grid cell size for biodiversity mapping in the state of Oregon. Biodiversity mapping in this study includes both species richness mapping and prioritization mapping. The study presented as Chapter 3 of this dissertation maps species richness and prioritization hexagons at three scales for analysis. This study will expand upon and contrast with the research reported in this previous chapter. It will expand upon this study by mapping biodiversity at seven as opposed to three scales, including scales of finer resolution not possible in the previous study.

The most important contrast between the previous research and this research is the source of data used in the analysis. Seven fold compositions used species range maps with the EMAP hexagonal grid as the minimum mapping unit (MMU). These grid cells were populated with confirmed and probable species determined from samples, sitings, and expert opinions. This method of smoothing species ranges to a regular grid was used in the initial stage of GAP analysis Oregon and other states (e.g. Kiester et. al., 1996)

This analysis uses species range maps based on interpretation of Landsat Multi-Spectral Scanner (MSS) imagery. The resulting natural vegetation polygons are then clustered into wildlife habitats, overlain with the original hexagon-based range maps, and

populated with species based on a Wildlife Habitat Relations (WHR) matrix. The resulting species range maps have a much smaller MMU which is equal to the smallest polygon interpreted from satellite imagery.

Analysis can now be expanded to use smaller grid cells for biodiversity mapping. Because the MMU in this study is much smaller than the EMAP hexagonal grid cell, biodiversity can be mapped at scales smaller than the EMAP grid cell. Some hexagonal compositions and decompositions also use fractions of EMAP grid cells (See **Figure 1.1**).The previous study was only able to compose the EMAP grid by a factor of 7, because a 7-fold composition is the only composition that uses an entire hexagon.

With species assigned to habitat polygons in this study, any grid made from the triangular building blocks derived from the smallest hexagonal grid can be used to construct other hexagonal grids. The two other possibilities for composing and decomposing a hexagonal grid are three and four fold compositions (**Figure 1.1**). Three fold was selected in order to minimize the scale change between biodiversity maps at successive steps.

Constructing richness maps at different scales is a combinatorial process. Grid cells at each scale will have a unique species list. These results cannot be predicted by traditional geostatistical techniques and are data dependent. Issues associated with such procedures are addressed by Stoms (1994) and expanded upon in **Chapter 3** of this dissertation.

Constructing prioritization maps at any given scale is also a combinatorial procedure. Prioritization mapping selects a given number of grid cells which maximize the number of different species present, an example of a maximum covering location problem (MCLP) (Church et. al., 1994). This analysis involves comparing species lists of multiple

grid cells. As grid cells and their associated species lists change with scale, new combinations may give geographically dissimilar results.

DATA

The species range maps used in this study are a second generation of maps developed for the state of Oregon. The maps used in this study are approximately equivalent to those in the *Atlas of Oregon Wildlife* (Csuti et. al., 1997).

Construction of these range maps began with LANDSAT MSS imagery of Oregon. Kagan and Caicco(1992) visually interpreted boundaries of vegetation cover types using MSS false color infrared positive prints at a scale of 1:250,000. Vegetation polygons were labeled with the assistance of a variety of ancillary maps. The MMU for this study was polygons of 133 hectares(ha.). A total of 6,916 vegetation polygons were mapped in vector format, with the average polygon size being 3,296 ha. 130 different actual vegetation types are represented in these polygons.

The actual vegetation map was then converted into a wildlife habitat map using a wildlife habitat relation (WHR) developed by O'Neil et. al. (1995). This WHR combined four existing WHR matrices and supplemented these data with "additional information from past biological surveys, museum collections, and published literature"(O'Neil et. al., 1995, p. 1484). This WHR matrix was used to assign 420 breeding species of terrestrial vertebrates to appropriate vegetation types.

Wildlife habitats were then generalized into 30 classes. Multivariable statistical analysis was used to find "consistent patterns of wildlife use within groups of vegetation types suggest[ing] that wildlife species perceive these groups as similar habitats"(O'Neil

et. al., 1995, p. 1484). A matrix of vegetation types and species allowed calculation of similarity for each element. This Jaccard coefficient "minimizes the within-cluster variance relative to the between-cluster variance" (O'Neil et. al., 1995, p. 1484).

A species may be present in a given habitat in one portion of the state, but not in the same habitat in another part of the state. The EMAP hexagonal grid was thus intersected with the wildlife habitat coverage. The resulting coverage was composed of over 15,000 polygons. Object oriented programming written by Kevin Sahr created lists of polygons for each species, based on the presence of the polygon within the species range hexagonal outline and presence of the appropriate habitats (Csuti et. al., 1997).

Some polygons selected were portions of larger parent polygons that extended outside of the range based on hexagonal outlines. A species range was extended into adjacent non-occurrence hexagons if the majority of the original parent polygon lay in an occurrence hexagon. This method of refining species boundaries may be an important factor in contributing to the increased variations in species richness and more efficient prioritization discussed later.

All sampling grids used in this study are based on a composition or decomposition of a portion of the Environmental Protection Agency EMAP hexagonal grid. The entire EMAP grid provides complete coverage for the contiguous United States. This Lambert azimuthal equal area map projection is composed of grid cells approximately 640 km^2. This size was selected as a "suitable compromise between the desired spatial resolution of sampling and the projected available financial resources" (White et. al., 1992, p. 18). Only one set of grid cells used in this study matches the EMAP grid. All others consist of

smaller, larger or offset hexagons resulting from geometric constructions of elements making up the EMAP grid and discussed in the methodology section of this paper.

METHODOLOGY

Species richness maps are created by summing the total number of species in each grid cell. Although these maps provide spatial information on what areas are rich or poor in number of species, they are not suited to answer important questions in conservation biology (Williams et. al., 1996, Prendergast et. al., 1993). Prioritization maps look to maximize the number of unique species in a given number of grid cells, an example of a maximum covering location problem (MCLP) (Church et. al., 1994). Analysis in Oregon uses a linear programming algorithm, which ensures "optimal solutions to the reserve selection algorithm" (Church et. al., 1994, p.83).

A change in the size of the grid cell will result in a new list of species associated with each new grid cell sample. Stoms (1994) recognizes that agglomerating sampling units and species contained within is not a classical spatial statistics problem that can be addressed by such methods as calculating seminarians; "aggregation is not a simple numerical averaging over different sampling sizes, but is a logical union of sets (species lists)" (p. 347). An example derived from Stom's (1994) explanation is presented as **Figure 3.1** in the previous chapter.

This study looks at biodiversity mapping on the EMAP hexagonal grid. Three geometries for the composition and decomposition of these grid cells are presented in **Figure 1.1**. All three of these geometries will preserve the important attributes found in a

hexagonal grid, such as grid cells filling 2-D space and all adjacent grid cells being equi-distant.

In the previous study, the MMU for species range maps was based on the EMAP grid cells. This limited the geometric constructions possible in two important ways. First, no decomposition was possible without further assumptions, as the MMU was defined by the EMAP grid cells. Also, 3-fold and 4-fold compositions would require further assumptions, as they involve taking fractions of surrounding hexagons. A 3-fold composition takes a central hexagon and 1/3 of all adjacent hexagons, while a 4-fold composition takes a central hexagon and 1/2 of all adjacent hexagons(See **Figure 1.1**).

In this study, the species range maps are not tied directly to the EMAP hexagonal grid. The wildlife habitat map must be overlain with a hexagonal grid at some point to assign wildlife habitat polygons to an equal area grid cell, but until this is done, any composition or decomposition of the EMAP hexagonal grid is possible. A three fold composition was selected to provide information on grid cells with the finest variations in size between scales of mapping. Each composition will result in hexagonal grid cells three times the area of the original hexagon.

This study was designed so that only one computationally intensive overlay of the wildlife habitat coverage with a base grid for building hexagons was necessary. To do this, the smallest elements that could be used as building blocks for all hexagonal grids were constructed. First, a hexagonal grid with grid cells 1/81 the size of the EMAP grid was obtained from Mike McDowell at the EPA. This would be equivalent to a 4 times 3 -fold decomposition (4X's 3-fold decomposition), and each grid cell would be approximately 8 km^2. Each of these hexagons has a unique address based on the EMAP code, plus a suffix

which uniquely identifies its location at this scale (Spence and White, 1992). Almost 33,000 of these hexagons were necessary to cover the state of Oregon.

This study used object oriented (C++) programming to divide each of these hexagons into 12 triangles. Each triangle was addressed using the number of the hexagon and the location of the triangle within the hexagon. It was necessary to divide the hexagon into 12 triangles, as 3-fold compositions rotate resulting hexagonal grid cells by 30 degrees, thus requiring different triangles at different compositions. The resulting triangular grid was composed of almost 400,000 triangles, each of approximately 0.67 km^2(67 ha.). The size of an building block for a given hexagonal grid is four of these triangles (i.e. 1/3 of a hexagon) with an area approximately 267 ha. This size comes close to the 133 ha. MMU used in the construction of the Oregon Actual Vegetation map (Kagan and Caicco, 1992). It should be noted, however, that the MMU for the habitat range maps is a function of not only the habitat maps, but also the original EMAP species range maps which have a MMU of 640 km^2.

This triangular grid was then intersected with the Wildlife Habitat map (O'Neil et. al., 1995) using ESRI Arc/Info software. The resulting coverage consisted of approximately 800,000 polygons. Each polygon identified a triangular grid cell and a polygon code from the wildlife habitat map. Each species had a list of polygons from the wildlife habitat map with which it was associated. An object oriented program was written to take these data and create a matrix file. This matrix file has approximately 400,000 rows representing each unique triangular grid cell and 424 columns representing the 420 species comprising the WHR matrix, and four additional species included in *The Atlas of Oregon Wildlife* (Csuti et. al., 1997).

The first scale at which a species richness map can be constructed is the 4X's 3-fold decomposition of the EMAP grid. The nature of the triangular grid will allow only one hexagonal grid to be constructed at this scale, a reconstruction of the decomposed grid from the EPA. The next scale at which species richness maps are constructed is 3X's 3-fold decomposition, with grid cells approximately 24 km^2. By using any three adjacent hexagons at the 4X's 3-fold decomposition scale as a center, it is possible to construct three unique and offset richness maps at this scale (See 7-fold example in **Figure 1.2**). Any other geometric constructions from the triangular grid at this scale would be redundant. Three maps are constructed at this scale, and statistics associated with all grid cells from the three maps are summarized into one set of numbers.

Each subsequent scale allows for the construction of three times as many unique richness maps. At the EMAP scale, for example, 81 (i.e. 3^4) possible maps could be constructed from the triangular grid. This study does not construct all possible richness maps, but rather three maps at all scales greater than 4X's 3-fold decomposition. This should be sufficient, as each map is an exhaustive sample (save edge effects) of the richness data. More grid cell values from the same data should not have a statistical impact on results.

The maximum grid cell size composed for species richness is approximately 5,760 km^2, or 2X's 3-fold composition of the EMAP grid. This maximum size avoids grid cells that approach the extent of the study area. If the next composition (i.e. 3X's 3-fold composition) were constructed, less than 10 grid cells of this size would fit on each map within the boundary of Oregon.

Species richness maps in this study divide the range of species richness values into classes for color map displays. Five classes are defined based on the statistical distribution

of species richness values. This study uses the combined statistics discussed above for dividing the distribution into classes. At any scale above 4X's 3-fold decomposition, therefore, three maps will exist, with each having classes based on grid cell values from all three maps.

Statistical measures can be made from all richness grid cells at each scale. The previous chapter argued for using coefficient of variance (CV) as a metric to compare maps of different scales. CV is defined as the sample standard deviation expressed as a percentage of the sample mean (Steel and Torrie, p. 27). It can provide a more stable measure of variation between scales of combinatorial maps, where variance and average are both changing. This is the same measure initially proposed by Stoms (1994) in his comparison of multi-scale richness maps.

Prioritization analysis uses a matrix of grid cells and species to determine which grid cells in combination will represent the most species for a given number of grid cells. This study uses species lists combined from all maps at a given scale.

This method of combining all data at a scale permits one comprehensive prioritization analysis to be done for each composition or decomposition level. Combining all species lists at one scale also allows for the overlap of grid cells in prioritization analysis. The implication of overlapping grid cells to families of hexagons in prioritization areas will be discussed later in this paper.

RESULTS

Richness Mapping

Statistics associated with the richness maps at seven different scales are presented in **Table 4.1.** Comp 0X's 3-fold is the EMAP scale, with decomposition grid cells decreasing in size to the left of the EMAP size and composition grid cells increasing in size to the right. The decomp 4X's 3 scale is the finest scale possible from the triangular grid. It was possible to construct only one geometry, resulting in a map with 32,899 hexagons. The richness map for this construction is presented as **Figure 4.1.**

The decomp 3X's 3-fold statistics represent the 3-fold decompositions of the EMAP grid cells. One of the three richness maps for this scale is presented as **Figure 4.2.** The statistics are derived from three unique maps generated at this scale. The number of hexagons reported (32,071) is a sum of all hexagons from the three maps (10,687 + 10,692 + 10,692). Each of these numbers is smaller than one-third of the original number of hexagons due to less edge hexagons lying completely within the area mapped for wildlife habitats (Compare **Figure 4.1** with **Figure 4.2**). Although the minimum number of species in a grid cell stays the same as in the finer grid cells, the maximum and average numbers increase. Variance, standard deviation and CV all decrease. The decrease in CV is the largest between any two consecutive scales, as the value drops by more than 7%.

Statistics for maps associated with larger grid cells show predictable decreases in number of hexagons and increases in minimum, maximum and average number of species in grid cells. Variance and standard deviation continue to decrease at each step.The CV values also decrease at each step, with larger decreases occurring between smaller grid cell scales and smaller decreases occurring as grid cells increase in size. One map of the

Table 4.1: Richness Map Statistics for 3-Fold EMAP Compositions

	Deomp 4X's 3 fold	Decomp 3X's 3 fold	Decomp 2X's 3 fold	Decomp 1X's 3 fold	**EMAP** 0X's 3 fold	Comp 1X's 3 fold	Comp 2X's 3 fold
Number of Hexagons	32,899	32,071	10,504	3,377	1,067	321	89
Min	2	2	37	99	117	174	196
Max	275	281	281	288	298	312	329
Mean	160.97	175.50	187.74	202.51	218.16	236.75	264.90
Variance	1946.66	1270.25	1105.58	988.44	923.12	835.42	821.25
Std Dev	44.12	35.64	33.25	31.44	30.38	28.90	28.66
Coeff of Variation	**27.40%**	**20.31%**	**17.72%**	**15.52%**	**13.93%**	**12.21%**	**10.82%**

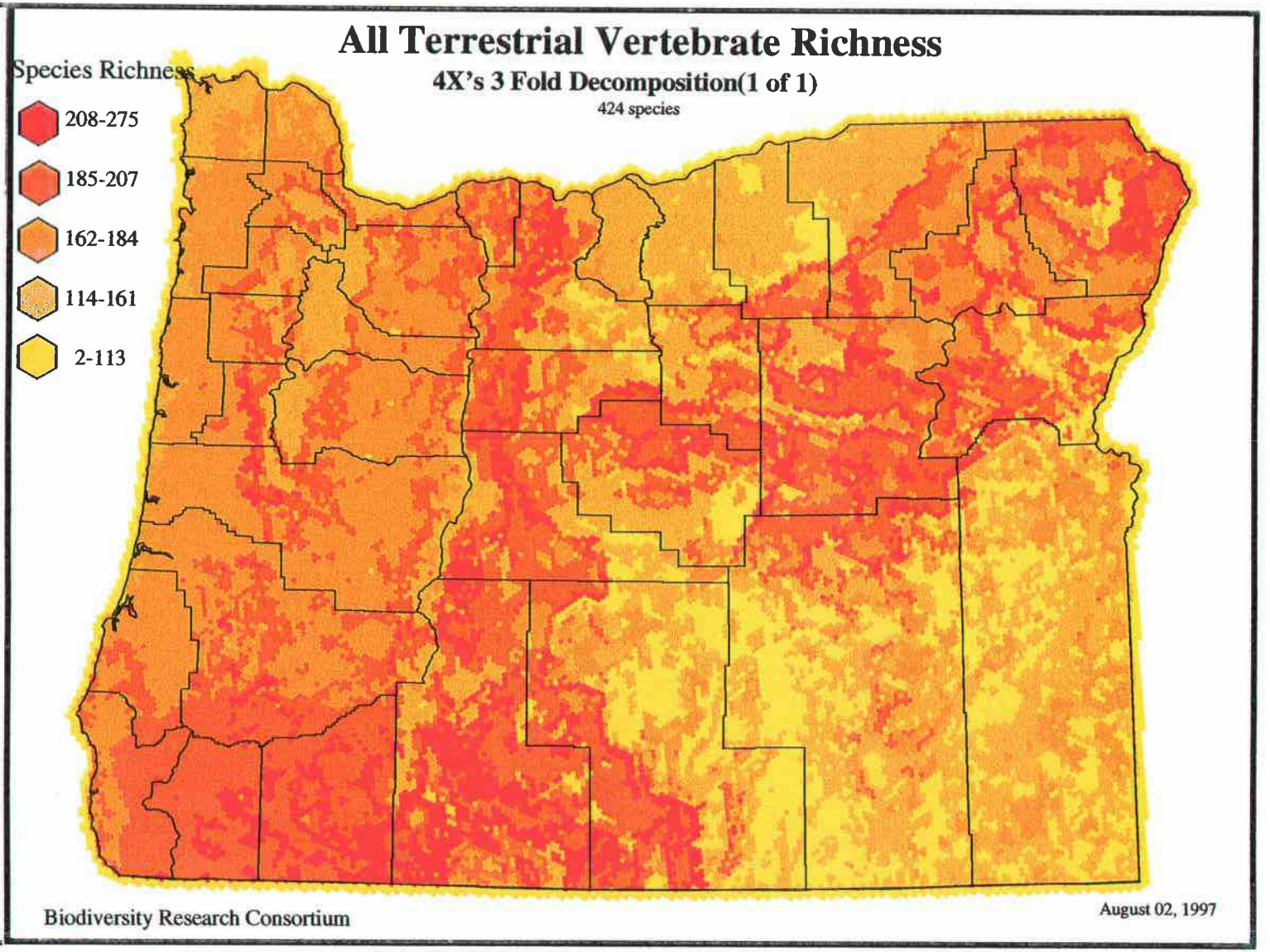

Figure 4.1: Richness map using 4 times a 3-fold decomposition of the EMAP grid.

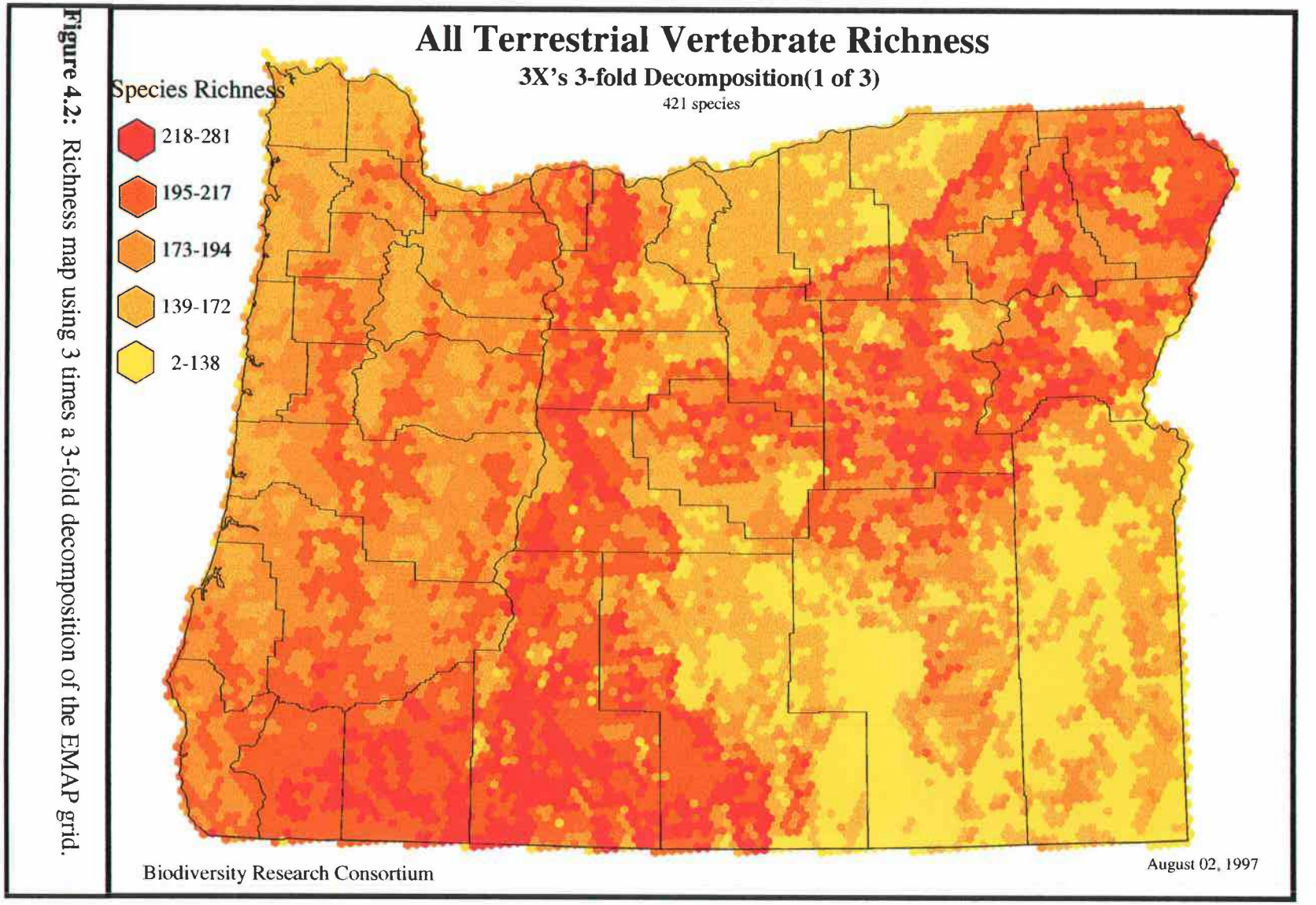

Figure 4.2: Richness map using 3 times a 3-fold decomposition of the EMAP grid.

2X's 3-fold decomposition, 1X's 3-fold decomposition, 0X's 3-fold composition, 1 X's 3-fold composition and 2X's 3-fold composition are included as **Figure 4.3**, **Figure 4.4**, **Figure 4.5**, **Figure 4.6**, and **Figure 4.7** respectively.

Figure 4.5 is a recreation of the EMAP grid which covers the state of Oregon. Labels on these grid cells are the EMAP hexagonal addresses, with a "01" suffix added to indicate which of the 81 smaller hexagons making up that EMAP hexagon was used as the center for the geometric construction. The other two maps at this scale are offset from the EMAP grid. This map, however, differs from the EMAP scale richness map presented in the previous chapter(Compare with **Figure 3.5**).

This EMAP scale richness map is different from the EMAP scale richness map presented in the previous chapter in that presence of species is now derived from a second generation of species range maps. Ranges are no longer based only on sitings and expert opinion mapped to a hexagonal grid. Wildlife habitat maps are now constructed from vegetation maps and a WHR matrix in conjunction with EMAP grid based range maps, as discussed in the methods section of this chapter. Thus, although the MMU of the Oregon Actual Vegetation map may be130 ha., the MMU of the wildlife range maps is more difficult to access.

This difference also results in the two maps having different extents. **Figure 4.5** includes EMAP hexagons whose entire area covers the wildlife habitat map used in this analysis. This is different than the previous richness map (**Figure 3.5**), which included all EMAP hexagons within or adjacent to the state of Oregon for which species presence or absence was determined. This map included several grid cells which would have areas outside of the wildlife habitat map (approximately equal to the boundary of Oregon). The

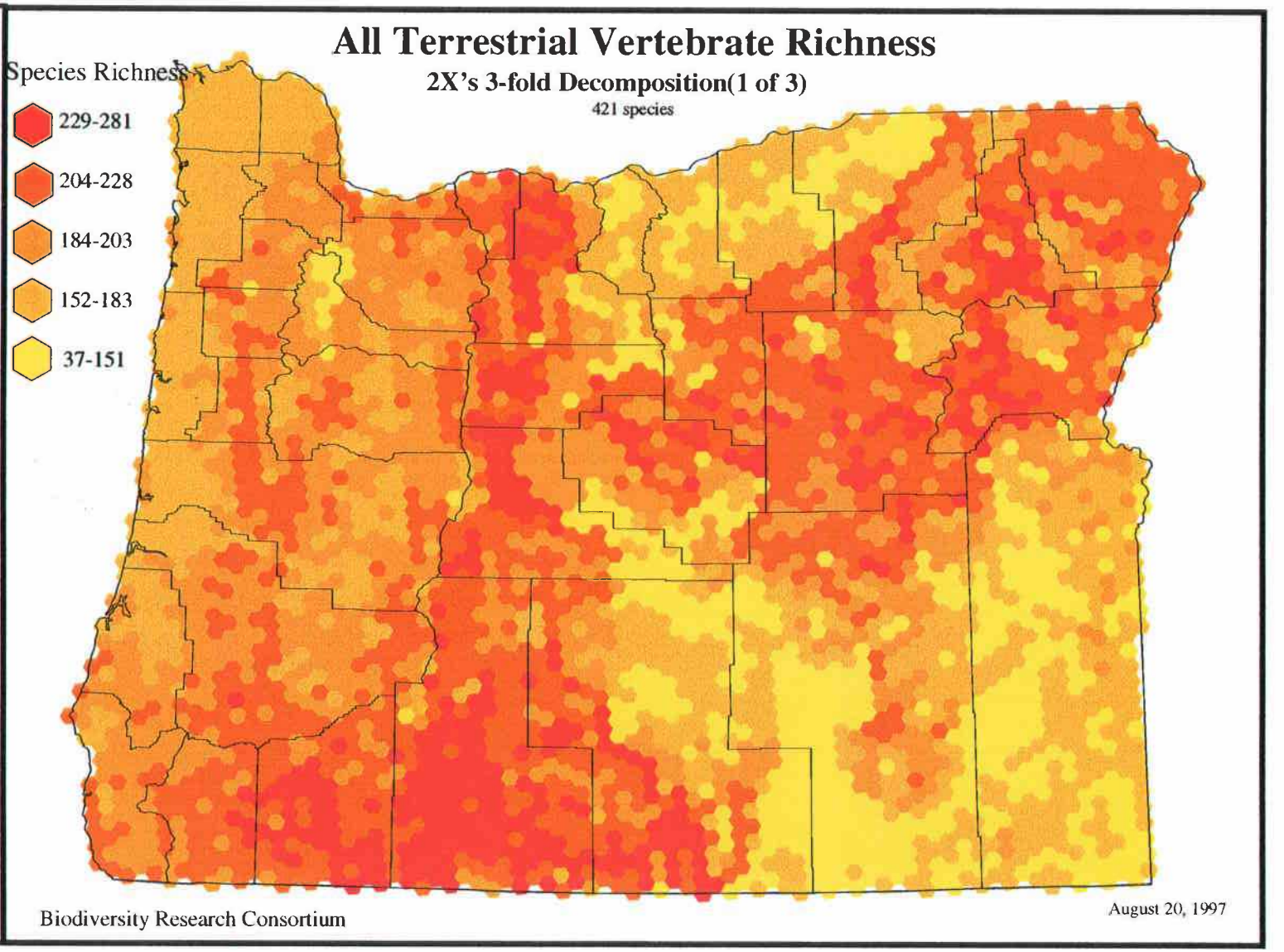

Figure 4.3: Richness map using 2 times a 3-fold decomposition of the EMAP grid.

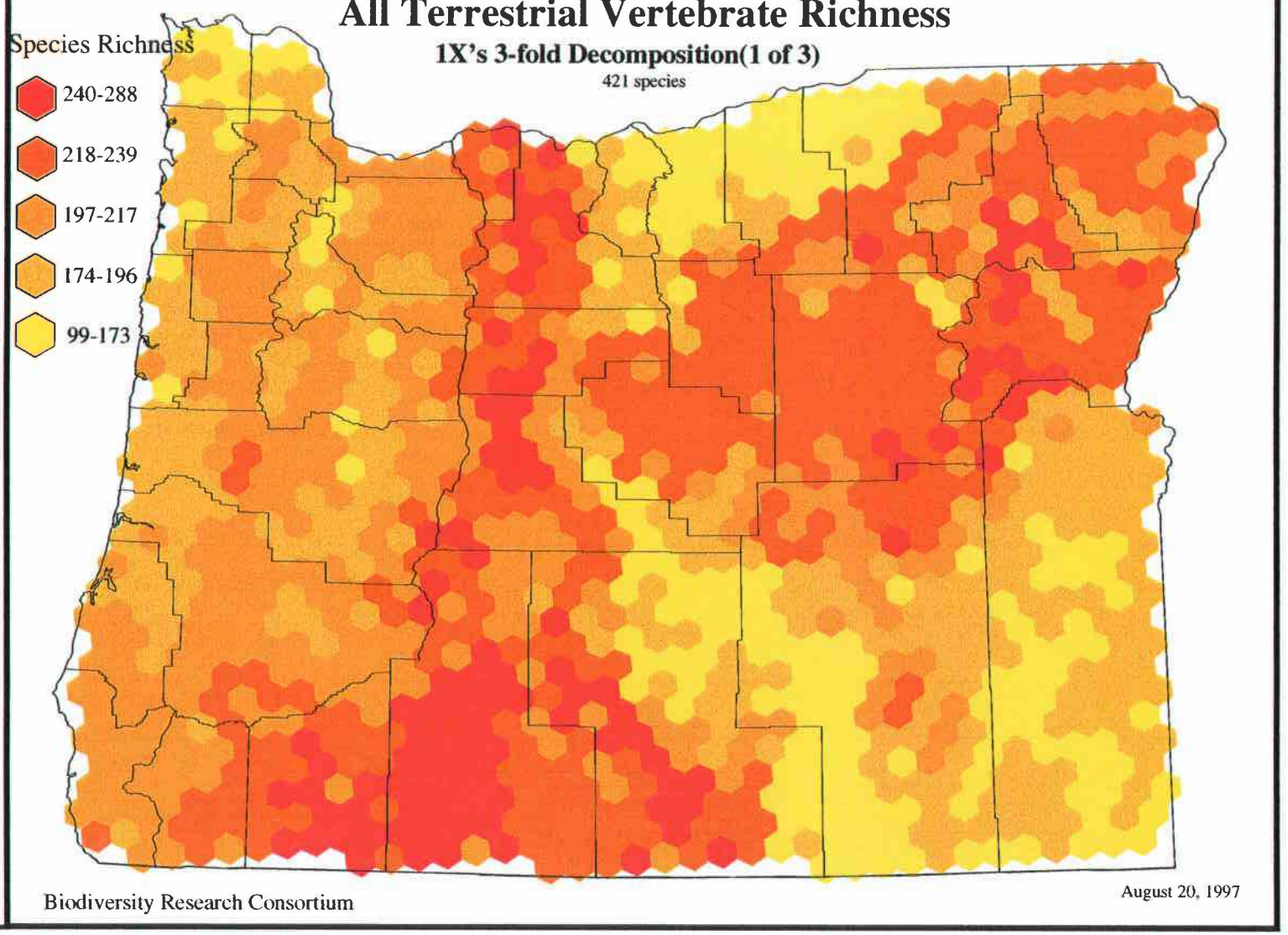

Figure 4.4: Richness map using 1 times a 3-fold decomposition of the EMAP grid.

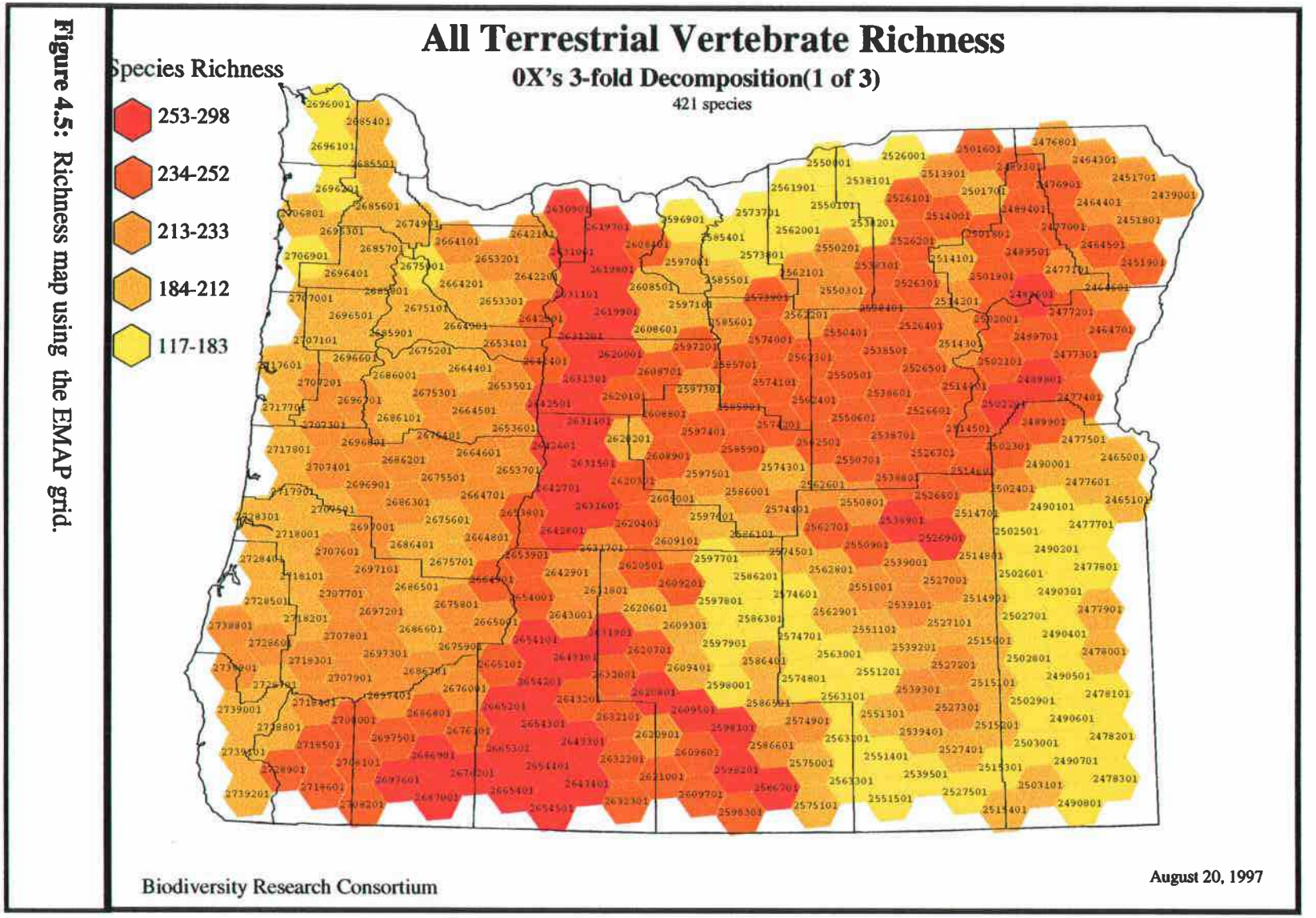

Figure 4.5: Richness map using the EMAP grid.

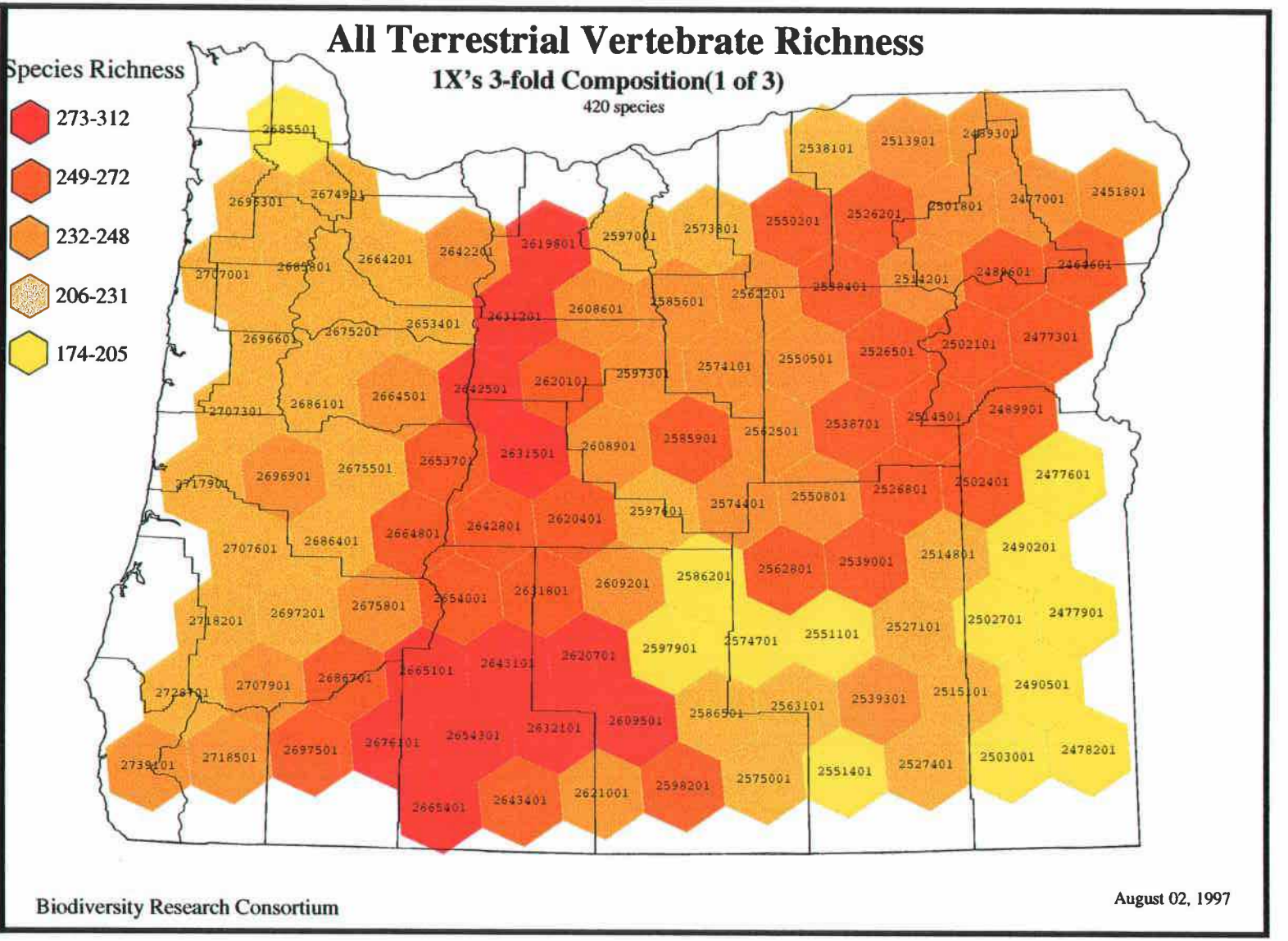

Figure 4.6: Richness map using 1 times a 3-fold composition of the EMAP grid.

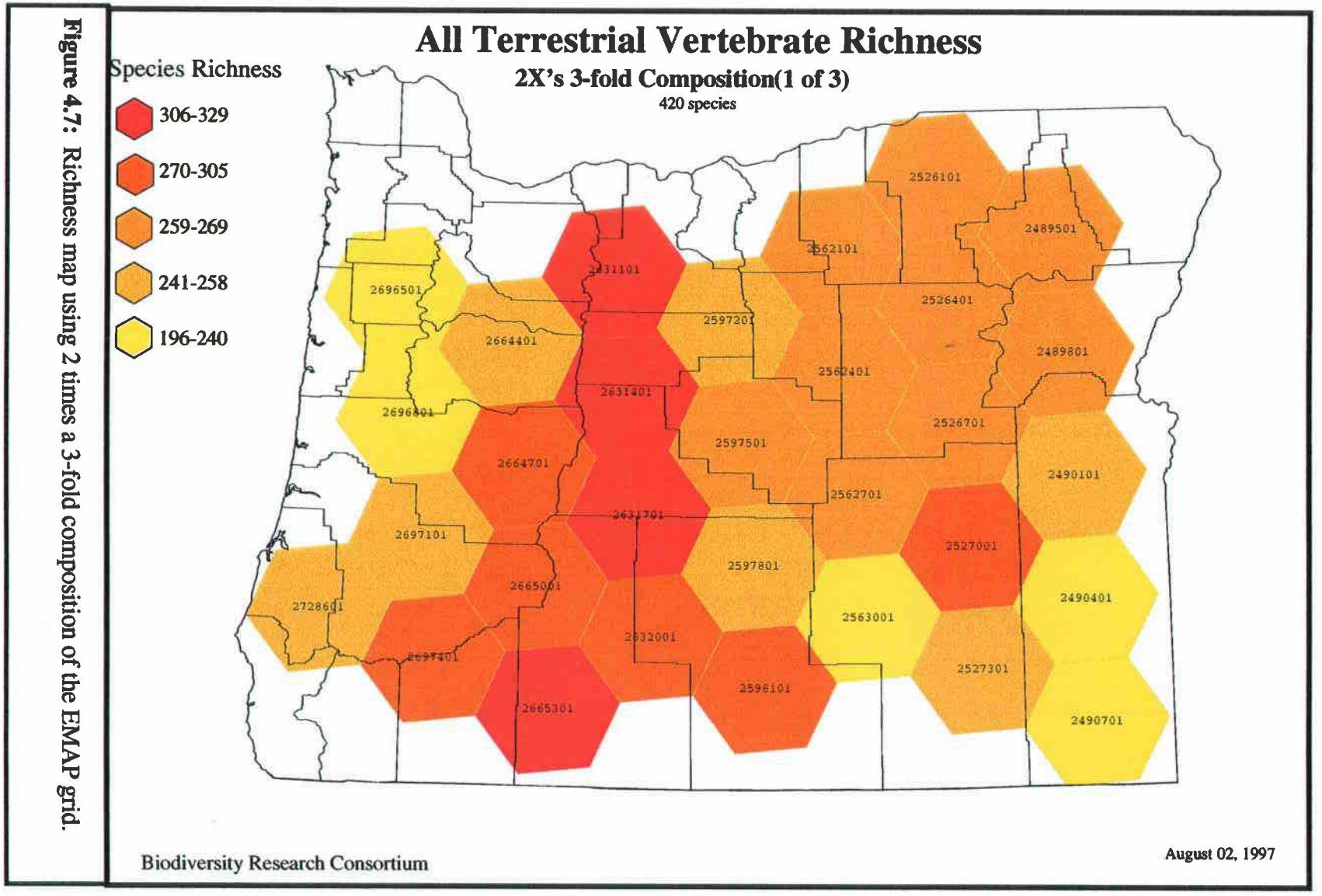

Figure 4.7: Richness map using 2 times a 3-fold composition of the EMAP grid.

result is a decrease in total richness hexagons from 441 in the original map in **Figure 3.5** to 352 in **Figure 4.5**.

Prioritization Analysis

Prioritization analysis was completed on five scales of maps from 2X's 3-fold decomposition to 2X's 3-fold composition. Summaries of species coverages at each cardinality of these analyses is included as **Table 4.2-Table 4.6** in this chapter's **Appendix**. The number of hexagons per path is called the cardinality of the analysis. One important observation from these tables is that all 424 species are not covered in analysis at any of these scales. This is due to the presence of species with ranges near state boundaries not being sampled by any hexagons at larger scales. The 2X's 3-fold decomposition, the 1X's 3-fold decomposition, and the 0X's 3-fold composition all sample a maximum of 421 species. The 1X's 3-fold composition and 2X's 3-fold compositions sample a maximum of 420 species as areas further inboard of state boundaries are no longer represented.

Because different numbers of species are covered in these prioritization analysis, the cardinality necessary to cover 420 species will be referred to as "full coverage" to compare prioritization at different scales. 420 species are covered at a cardinality of 14, 12, 12, 11, and 10 for scales 2X's 3-fold decomposition, 1X's 3-fold decomposition, 0X's 3-fold decomposition, 1X's 3-fold decomposition and 2X's 3-fold decomposition, respectively. The significance of two scales covering the same number of species at a cardinality of 12, even with one analysis using one-third the area will be discussed in the next section.

A benchmark for prioritization analysis comparisons in Oregon is the coverage achieved at cardinality 5. Five areas are consistently able to cover over 90% of total spe-

cies. This is consistent with prioritization analysis being used as a coarse filter to guide conservation efforts(See Csuti, 1994 and Csuti and Kiester, 1996). The numbers of species covered at cardinality 5 are 395, 397, 399, 404, and 412 species for scales 2X's 3-fold decomposition, 1X's 3-fold decomposition, 0X's 3-fold decomposition, 1X's 3-fold composition and 2X's 3-fold composition respectively. These numbers reflect a cost associated with the benefit of mapping smaller areas with a finer grid. The cost is the loss of species covered, which is eight species in moving from the 2X's 3-fold decomposition scale to the 1X's 3-fold decomposition scale, five species in moving from the 1X's 3-fold decomposition scale to the 0X's 3-fold decomposition scale, and two species in moving from both the 0X's 3-fold decomposition scale to the 1X's 3-fold decomposition scale and from the 1X's 3-fold decomposition scale to the 2X's 3-fold decomposition scale. The significance of these steps will also be discussed in the next section.

The cardinality 5 prioritization map for the coarsest grid (2X's 3-fold composition) is presented as **Figure 4.8**. 98.1% of all species with ranges within this grid are represented within the selected hexagons. The three areas to the west of the state are represented by a single hexagon. The two areas in the east of the state are defined by multiple hexagons. These hexagons overlap, with each of these families of hexagons defining a large, continuous area.

The cardinality 5 prioritization map for the 1X's 3-fold composition is presented as **Figure 4.9.** This analysis uses only one-third the area of the previous analysis, and is able to cover 96.2% of the species. All five of these new areas are contained partially or completely within the areas selected using larger grid cells in **Figure 4.8**. Only one area in the northeast of the state is now comprised of an overlapping family of hexagons.

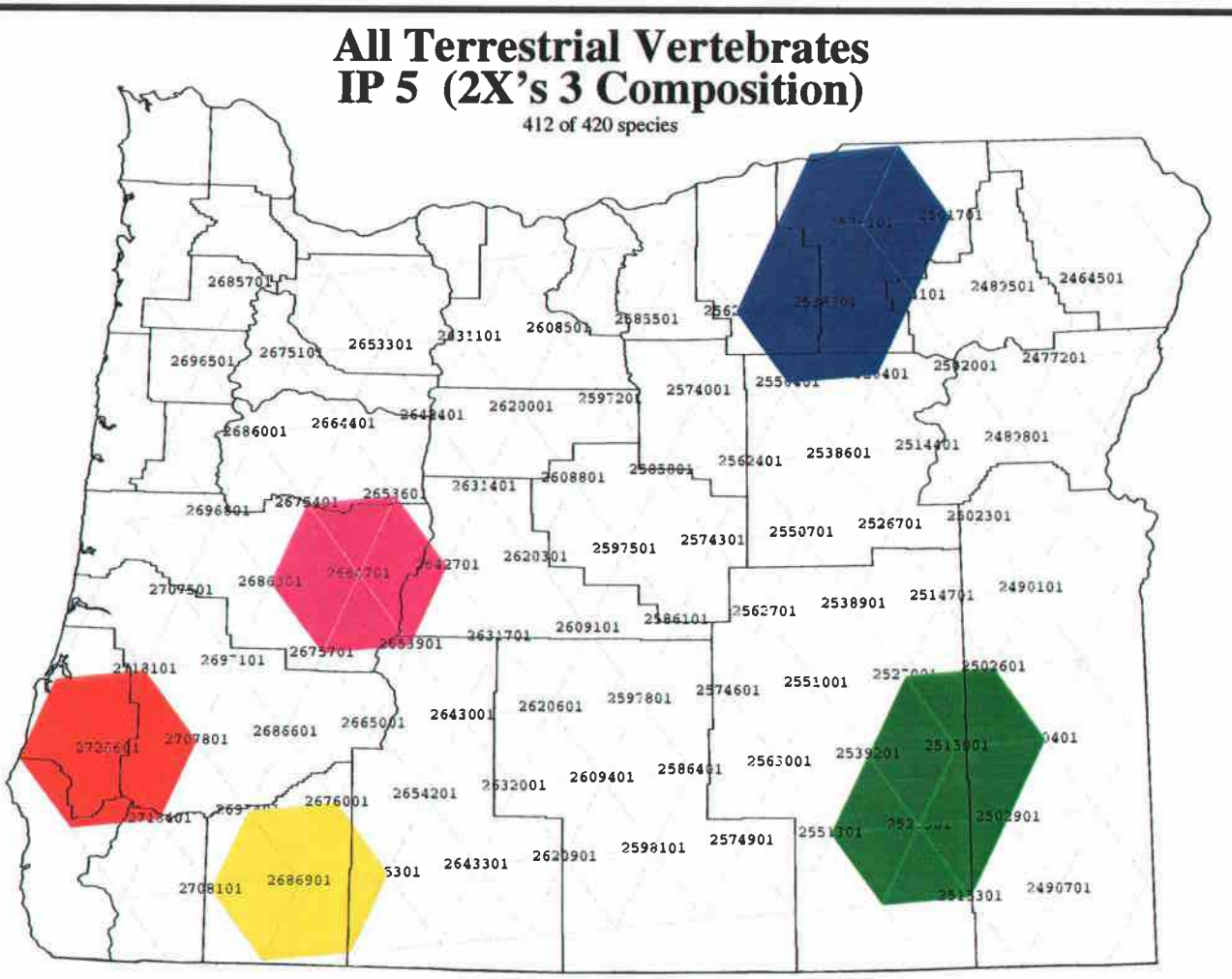

Figure 4.8: Cardinality 5 prioritization hexagons for 2 times 3-fold composition.

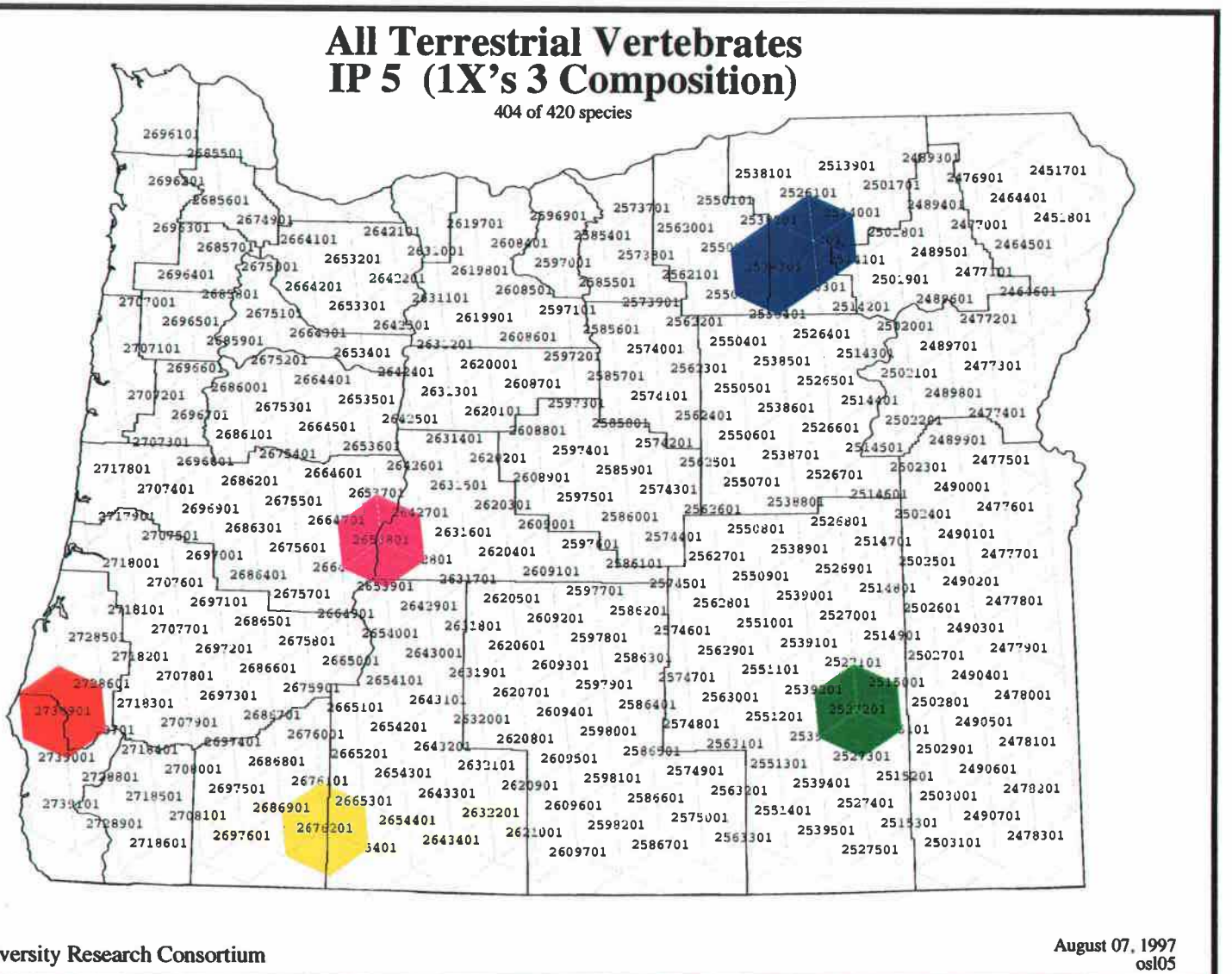

Figure 4.9: Cardinality 5 prioritization hexagons for 1 times 3-fold composition.

Figure 4.10 illustrates the cardinality 5 prioritization maps at the EMAP scale (0X's 3-fold composition). Of all species with a range within this grid, 94.8% are covered, with the decrease due again to using an area one-third the size of the previous analysis. This step is significant, as for the first time two of the areas, the blue areas to the northeast, and the east-central magenta areas, have each splintered into two areas with significant separation. Although these two new areas show no overlap with other prioritization hexagons, a portion of all five prioritization areas still lie partially or completely within the areas selected using the next largest grid cell size. Overlapping families of hexagons have also appeared for the first time to define the red and yellow prioritization areas in the southwest corner of the state.

Figure 4.11 illustrates the cardinality 5 prioritization map at the 1X's 3-fold decomposition. Using a total area one-third of the previous analysis allows 94.3% of the species within the grid to be selected. Once again, portions of all five prioritization areas, including the two disjoint areas, are at least partially within areas selected using the next largest grid cell size. One area has again splintered, the blue area furthest to the northeast. The separation between these two new areas, however, is much smaller than the distance between disjoint areas created at the previous level. It is also worth noting that two new areas are now comprised of overlapping families of hexagons. These are the magenta area in the east-central portion of the state, and the more western blue area. Both of these areas are narrow and elongate.

The finest resolution prioritization map for cardinality 5 is presented as **Figure 4.12**. 93.8% of all species with ranges within this grid are represented within the selected hexagons. The two disjoint, elongate prioritization areas discussed at the previous scale

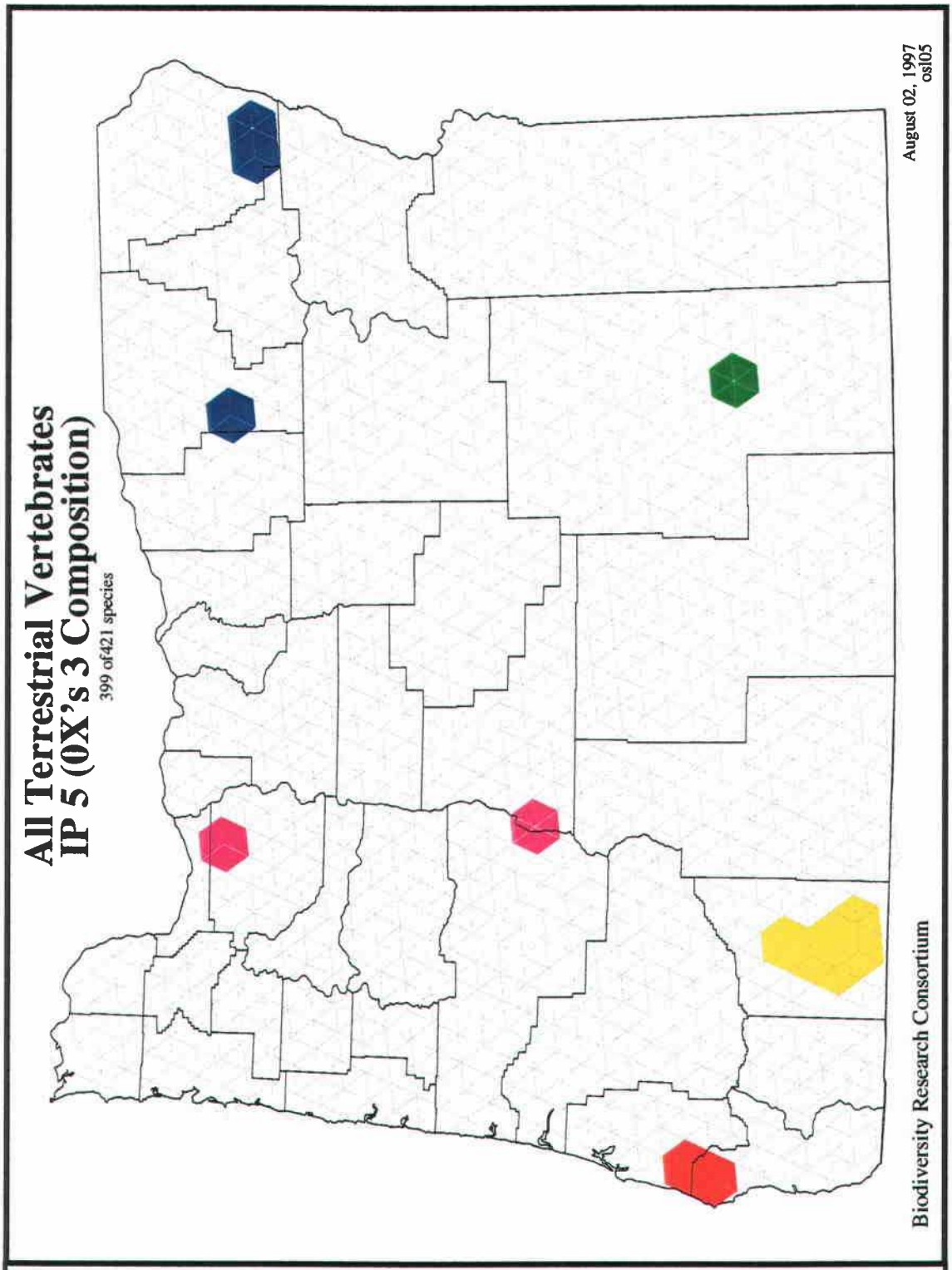

Figure 4.10: Cardinality 5 prioritization hexagons for EMAP grid.

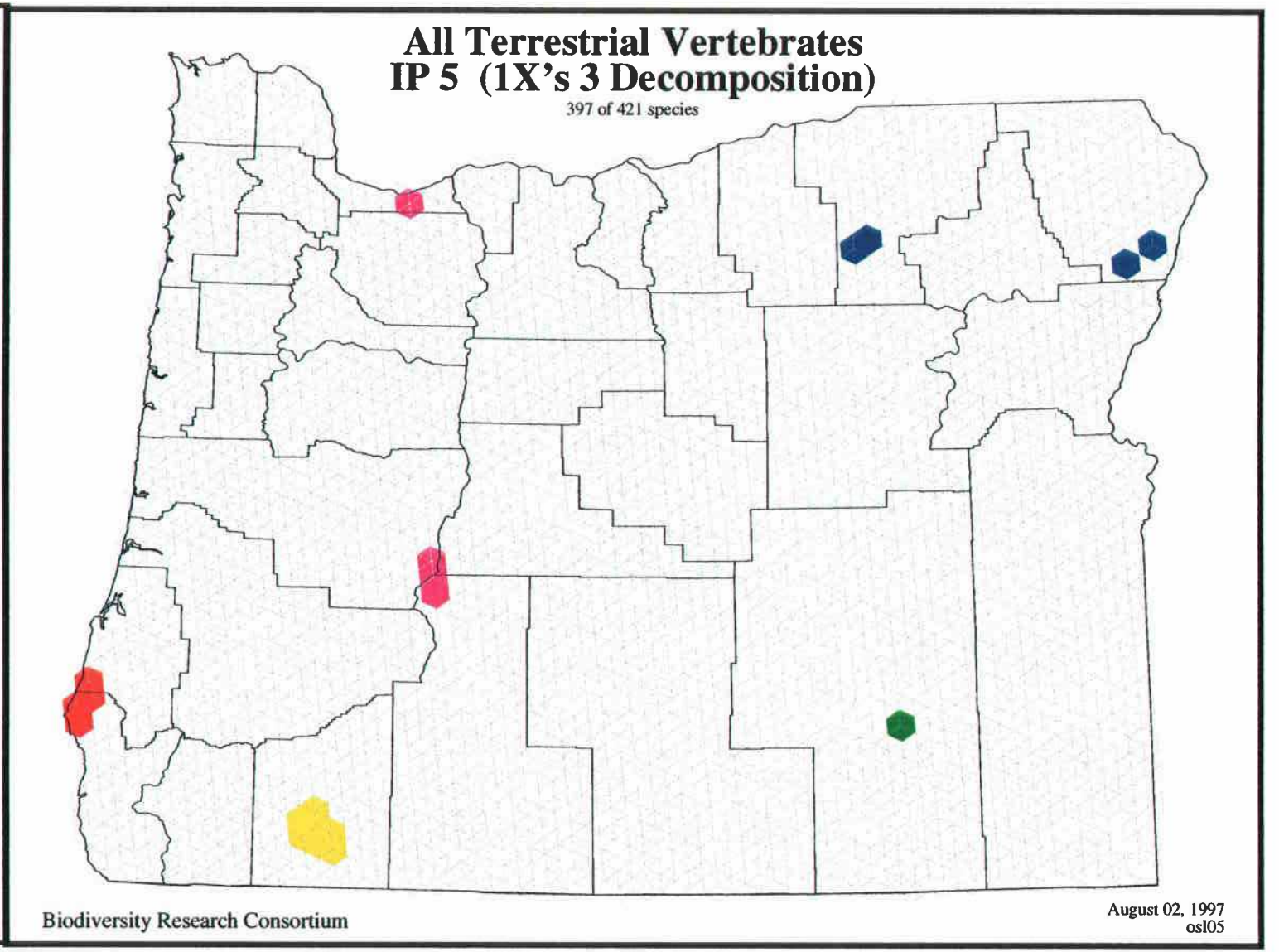

Figure 4.11: Cardinality 5 prioritization hexagons for 1 times 3-fold decomposition.

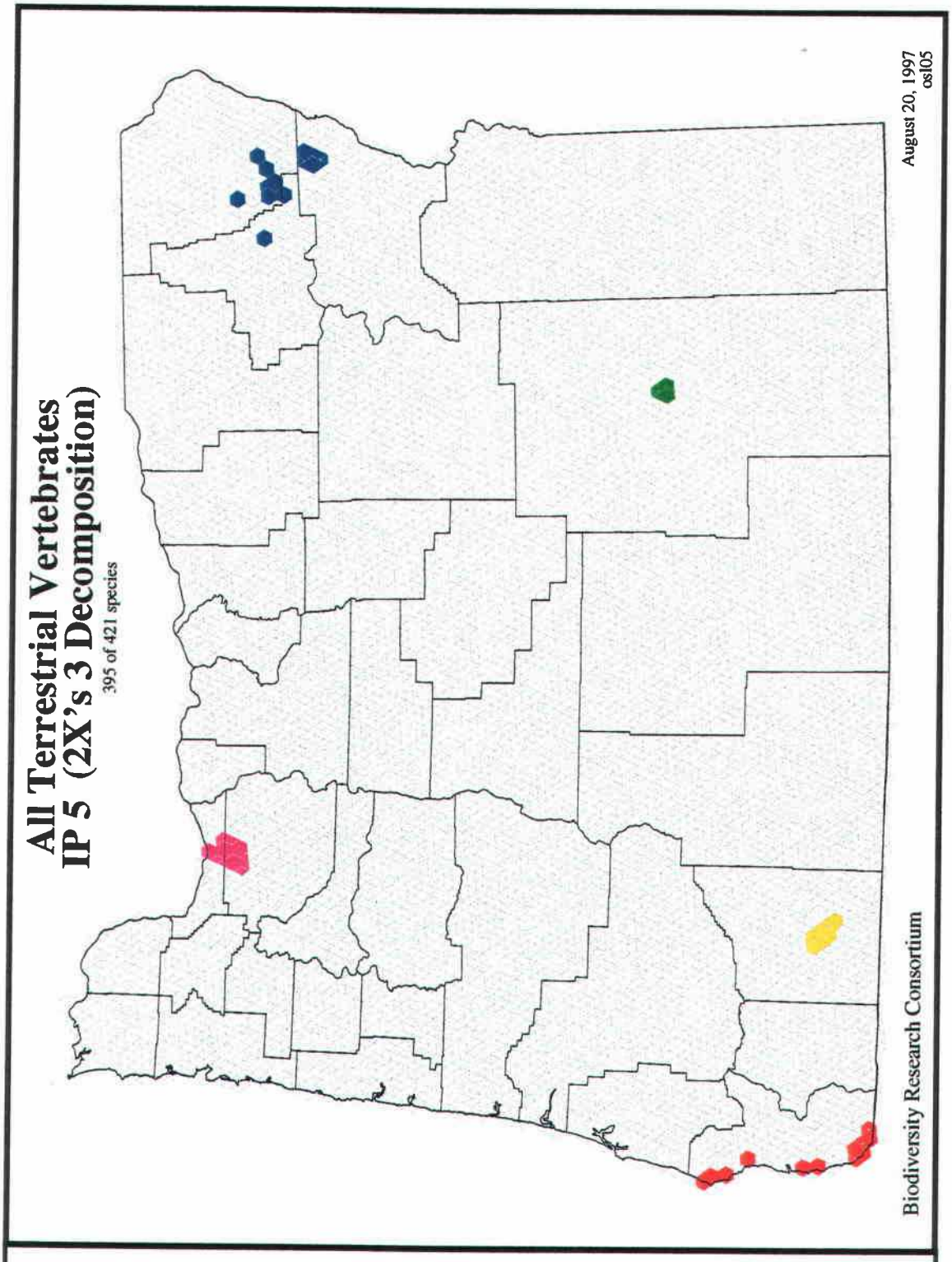

Figure 4.12: Cardinality 5 prioritization hexagons for 2 times 3-fold decomposition.

are no longer present. Two of the areas have each splintered into four disjoint areas, although distance between these areas is again on the scale of a few miles. In both cases, only one of the new disjoint areas is contained within the prioritization area from the previous scale. Two other prioritization areas, the magenta area and the yellow area, are also contained within the prioritization areas from the previous scale. The green area to the southeast of the state has actually shifted some distance to the north. Not only is this new green area not within the green prioritization area from the previously discussed scale, it is not within any of the prioritization areas discussed above. All prioritization areas at this scale are composed of overlapping or non-overlapping families of hexagons.

DISCUSSION

The most appropriate scales for mapping biodiversity in Oregon can be inferred from the results of this study. This will be done by analyzing statistics associated with both the species richness maps and the prioritization maps. Spatial patterns in all of these maps will also be discussed quantitatively as indicators of preferred scales for biodiversity mapping.

Optimal Scale for Richness Mapping

The best scale for richness mapping would preserve as much information as possible while using the maximum sized grid cell. Stoms (1994) recognizes this relative "little loss of information (in terms of variability)" by graphing the log10(CV) vs. log10(Grid cell size). The results are graphs that show a small drop in CV at smaller grid cells and a

greater drop at larger grid cells. The edge of the flat area before the sharp dropoff would be the most appropriate scale for richness mapping from a statistical perspective.

Results of this study follow a very different pattern, as illustrated by the blue line in **Figure 4.13**. The steep slope at the smallest grid cells continues to slowly decrease

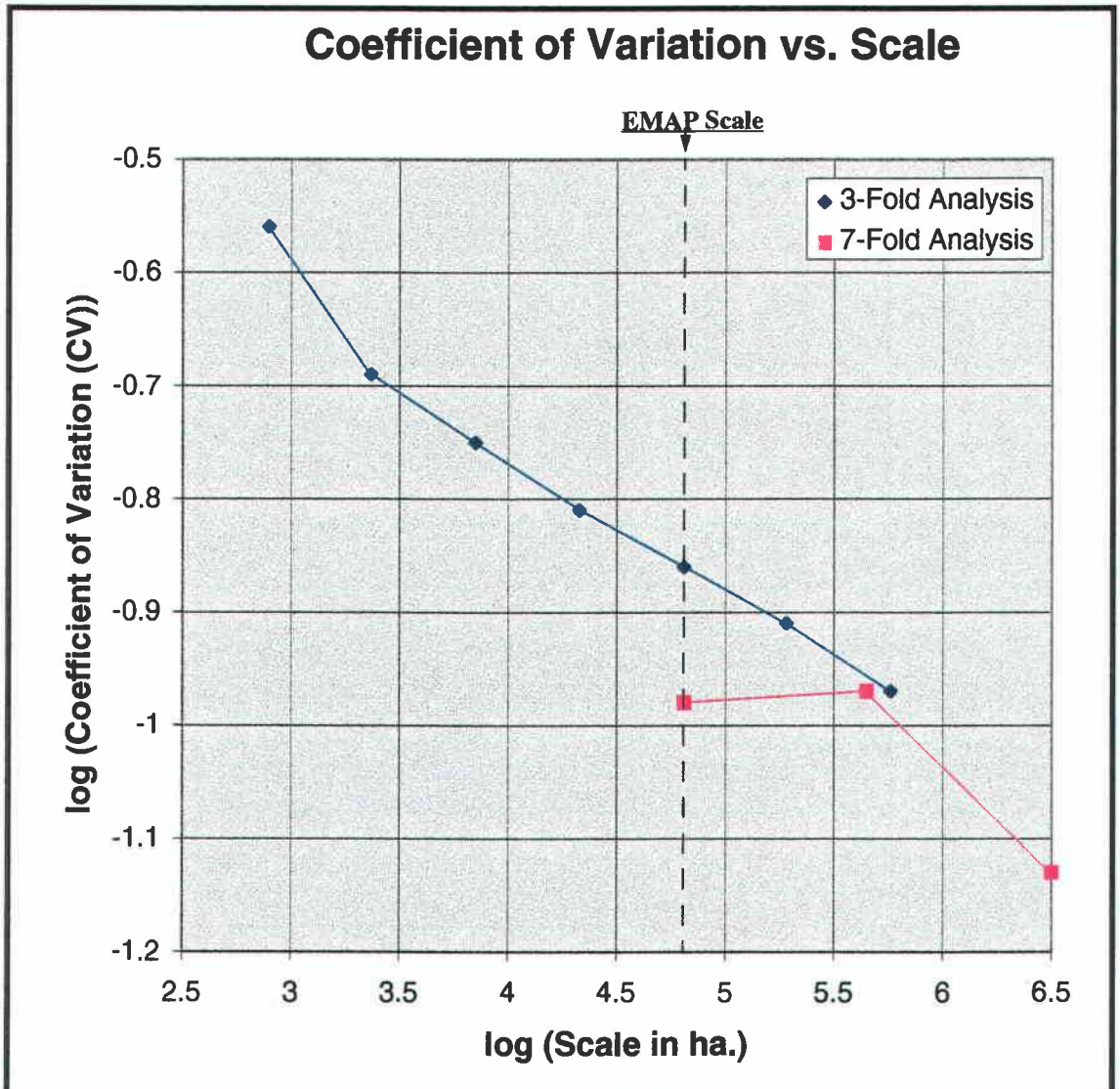

Figure 4.13: Coefficient of Variation vs. scale for 7-fold and 3-fold richness maps.

with increase in grid cell size. The sharp decrease in CV between the two smallest grid cells may be due to the smallest grid cells being able to sample within as well as on the boundary of adjacent wildlife habitat polygons. Most triangles sampled only one or two polygons from the wildlife habitat map. If the smallest hexagons also only sample one or two polygons, then each hexagon would either contain the species list of one or two adjacent polygons. As grid cell samples become larger, more polygons would be covered in a single grid cell. This argument seems to be supported by the observation that the richness map using the smallest grid cells appears to have the most narrow linear patterns, possibly associated with habitat boundaries (See **Figure 4.1**).

The absence of a sharp dropoff at higher scales may be the result of this study using a maximum grid cell size nine times the size of the EMAP grid cells. In the previous study, a map seven times the scale of the EMAP grid showed no change in CV. It was not until the next scale, with grid cells 49 times as large, that CV dropped off considerably. The results of CV calculations for the seven fold compositions are included for comparison in **Figure 4.13**.

Comparison of these two curves also reveals that overall, the new series of richness maps has a significantly higher CV than the previous set. The shift of CV at the EMAP scale from 10.45 to 13.93 represents an increase of 33%. This is due to the basis of species range maps changing from the EMAP hexagonal grid to the wildlife habitat maps. These finer detailed maps with better defined edges and internal boundaries allow a greater quantity of information to be captured as measured by statistical variability in species richness values at the EMAP scale.

Optimal Scale for Prioritization Mapping

The question of which scale is best suited for prioritization mapping can be addressed in two ways. The first is to look at the relative efficiency of prioritization analysis between each two adjacent scales. The second is to look at the locations of prioritization hexagons and the nature of their change with changes in scale.

Two measures of efficiency of prioritization analysis indicate that 1X's 3-fold decomposition would be the most efficient scale. The first of these is that no additional hexagons are required for "full coverage" of all species at the 1X's 3-fold decomp scale than at the next largest EMAP scale (See **Appendix 3**). Both analyses require 12 cardinalities to cover 420 species and 13 cardinalities to cover 421 species, despite the 1X's 3-fold scale using grid cells and a total prioritization area one-third the size of the EMAP scale analysis. Between all other scales, cardinalities must increase by one or two to cover the 420 species given the decrease in area associated with their scale.

A second measure of efficiency would be the decrease in the number of species covered with decreasing grid cell size at a given cardinality. All five scales of prioritization are made up of at least 10 cardinalities. Comparisons between scales show which two successive scales have the least change in species covered. For the 10 cardinalities, no change is smaller than the change from the 1X's 3-fold decomposition to the EMAP scale for seven of the ten cardinalities, a maximum between any two successive scales. **Figure 4.14** graphs this trend for cardinalities 3 through 5 as an example.

The cardinality of 5, which covers 93.8% to 98.1% of species (depending on scale) and is illustrated in **Figures 4.8 - Figure 4.12** can be used as an example. The decrease in number of species between the two largest scales is 8, the result of using only one third the

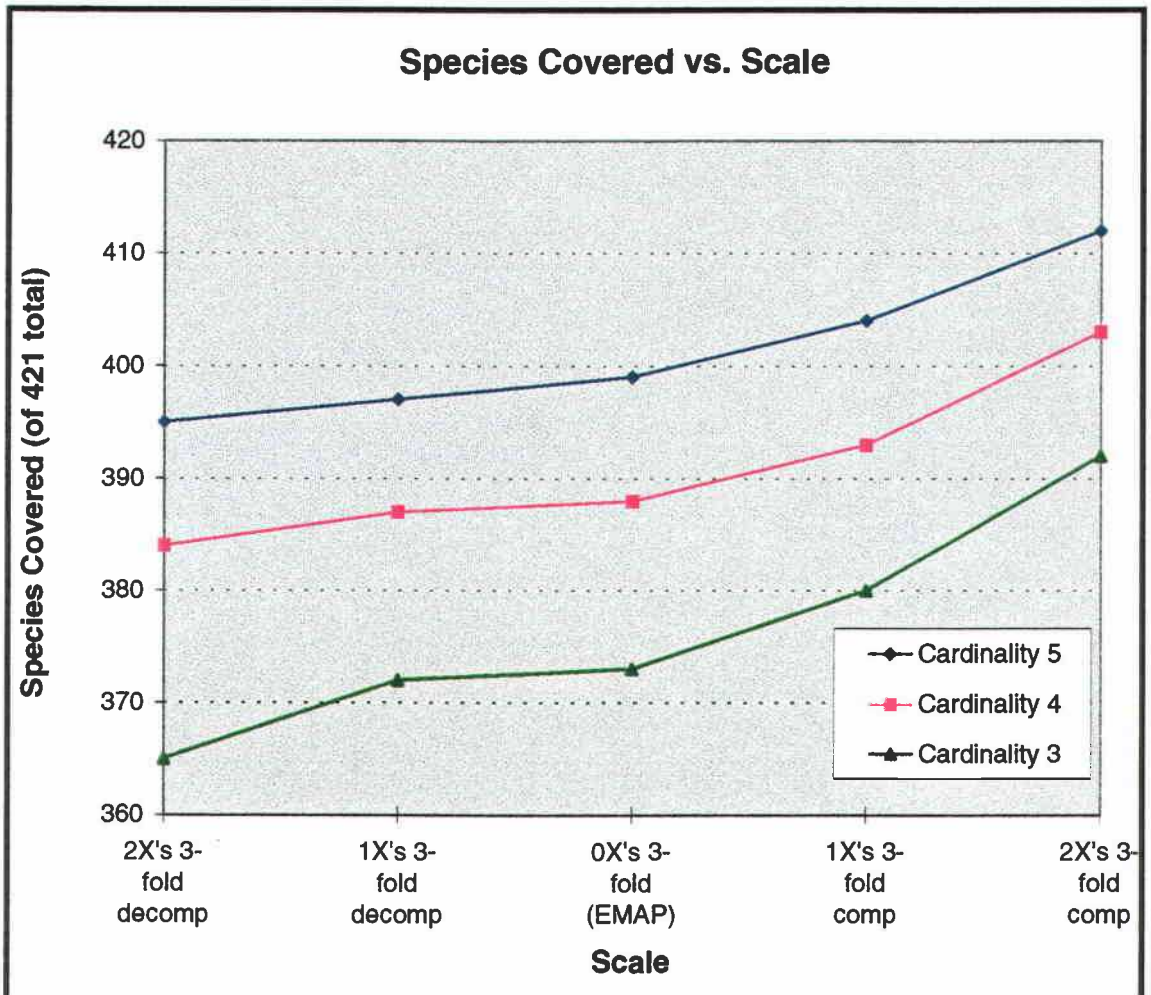

Figure 4.14: Species covered vs. scale for three cardinalities of prioritization.

area for prioritization. The decrease for the next step down in scale is 5. The next 2 steps down in scale, however, show a net decrease of 2 species at each step. The change from the EMAP scale to the 1X's 3-fold decomp scale is the first step that shows this relatively small decrease of 2 species, indicating the efficiency of this scale of prioritization mapping.

A different approach for determining an appropriate scale for prioritization mapping is to look at the changes in location and pattern of prioritization hexagons with scale. Based on qualitative observations, locational information may be equally important in determining proper scale for prioritization analysis. This discussion will refer to the prioritization maps for cardinality 5 presented in the results portion of this study as **Figures 4.8 - 4.12.**

The analysis using the largest grid cells define large areas whose boundaries directly reflect the shape of the hexagonal grid cells (See **Figure 4.8**). These sets of five hexagons capture the most species, but possibly not in the most efficient manner. If no other areas could contend to be included in prioritization analysis, prioritization analysis using smaller grid cells would simply refine the area within these larger hexagons.

Figure 4.9 shows this process of refining, as five areas are selected within the previous areas. Shapes of prioritization areas continue to reflect the shape of the grid cells. **Figure 4.10,** however, shows an important change in location and shape of prioritization areas. Prioritization areas within other previous prioritization areas continue to be refined, but now two new and separate areas have been identified. By relaxing the number of species that can be covered (because they will no longer all fit in a grid cell one-third the size), new areas can be included in the analysis. Also, for the first time, the yellow family of grid cells define an area that begins to look somewhat natural, as opposed to a relic of the grid cells defining the area.

It can be argued that the loss of species at any of these levels is not significant. With an increase of one cardinality, the 6 hexagons at this scale will now cover more species than the five hexagons at the larger scale. This is accomplished by increasing the pri-

oritization area by 20% (by adding one hexagon) versus 200% (by mapping at the same cardinality at a scale three times as large). The introduction of two new areas vying for inclusion in prioritization results seems a much more important issue.

Figure 4.11 illustrates the smallest grid cells which represents all seven of the prioritization areas at all scales examined. In addition to the yellow area, the coastal red area is now taking on a more natural, less hexagonal shape. The furthest northeast blue area has now split in two. This split, however, is very different from the two separations seen at the previous scale. At this scale, both new blue hexagons are within the area selected at the previous scale. Although separated, they do not define a new prioritization area, an important difference from the splintering seen at the previous scale.

Figure 4.12 shows prioritization analysis at the finest scale. The most obvious difference here is that neither of two areas, the magenta area in the west-central state and the eastern blue area, have been selected. At the previous scale, both of these areas consisted of elongate patterns of hexagons. This could indicate that prioritization analysis would only select these areas if a central area and peripheral areas almost out of reach at that scale were included. Once the grid cell decreased in size again, an area large and diverse enough to be included in prioritization could no longer be selected. It is also interesting to note that the two areas that are no longer selected were areas originally selected with the largest grid cells.

All prioritization areas in **Figure 4.12** now look more natural, with less of a hexagonal pattern outlining most areas. Three of these areas are compact. Two areas, the red coastal area and the blue area to the northeast, are broken into four localized but disjoint

areas. Both of these areas in part overlap areas selected with larger grid cells, but both are expanding locally outside of areas selected at any other scale.

Although more detailed information is generally preferable in spatial analysis, this scale may be of too fine a resolution for statewide biodiversity analysis. The creation of these two disjoint areas at this scale may indicate that factors influencing selection are now working on a habitat-type scale as opposed to a more regional ecoregion-type scale seen in all other analyses. Also, with hexagons of approximately 72 km^2, other issues such as minimum area requirements(Csuti and Kiester, 1996) may come into play. Such a scale may be more suited for reserve design as opposed to prioritization reserve selection (See Csuti, 1994).

EMAP Scale Prioritization Analysis from Two Datasets

The prioritization at the EMAP scale can also be compared with the prioritization done at the EMAP scale using the previous species range maps. A comparison of **Figure 4.10** with **Figure 2.9** gives an idea of the locational stability. All five prioritization areas from **Figure 2.9** overlap or are adjacent to prioritization areas from **Figure 4.10**. The two splintered areas in **Figure 4.10** are not represented in **Figure 2.9**. The addition of these two areas in the new analysis could be the result of a more comprehensive and varied species list resulting from more detailed habitat based species range mapping.

The most salient difference between these analyses, however, is the efficiency of species coverage. The previous analysis was able to obtain full coverage of all 422 terrestrial vertebrates in 23 cardinalities, and 421 species in 22 cardinalities. This study required

only 13 cardinalities to cover 421 species. This study, therefore, covered as many species while using less than 60% of the hexagons of the other study.

The two differences between these analyses is that the species range maps were based on different criteria, and that the new analysis used three sets of overlapping hexagons. These sets of offset hexagons could have found more efficient representations of species.

To test this hypothesis, a second prioritization analysis was done with the new data at the EMAP scale. For this analysis, only one of the three sets of prioritization hexagons was used, the set with no offset from the EMAP grid. This new prioritization was somewhat less efficient. The new total, 420 total species, were now covered at a cardinality of 13. Previously, 420 species were covered at a cardinality of 12. Also, at any cardinality above 1, 1 to 8 less species were covered with the new analysis. This effect, however, is minimal compared with the drop from 22 to 13 cardinalities to cover 421 species between the old and new analysis

The most likely explanation for this drop would be the difference in the species range maps. The new species range maps are based on habitat extents. The EMAP hexagon is no longer the MMU. With this finer scale mapping, species ranges can be extended into portions of neighboring hexagons, allowing the hexagon to include a greater variation of species. This interpretation is also consistent with the increase in CV between old and new maps at the EMAP scale. In this case, the increased resolution of the species range maps allows more species richness variations information to be captured in the new analysis.

CONCLUSIONS

The proper scale for biodiversity mapping can be determined by looking at maps and statistics associated with these maps at several scales. This analysis indicates that the EMAP scale is an appropriate scale for mapping species richness in Oregon. This study also sees improvements in a grid cell 1/3 the EMAP cell being used for prioritization mapping in the state of Oregon.

Seven scales of richness maps were produced with grid cells varying by a factor of three from 1/81 the size of the EMAP hexagon to 9 X's its size. A coefficient of variation (CV) graph shows no strong patterns of the CV curve flattening, indicating that each scale of richness map retains a relatively similar amount of information on the variation of richness values present as at the previous level. A subtle change in slope in moving to the EMAP scale from the scale with grid cells 1/3 the size indicates that, relatively, the EMAP scale is a marginally better scale for mapping species richness.

The grid cell one third the size of the EMAP hexagon is the best scale for prioritization mapping for two reasons. First, it is more efficient than the larger EMAP grid cells. Both take the same number of cardinalities (12) to cover all 421 species. In examining species covered at several cardinalities, this scale is also most consistent at defining a change in slope of number of species covered vs. size of grid cell.

The map pattern and location of prioritization hexagons could also be used to argue for the use of this scale. This scale identifies a maximum number of prioritization areas at cardinality 5 using a minimum grid cell size. Prioritization areas are specifically located but not yet fragmented within an area, as occurs with prioritization areas selected

by smaller grid cells. All of this points to a grid cell 1/3 the size of the EMAP grid as being most appropriate for prioritization mapping in Oregon.

It can also be concluded from this analysis that mapping species ranges based on habitat maps is preferable to range maps based on EMAP grid cells. Comparing richness maps at the EMAP scale indicates the new maps have a greater variation of value, indicating more diversity information was captured. Prioritization analysis was also much more efficient with the new maps, the probable result of increased diversity information within the data, which results from refining species range boundaries.

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Appendix

Results of Multi-Scale Three-Fold Prioritization Analysis

Table 4.2: 2X's 3-Fold Decomposition Prioritization Statistics

Oregon All Vertebrates Prioritization
10504 hexagons and 421 total species

# of hexes/path	# of paths	# of hexagons	# species covered	% species covered
1	2	2	281	66.75
2	1	2	338	80.29
3	4	6	365	86.70
4	50	25	384	91.21
5	50	46	395	93.82
6	50	27	403	95.72
7	50	37	408	96.91
8	>=1	>=9	411	97.62
9	>=1	>=9	414	98.34
10	>=1	>=10	415	98.57
11	>=1	>=11	417	99.05
12	>=1	>=12	418	99.29
13	>=1	>=13	419	99.52
14	>=1	>=14	420	99.76
15	>=1	>=15	421	100.00

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Table 4.3: 1X's 3-Fold Decomposition Prioritization Statistics

Oregon All Vertebrates Prioritization
3377 hexagons and 421 total species

# of hexes/path	# of paths	# of hexagons	# species covered	% species covered
1	1	1	288	68.41
2	1	2	343	81.47
3	2	4	372	88.36
4	53	15	387	91.92
5	50	20	397	94.30
6	50	26	404	95.96
7	50	40	409	97.15
8	50	31	413	98.10
9	50	35	416	98.81
10	50	44	417	99.05
11	50	42	419	99.52
12	50	51	420	99.76
13	50	63	421	100.00

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Table 4.4: 0X's 3-Fold Decomposition (EMAP) Prioritization Statistics

Oregon All Vertebrates Prioritization
1067 hexagons and 421 total species

# of hexes/path	# of paths	# of hexagons	# species covered	% species covered
1	2	2	298	70.72
2	2	3	348	82.66
3	3	5	373	88.60
4	10	9	388	92.16
5	36	14	399	94.77
6	36	14	407	96.67
7	50	26	411	97.62
8	50	34	414	98.34
9	50	36	416	98.81
10	50	38	418	99.29
11	50	66	419	99.52
12	50	54	420	99.76
13	50	55	421	100.00

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Table 4.5: 1X's 3-Fold Composition Prioritization Statistics

Oregon All Vertebrates Prioritization
321 hexagons and 420 total species

# of hexes/path	# of paths	# of hexagons	# species covered	% species covered
1	2	2	312	74.29
2	4	5	356	84.76
3	2	4	380	90.48
4	1	4	393	93.57
5	2	6	404	96.19
6	40	16	409	97.38
7	50	25	413	98.33
8	53	18	417	99.29
9	50	27	418	99.52
10	50	32	419	99.76
11	50	38	420	100.00

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Table 4.6: 2X's 3-Fold Composition Prioritization Statistics

Oregon All Vertebrates Prioritization
89 hexagons and 420 total species

# of hexes/path	# of paths	# of hexagons	# species covered	% species covered
1	1	1	329	78.33
2	2	3	369	87.86
3	2	4	392	93.33
4	14	12	403	95.95
5	4	7	412	98.10
6	20	13	415	98.81
7	58	16	417	99.29
8	50	26	418	99.52
9	50	27	419	99.76
10	50	27	420	100.00

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CHAPTER 5. SUMMARY

SUMMARY STATEMENT

The scale of study has a strong effect on biodiversity mapping, due to its combinatorial nature. The proper scale for mapping can be determined by looking at both the extent used for analysis and the grid cell size. Using geopolitical extents such as the state of Oregon is not detrimental to prioritization analysis. Internal natural boundaries such as the ecoregion boundaries of Oregon are not preferentially selected as prioritization areas. These regions instead tend to break up the extent into areas where species data are more homogenous within areas and heterogeneous between areas.

Proper grid cell size can be determined for richness mapping, and for prioritization analysis if the change between scales is small. Proper grid cell size is also dependent on the scale of species range maps used for analysis. Seven-fold analysis for range maps based on the EMAP grid indicates grid cells seven times the EMAP size show no loss of species richness information. No determination of proper prioritization scale can be made, as the change in scale by a factor of seven is too large to see important changes.

Three-fold analysis indicates no strongly preferred grid cell size for richness maps based on species range maps from wildlife habitat relationships. A proper scale, however, was identified for these data from prioritization analysis. Grid cells one-third the size of the EMAP grid are relatively the most efficient, as well as presenting the most choices for prioritization areas.These areas are not simply alternative choices of wildlife habitat poly-

gons, but rather areas showing significant separation, possibly representing habitat assemblages from different ecoregions.

ECOREGION BOUNDARY EFFECTS

Two major conclusions have resulted from looking at the effect of ecoregion boundaries on prioritization analysis. The first is that prioritization hexagons do not fall preferentially on most ecoregion boundaries. The second is that prioritization analysis results remain geographically stable after eliminating hexagons along ecoregion boundaries.

These results have interesting implications concerning the scale of biodiversity processes affecting prioritization analysis. First, hexagons straddling ecoregion boundaries and sampling different biotic assemblages are not a driving factor in prioritization analysis. If this were true, percentages of prioritization hexagons on ecoregion boundaries would be higher than percentage of total hexagons that are prioritization hexagons. The Jaccard buffer analysis also indicates that localized changes in species list on the order of adjacent hexagons are also not of a scale which drives prioritization analysis.

Inferences can also be drawn from the geographic stability of results. This implies that geographic areas on the scale of ecoregions may be an important factor in prioritization analysis. Also, when multiple paths are selected, hexagons are often proximal and within the same ecoregion. This may imply that the most important heterogeneity for prioritization analysis may be differences found at a scale similar to the sizes of ecoregions in Oregon.

SCALE EFFECTS USING SEVEN-FOLD EMAP HEXAGON COMPOSITIONS

Seven-fold compositions of the EMAP grid identifies proper scales for mapping species richness for species range maps based on the EMAP grid. An optimal scale would maximize variation and grid cell size while minimizing the number of grid cells required for mapping. It cannot, however, be used to determine proper scales for prioritization analysis.

The grid cell size for mapping richness of terrestrial vertebrates in Oregon could be increased by a factor of 7 over the EMAP grid cell without losing any statistically significant information on species richness variation. Local changes in variation from the EMAP grid to one 7 times as large are not influenced by any single area within the mapping extent. If the grid cell size is increased again by a factor of 7, variations previously present in the map would be lost, as measured by the coefficient of variation.

The proper scale for prioritization analysis cannot be determined with this method. It was necessary to create maps with less change in grid cell size between scales (i.e. three-fold analysis) and to look at grid cells smaller and larger than the EMAP grid, to find geographically consistent prioritization results. Richness maps based on more homogenous extents may also help to relate proper scale and extent of species richness mapping to prioritization mapping.

SCALE EFFECTS USING THREE-FOLD EMAP HEXAGON COMPOSITIONS AND DECOMPOSITIONS

The proper scale for biodiversity mapping can be determined by looking at maps and statistics associated with these maps consisting of three-fold compositions and decompositions of the EMAP grid. This analysis indicates that the EMAP scale is an appropriate scale for mapping species richness in Oregon. This study also sees improvements in a grid cell 1/3 the size of the EMAP cell being used for prioritization mapping in the state of Oregon. Additionally, research indicates that more variation is captured in species range maps based on wildlife habitat relationships, as the coefficient of variance of species richness values at the EMAP scale and the efficiency of prioritization both increase.

Seven scales of richness maps were produced with grid cells varying by a factor of three from 1/81 the size of the EMAP hexagon to 9 X's its size. A graph of coefficient of variation (CV) shows no strong patterns of the CV curve flattening, indicating that each scale of richness maps retains a relatively similar amount of information on the variation of richness values present as at the previous level.

The grid cell one third the size of the EMAP hexagon is the best scale for prioritization mapping for two reasons. First, it is more efficient than the larger EMAP grid cells. Both take the same number of cardinalities (12) to cover all 421 species. In examining species covered at several cardinalities, this scale is also most consistent at defining a change in slope of number of species covered vs. size of grid cell.

The map pattern and location of prioritization hexagons could also be used to argue for the use of this scale. This scale identifies a maximum number of prioritization

areas at cardinality 5 using a minimum grid cell size. Prioritization areas are specifically located but not yet fragmented within an area, as occurs with prioritization areas selected by smaller grid cells. All of this points to a grid cell 1/3 the size of the EMAP grid as being most appropriate for prioritization mapping in Oregon.

It can also be concluded from this analysis that mapping species ranges based on habitat maps is preferable to range maps based on EMAP grid cells. Comparing richness maps at the EMAP scale indicates the new maps have a greater variation of value, indicating more diversity information was captured. Prioritization analysis was also much more efficient with the new maps, the probable result of increased diversity information within the data, which results from refining species range boundaries.

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