Figure 1. ACE-II Biological Index Model Flow Chart.

The *Biological Index* is based on four indices relevant to conservation value, native species richness, rare species richness, irreplaceability, and the presence of sensitive habitats, summed in a weighted-additive model framework. Data were normalized to give each taxonomic group and each of the four indices equal weight in the analysis. The analysis was done by ecoregion, to identify areas of high biological richness within each ecoregion of the state. The analysis unit used was 2.5 square mile hexagons.

	Dataset	Data group	Source		Process	
1	Native	Birds	CWHR ranges		Count of number of native	
2	species	Amphibians	CWITK langes		species per hexagon based	
3	richness	Reptiles	1		on range maps.	
4	Tielmess	Mammals	4		on range maps.	
			D 0.16 1		-	
5		Fish	Brown & Moyle ranges			
6	Plants		Jepson Ecoregions based on The			
_	5	D: 1	Jepson Manual (Hickman 1993).		DVI 54////	
7	Rarity-	•			[RWI=Σ 1/(# hexagons occupied per species)] Based on occurrence data. The species found in the	
8	weighted	Amphibians	records and records with accuracy of >1 mile) and additional museum records. All records were buffered by			
9	richness	Reptiles				
10	index	Mammals				
11	(RWI)	Fish	1 mile to standardize accurac	y.	fewest number of hexagons	
12		Plants			have the highest values.	
13	Rare	Birds	1		Count of number of rare	
14	Species	Amphibians			species per hexagon based on occurrence data.	
15	Richness	Reptiles				
16	1	Mammals	1			
17	1	Fish	1			
18	1	Plants				
19	Sensitive	Riparian	Habitat mapped by Calveg, CNDDB, DWR, NWI, some local maps.		All hexagons with a mapped location of the habitat type marked as presences (0=not present; 1=present).	
20	habitats	Wetlands				
21		Rare natural	CNDDB mapped rare natural communities excluding riparian and wetland habitats. Additional rare natural communities from local vegetation maps were also added.			
2.1		communities				
22	1	High value	COHO, steelhead, and heritage native			
		salmonid	trout watersheds.			
		habitat				
		1	· 			
A. Normalize data layers 1-22 from 0-1 by ecoregion.					h layer was normalized	
71. I Tormanze data layers 1 22 from 0 1 by ecolegion.				ecoregionally, meaning the data values in each layer were scaled from 0-1 based on all values within the ecoregion. Normalizing by taxonomic group remove any potential bias caused by differences in the number of taxa per taxonomic group.		
B. Sum normalized data layers in each of 4 dataset						
categories to obtain the four final data layers.						
The state of the s						
C	C. Normalize the 4 final data layers from 0-1 by ecoregion.				Normalization of the four final data layer	
L	C. 1301manze the 4 final data layers from 0-1 by ecolegion.				was done to standardize the weights of the	

Step 1.Data compilation

Step 2.

Model development

biological index.

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D. Sum the normalized final data layers to calculate the

data values input into the weighted-additive

model.