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			species per hexagon based	
	3	richness	Reptiles			on range maps.	
	4		Mammals				
	5		Fish	Brown & Moyle ranges			
	6		Plants	Jepson Ecoregions based on The			
	_			Jepson Manual (Hickman 1993).			
	7	Rarity-	Birds	CNDDB records (excluding extirp		[RWI= Σ 1/(# hexagons	
	8	weighted richness			OI	occupied per species)] Based on occurrence data. The species found in the fewest number of hexagons	
	9	index	Reptiles	records. All records were buffered by 1 mile to standardize accuracy.			
S4 1	10	(RWI)	Mammals				
Step 1.	11	(1(),1)	Fish			have the highest values.	
Data	12	Rare	Plants Birds	4	ŀ	Count of number of rare	
compilation {	13 14	Species	Amphibians	-		species per hexagon based	
	14	Richness	Reptiles	4		on occurrence data.	
	16	1	Mammals				
	17	4	Fish				
	18		Plants	4			
	19	Sensitive	Riparian	Habitat mapped by Calveg, CNDD)B	All hexagons with a	
	20	habitats	Wetlands	DWR, NWI, some local maps.		mapped location of the	
	21		Rare natural	CNDDB mapped rare natural		habitat type marked as	
			communities	communities excluding riparian and		presences (0=not present;	
				wetland habitats. Additional rare		1=present).	
				natural communities from local			
				vegetation maps were also added.			
	22		High value	COHO, steelhead, and heritage nat	tive		
			salmonid	trout watersheds.			
			habitat				
(v Fach	laver was normalized	
	A	A. Normalize data layers 1-22 from 0-1 by ecoregion.				<u>Note:</u> Each layer was normalized ecoregionally, meaning the data values in each layer were scaled from 0-1 based on	
		Ţ					
	П					within the ecoregion.	
Step 2.		B. Sum normalized data layers in each of 4 dataset categories to obtain the four final data layers.				 Normalizing by taxonomic group removed any potential bias caused by differences in the number of taxa per taxonomic group. Normalization of the four final data layers was done to standardize the weights of the data values input into the weighted-additive model. 	
Model \langle	00						
development		\Box					
-	C	C. Normalize the 4 final data layers from 0-1 by ecoregion.					
		D. Sum the normalized final data layers to calculate the					
	b	iological inde	Х.				