



# Landscape genetic analysis and population structure of three sympatric amphibians in managed redwood forest of northwestern California

Cindy Castañeda and Dr. Andres Aguilar  
Department of Biological Sciences, California State University, Los Angeles



## ABSTRACT

In this study, we are currently estimating sequence divergence, gene flow, and dispersal capabilities among 28 southern torrent salamanders (*Rhyacotriton variegatus*), 94 tailed frogs (*Ascaphus truei*), and 99 coastal giant salamanders (*Dicamptodon tenebrosus*) sampled from Mendocino County, CA USA. Geographical Information System (GIS) was used to create least cost paths (LCPs) as an estimate of dispersal among the three species. To estimate genetic differentiation among sites pairwise  $F_{ST}$  is being calculated. Nucleotide ( $\pi$ ) and haplotype diversity ( $h$ ) indices will be calculated using DnaSP v. 5<sup>6</sup> to measure sequence divergence. These data will provide valuable insight into patterns of genetic structure and identify threats to the persistence of these amphibians. In highlighting threats to the evolutionary heritage of these species related to habitat fragmentation, risk of localized extinction will be decreased.

## INTRODUCTION

- Only a few studies have examined population genetic characteristics of southern torrent salamanders, tailed frogs, and coastal giant salamanders on a landscape facing pressure from timber harvest.
- The home range of the southern torrent salamander, the coastal giant salamander, and the tailed frog expands a heavily logged forest making these species of concern.
- Amphibians are important indicators of ecosystem health due to their high sensitivity to environmental changes and human impacts<sup>9</sup>.
- Landscape may influence viability and abundance of a species by impacting foraging, reproduction, overwintering habitat, and dispersal<sup>7</sup>.
- Once the link between habitat structure and constraints on amphibian dispersal is identified, appropriate conservation strategies can be developed and implemented that meet ecological requirements of stream amphibians<sup>7</sup>.

### Objectives:

1. Determine landscape features which limit migration and gene flow in a disturbed landscape
2. Compare the similarities and differences in landscape features and gene flow among the three species

## METHODS

- Polymerase Chain Reactions (PCR's) with previously extracted whole genomic DNA using a series of mitochondrial markers
- PCR product sequenced by Laragen, Inc.
- Align sequence using Geneious v7.0<sup>5</sup>
- Calculate LCPs with SDMToolbox v.1.0<sup>2,8</sup> in ArcMap 10.2<sup>3</sup>
- Use SAMOVA 2.0<sup>4</sup> to define groups of populations

## PRELIMINARY RESULTS

In the first analysis (Fig. 1A) cost was based on a landscape where CTI (wetness) was maximized and HLI (solar radiation) was minimized. Canopy path (Fig. 1B) was based on a raster indicating percent canopy cover. Dispersal paths varied depending on the cost raster.

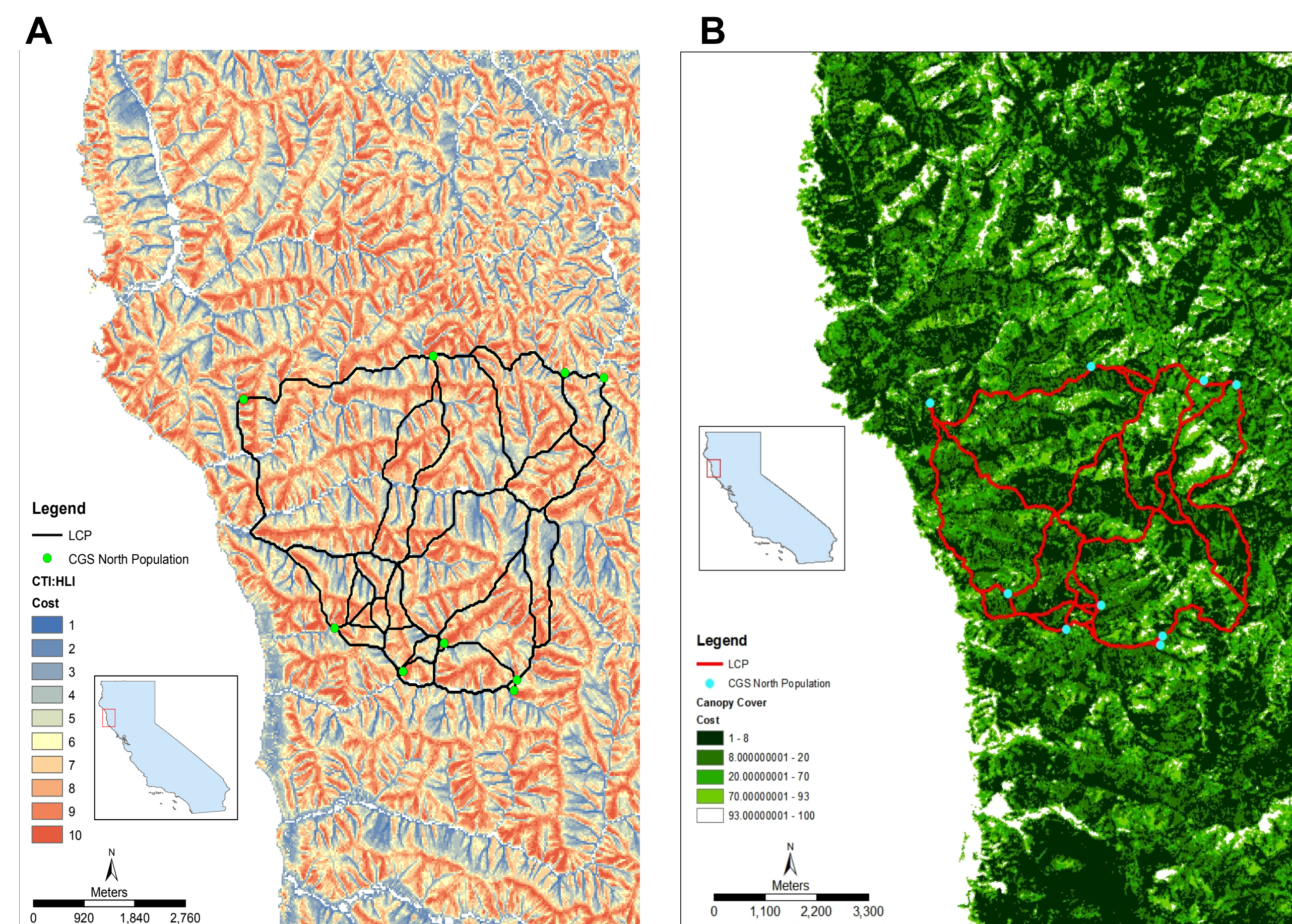


Figure 1. Least cost paths (LCPs) for coastal giant salamanders (CGS) in the northern part of their sampling location based on (A) HLI (solar radiation) and CTI (wetness) and (B) percent canopy cover. A cost of 1 equals the least cost or most favorable conditions and a cost of 10 or 100 equals the greatest cost.

SAMOVA found ten ( $K=10$ ) genetically differentiated groups of populations. These groups seemed to cluster based on geography (Fig. 2)<sup>4</sup>.

## RESULTS (cont.)

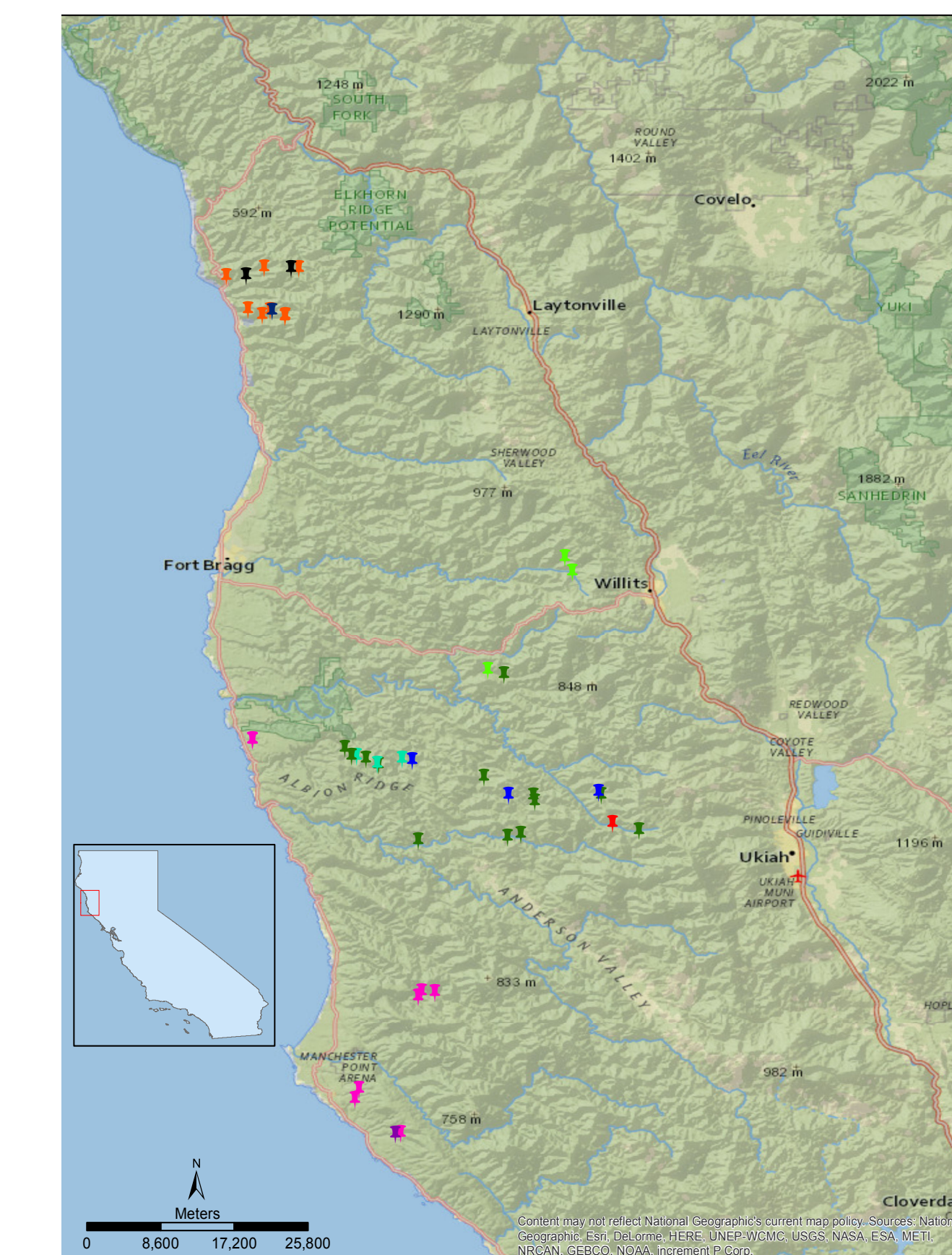


Figure 2. SAMOVA results illustrating clustering of populations for CGS.

## DISCUSSION

Landscape variables played an important role in least cost paths modeling suggesting that potential gene flow routes between sites depend on landscape features. Overall, SAMOVA analyses suggests a general north-south clustering.

Future steps:

- Create linear regressions between geographic distance and genetic distance ( $F_{ST}$ ) for a given LCP
- Determine the best LCP model using AIC scores<sup>1</sup>

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