Adaptation is RAD...seq

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Overview

Funk, W. C. et at. (2016), Adaptive divergence despite strong genetic drift: genomic analysis of the evolutionary mechanisms causing genetic differentiation in the island fox (Urocyon littoralis). Mol Ecol, 25: 2176–2194. doi:10.1111/mec.13605

Sampled Populations

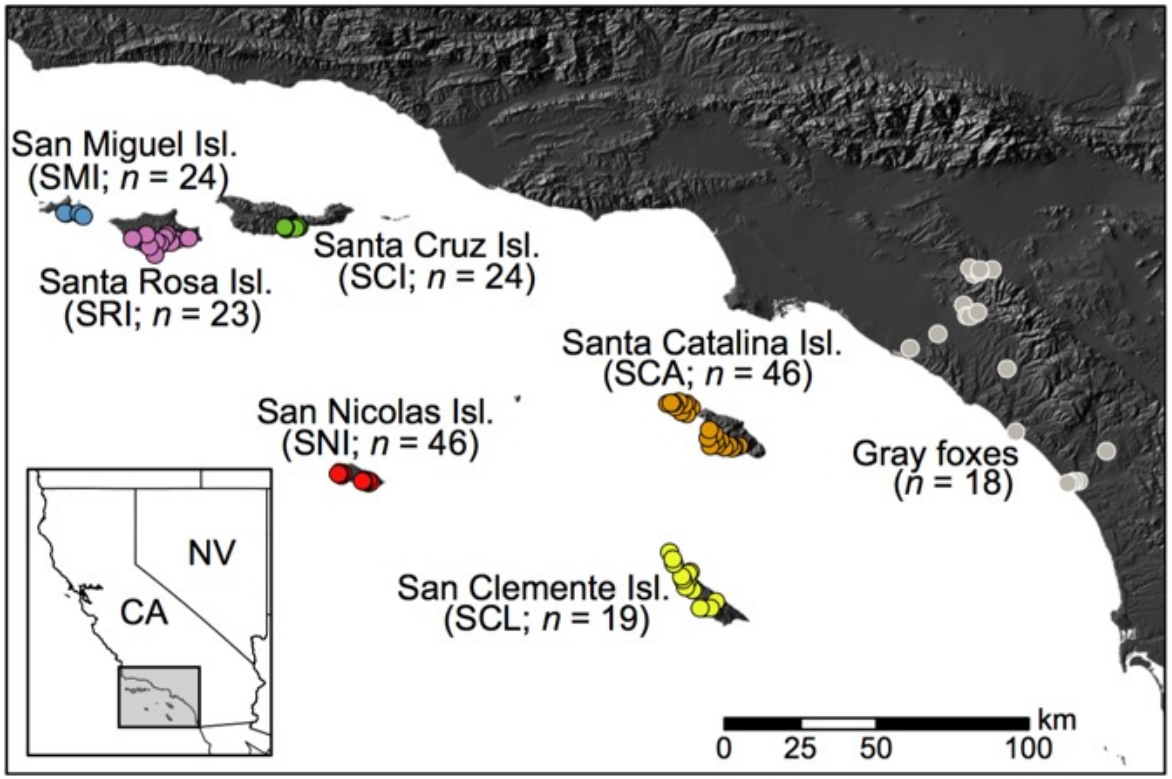

Fig. 1 Map of island fox and grey fox individuals included in genomic analyses. Abbreviations and sample sizes are shown in parentheses. Inset shows location of study area in southern California, USA.

Figure: Map of Island foxes and Grey foxes.

Island foxes

Figure: Island foxes

Introduction

Island Fox Adaptation

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1. Genetic Drift
    1. Founder Effect -variation due to random sampling
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Island Fox Adaptation

1. Genetic Drift
    1. Founder Effect -variation due to random sampling
    1. Greater effects on small populations
2. Natural Selection
    2. Environmental differences between islands cause adaptation
    2. Similar to adaptive radiation in Darwin's finches

Goals

1. Characterize the population genetic structure of island foxes **
2. Test hypothesis that genetic drift contributes to genetic differentiation among populations
3. Test hypothesis that divergent selection caused by environmental differences among islands contributes to genetic differentiation among populations
4. Characterize patterns of population divergence at neutral vs. any detected adaptive loci

Dataset from Funk et al.

1. Two SNP data sets in Genepop file format
    1. With Grey Fox: 4,858 SNPs
    1. Without Grey Fox: 5,293 SNPs
2. SNPs are result of filtering

Fst Values from Arlequin

1. Fst
    1. Genetic measure of differentiation among populations
    1. 0 = no differentiation, 1 = complete differentiation

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    1. Genetic measure of differentiation among populations
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2. Arlequin 3.5
    2. 1,000 permutations
    2. Default parameters

Fst Values from Arlequin

	Grey	SMI	SRI	SCI	SCA	SCL	SNI
Grey	0.000						
SMI	0.688	0.000					
SRI	0.590	0.551	0.000				
SCI	0.623	0.804	0.592	0.000			
SCA	0.463	0.689	0.587	0.546	0.000		
SCL	0.661	0.898	0.772	0.789	0.471	0.000	
SNI	0.825	0.972	0.916	0.931	0.651	0.942	0.000

	Grey foxes	SMI	SRI	SCI	SCA	SCL	SNI
Grey foxes	—	0.376	0.345	0.346	0.282	0.357	0.384
SMI	0.664	—	0.136	0.325	0.457	0.460	0.603
SRI	0.589	0.515	—	0.199	0.368	0.392	0.547
SCI	0.623	0.773	0.584	—	0.291	0.362	0.527
SCA	0.462	0.676	0.596	0.558	—	0.204	0.237
SCL	0.629	0.884	0.749	0.778	0.463	—	0.239
SNI	0.814	0.963	0.902	0.919	0.646	0.914	—

Figure: Left) Our Fst Values Right) Original Fst Values

PCA Analysis

1. File Set-up
    1. Unix: sed, grep
    1. Used both data sets

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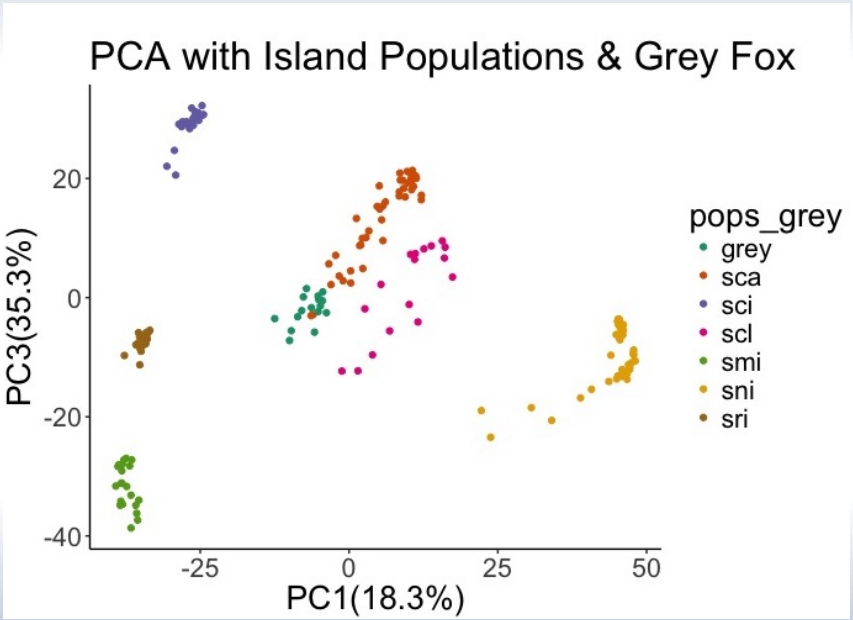
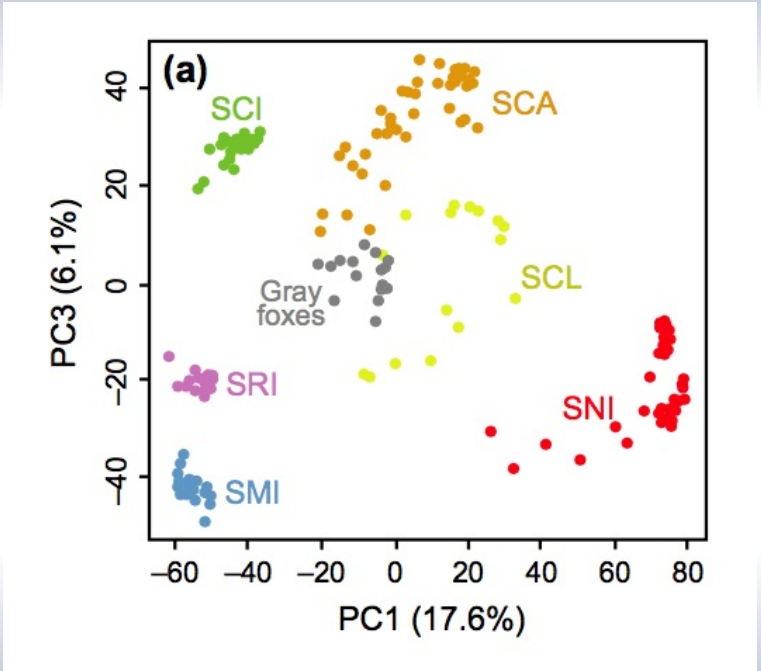
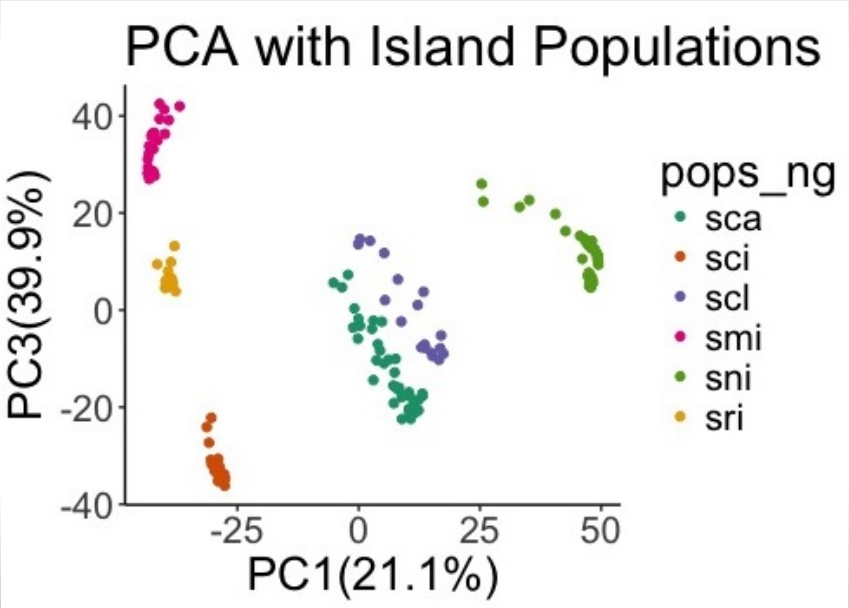
2. PCA Plot Creation
    2. Used prcomp in R
    2. Used ggplot to visualize

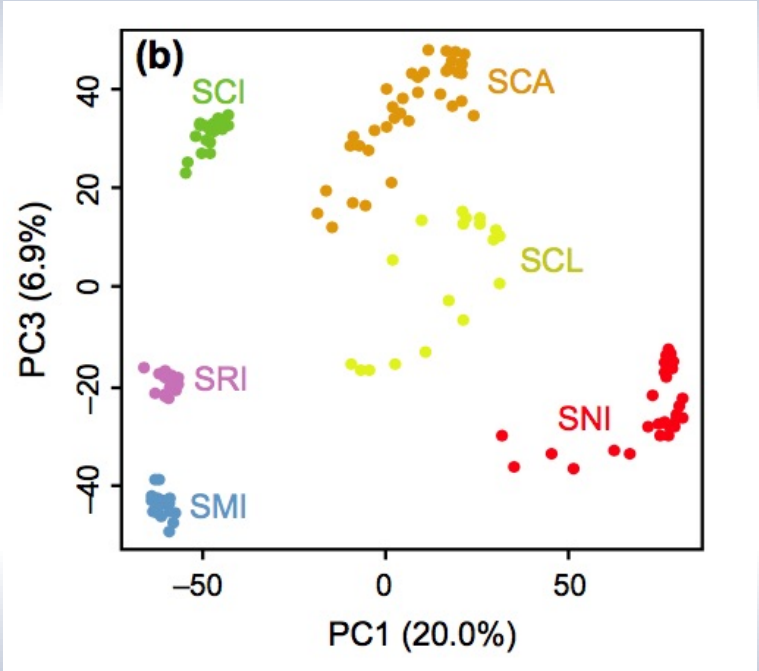
PCA Plot including Grey Foxes





PCA Plot not including Grey Foxes





STRUCTURE Analysis

1. PGDSpyder
    1. Reformatted genepop file format to STRUCTURE file format

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3. STRUCTURE HARVESTER
    3. Shows likelihood for each grouping of individuals from STRUCTURE output

STRUCTURE Comparison

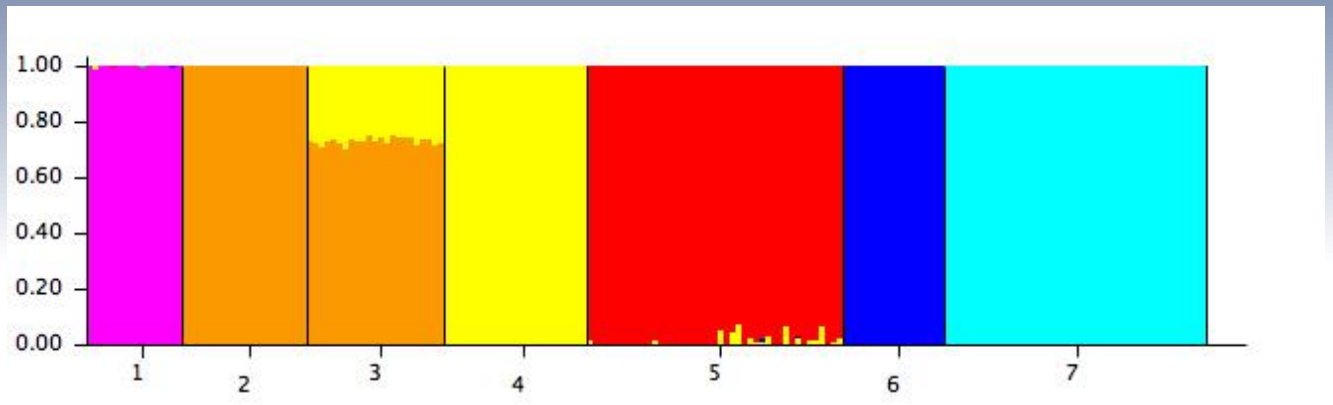


Figure: Our results from structure analysis.

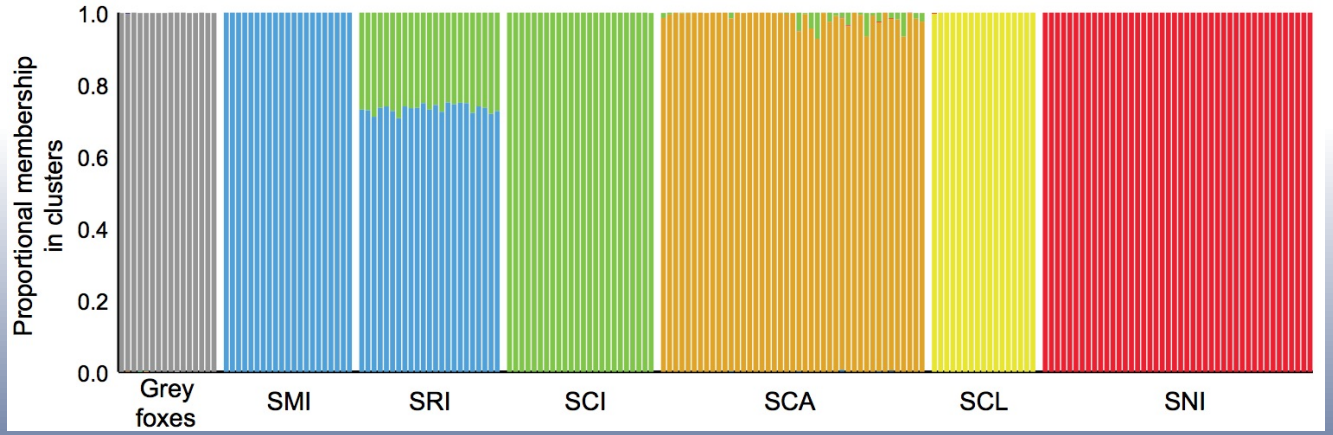
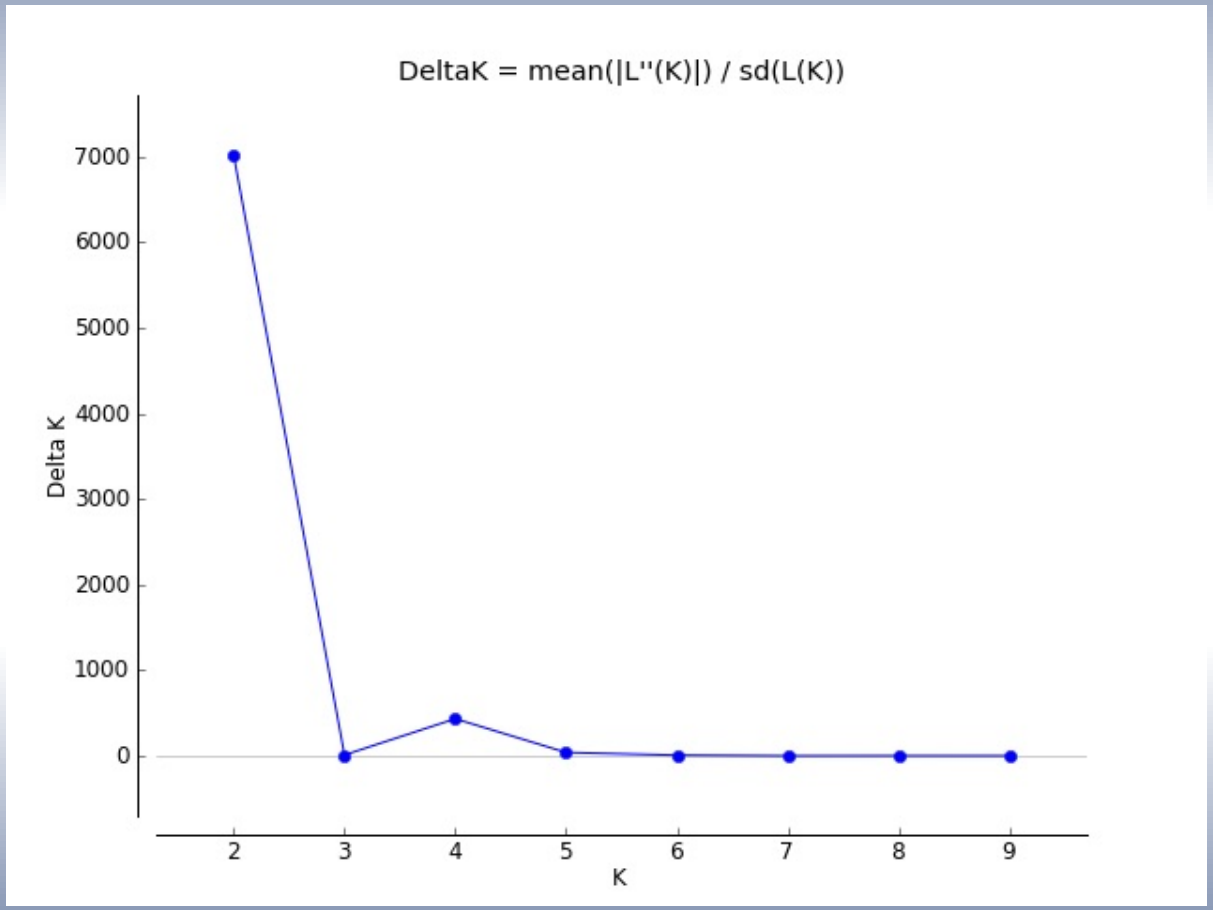


Figure: Original structure analysis results.

STRUCTURE Analysis



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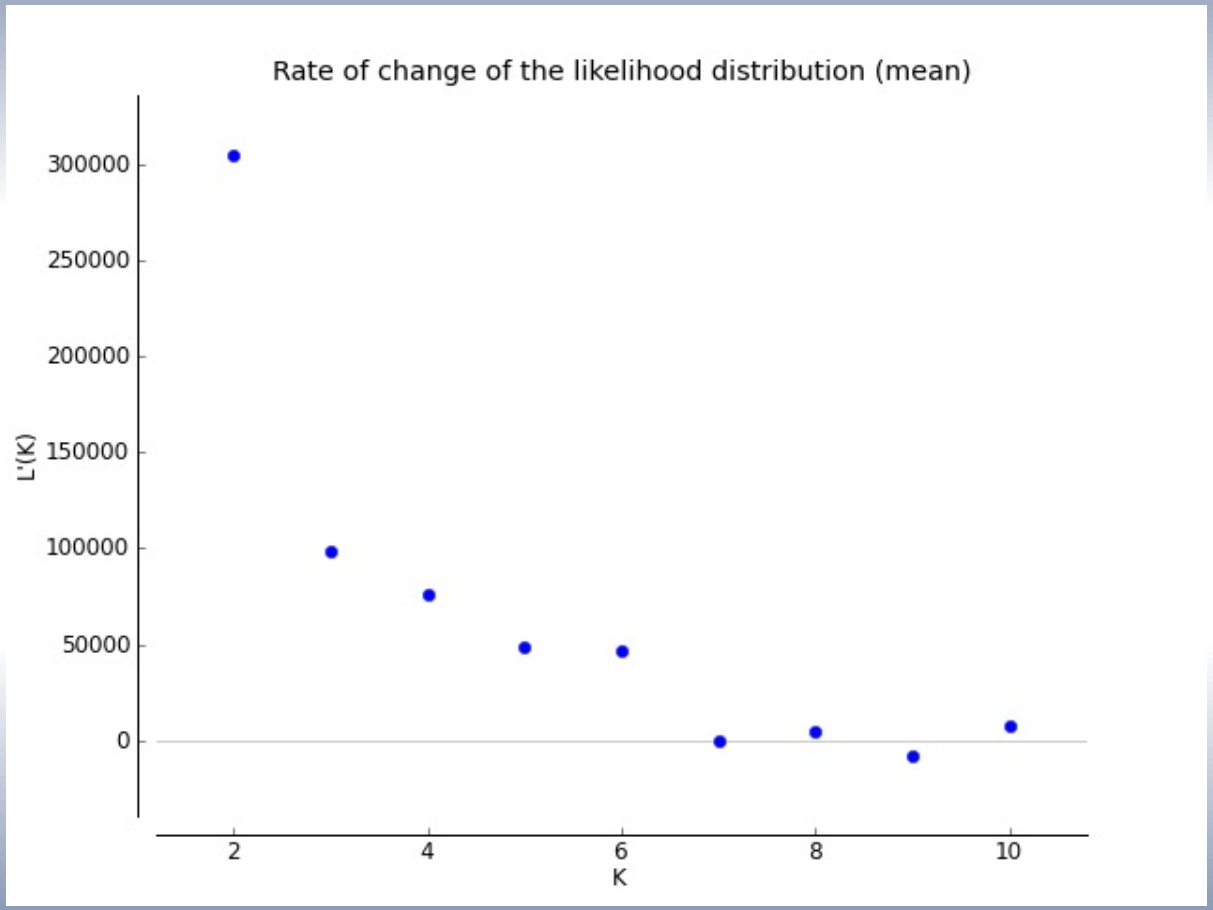

Conclusions

1. Genepop file format is difficult to manipulate in R
2. Arlequin requires very specific file formatting
3. Our results were similar with respect to overall interpretation
4. However, we could not exactly replicate some of their analyses