



# Estimating effective population size (Ne) of wild Delta Smelt using RAD-seq

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## Purpose

- The effective population size (Ne) of a population provides insights into demography history and extinction risk of species of interest and is an important parameter in conservation biology
- The purpose of this study is to develop techniques to sensitively estimate Ne in Delta Smelt using RAD-seq data
- Develop a bioinformatics pipeline to be used to monitor the genetic diversity of non-model organisms
- Determine if declining abundances of Delta Smelt has affected the species' genetic diversity

## Background

### Species

- Hypomesus transpacificus* (Delta Smelt) is a small translucent estuarine fish endemic to the San Francisco Estuary
- Delta Smelt population abundances have been declining since the 1970s and have been protected under the federal and California Endangered Species Act since 1993
- Currently, Delta Smelt abundances are monitored through regular surveys<sup>1</sup>
- Despite an intense amount of research into the species the population abundances continue to decline

### Techniques

- Previous studies have used **temporal** ( $Ne_T$ ) and **linkage disequilibrium** ( $Ne_{LD}$ ) methods to estimate Ne of the wild Delta Smelt population using 12-15 microsatellite markers<sup>2-3</sup>

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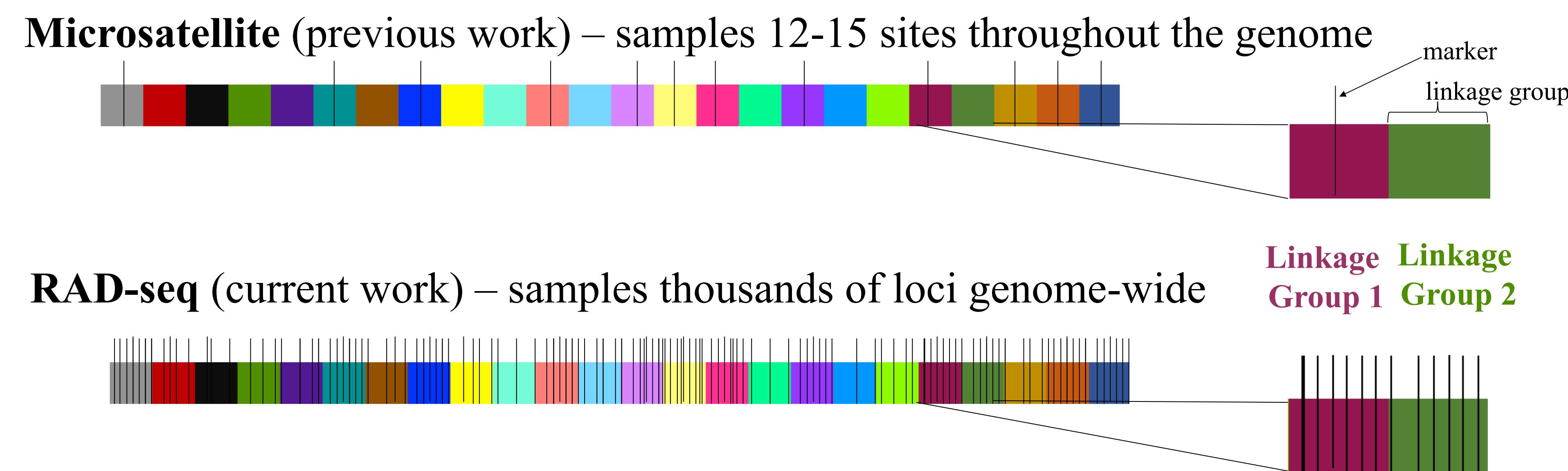
<http://github.com/shannonekj>

Okay to photograph

## Research Questions:

- Are lower abundances of Delta Smelt negatively affecting the species genetic diversity?
- What is the most sensitive and accurate way to estimate the effective population size of Delta Smelt?

## Sequencing Methods



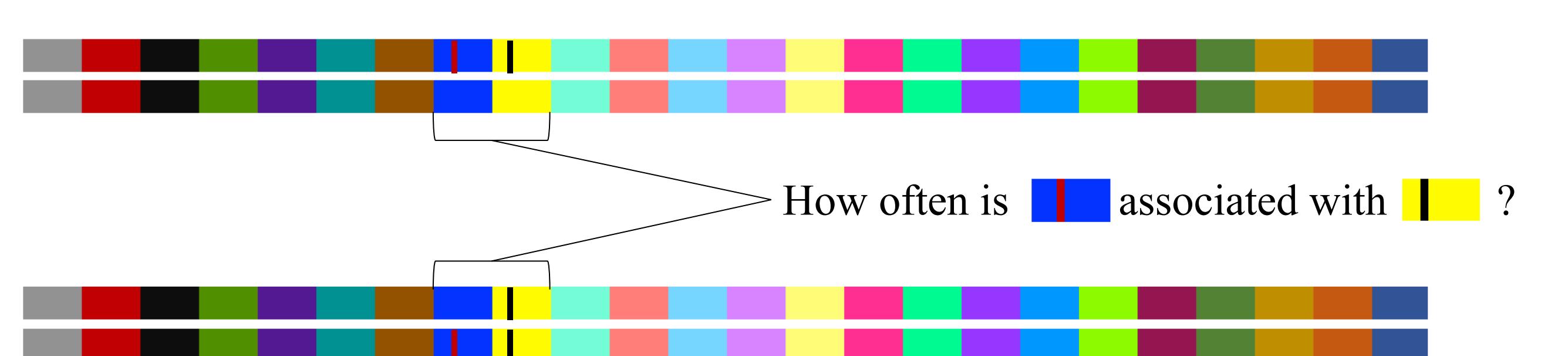
## Estimation of Ne

### Temporal Multiple Generations



Compare allele frequencies genome wide to measure degree of genetic drift.

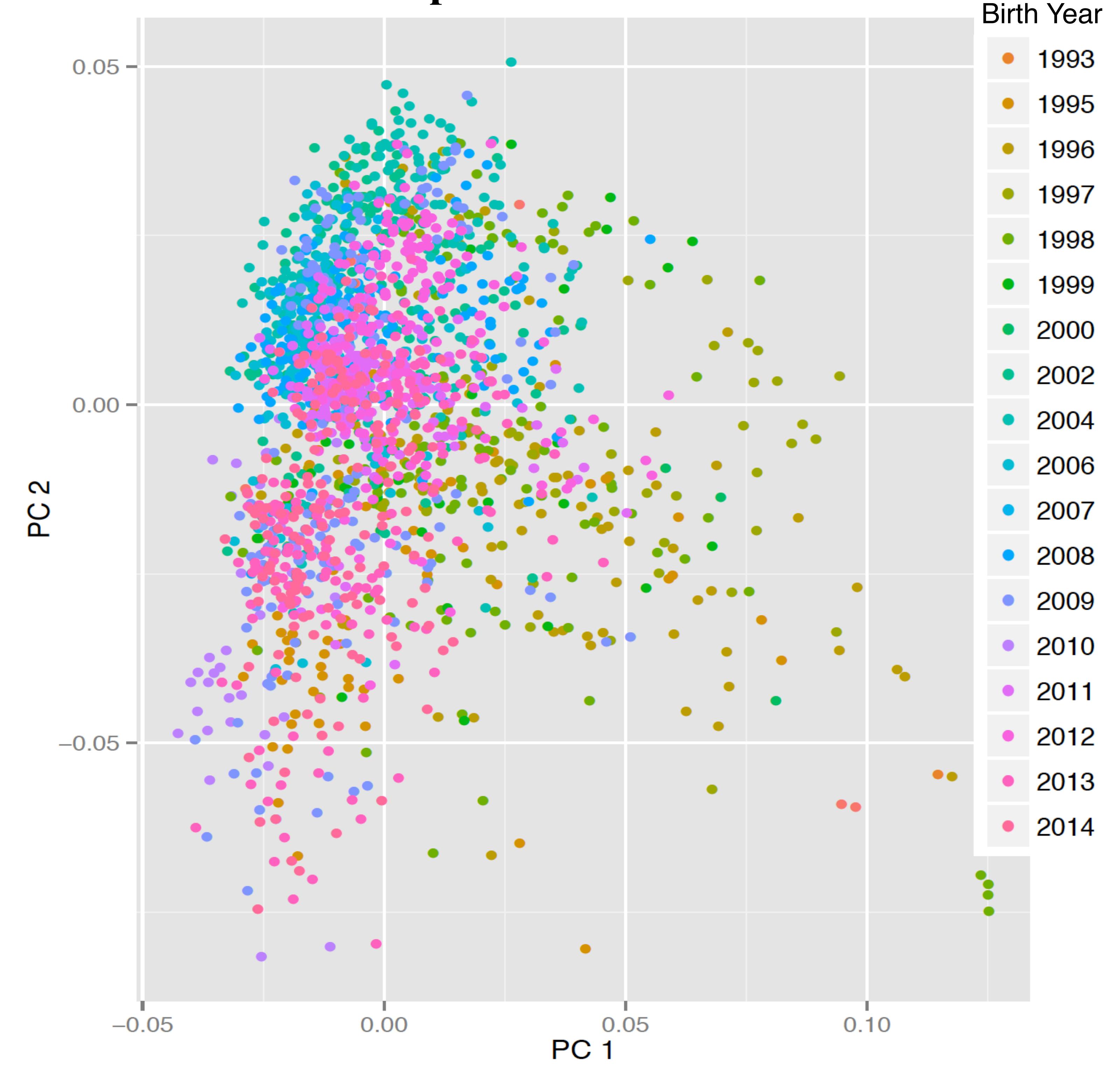
### Linkage Disequilibrium Single Generation



$$\hat{N}_e = \frac{1}{3(\hat{r}^2 - \frac{1}{S})}$$

S= # individuals sampled  
 $\hat{r}^2$  = mean squared inter-locus correlation of allele frequencies

## PCA plot of wild Delta Smelt



## Terms Defined

**Ne:** The effective population size of an ideal population. This term measures the amount of genetic diversity maintained within a population.

**Ne<sub>LD</sub>:** A temporal method of estimating effective population size. This method uses samples from different generations.

**Ne<sub>T</sub>:** A linkage disequilibrium method of estimating effective population size. This method uses samples from a single generation.

**Linkage Disequilibrium:** The nonrandom association of alleles at different loci in a given population.

**RAD-seq:** Restriction site Associated DNA Sequencing

## References

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