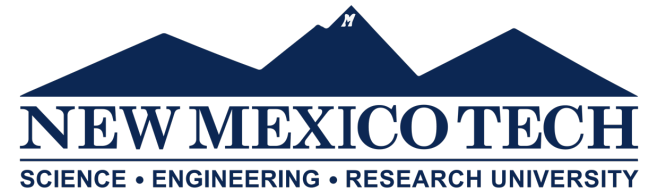


# Exploring conservation genomic data in R

Josh Jahner  
jpjahner@gmail.com



UNIVERSITY  
OF WYOMING



# Outline of today's topics

- 1) Big questions in conservation genetics
- 2) Types of conservation genetic data
- 3) Simulating data with the beta distribution
- 4) Exploring conservation genetic analyses

# Genetic diversity and inbreeding

FROM THE COVER

MOLECULAR ECOLOGY  
RESOURCES WILEY

## Genomics-informed captive breeding can reduce inbreeding depression and the genetic load in zoo populations

Samuel A. Speak<sup>1,2,3</sup>  | Thomas Birley<sup>1</sup> | Chiara Bortoluzzi<sup>4,5</sup> | Matthew D. Clark<sup>2,6</sup> |  
Lawrence Percival-Alwyn<sup>7</sup> | Hernán E. Morales<sup>8</sup>  | Cock van Oosterhout<sup>1</sup> 

# Identifying adaptive genetic variation


Received: 30 January 2024 | Revised: 23 April 2024 | Accepted: 30 April 2024

DOI: 10.1111/mec.17383

**ORIGINAL ARTICLE**

**MOLECULAR ECOLOGY** WILEY

## Natural selection on feralization genes contributed to the invasive spread of wild pigs throughout the United States

Niek W. G. Barmantlo<sup>1,2</sup>  | Patrick G. Meirmans<sup>2</sup>  | William H. Stiver<sup>3</sup> |  
Joseph G. Yarkovich<sup>3</sup> | Blake E. McCann<sup>4</sup> | Antoinette J. Piaggio<sup>5</sup> | Dominic Wright<sup>6</sup>  |  
Timothy J. Smyser<sup>5</sup>  | Mirte Bosse<sup>1,7</sup> 

# Population structure and connectivity



*Molecular Ecology*

WILEY

MOLECULAR ECOLOGY

ORIGINAL ARTICLE **OPEN ACCESS**

## Shared Dispersal Patterns but Contrasting Levels of Gene Flow in Two Anadromous Salmonids Along a Broad Subarctic Coastal Gradient

Raphaël Bouchard<sup>1,2</sup>  | Charles Babin<sup>1,2</sup> | Eric Normandeau<sup>3</sup> | Amanda Xuereb<sup>1,2</sup> | Félix Boulanger<sup>4</sup> | Angela Coxon<sup>4</sup> | Sanford Diamond<sup>5</sup> | Robert Fireman<sup>5</sup> | John Lameboy<sup>5</sup> | Natasha Louttit<sup>4,5</sup> | George Natawapineskum<sup>5</sup> | Derek Okimaw<sup>5</sup> | Dante Torio<sup>6</sup> | Stephanie Varty<sup>5</sup> | Jean-Sébastien Moore<sup>1,2</sup> | Dylan Fraser<sup>7</sup>  | Louis Bernatchez<sup>1,2</sup>

# Population size estimation










*Evolutionary Applications*

WILEY

Evolutionary Applications 




ORIGINAL ARTICLE **OPEN ACCESS**

## Estimating the Effective Size of European Wolf Populations

Joachim Mergeay<sup>1,2</sup>  | Sander Smet<sup>2</sup> | Sebastian Collet<sup>3</sup>  | Sabina Nowak<sup>4</sup>  | Ilka Reinhardt<sup>5</sup>  | Gesa Kluth<sup>5</sup> |  
Maciej Szewczyk<sup>6</sup>  | Raquel Godinho<sup>7</sup>  | Carsten Nowak<sup>3</sup>  | Robert W. Mysłajek<sup>4</sup>  | Gregor Rolshausen<sup>3</sup> 

# Demographic history reconstruction

## Whole Genomes Inform Genetic Rescue Strategy for Montane Red Foxes in North America

Cate B. Quinn <sup>1,2,3,\*</sup> Sophie Preckler-Quisquater,<sup>1</sup> Michael R. Buchalski <sup>2</sup>  
Benjamin N. Sacks <sup>1,4</sup>

# Species delimitation



Current Biology

## Report

# Comparative species delimitation of a biological conservation icon

Ava Ghezelayagh,<sup>1,2,13,14,\*</sup> Jeffrey W. Simmons,<sup>3</sup> Julia E. Wood,<sup>1</sup> Tsunemi Yamashita,<sup>4</sup> Matthew R. Thomas,<sup>5</sup>  
Rebecca E. Blanton,<sup>6</sup> Oliver D. Orr,<sup>1</sup> Daniel J. MacGuigan,<sup>7</sup> Daemin Kim,<sup>1</sup> Edgar Benavides,<sup>8,9</sup> Benjamin P. Keck,<sup>10</sup>  
Richard C. Harrington,<sup>1,11</sup> and Thomas J. Near<sup>1,12</sup>



# Hybridization and admixture




*Evolution Letters*, 2025, 9(1), 1–12

<https://doi.org/10.1093/evlett/qrae057>

Advance access publication 19 October 2024

**Letter**

## Genetic structure and common ancestry expose the dingo-dog hybrid myth

Andrew R. Weeks<sup>1,2</sup> , Peter Kriesner<sup>1</sup>, Nenad Bartonicek<sup>1,†</sup>, Anthony van Rooyen<sup>1</sup>, Kylie M. Cairns<sup>3</sup>, Collin W. Ahrens<sup>1</sup>

# Assisted gene flow, genetic rescue, translocations





*Evolutionary Applications*

WILEY

Evolutionary Applications 

ORIGINAL ARTICLE **OPEN ACCESS**

## Genetic Rescue of the Dinaric Lynx Population: Insights for Conservation From Genetic Monitoring and Individual-Based Modelling

Elena Pazhenkova<sup>1,2</sup>  | Matej Bartol<sup>3</sup> | Barbara Boljte<sup>1,2</sup> | Urša Fležar<sup>1</sup> | Andrea Gazzola<sup>4</sup> | Tomislav Gomerčič<sup>5</sup> | Marjeta Konec<sup>1,2</sup> | Ivan Kos<sup>1</sup> | Miha Krofel<sup>1</sup> | Jakub Kubala<sup>6</sup> | Ladislav Paule<sup>6</sup>  | Mihai Pop<sup>4</sup> | Hubert Potočník<sup>1</sup> | Barbara Promberger<sup>7</sup> | Robin Rigg<sup>1,8</sup> | Teodora Sin<sup>4</sup>  | Magda Sindičić<sup>5</sup> | Vedran Slijepčević<sup>9</sup> | Astrid Vik Stronen<sup>1,2,10</sup>  | Ira Topličanec<sup>5</sup> | Tomaž Skrbinšek<sup>1,2</sup>

# Genetic monitoring

Received: 26 September 2023 | Revised: 1 December 2023 | Accepted: 19 January 2024

DOI: 10.1002/ece3.10934

## RESEARCH ARTICLE

Ecology and Evolution

Open Access

WILEY

## Evaluating genotyping-in-thousands by sequencing as a genetic monitoring tool for a climate sentinel mammal using non-invasive and archival samples

Kate E. Arpin<sup>1</sup> | Danielle A. Schmidt<sup>1</sup> | Bryson M. F. Sjodin<sup>1</sup> | Anthony L. Einfeldt<sup>2</sup> |  
Kurt Galbreath<sup>3</sup> | Michael A. Russello<sup>1</sup> 

# Outline of today's topics

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# Mitochondrial DNA (Sanger sequencing)

Individual 1

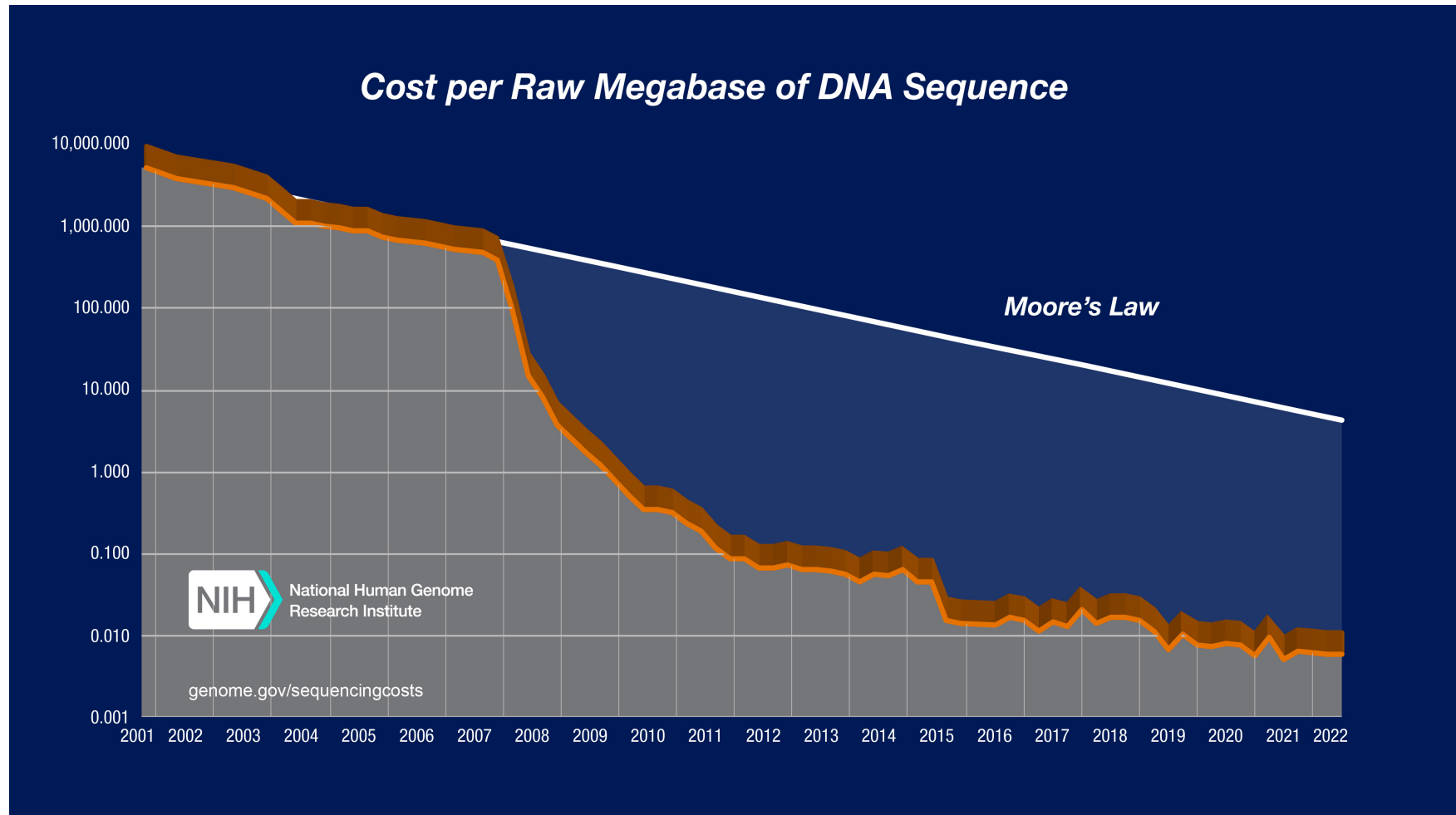
ACTTTGAGCTTTCTGA ...  
ACTCTGAGCTTTCTGA ...

Individual 2

ACTCTGGGCTATCTGA ...  
ACTCTGGGCTATCTGA ...



# Availability of massive data sets in the life sciences



# Reduced representation sequencing

Section of a chromosome



Sequences  
from one cut site

CCATGGTGAATCACCCTG  
CCATGGGTAATCACCCTG  
CCATGGTGAATCACCCTG  
CCATGGTGAATCACCCTG  
CCATGGGTAATCACCCTG  
CCATGGTGAATCACCCTG  
CCATGGGTAATCACCCTG  
CCATGGGTAATCACCCTG



Single nucleotide  
polymorphism (SNP)



# Reduced representation sequencing

Section of a chromosome



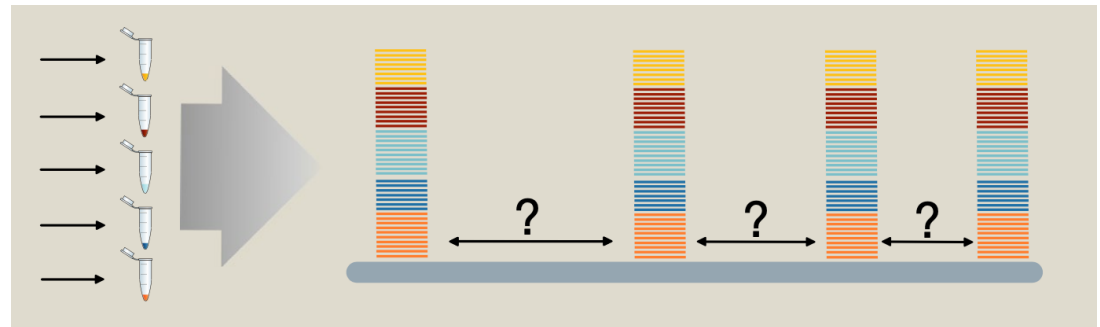
Sequences  
from one cut site

CCATGGTGTAAATCACCCCTG  
CCATGGGTAATCACCCCTG  
CCATGGTGTAAATCACCCCTG  
CCATGGTGTAAATCACCCCTG  
CCATGGGTAATCACCCCTG  
CCATGGTGTAAATCACCCCTG  
CCATGGGTAATCACCCCTG  
CCATGGGTAATCACCCCTG  
CCATGGGTAATCACCCCTG



Single nucleotide  
polymorphism (SNP)

RADseq approaches



# Reduced representation sequencing

Section of a chromosome

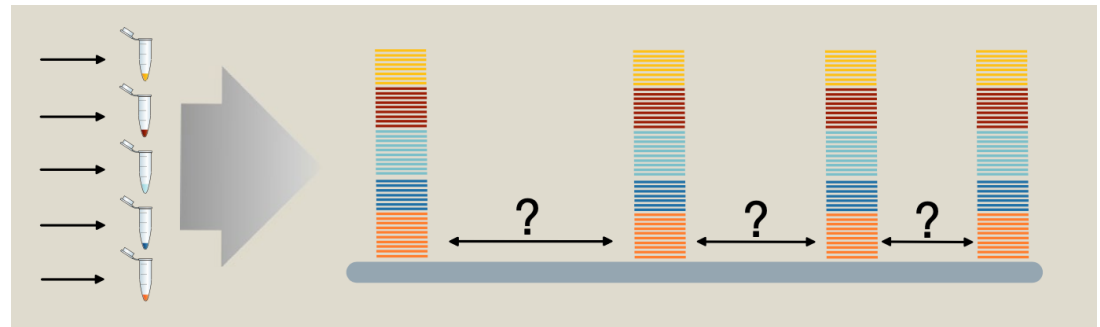


Sequences  
from one cut site

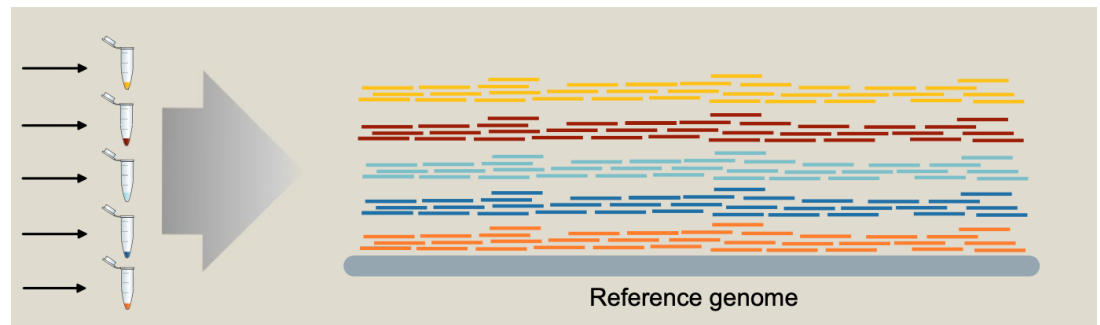
CCATGGT**I**GTAATCACCCCTG  
CCATGG**G**GTAATCACCCCTG  
CCATGGT**I**GTAATCACCCCTG  
CCATGGT**I**GTAATCACCCCTG  
CCATGG**G**GTAATCACCCCTG  
CCATGGT**I**GTAATCACCCCTG  
CCATGG**G**GTAATCACCCCTG  
CCATGG**G**GTAATCACCCCTG

↑  
Single nucleotide  
polymorphism (SNP)

RADseq approaches



Whole genome resequencing



# Outline of today's topics

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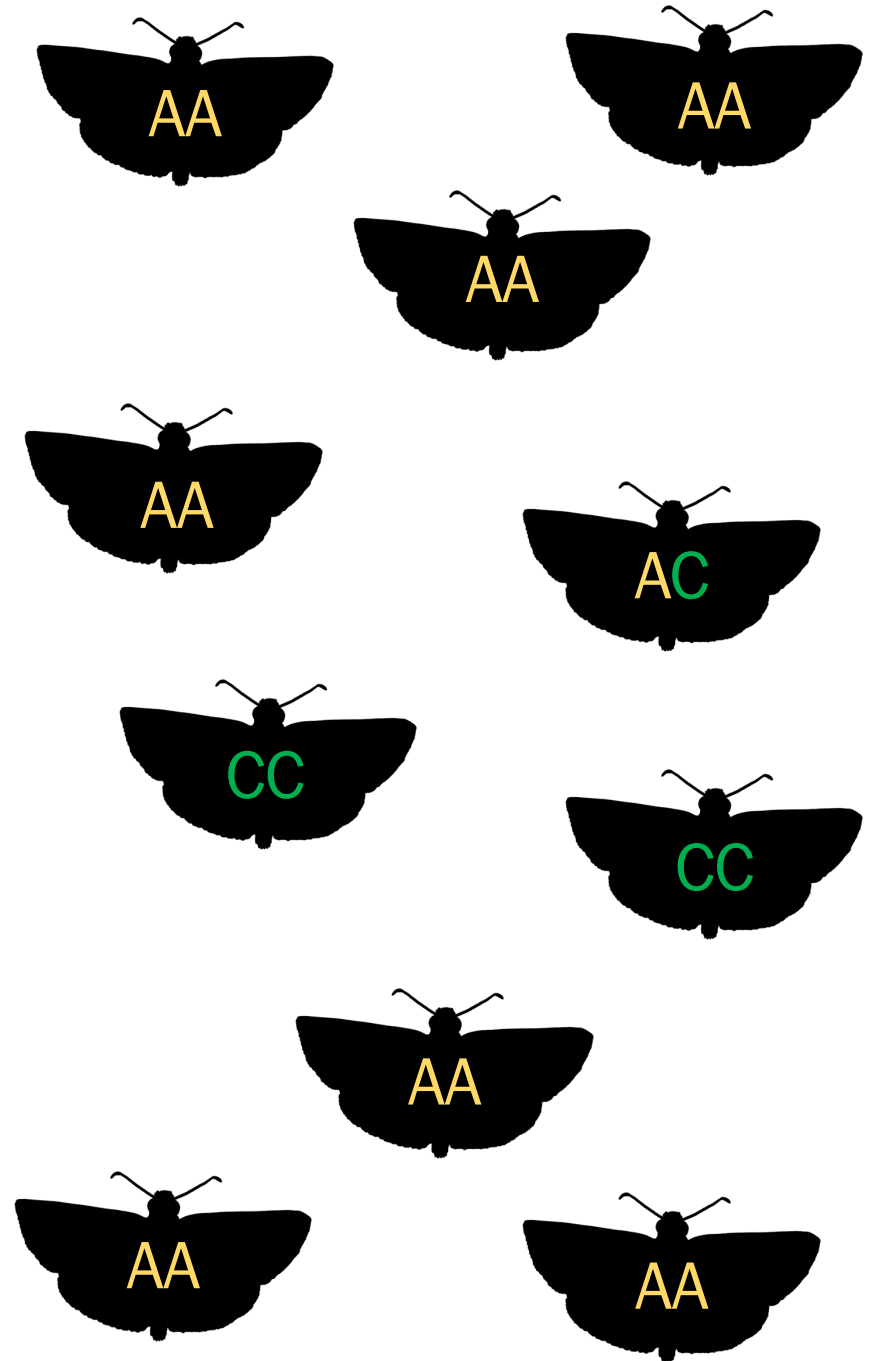
Find the R scripts at:

[https://github.com/jpjahner/congen\\_workshop](https://github.com/jpjahner/congen_workshop)

01\_beta\_simulate.R

02\_explore\_analyses.R

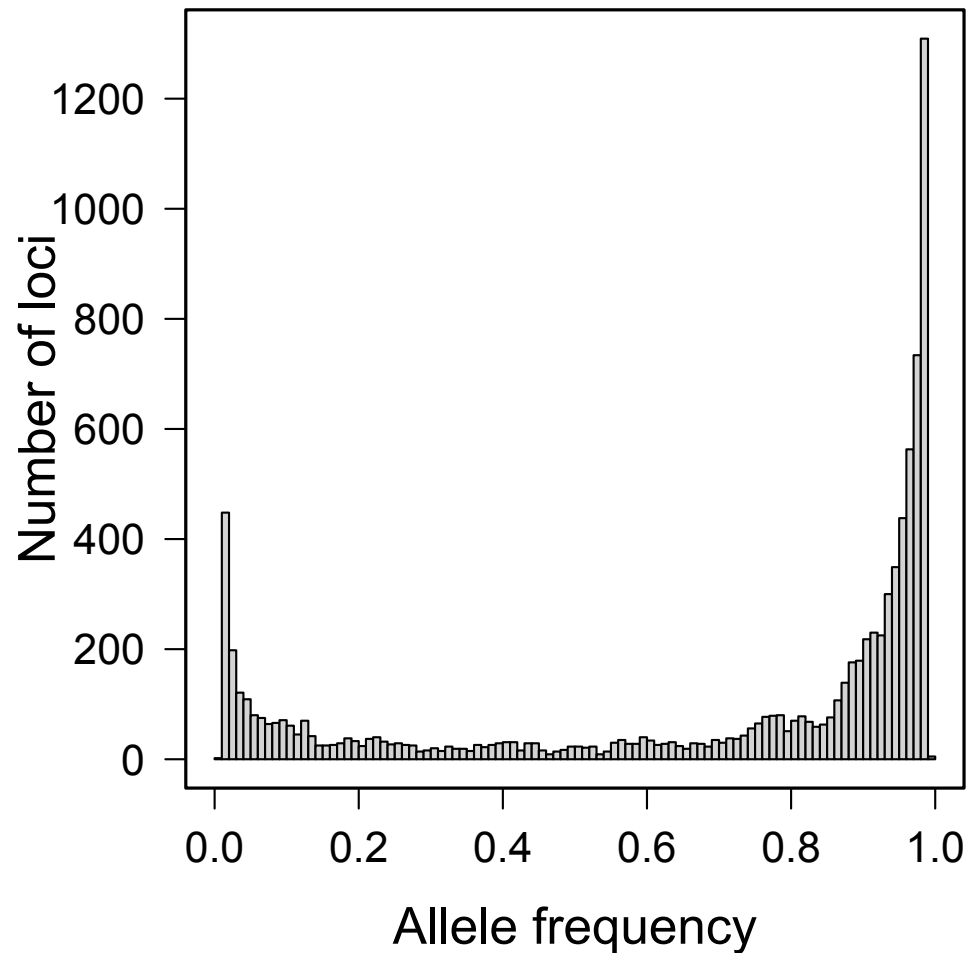
Allele frequency of A:  
 $15 / 20 = 0.75$

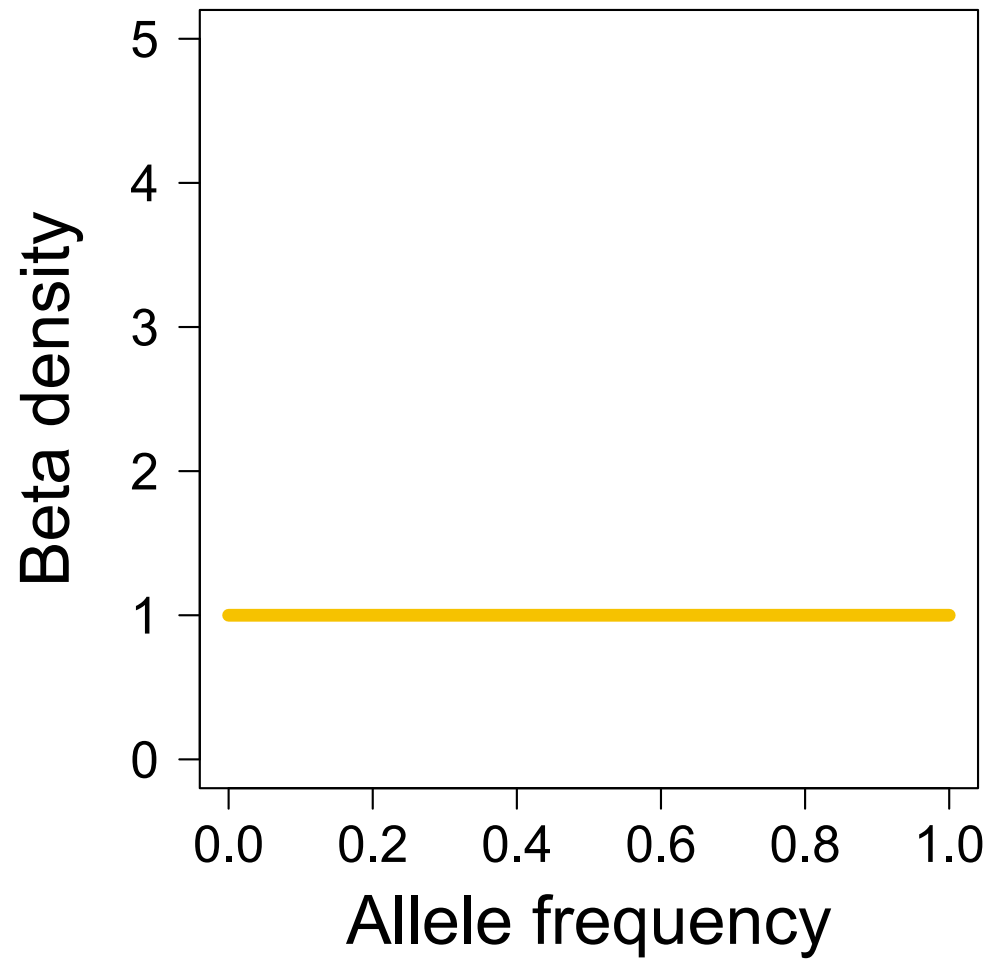


# Influence of dams on sauger population structure and hybridization with introduced walleye

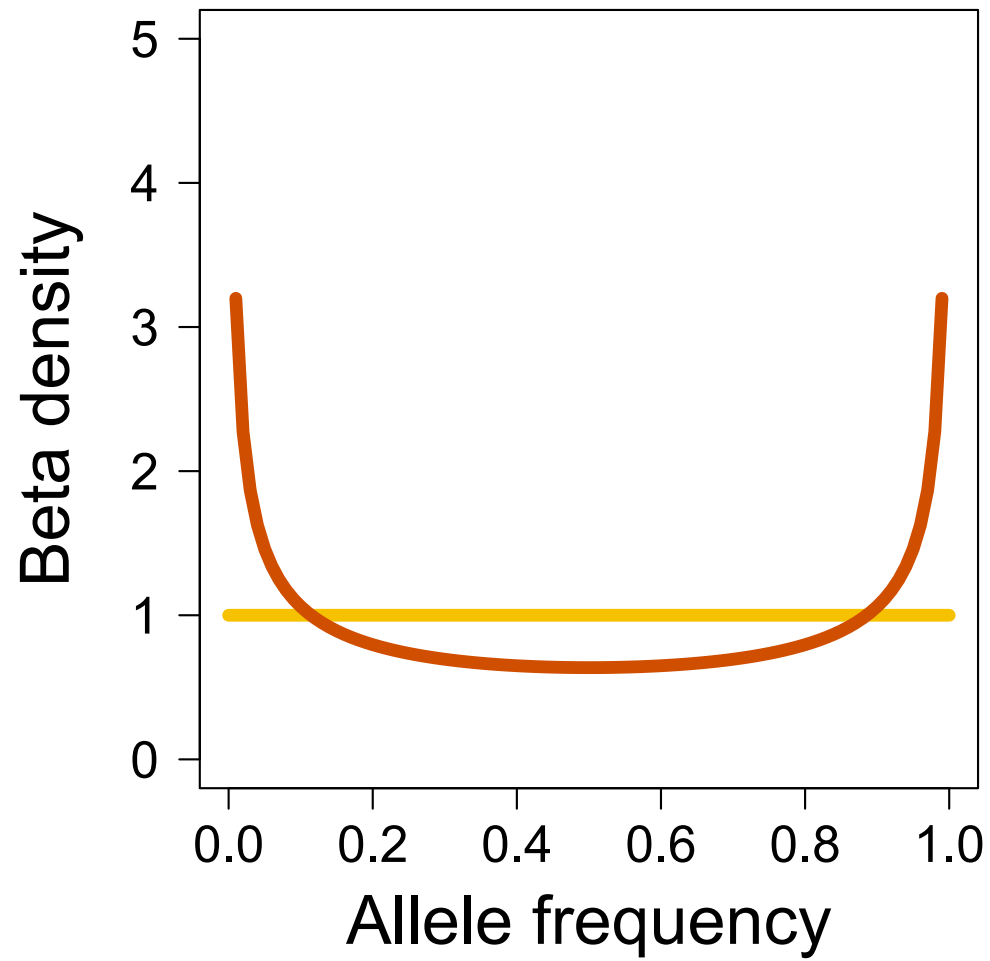
William C. Rosenthal<sup>1,2</sup>  | Elizabeth G. Mandeville<sup>1,3</sup> | Ashleigh M. Pilkerton<sup>2,4,5</sup>  |  
Paul C. Gerrity<sup>6</sup> | Joseph A. Skorupski<sup>6</sup> | Annika W. Walters<sup>2,4,5,7</sup>  |  
Catherine E. Wagner<sup>1,2</sup>

## Site Frequency Spectrum (SFS)



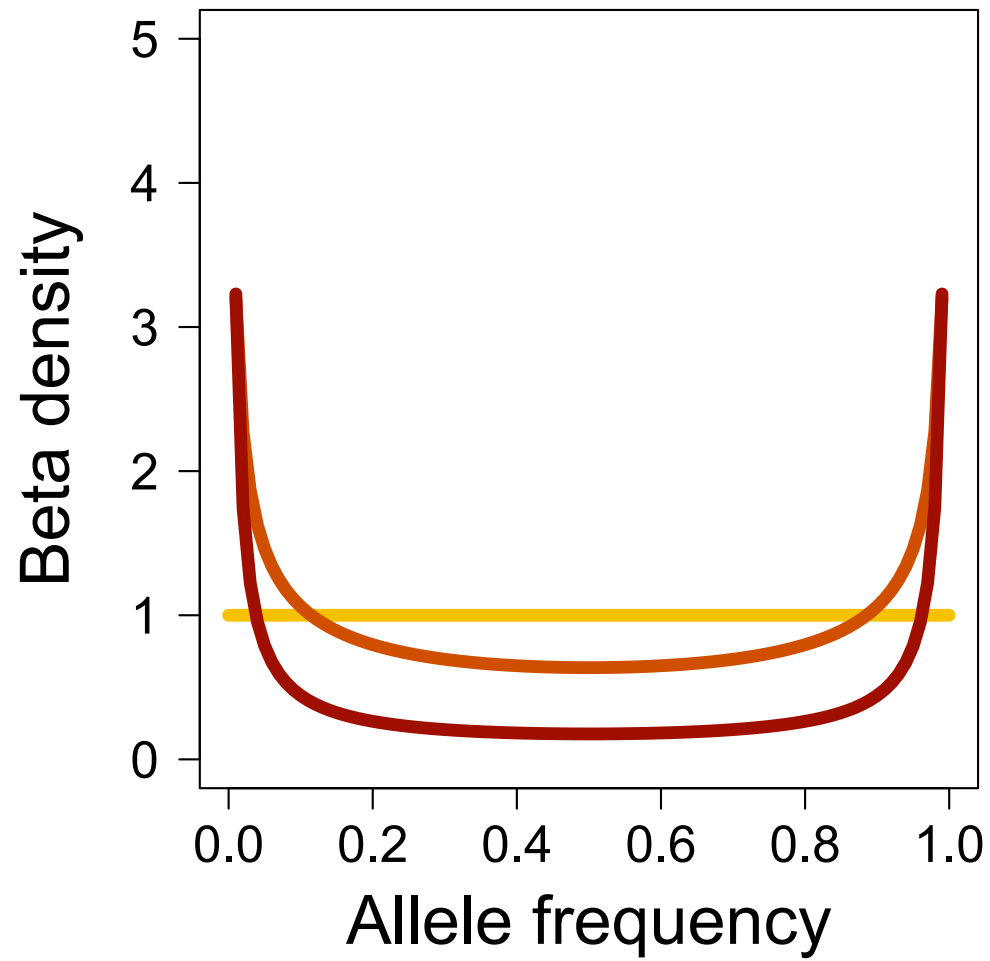


$$\alpha = 1 \quad \beta = 1$$

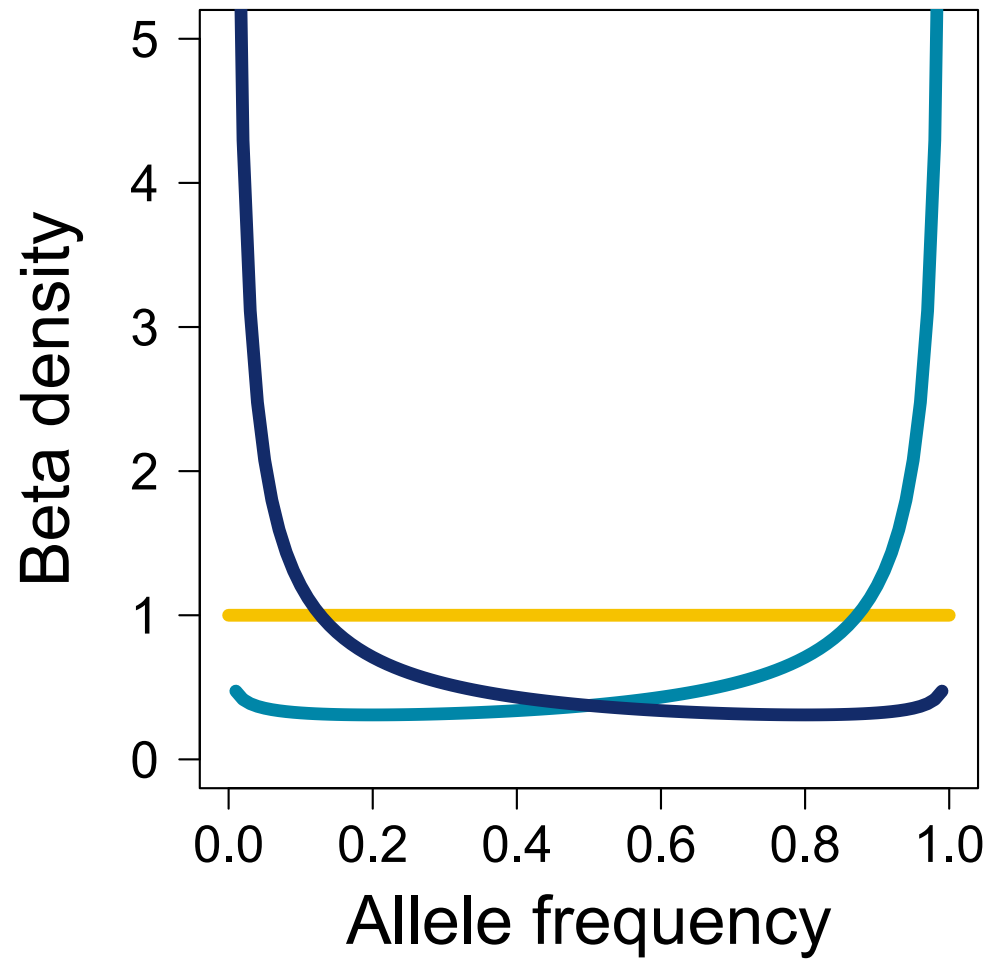


$\alpha = 1$   $\beta = 1$   
 $\alpha = 0.5$   $\beta = 0.5$

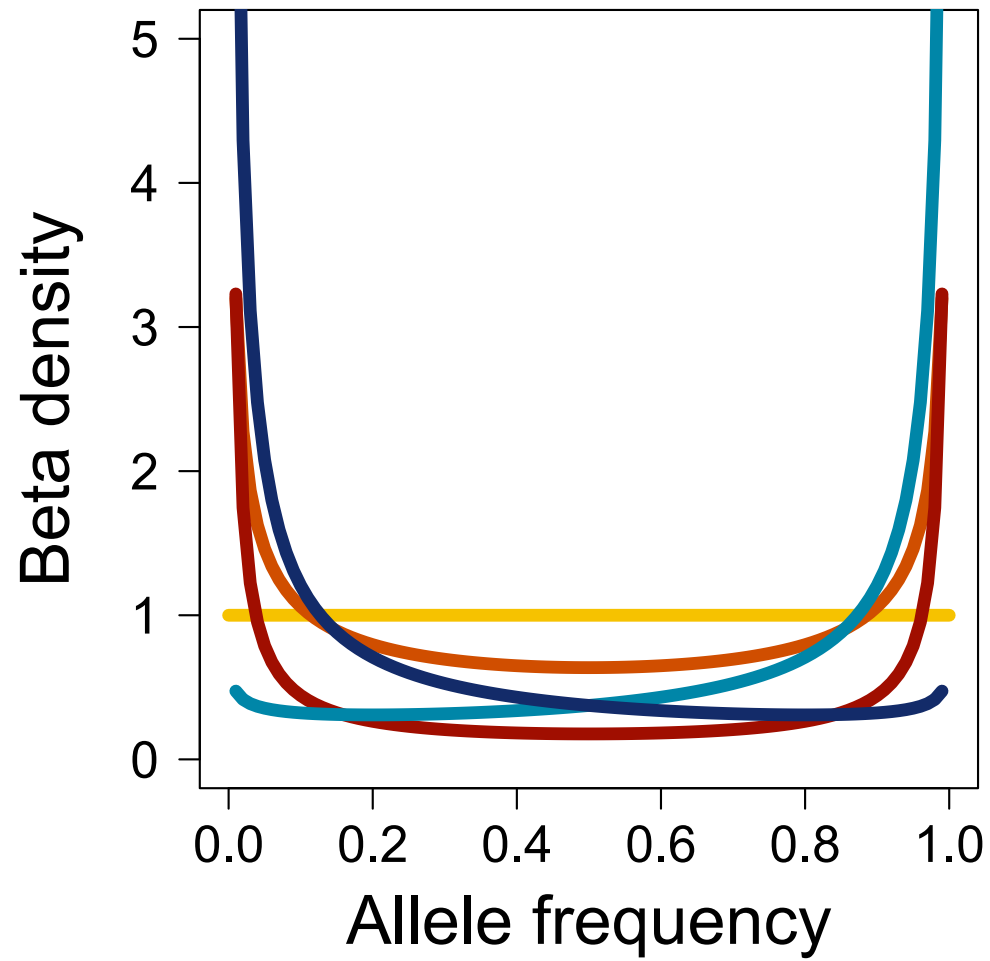




$\alpha = 1 \quad \beta = 1$   
 $\alpha = 0.5 \quad \beta = 0.5$   
 $\alpha = 0.1 \quad \beta = 0.1$



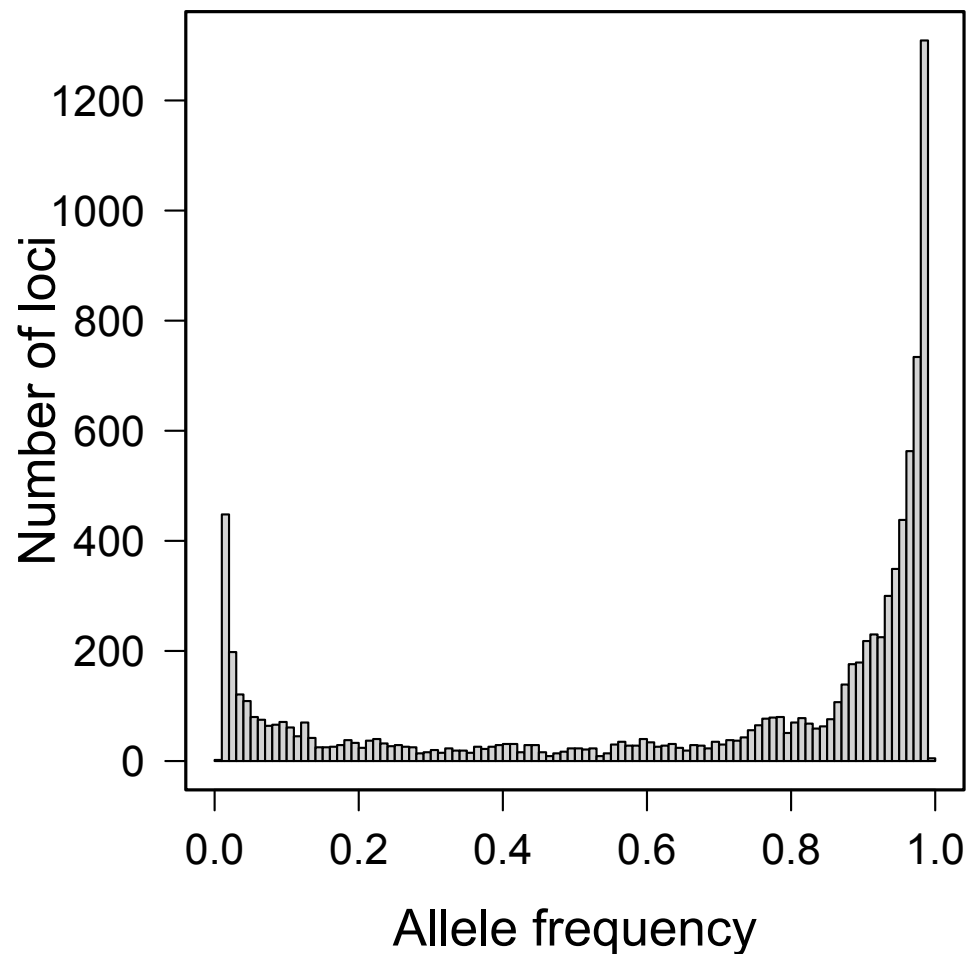
$\alpha = 0.2$     $\beta = 0.8$   
 $\alpha = 0.8$     $\beta = 0.2$   
 $\alpha = 1$     $\beta = 1$



$\alpha = 0.2$   $\beta = 0.8$   
 $\alpha = 0.8$   $\beta = 0.2$   
 $\alpha = 1$   $\beta = 1$   
 $\alpha = 0.5$   $\beta = 0.5$   
 $\alpha = 0.1$   $\beta = 0.1$

# Influence of dams on sauger population structure and hybridization with introduced walleye

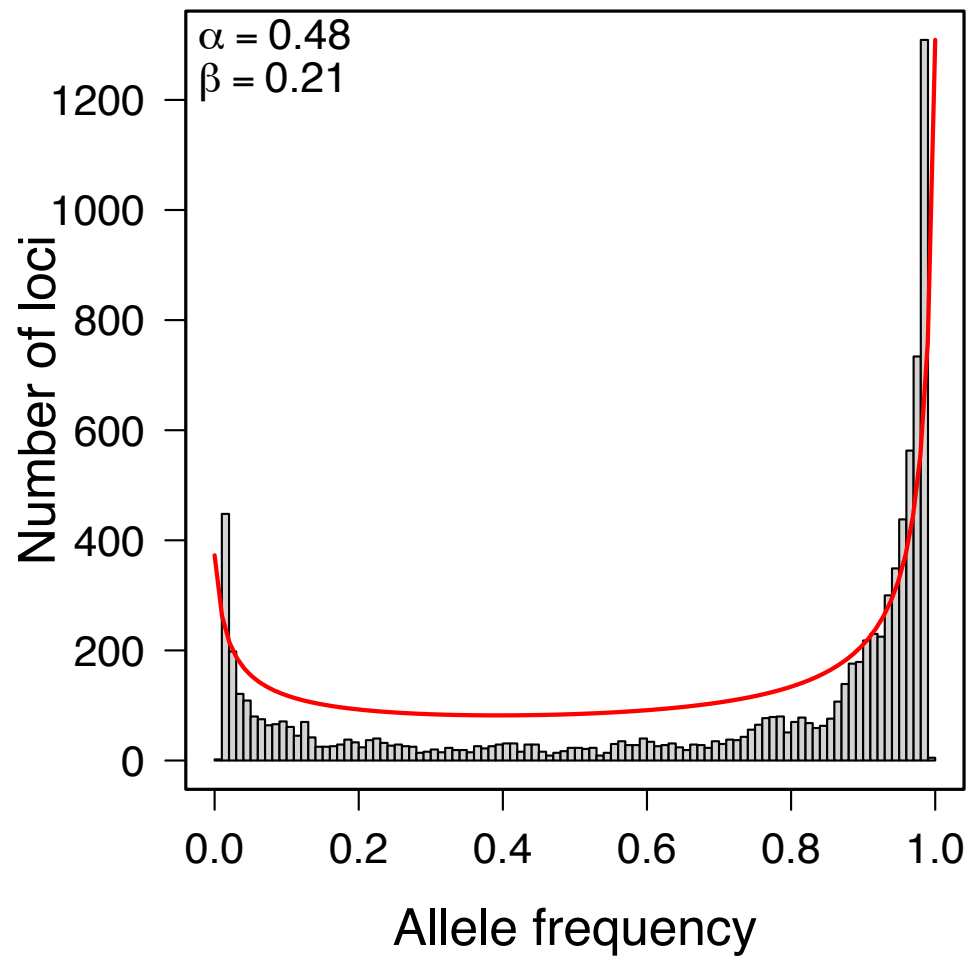
William C. Rosenthal<sup>1,2</sup>  | Elizabeth G. Mandeville<sup>1,3</sup> | Ashleigh M. Pilkerton<sup>2,4,5</sup>  |  
Paul C. Gerrity<sup>6</sup> | Joseph A. Skorupski<sup>6</sup> | Annika W. Walters<sup>2,4,5,7</sup>  |  
Catherine E. Wagner<sup>1,2</sup>



`dbeta(xvals, shape1=NA, shape2=NA)`

# Influence of dams on sauger population structure and hybridization with introduced walleye

William C. Rosenthal<sup>1,2</sup>  | Elizabeth G. Mandeville<sup>1,3</sup> | Ashleigh M. Pilkerton<sup>2,4,5</sup>  |  
Paul C. Gerrity<sup>6</sup> | Joseph A. Skorupski<sup>6</sup> | Annika W. Walters<sup>2,4,5,7</sup>  |  
Catherine E. Wagner<sup>1,2</sup>




```
## Function for simulating genetic data from the beta distribution
```

```
single_pop_sim <- function(nloci=NA, ninds=NA, alpha=NA, beta=NA){  
  genotypes <- matrix(NA, ninds, nloci)  
  for (i in 1:nloci){  
    afreq <- rbeta(1, alpha, beta)  
    for (j in 1:ninds){  
      genotypes[j,i] <- sum(rbinom(2, 1, afreq))  
    }  
  }  
  return(genotypes)  
}
```

```
## Function for simulating genetic data from the beta distribution
```

```
single_pop_sim <- function(nloci=NA, ninds=NA, alpha=NA, beta=NA){  
  genotypes <- matrix(NA, ninds, nloci)  
  for (i in 1:nloci){  
    afreq <- rbeta(1, alpha, beta)  
    for (j in 1:ninds){  
      genotypes[j,i] <- sum(rbinom(2, 1, afreq))  
    }  
  }  
  return(genotypes)  
}
```




Draw an allele  
freq from the  
beta distribution


```
## Function for simulating genetic data from the beta distribution
```

```
single_pop_sim <- function(nloci=NA, ninds=NA, alpha=NA, beta=NA){  
  genotypes <- matrix(NA, ninds, nloci)  
  for (i in 1:nloci){  
    afreq <- rbeta(1, alpha, beta)  
    for (j in 1:ninds){  
      genotypes[j,i] <- sum(rbinom(2, 1, afreq))  
    }  
  }  
  return(genotypes)  
}
```

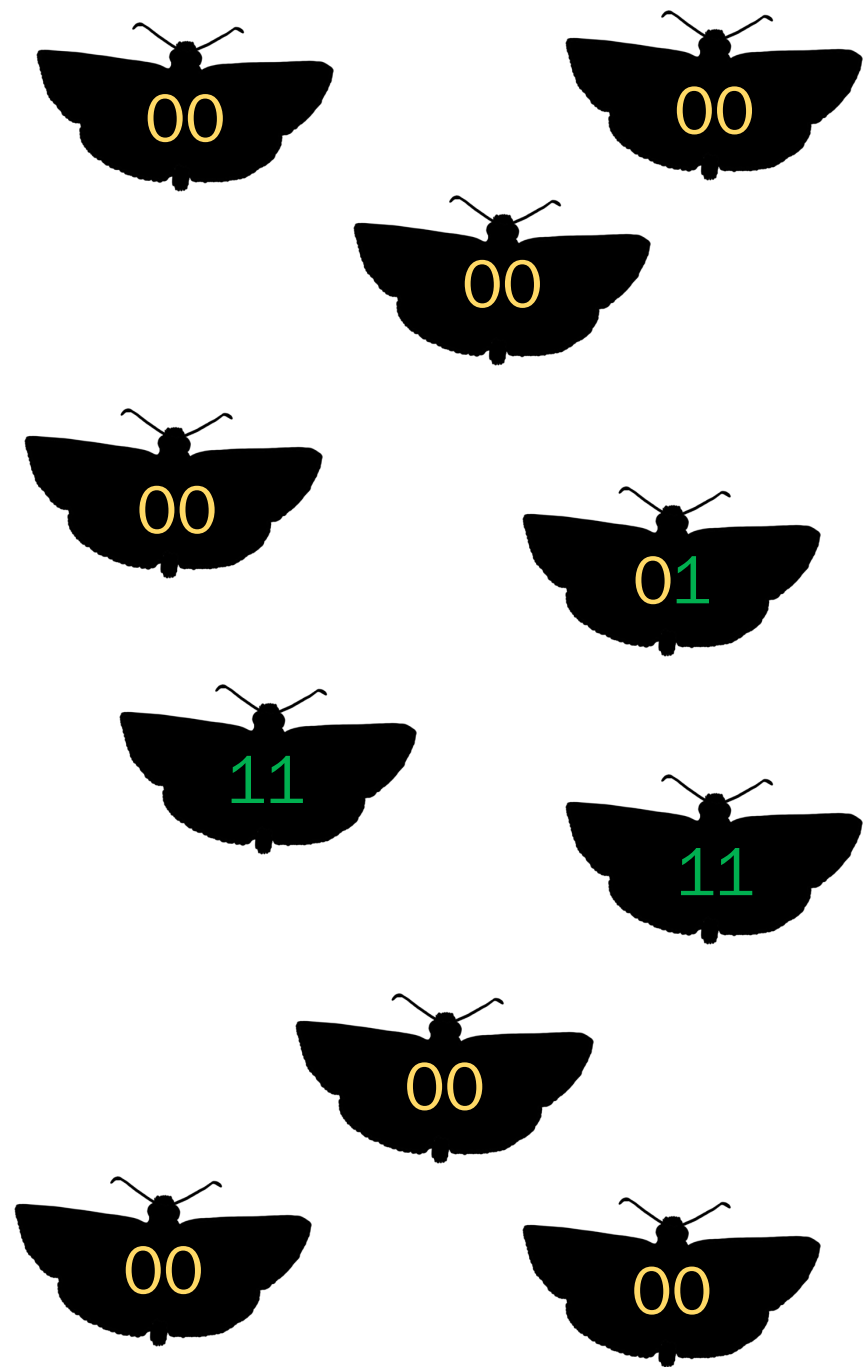
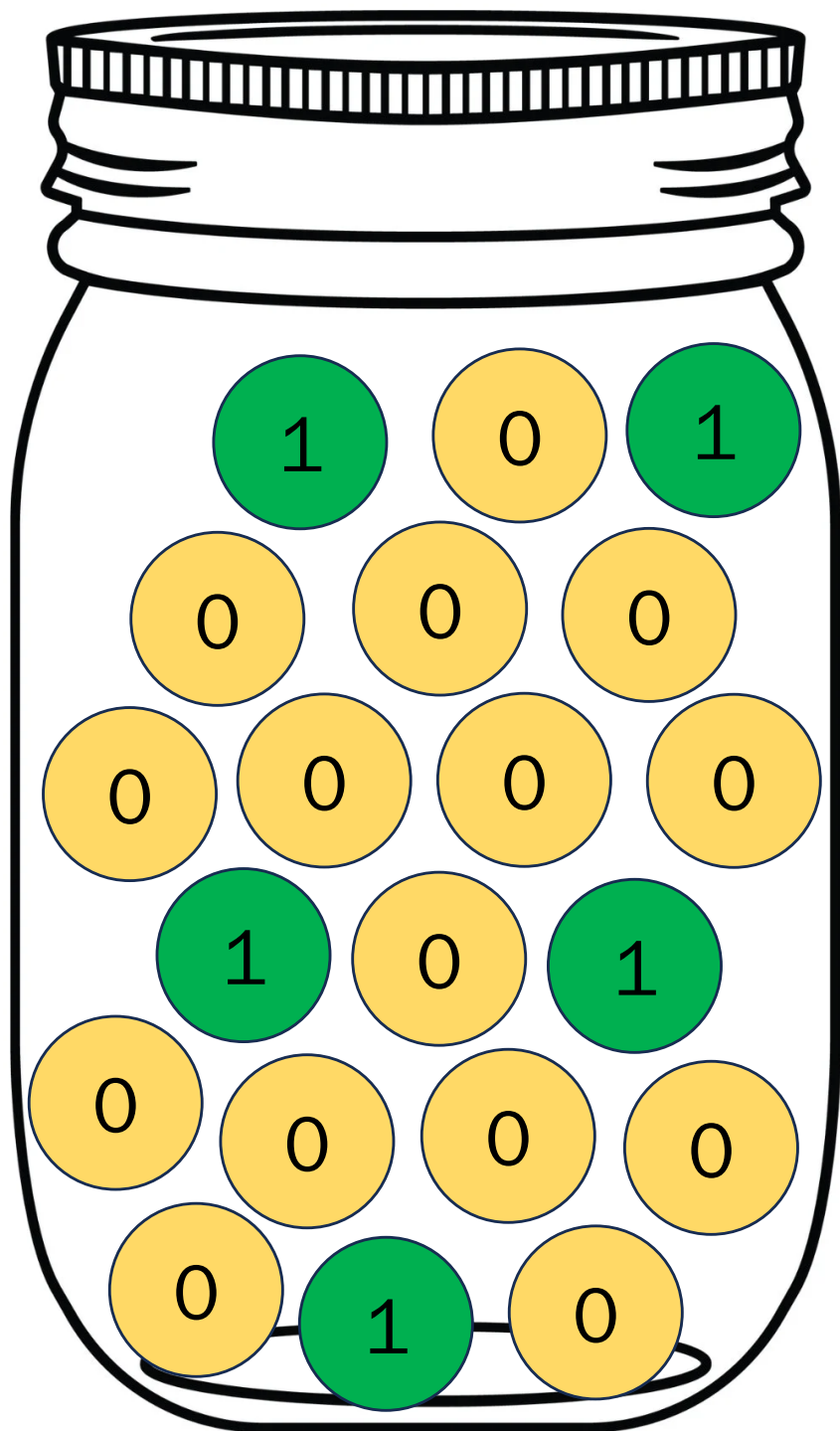
Draw an allele  
freq from the  
beta distribution



Draw twice from the  
binomial distribution to  
determine genotype  
(0, 1, or 2)









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- 1) Big questions in conservation genetics
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Goals for the rest of our time:

1. Simulate genetic data using the beta distribution
2. Explore the data with three different genetic analyses

Goals for the rest of our time:

1. Simulate genetic data using the beta distribution
2. Explore the data with three different genetic analyses

How are genetic analyses  
affected by the shape of the  
site frequency spectrum?

How many genetic markers  
do I need to detect a signal?