

Describing Variation & Patterns of Diversity

BIOL 1435

January 31, 2023

Icebreaker

Name, Year, Major, and what was the last song you listened to today?

Overview

1. ATGC's of life & encoding DNA
2. Measures of sequence diversity
3. In class coding exercise

Overview

1. ATGC's of life & encoding DNA

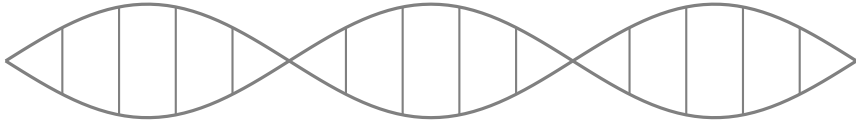
2. Measures of sequence diversity

3. In class coding exercise

DNA consists of four nucleotides

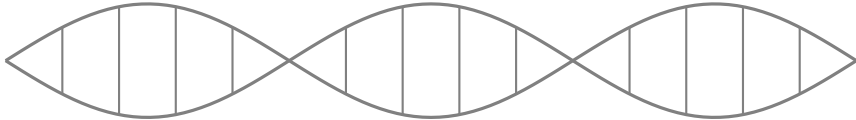
ATGC

DNA is organized onto chromosomes



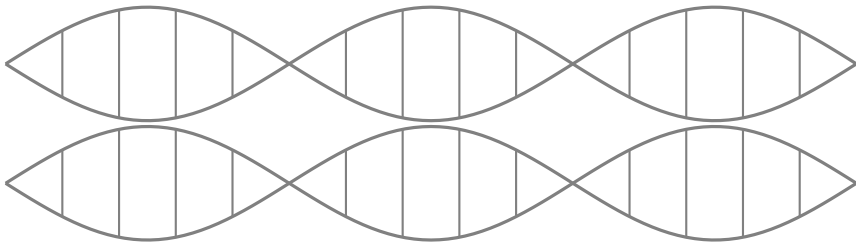
Ploidy (#N): number of sets of chromosomes

$N = \text{haploid}$



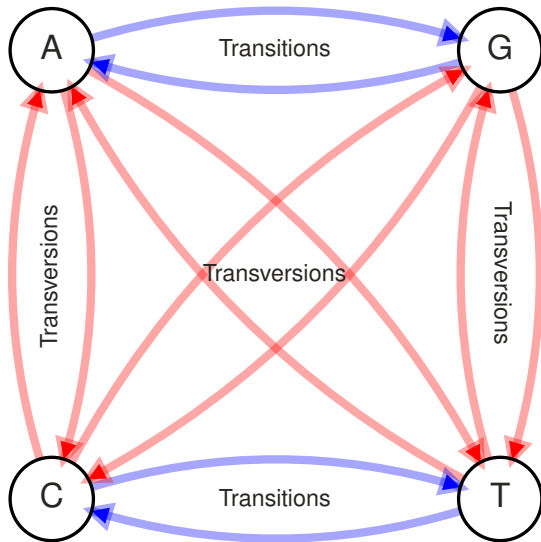
Ploidy (#N): number of sets of chromosomes

$2N = \text{diploid}$



**Q: How does genetic variation
arise?**

A: Mutations



How do we encode DNA?

$$m \text{ (sites)} \times n \text{ (chromosomes)}$$

How do we encode DNA?

	<i>ind₁</i>	<i>ind₂</i>	<i>ind₃</i>	<i>ind₄</i>	<i>ind₅</i>
<i>pos₁</i>	T	T	T	T	T
<i>pos₂</i>	C	G	G	C	G
<i>pos₃</i>	A	T	A	T	T
<i>pos₄</i>	G	G	G	G	C
<i>pos₅</i>	T	A	A	A	A

Genotype matrices

$$\begin{array}{c} \text{pos}_1 \\ \text{pos}_2 \\ \text{pos}_3 \\ \text{pos}_4 \\ \text{pos}_5 \end{array} \begin{array}{c} \text{ind}_1 \\ \text{ind}_2 \\ \text{ind}_3 \\ \text{ind}_4 \\ \text{ind}_5 \end{array} \begin{bmatrix} T & T & T & T & T \\ C & G & G & C & G \\ A & T & A & T & T \\ G & G & G & G & C \\ T & A & A & A & A \end{bmatrix} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix}$$

0 = reference or ancestral allele

1 = alternative or derived allele

Genotype matrices

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Genotype matrices

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} = \begin{bmatrix} 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Some terminology...

- Single nucleotide polymorphism (SNP)
- Single nucleotide variant (SNV)
- Variant site
- Segregating site

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How would you summarize this genotype matrix?

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Measurements of genetic variation

- Segregating sites (S)
- Site frequency spectrum (SFS)
- Gene diversity (h & H)
 - Also referred to as *expected heterozygosity*
- Nucleotide diversity (Π & π)

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Segregating sites (S)

Definition

A segregating site is a site that is polymorphic in the data—i.e., there are multiple alleles observed.

Segregating sites (S)

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Segregating sites (S)

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} \rightarrow \begin{bmatrix} 0 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix}$$

Segregating sites (S)

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} \rightarrow \begin{bmatrix} 0 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \rightarrow S = 4$$

Measurements of genetic variation

- Segregating sites (S)
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Site frequency spectrum (SFS)

Definition

Minor allele frequency spectrum: Histogram of the frequency of the less common allele which range from $1/n$ to 0.5 where n is the total number of chromosomes.

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Derived allele frequency spectrum: Histogram of the frequency of the derived allele—normally determined by the use of an outgroup—which range from $1/n$ to $(n-1)/n$.

Site frequency spectrum (SFS)

Definition

Minor allele frequency spectrum: Histogram of the frequency of the less common allele which range from $1/n$ to 0.5 where n is the total number of chromosomes.

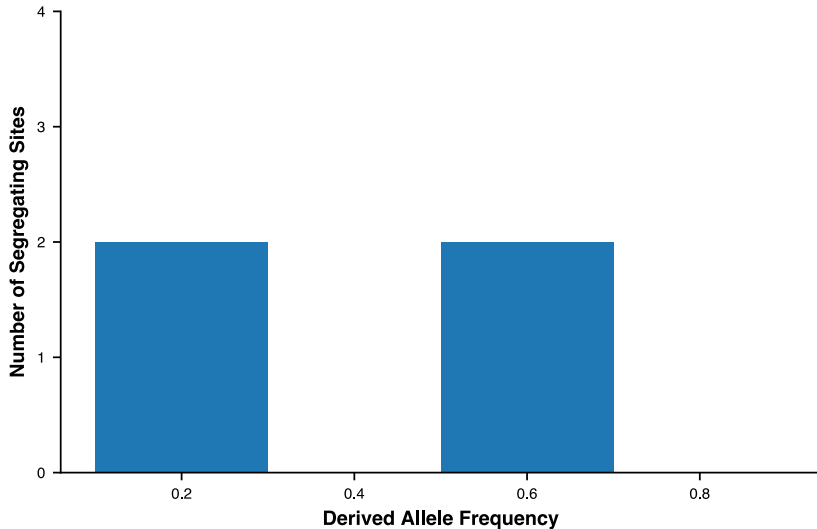
Derived allele frequency spectrum: Histogram of the frequency of the derived allele—normally determined by the use of an outgroup—which range from $1/n$ to $(n-1)/n$.

Note

Minor allele frequency spectrum = Folded SFS

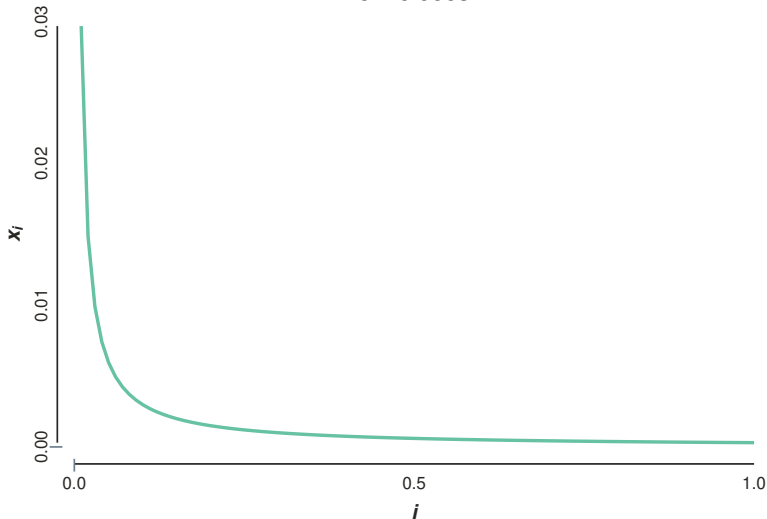
Derived allele frequency spectrum = Unfolded SFS

Site frequency spectrum (SFS)



Site frequency spectrum has the shape $\frac{\theta}{i}$

$\theta = 0.0003$



Measurements of genetic variation

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Gene diversity (h & H)

Definition

Gene diversity is the probability that two random DNA sequences are different.

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Equation

$$h = 1 - \sum_{i=1}^m p_i^2 \quad (1)$$

Where p_i is the frequency of the i^{th} allele out of m observed alleles.

$$H = \frac{1}{L} \sum_{j=1}^L h_j \quad (2)$$

Where h_j is the gene diversity for site j and L is to the total number of sites.

Dave's tips and tricks

Note

$$h = 1 - (p^2 + q^2)$$

Where p is the frequency of the derived/alternate allele and $q = (1 - p)$

Gene diversity (h & H)

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Gene diversity (h & H)

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} \rightarrow \begin{bmatrix} 1 - (1^2 + 0^2) \\ 1 - (2^2/5^2 + 3^2/5^2) \\ 1 - (2^2/5^2 + 3^2/5^2) \\ 1 - (1^2/5^2 + 4^2/5^2) \\ 1 - (1^2/5^2 + 4^2/5^2) \end{bmatrix}$$

Gene diversity (h & H)

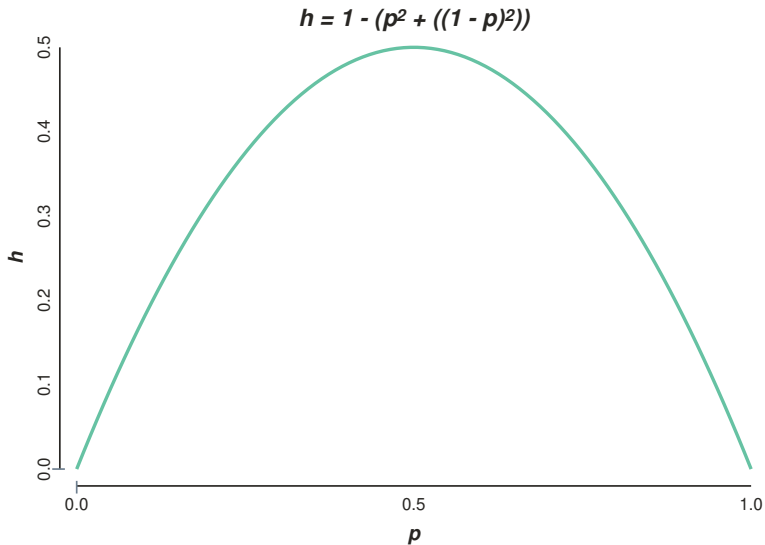
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Gene diversity (h & H)

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} \rightarrow \begin{bmatrix} 1 - (1^2 + 0^2) \\ 1 - (2^2/5^2 + 3^2/5^2) \\ 1 - (2^2/5^2 + 3^2/5^2) \\ 1 - (1^2/5^2 + 4^2/5^2) \\ 1 - (1^2/5^2 + 4^2/5^2) \end{bmatrix} \rightarrow h_j = \begin{bmatrix} 0 \\ 12/25 \\ 12/25 \\ 8/25 \\ 8/25 \end{bmatrix}$$

$$H = 40/25 \times 1/5 = 8/25$$

Behavior of h



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Definition

Nucleotide diversity is the average number of pairwise differences between genotypes drawn from the same population.

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Equation

$$\Pi = \frac{\sum_{i < j} k_{ij}}{\binom{n}{2}} \quad (3)$$

Where k_{ij} is the number of nucleotide differences between the i^{th} and j^{th} sequence in the sample and the denominator represents the number of unique comparisons being made between n sequences.

$$\pi = \frac{\Pi}{L} \quad (4)$$

Where L is to the total number of sites.

Dave's tips and tricks

Note

$$\binom{n}{2} = \frac{n(n-1)}{2}$$

Nucleotide diversity (Π & π)

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Nucleotide diversity (Π & π)

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} \rightarrow \begin{array}{l} (0 + 0 + 0 + 0) = 0 \\ (3 + 1 + 1 + 1) = 6 \\ (3 + 1 + 2 + 0) = 6 \\ (1 + 1 + 1 + 1) = 4 \\ (4 + 0 + 0 + 0) = 4 \end{array}$$

Nucleotide diversity (Π & π)

$$\begin{array}{cc} \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} & \begin{array}{l} (0 + 0 + 0 + 0) = 0 \\ (3 + 1 + 1 + 1) = 6 \\ (3 + 1 + 2 + 0) = 6 \\ (1 + 1 + 1 + 1) = 4 \\ (4 + 0 + 0 + 0) = 4 \end{array} \end{array} \rightarrow \Pi = 20 \div \frac{5(5-1)}{2} = 2$$

Nucleotide diversity (Π & π)

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$$\pi = 2 \times 1/5 = 2/5$$

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