

Computational Exercise #1

SEPTEMBER 5, 2019

EVOLUTIONARY GENETICS 462



https://github.com/jjudson28/GEN_462_2019

On your computer:

- Move into the GEN_462_2019 Folder
 - `cd GEN_462_2019`
- Type `ls` to list the folder's contents
- To update your repository to be consistent with what is online, type `git pull` and then press enter



If you are on a cart computer:


- Go to the website for the github repository on your browser
- Click the files you want to download

Branch: master ▼

ISUEvoGen462 / Week_1 / Example_Data / Basics_of_R.Rmd

Find file

Copy path

 **jjudson28** Introductory Materials

acd77c1 3 days ago

1 contributor

55 lines (41 sloc) | 3.01 KB

Raw

Blame

History



Go to File, Save as in your web browser

Choose location to save that you can find easily

Don't append the ".txt" file ending

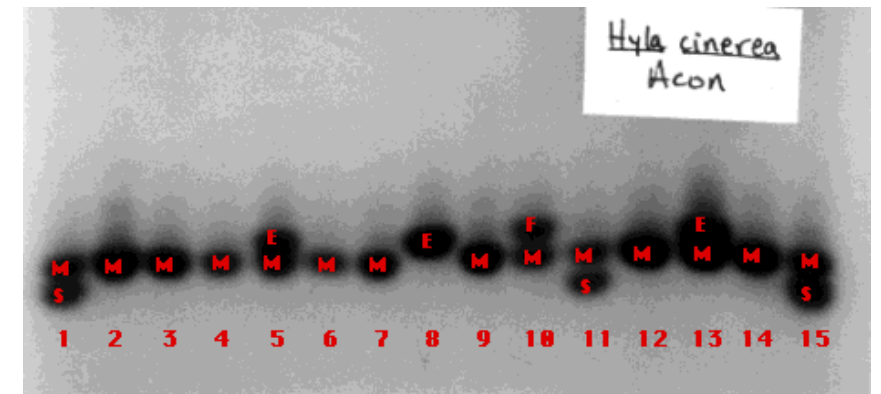
Objectives for Today

1. Review different marker types and their pros/cons
2. Brief HWE reminder
3. Use R Studio and the packages "adegenet" and "pegas" to generate basic statistics and HWE estimates
4. Interpret these values in a biological context

Common Marker Types

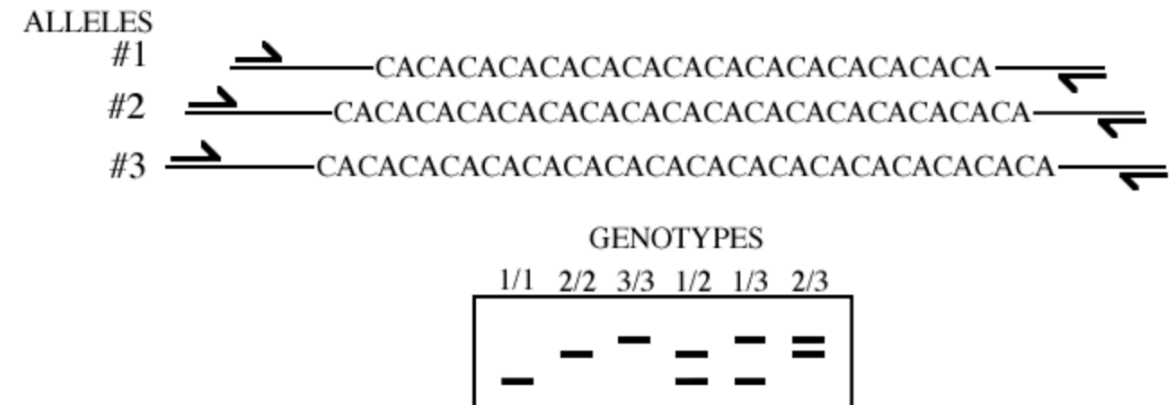
Allozymes

- Different forms of an enzyme coded by different alleles at the same locus
- Not very variable, not good for recent divergence
- Potentially under selection
- In class exercise from last week is example



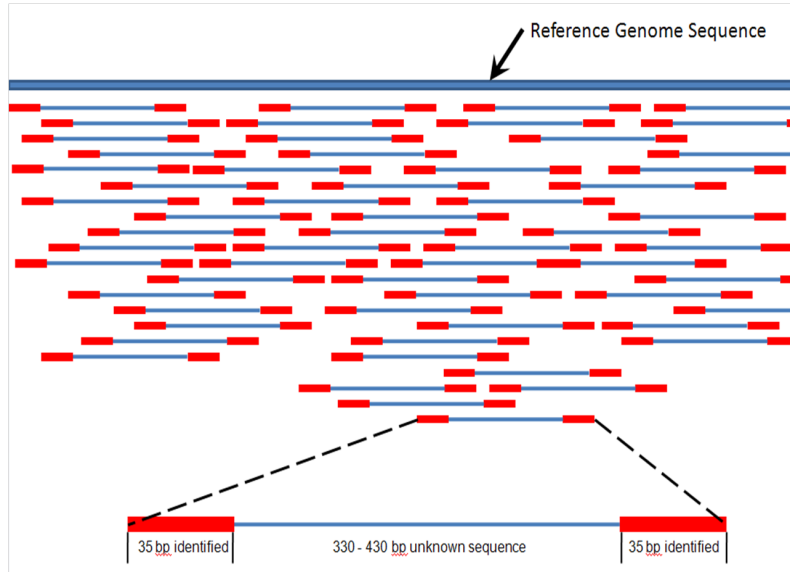
Microsatellites

- Tandem repeats in DNA sequence
- Rapidly evolving, good for recent divergence
- Neutral (?)
- Data is depicted as lengths or as number of repeats (numbers instead of letter bases)



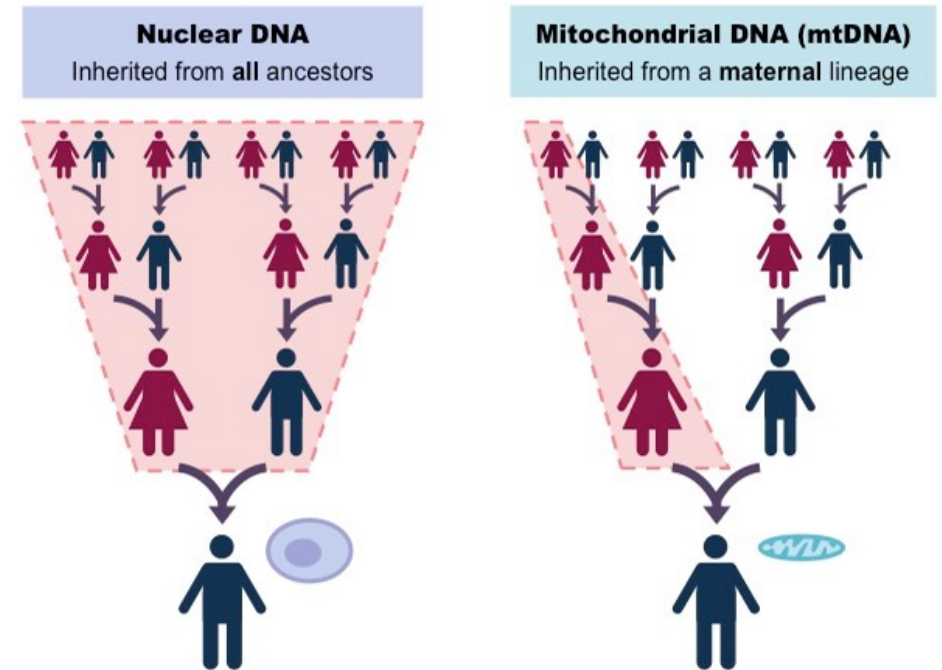
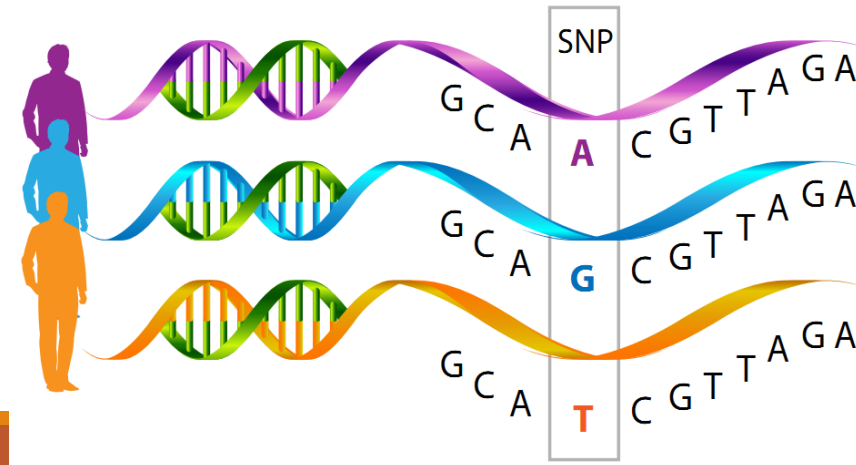
Sequence data (shorter or genomic sequence data)

- Mitochondrial or Chloroplast
- Full genome sequence data



Single Nucleotide Polymorphisms (SNPs)

- An example of use of sequence data
- Data depicted as letters representing DNA base



SNPs

Can have lots of data for fine-scale population structure / recent divergence

Not as rapidly evolving as microsatellites

Can be in coding regions (genes) or in neutral regions

Common way of assessing variation today

Hardy-Weinberg Equilibrium

What does it mean for a population to be in HWE?

- Assumptions are being met:
 - No natural selection
 - No mutation
 - No drift
 - No migration
 - Random mating

What does it mean when a population is not in HWE?

- Assumptions are NOT being met
- Evolution is occurring

Interpreting Values of HWE

When analyzing HWE, we use p-values to assess whether the population allele frequencies deviate from HWE:

$P < 0.05 \rightarrow$ Population is not in HWE

$P \geq 0.05 \rightarrow$ Population is in HWE

References

Sayres, M. A. W. *et al.* Bioinformatics Core Competencies for Undergraduate Life Sciences Education. *bioRxiv* 170993 (2017).

<http://www.biology-pages.info/P/Polymorphisms.html>

<http://www.informatics.jax.org/silver/figures/figure8-10.shtml>

<https://neuroendoimmune.wordpress.com/2014/03/27/dna-rna-snp-alphabet-soup-or-an-introduction-to-genetics/>