



# Geonomics Lab (Part 2)

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*Lab created by: Drew Terasaki Hart, Natalie Graham, Monica Wilkinson  
and Keeley Takimoto*


# Creating a GitHub account

1. Go to <https://github.com/>
2. Click Sign up
3. Sign up with your **berkeley email**
4. Follow the prompts to create your personal account.
5. Pick your username carefully, you will likely not want to change it (but you can). Some recommendations:
  - a. Use part of your real name so it is easier for people to know who you are
  - b. Try and keep it short, you may have to type it a lot
  - c. Keep everything lowercase. If you really want to separate words, use a hyphen (-) or an underscore (\_)

# GitHub Codespaces

1. Go to <https://github.com/TheWangLab/espm154>
2. Click the green "Code" button in the top right
3. Click "Open with Codespaces".
4. Wait for the codespace to load. This will take several minutes.
5. Open the "espm154\_lab6" ipynb file

## Tips:

1. If you hover over the plots, you can copy the image by clicking this icon:  *This may be useful in answering the lab exercises and keeping track of the simulations.*
2. You can download your notebook by right clicking on the file and selecting "Download" (you may have to click "Accept" on a pop-up first)

# Evolutionary Simulations in **Geonomics**

## Geonomics: Forward-Time, Spatially Explicit, and Arbitrarily Complex Landscape Genomic Simulations

Drew E Terasaki Hart , Anusha P Bishop, Ian J Wang

*Molecular Biology and Evolution*, Volume 38, Issue 10, October 2021, Pages 4634–4646,  
<https://doi.org/10.1093/molbev/msab175>

**Published:** 12 June 2021

*Simulation of **local adaptation** and **speciation** across realistic landscapes*

# Parameters = Recipe

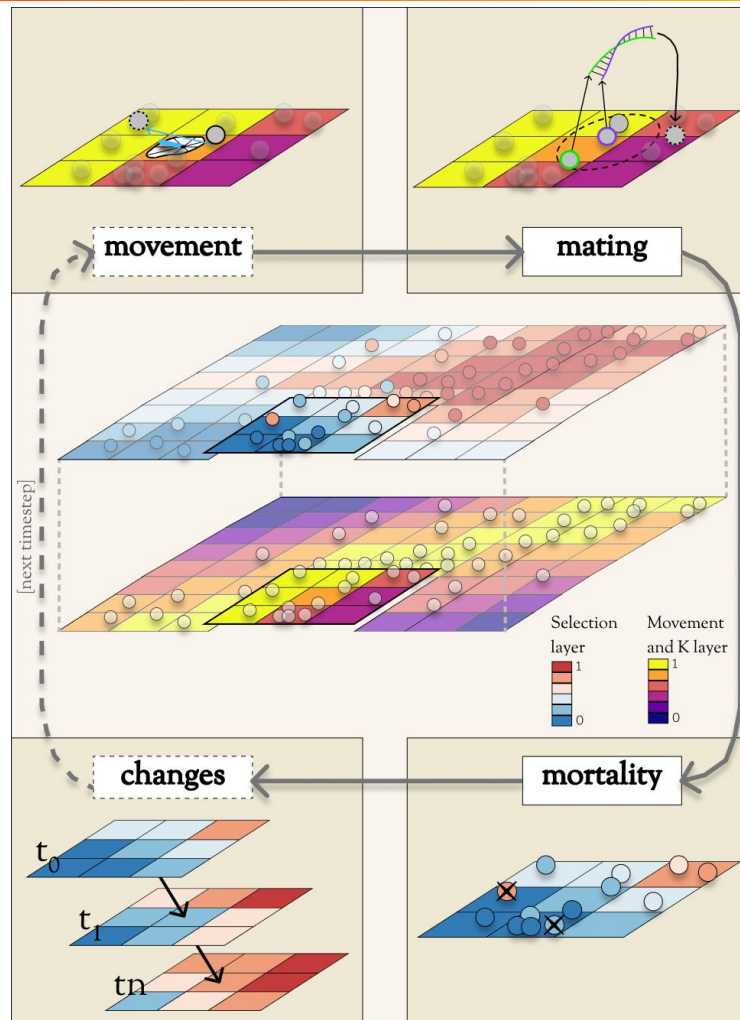


## Brownie in a Mug

- 3 tablespoons sugar
- 3 tablespoons flour
- 1 ½ tablespoons cocoa powder
- 1 ½ tablespoons melted butter
- 3 tablespoons milk
- ¼ teaspoon vanilla extract

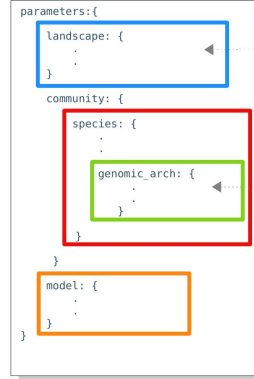
=

```
'mug_brownie': {  
  'sugar': 3  
  'flour': 3  
  'cocoa_powder': 1.5  
  'melted_butter': 1.5  
  'milk': 3,  
  'vanilla_extract': 0.25  
}
```



## 1.) Create and edit a parameters file

*parameters file:*



*Optional: Include paths to raster files and/or directories of environmental-change rasters*

*raster file:*



*raster directory:*

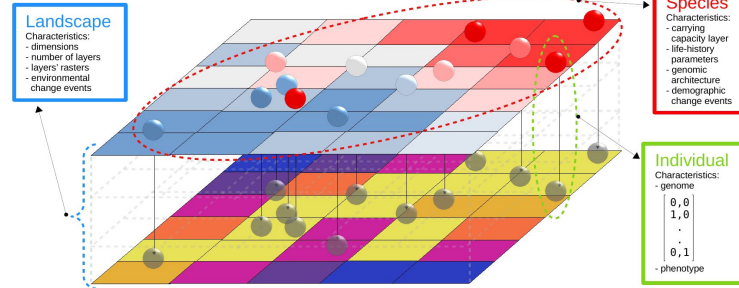


*Optional: include path to a genomic architecture file (.csv)*

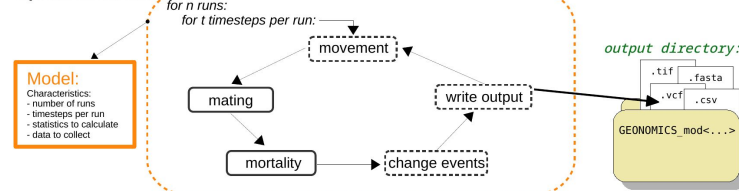
*genomic architecture file:*

loc,	p,	dom,	r,	trait,	alpha,
1,	0.5,	0,	0.5,	,	,
1,	0.5,	0,	0.5,	,	,
1,	0.5,	0,	0.01,	0,	0.5,
1,	0.5,	0,	0.01,	1,	0.5,
1,	0.5,	0,	0.01,	2,	0.5,
1,	0.5,	0,	0.5,	,	,
1,	0.5,	0,	0.5,	,	,
,	,	,	,	,	,
,	,	,	,	,	,

## 2.) Use the parameters file to create a model



## 3.) Run the model



# How does speciation occur?

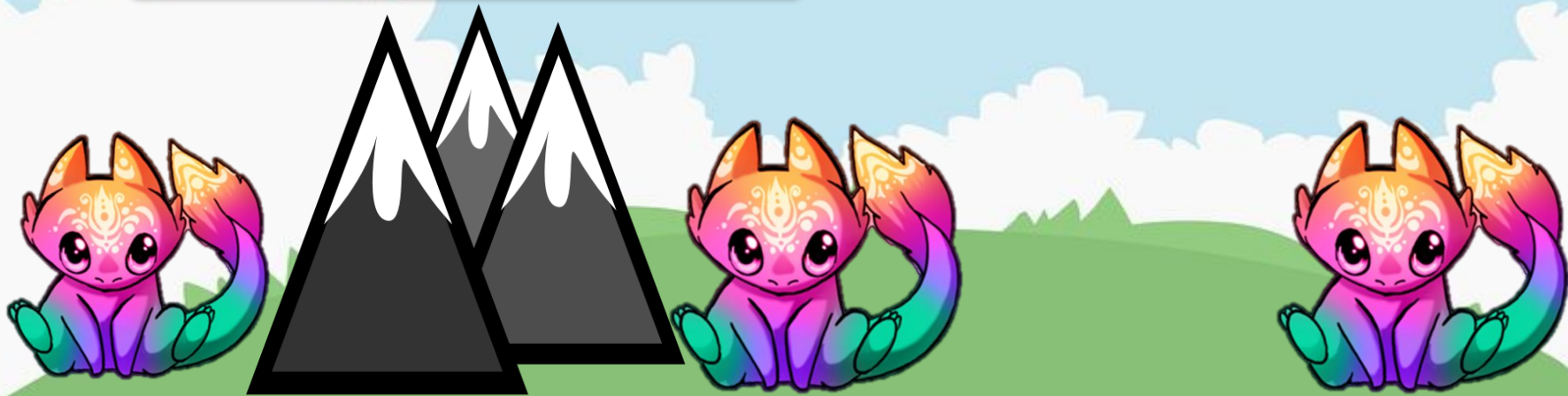




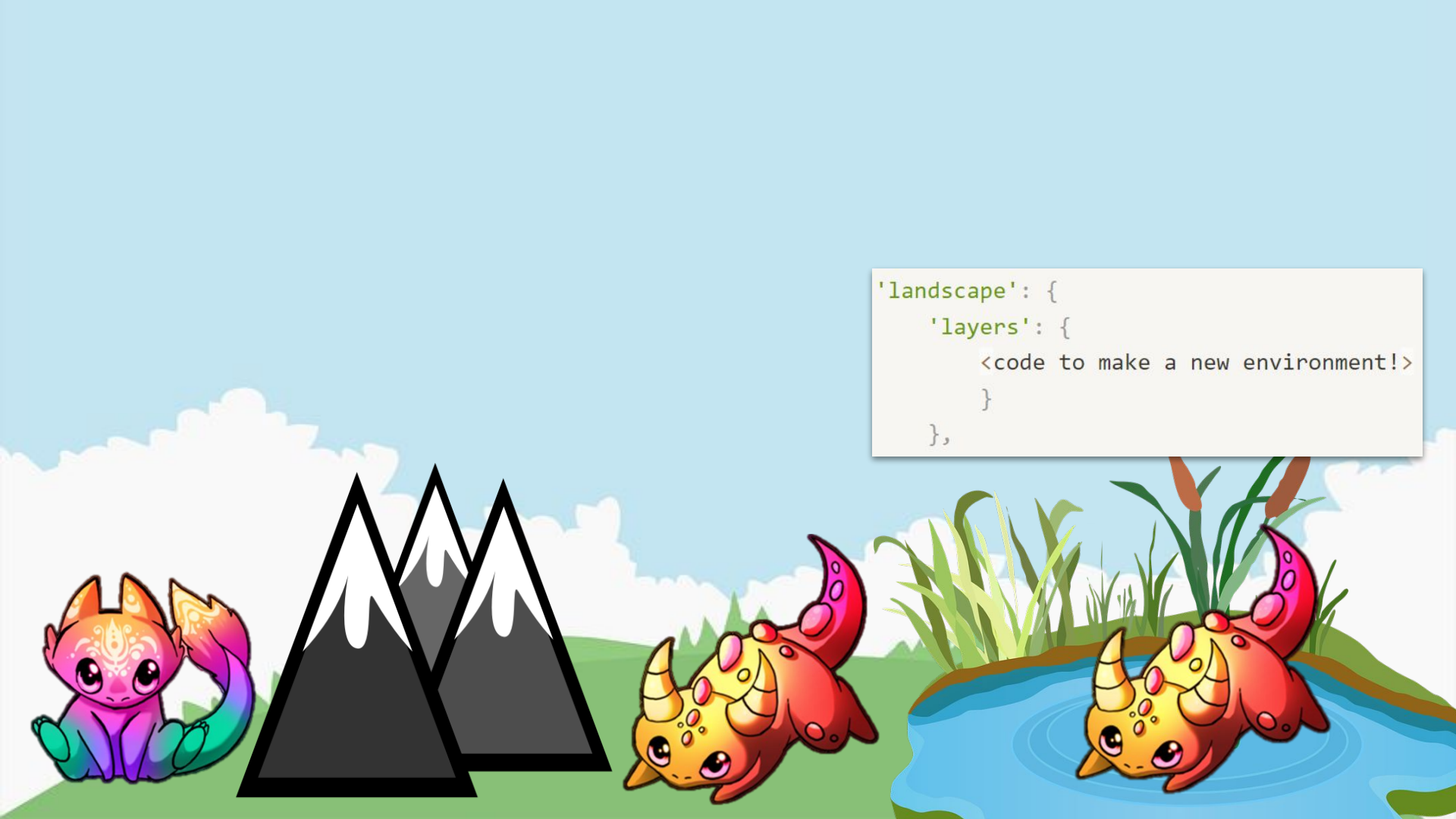
# How does speciation occur?



```
'landscape': {  
  'layers': {  
    <code to make a barrier!>  
  }  
},
```



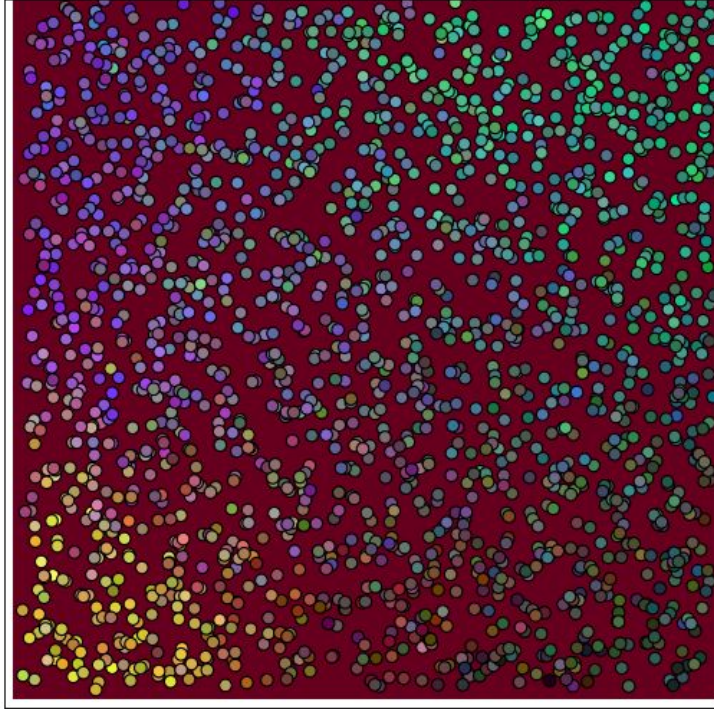




```
'landscape': {  
  'layers': {  
    <code to make a new environment!>  
  }  
,
```



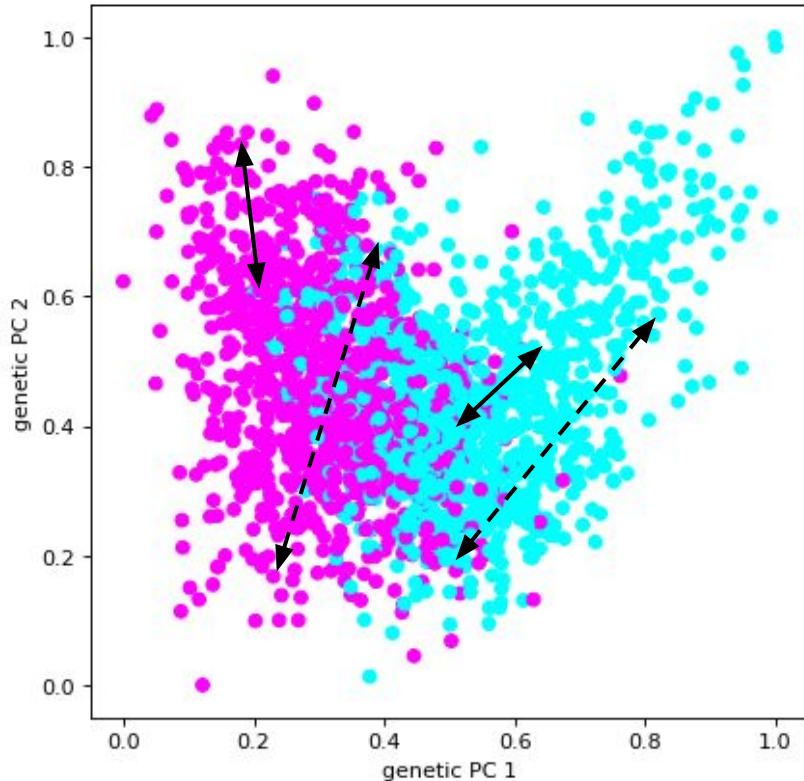
# PCA plots



**Individuals that have more similar colors are more similar**



# PCA plots



**Individuals that are closer on the plot are more similar**

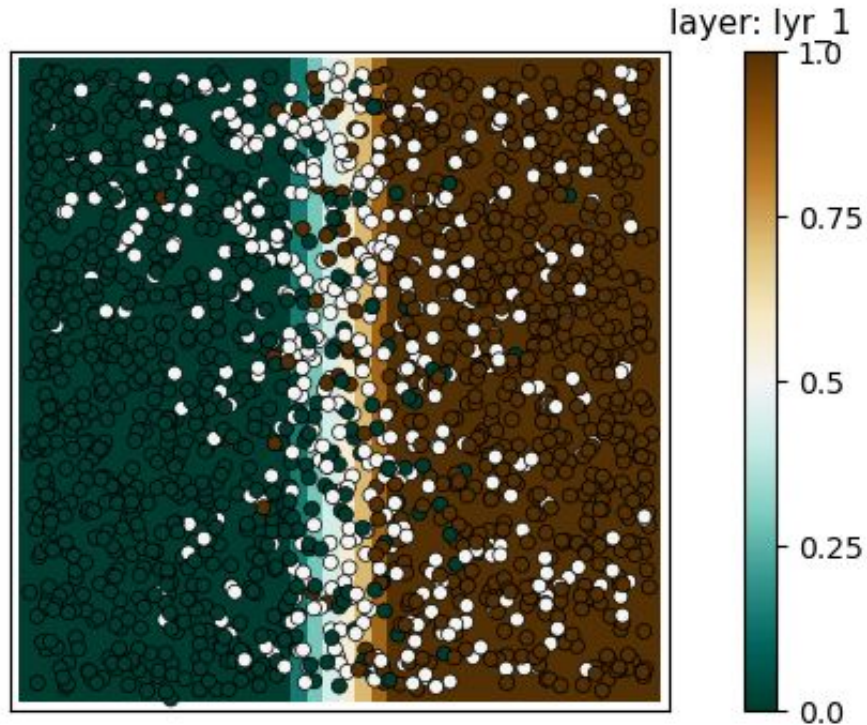
**Blue** = individuals on right side of barrier  
**Pink** = individuals on left side of barrier



## **Part 2:** Natural Selection



# Selection plots



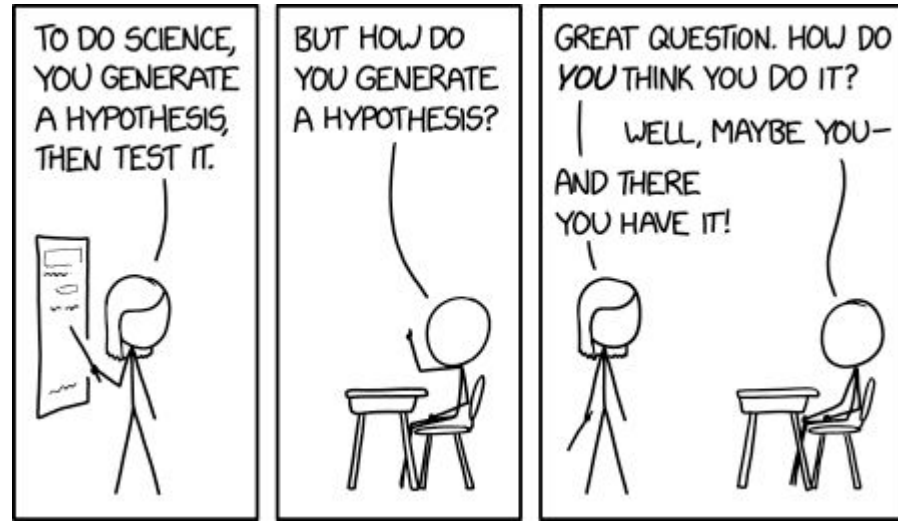
Individual color = trait  
Landscape color = env

*Individual color matches the  
background color = local  
adaptation*



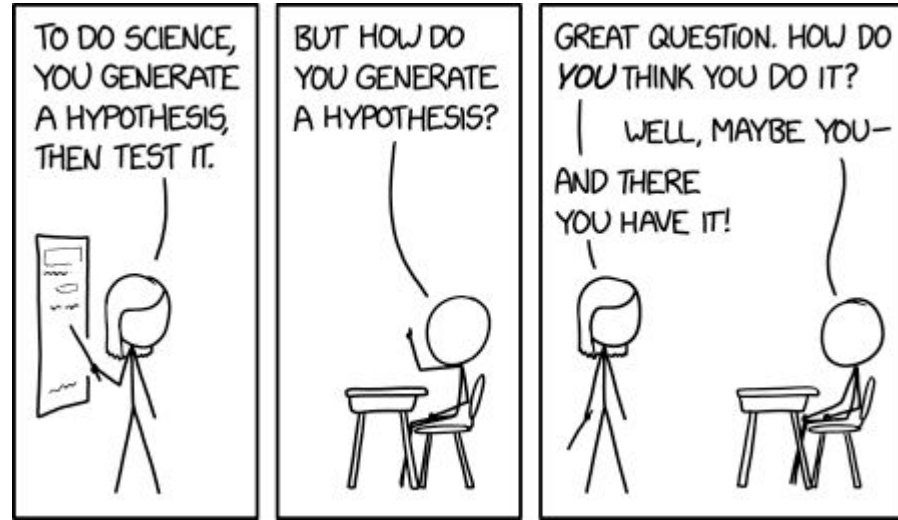
## **Part 3:** Hypothesis Testing

# Generating Hypotheses



If we [parameter change], then [outcome with evidence] because [justification]

# Generating Hypotheses



If we [parameter change], then [outcome with evidence] because [justification]

If we *add a barrier to our landscape*, then we will observe *differentiation of the populations on either side of the barrier in our PCA plot* because of *drift*

# Think-pair-share

1. THINK [5 minutes]: Pick one of the parameters listed in the lab to change and generate a hypothesis.

For ex: if we [*increase/decrease parameter X*] then we will observe that [*mismatch increase/decreases*] because [*justification*]

2. PAIR [5 minutes]: Share your hypothesis with the person next to you. See if you agree with each others expected outcomes.
3. SHARE: Be prepared to share one of your hypotheses with the class.

*(Before you start running you simulations, answer Question 2)*

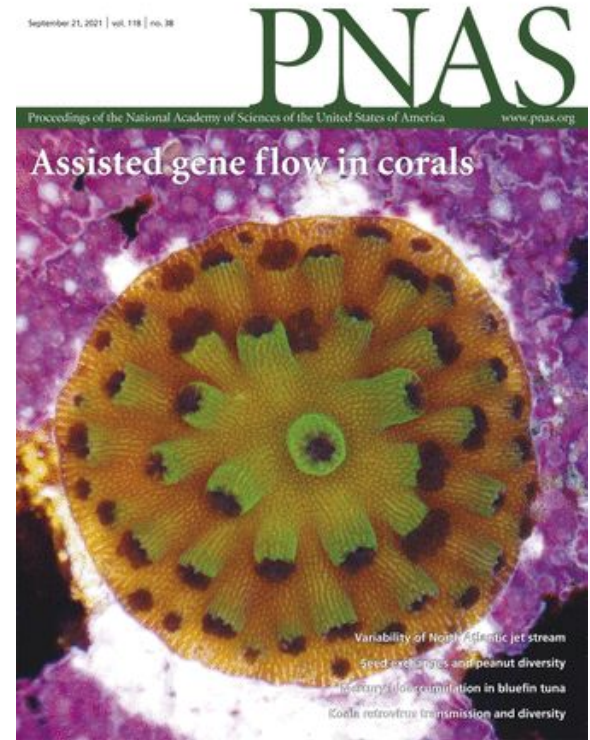


# Why does this matter?

Real world conservation question:  
**Is gene flow always good?**

Testable question:  
**What is the effect of movement distance on phenotype-environment mismatch?**

**CLASSROOM POLL:** Do you hypothesize that increasing movement distance will increase or decrease phenotype-environment mismatch in our simulations?



<https://www.pnas.org/doi/full/10.1073/pnas.2110559118>

# Why does this matter?

A real world conservation question: **Is gene flow always good?**

Testable question: **What is the effect of movement distance on phenotype-environment mismatch?**

Hypothesis A: If we have more movement, then adaptive alleles can spread more easily through the population, increasing fitness/decreasing mismatch

Hypothesis B: If we have more movement, then alleles that are not adapted to the local environment (i.e., maladaptive alleles) can spread more easily, decreasing fitness/increasing mismatch



I HAVE A QUESTION.

WELL, LESS OF A QUESTION  
AND MORE OF A COMMENT.

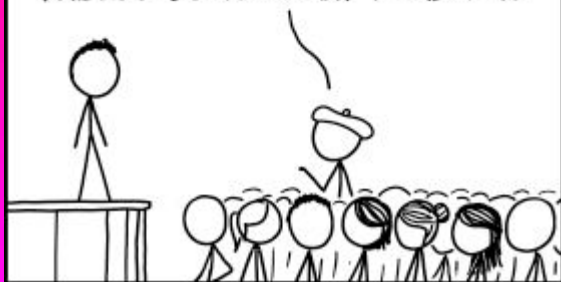
I GUESS IT'S LESS OF A COMMENT  
AND MORE OF AN UTTERANCE

REALLY IT'S LESS AN UTTERANCE,  
MORE AN AIR PRESSURE WAVE.

IT'S LESS AN AIR PRESSURE WAVE  
AND MORE A FRIENDLY HAND WAVE.

I GUESS IT'S LESS A FRIENDLY  
WAVE THAN IT IS A FRIENDLY BUG.

I FOUND THIS BUG AND NOW WE'RE  
FRIENDS. DO YOU WANT TO MEET IT?



Thanks! Questions?