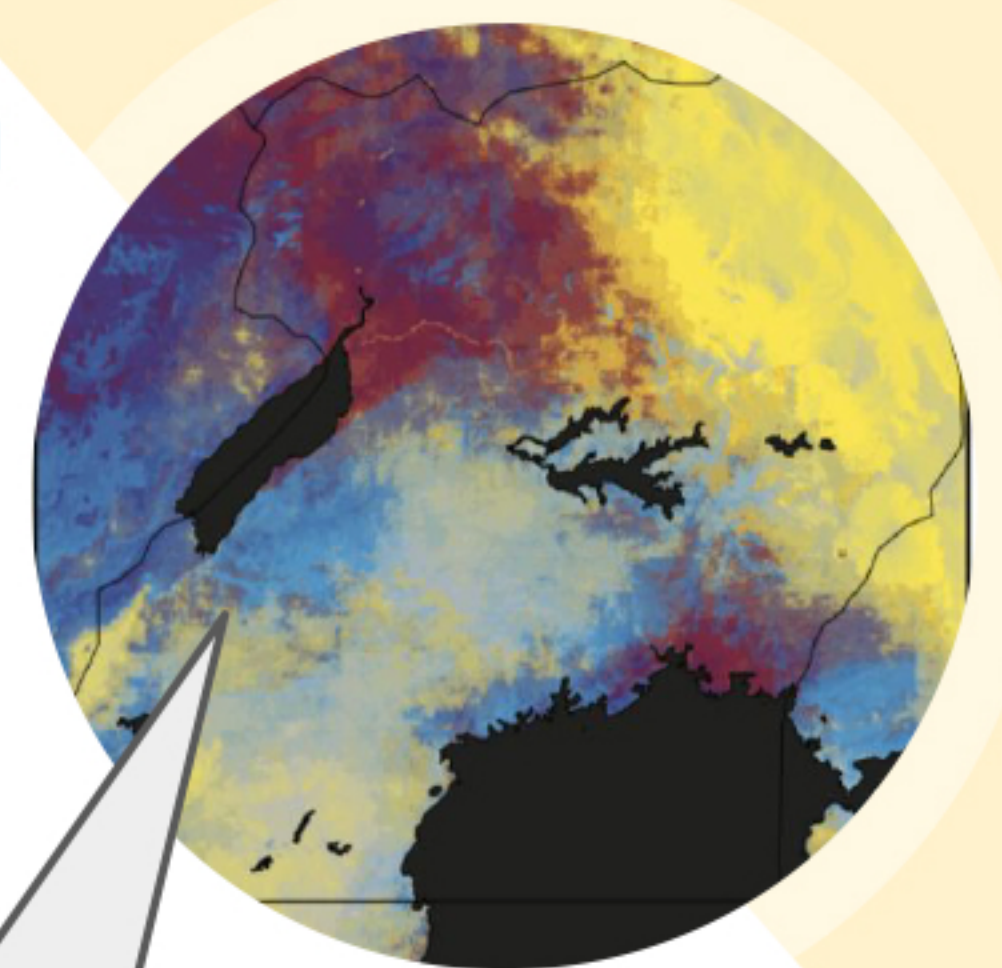




Dr. Norah Saarman

**Saarman Lab**  
 We investigate where species live and variation across space in the genetic diversity and phenotypic traits that allow species to be successful in their environment.



**Tsetse flies in Uganda –**

We are investigating the genetic connectivity, adaptive potential, and distribution of the tsetse fly *Glossina fuscipes fuscipes*, the major vector of sleeping sickness and Animal African trypanosomiasis, as well as the sand fly *Lutzomyia donovani*, a major vector of leishmaniasis. We are focusing on these vectors in northern Uganda, a region of sub-Saharan Africa that has had many challenges in the 21st century due to recent civil unrest. This is a vital time for northern Uganda to realize its potential in promoting human health and well-being, as well as conserving its stunning biodiversity and rich cultural heritage. We have funding pending to develop a workflow that incorporates genetic and field data into spatial models of vector movement and density and translate these findings into decision-relevant estimates of the key drivers of vector-borne disease transmission in response to climate change. Results from this proposal will be of immediate public health significance in Uganda by providing predictive maps, estimates of vector population biology and epidemiological models of disease transmission.

**Glossina fuscipes fuscipes in Uganda**

Population genomics data  
 ~50,000 SNPs  
 658 flies

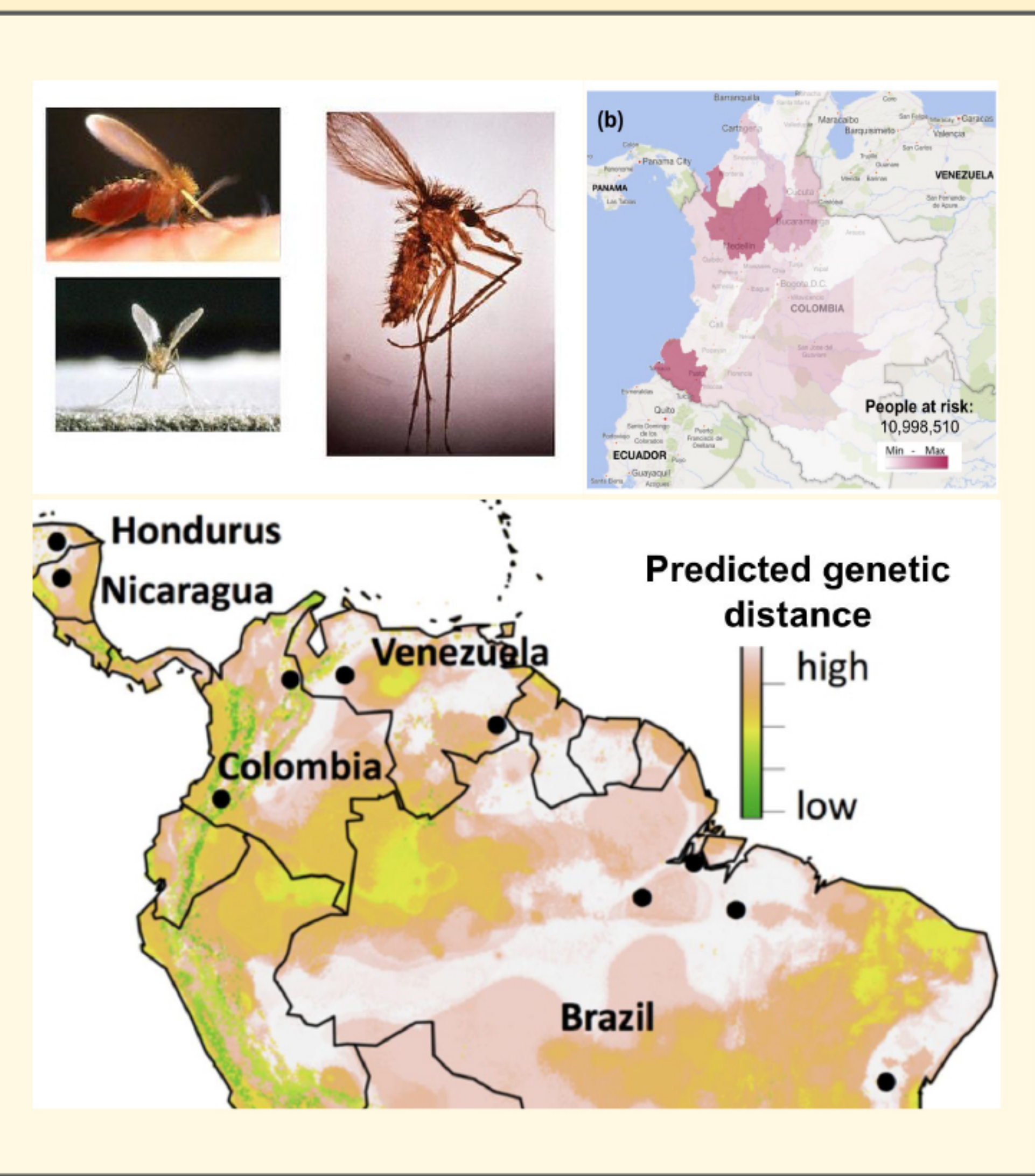
**Genetic diversity and distance patterns**

**Machine learning finds which x variables best predict y variable(s)**

Genetic distance (y)  
 Environmental data (x)

Machine learning  
 Random forest regression

Collaborators: Edyta Piers, Giuseppe Amadori, Anusha Bishop, Sampa Akora, Jeff Powell, Giulio Corbelli

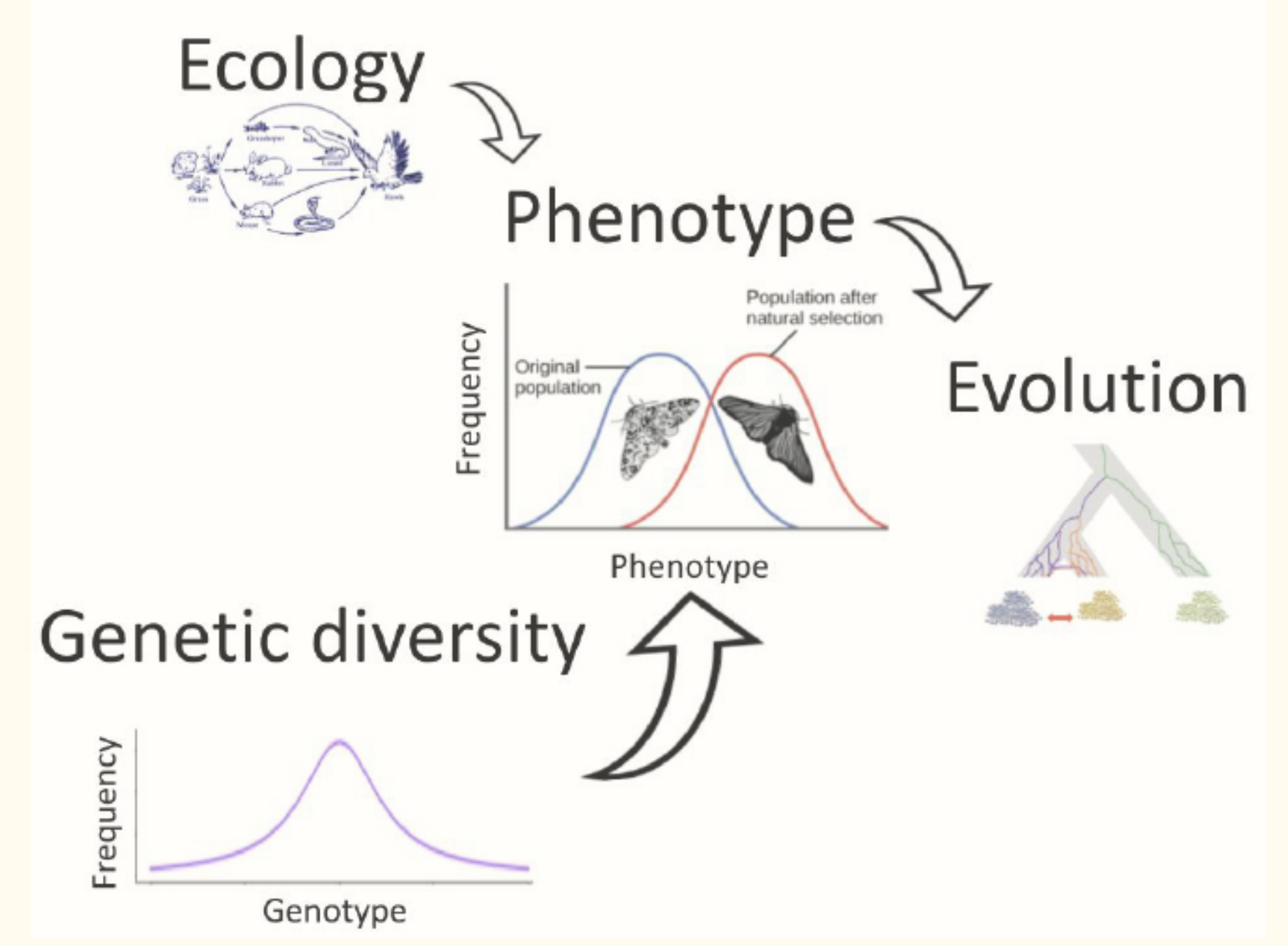
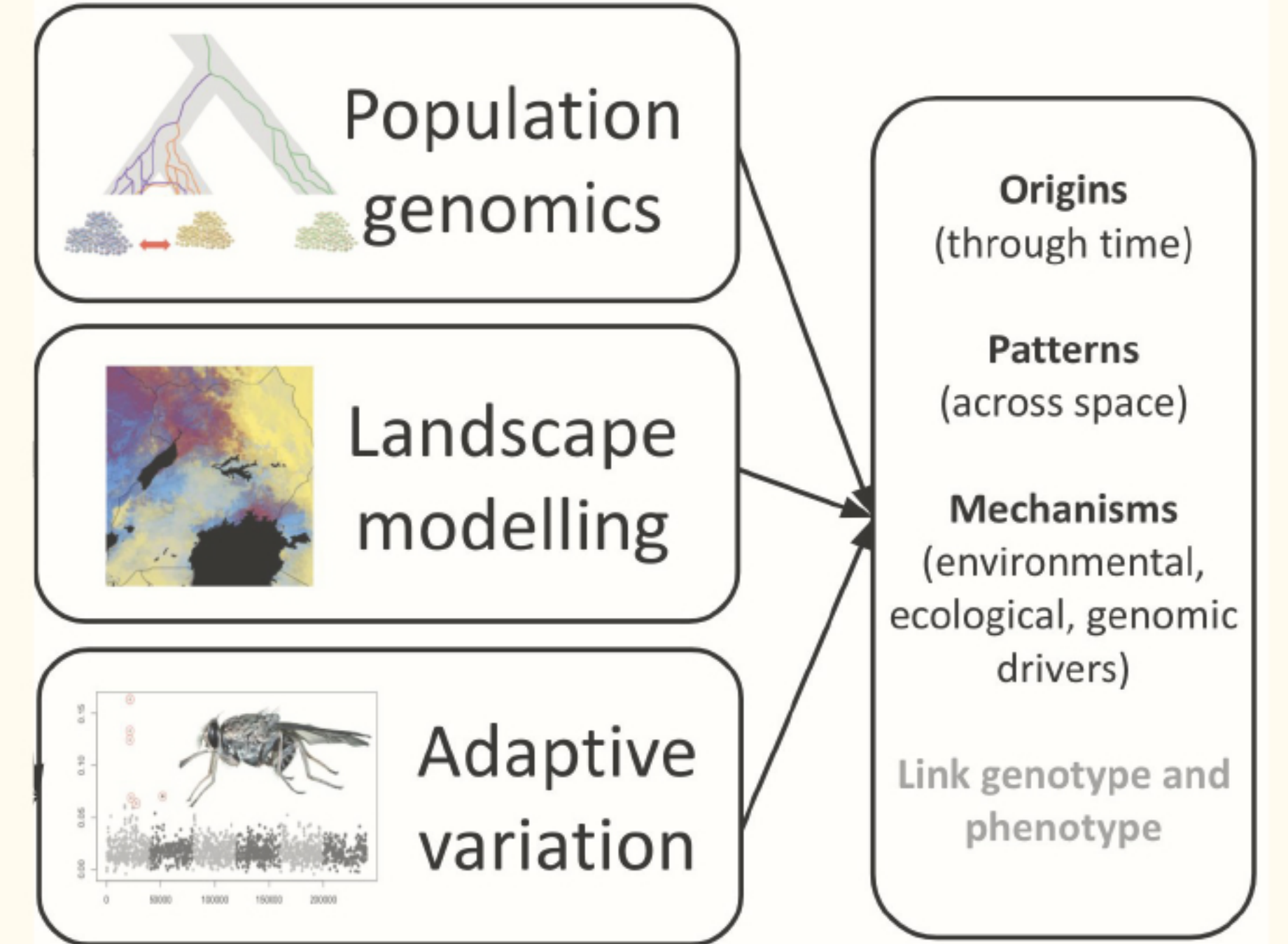


**Sand flies in the Magdalena Valley –**

We are investigating the genetic connectivity, adaptive potential, and distribution of the sand fly *Lutzomyia longipalpis* in the Magdalena Valley in Colombia. This sand fly is the vector of two types of leishmaniasis: the deadly form of the disease known as visceral leishmaniasis, and the more widespread but mild form of the disease known as cutaneous leishmaniasis. There is very little known about the distribution, ecology, and genomics of *Lutzomyia longipalpis*, leaving an urgent need for basic knowledge.



**Applications to vector control and human well being**



- Population genetics**
- Origins of genetic diversity?
  - What mechanisms shape and maintain diversity?
- Landscape Modelling**
- How is diversity distributed over space?
  - What are the environmental drivers?
  - How will climate change impact diversity?

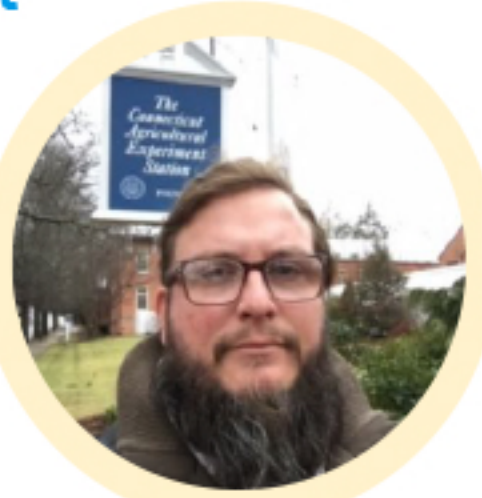
Find out more at [www.saarmanlab.com](http://www.saarmanlab.com)



Anusha Bishop



Dr. Robert Opiro



Dr. Andres Gomez

