

# Scenario 1

## Eastern indigo snake vector-borne disease



### Project Description:

Florida wildlife officials have recently recorded an increased mortality in populations of the native, endangered Eastern indigo snake (*Drymarchon couperi*). Upon necropsy, veterinarians have discovered that much of the pathology is consistent with an infectious disease. Initial work has also noticed unusually large numbers of ticks recently, especially on the deceased snakes. It has been suggested that the pathogen may be transmitted by ticks of the genus *Amblyomma*. In other countries, like Thailand, ticks of the genus *Amblyomma* are known to transmit infectious diseases to snakes ([read more here](#)). You have been awarded a grant to characterize this potential outbreak in hopes of mitigating future loss of this endangered and iconic reptile species of Florida.

### Additional Facts:

- 1) Florida is famous for its invasive populations of reptiles due to the import of wild animals from overseas for the pet trade
- 2) Florida has two native *Amblyomma* tick species, *A. americanum* and *A. maculatum*
- 3) The only snake genomes available are distantly related to the indigo snake, but one of them, the Burmese python, is also invasive in Florida.
- 4) Florida officials can provide you with any and all snake samples you need.

### Goals:

Using **genomic tools only**, we would like to characterize the pathogen, the vector, and its origin. Carefully consider the following:

- Which samples will be collected and how will they be documented?
- Which genomic methods/tools will be used and why were they chosen?
- What other sources of data/information are needed (e.g., GenBank)?
- How will the data and results be archived and/or disseminated?
- How should the findings be validated?

## Scenario 2

### Permafrost pathogen outbreak!



#### Project Description:

You are part of an international response team that is investigating a fatal disease cluster in both wild and domestic ungulates in a remote corner of Siberia. The disease seems to have an infectious origin, and regional public health experts suspect it was caused by a pathogen contained in a reindeer carcass frozen for thousands of years in permafrost that is now melting because of climate change (Note that this is a not implausible scenario: [Anthrax Outbreak In Russia Thought To Be Result Of Thawing Permafrost](#)). Your team's task is to investigate this cluster. You will use an NGS-based approach to attempt to identify the possible pathogen.

#### Additional Facts:

1. The index case is believed to be from a feral domestic goat that had fed near the carcass.
2. Unfortunately, all verified cases have died, and there is no access to samples from them.
3. The only samples you have are from the partially thawed reindeer carcass.

#### Goals:

Using **genomic tools only**, we would like to characterize the potential pathogen. Since the ultimate theme of this exercise is to design 'Best Practices', carefully consider the following:

- Which samples will be collected and how will they be documented?
- Which genomic methods/tools will be used and why were they chosen?
- What other sources of data/information are needed (e.g., GenBank)?
- How will the data and results be archived and/or disseminated?
- How should the findings be validated?