

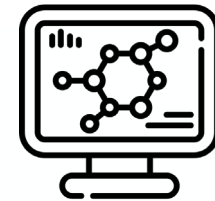
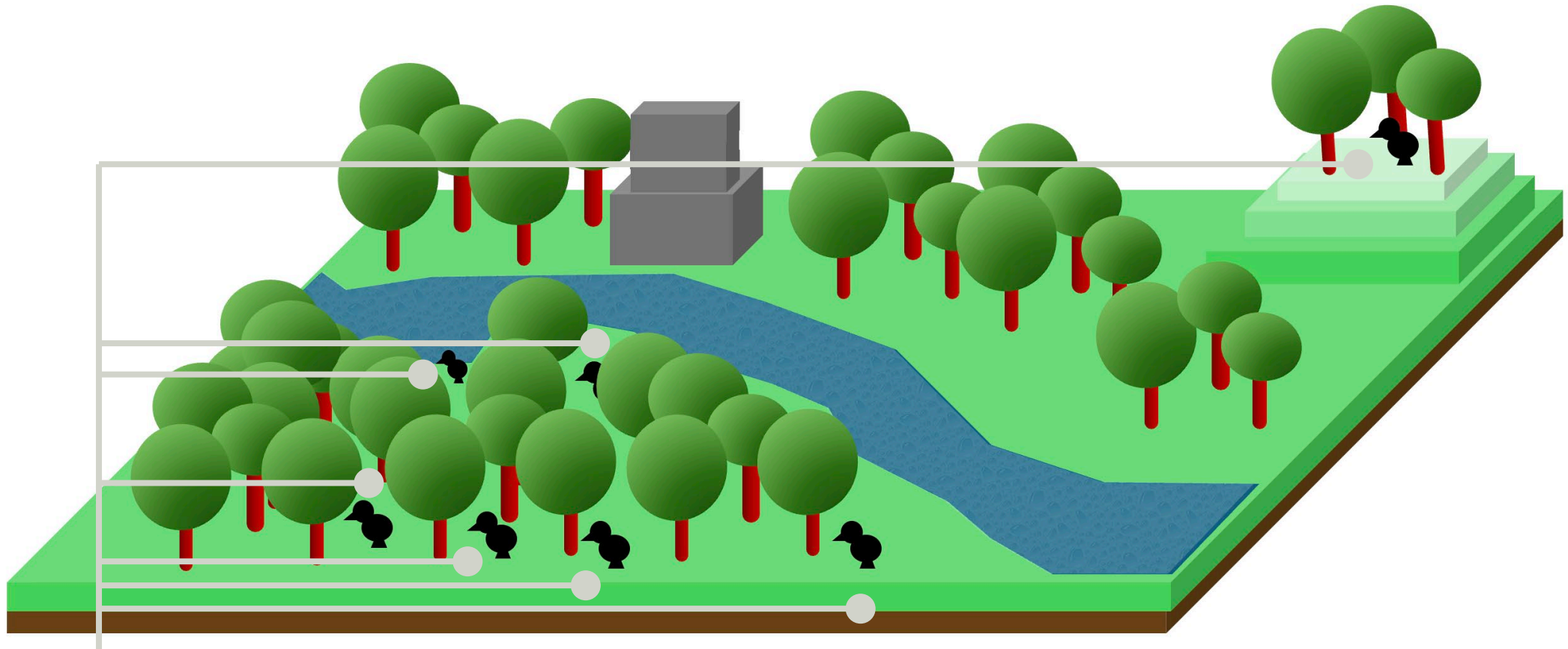
**BioSpace25 - Biodiversity insight from Space**  
**10 - 14 February 2025 | ESA-ESRIN | Frascati - Italy**



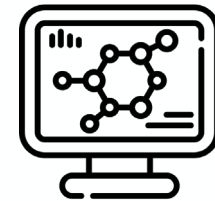
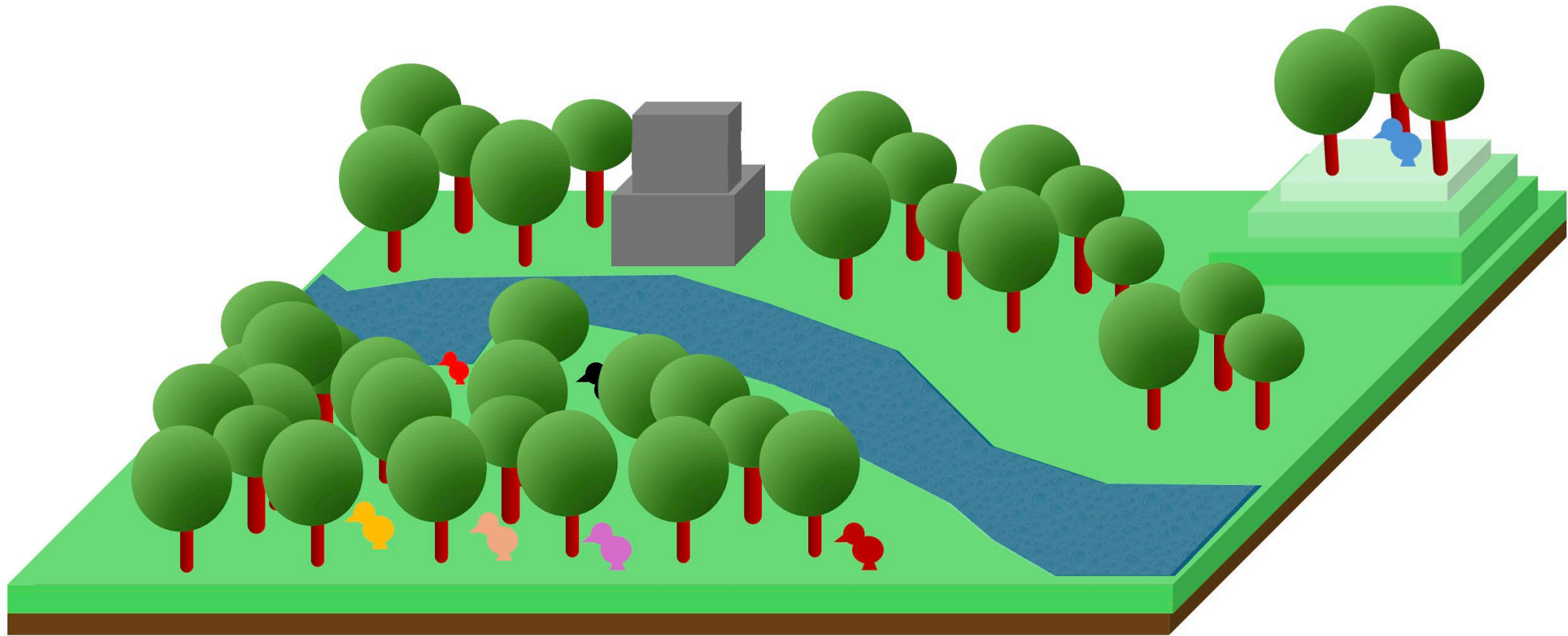
# An interactive tool to monitor species genetic diversity from Earth observations

**Oliver Selmoni, University of Zurich**  
**ISSI Genes from Space team**

# Measuring genetic diversity with DNA is demanding

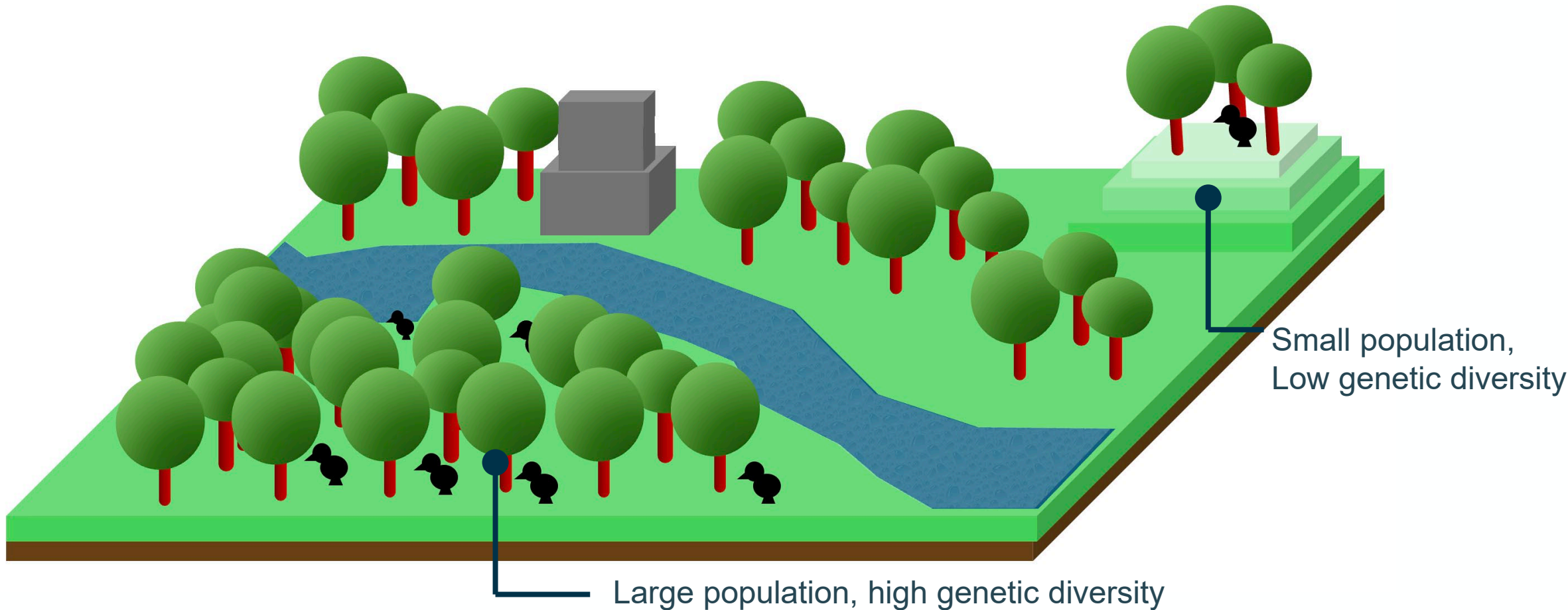


# Measuring genetic diversity with DNA is demanding



# Genetic diversity without DNA sequencing

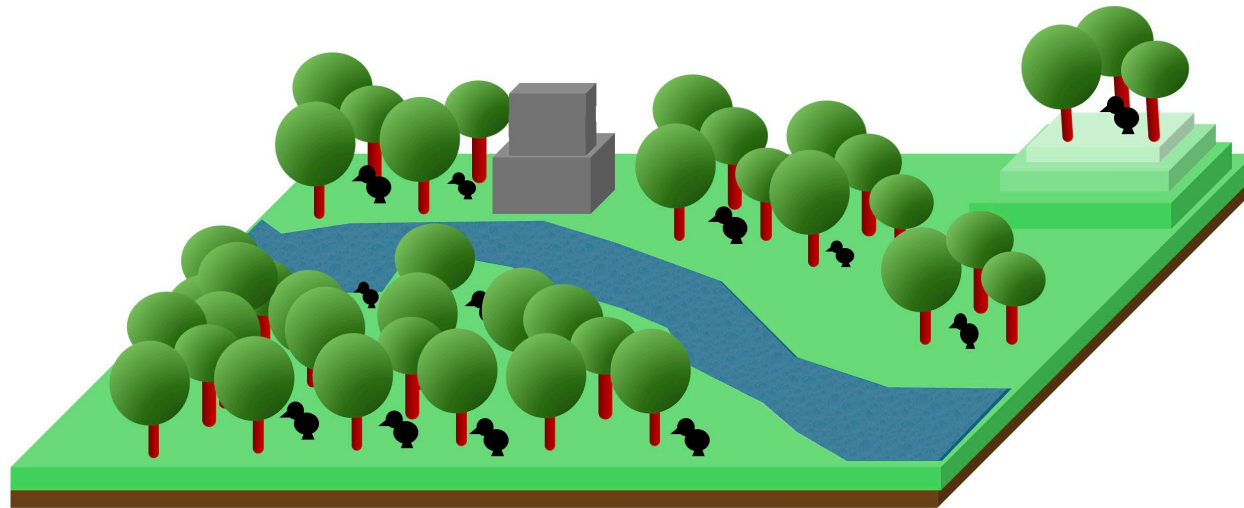
Genetic diversity is proportional to **the size of populations**



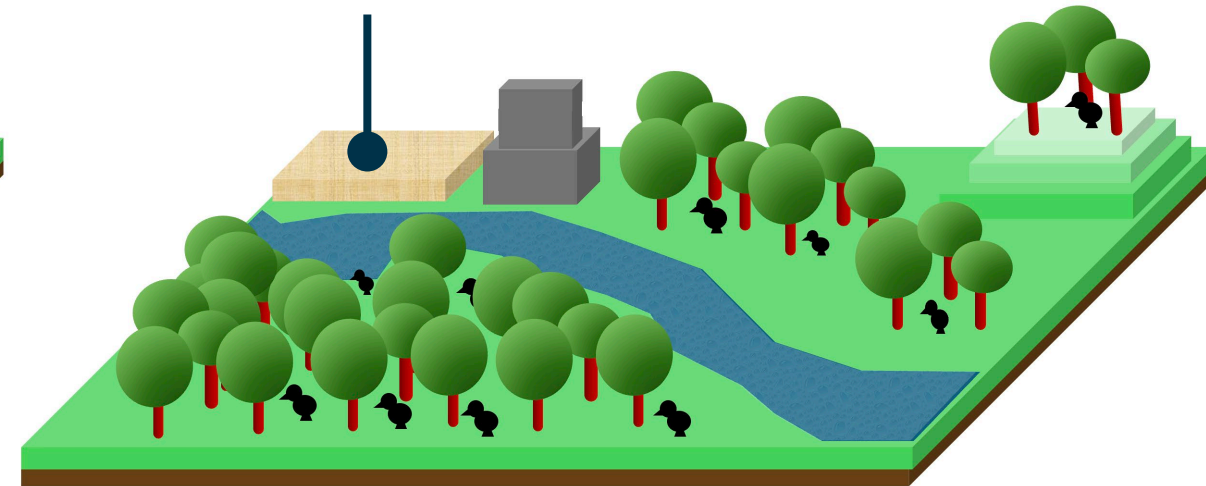
Headline indicator  $N_e > 500$  – how many populations are large enough?

# Genetic diversity without DNA sequencing

Genetic diversity is proportional to **the number of populations**



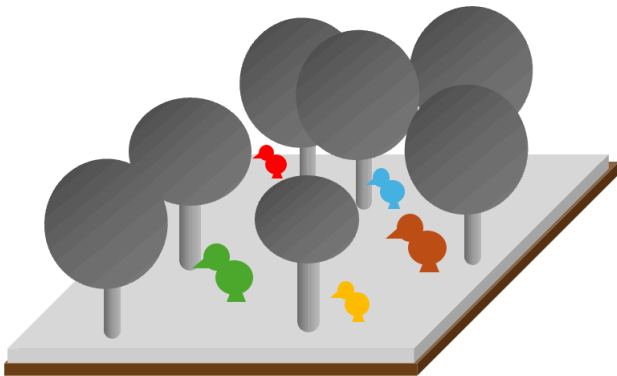
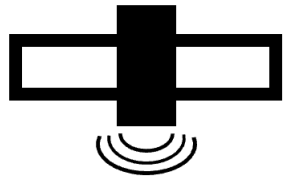
When populations are lost,  
genetic diversity declines



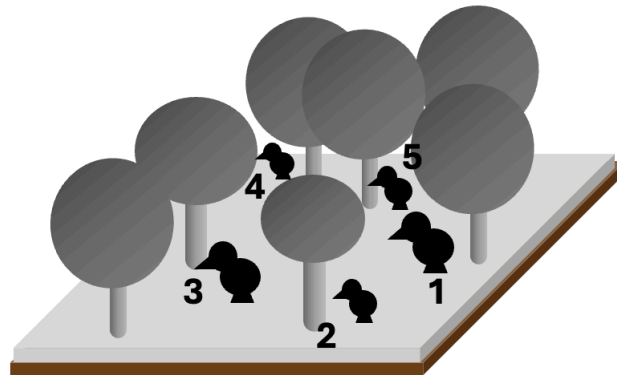
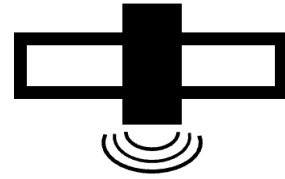
Complementary indicator **PM** – how many populations still exist?

# Genes from space?

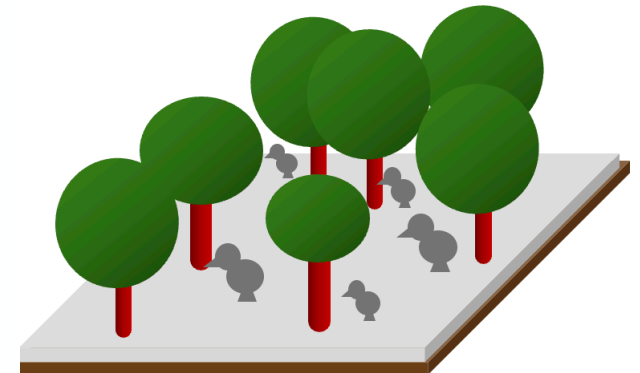
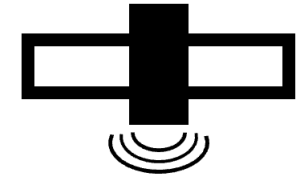
Earth observations...



**✗** ... can not measure genetic diversity



**✗** ... can not measure populations size



**✓** ... can measure habitat size

# The proposed framework

Step 1) Define populations



Step 2) Estimate populations size

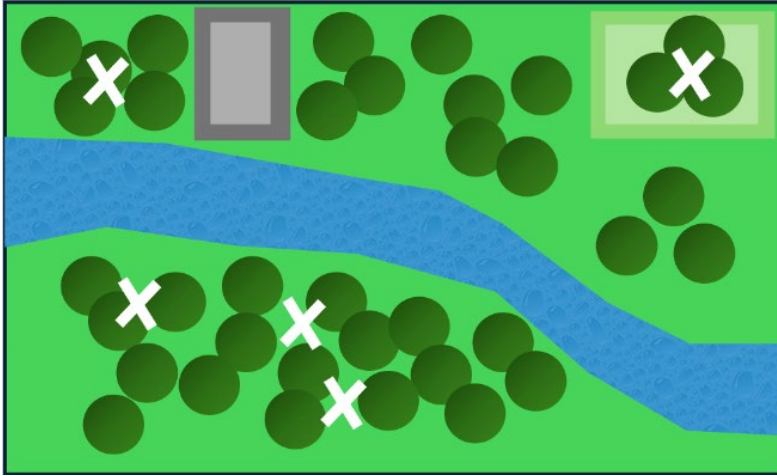


Step 3) Monitor change over time



# 1) Define species populations

2000



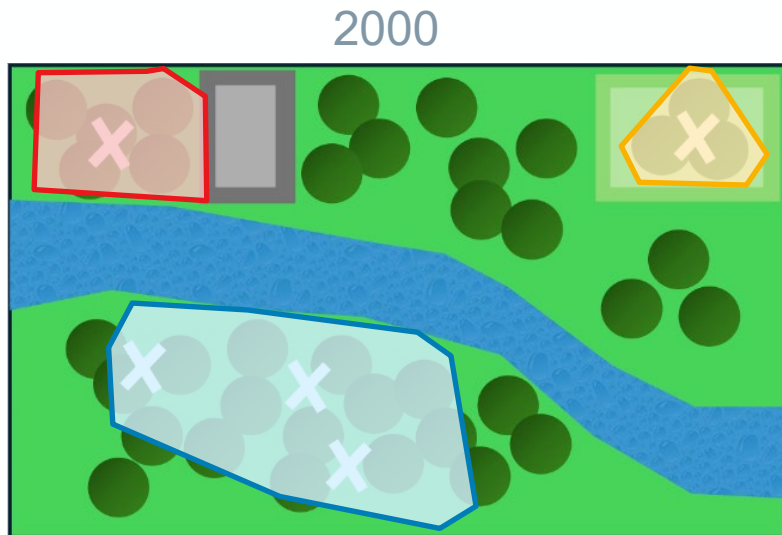
X = field observations of the species



Species occurs in broadleaved forests



## 2) Estimate populations size

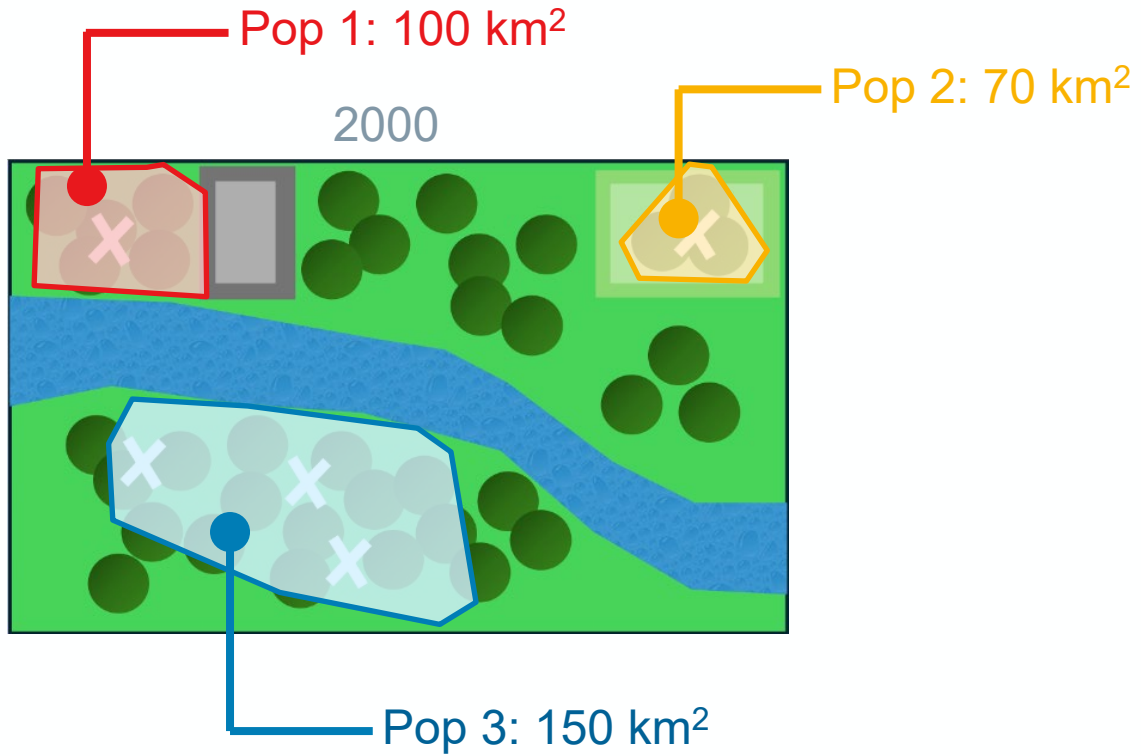


Species occurs in broadleaved forests

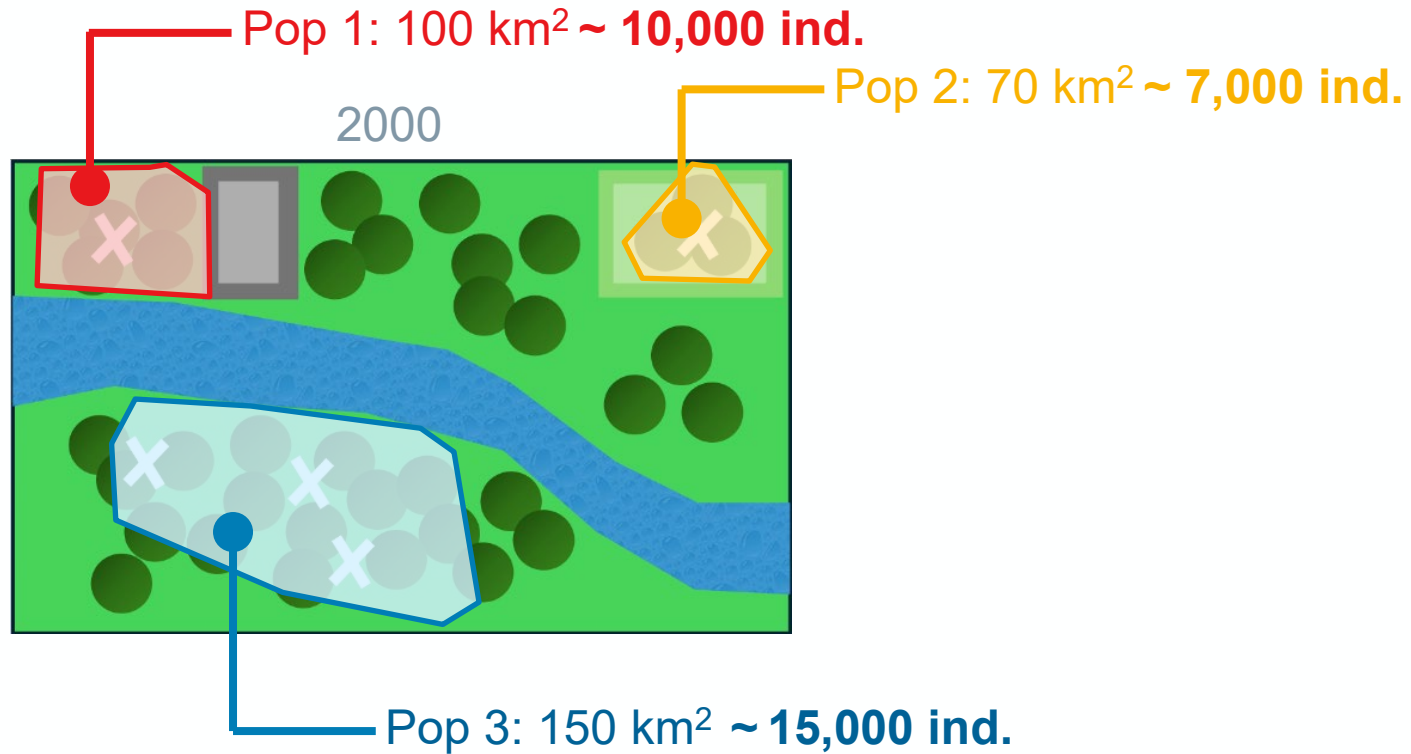


No dispersal across rivers and mountains

## 2) Estimate populations size

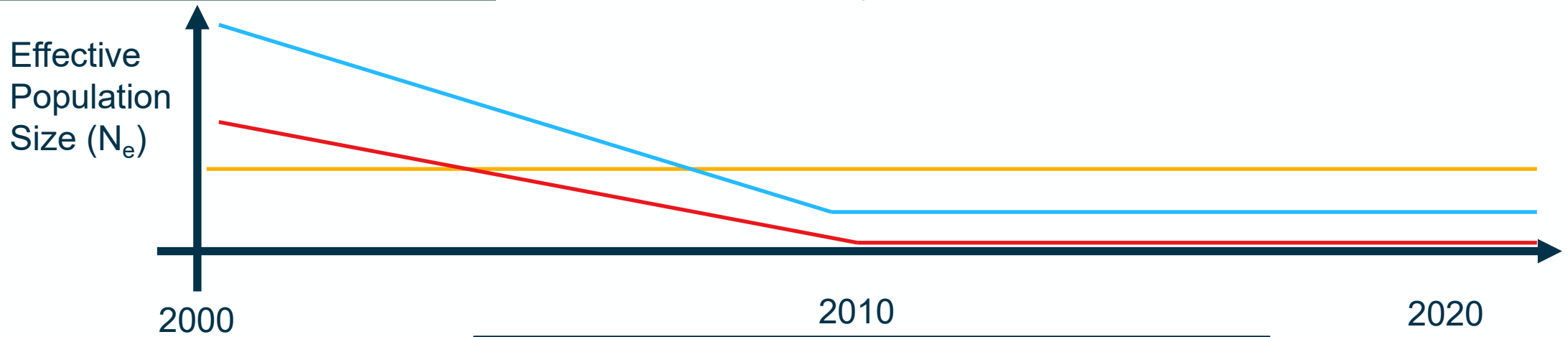
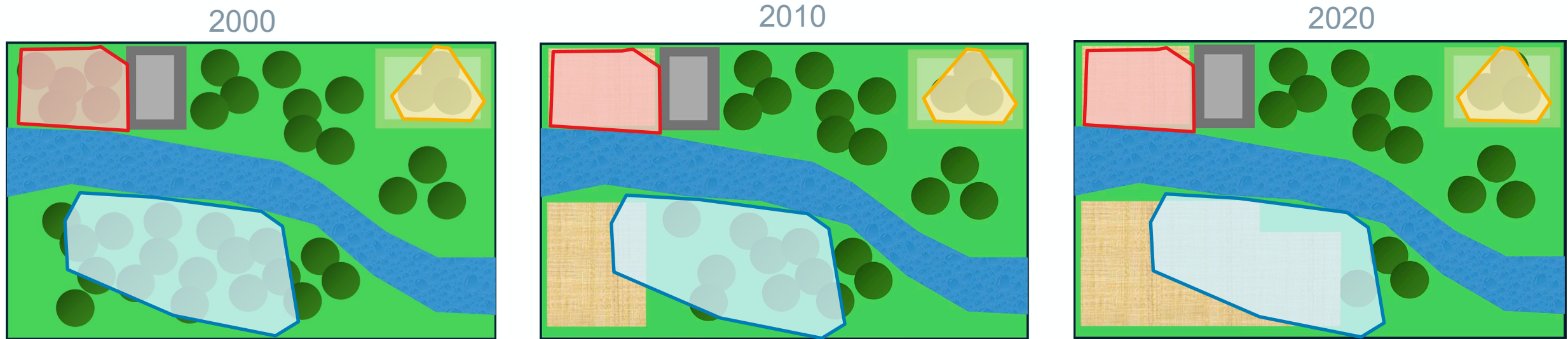


## 2) Estimate populations size



Population density ~ 100 individuals / km<sup>2</sup>

# 3) Monitor change over time



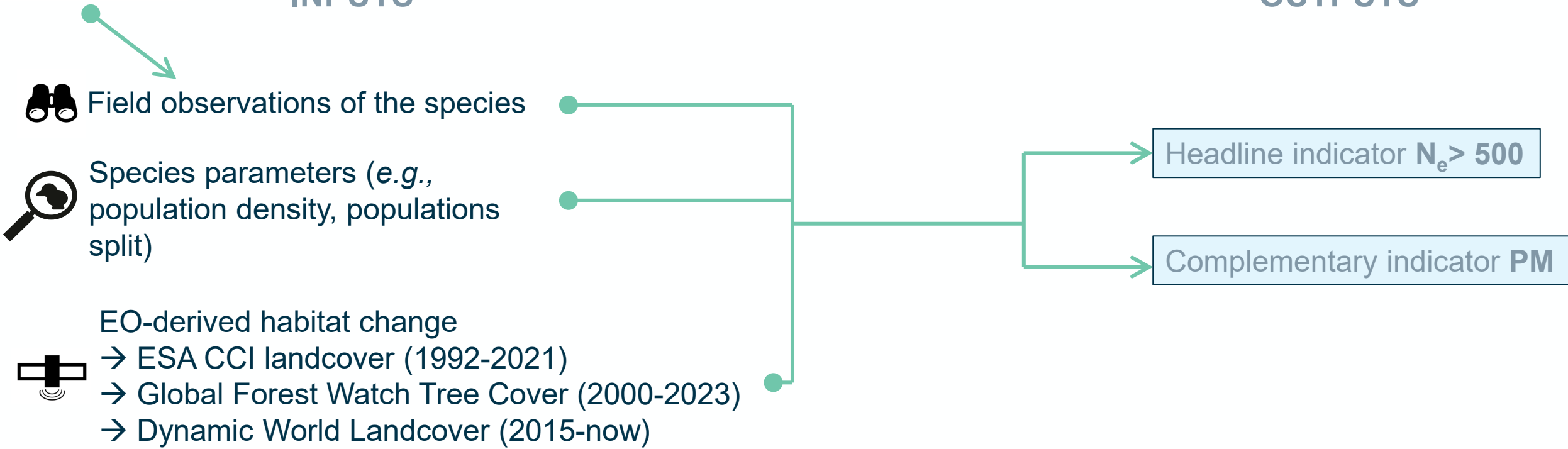
Ne500 Indicator: 1/3 population is large enough  
PM Indicator: 2/3 populations still exist

# The monitoring tool



## INPUTS

## OUTPUTS





# The monitoring tool

The screenshot shows the web interface of the monitoring tool. At the top, there is a browser address bar with the URL <https://www.genesfromspace.org>. Below the address bar, the page content is organized into sections:

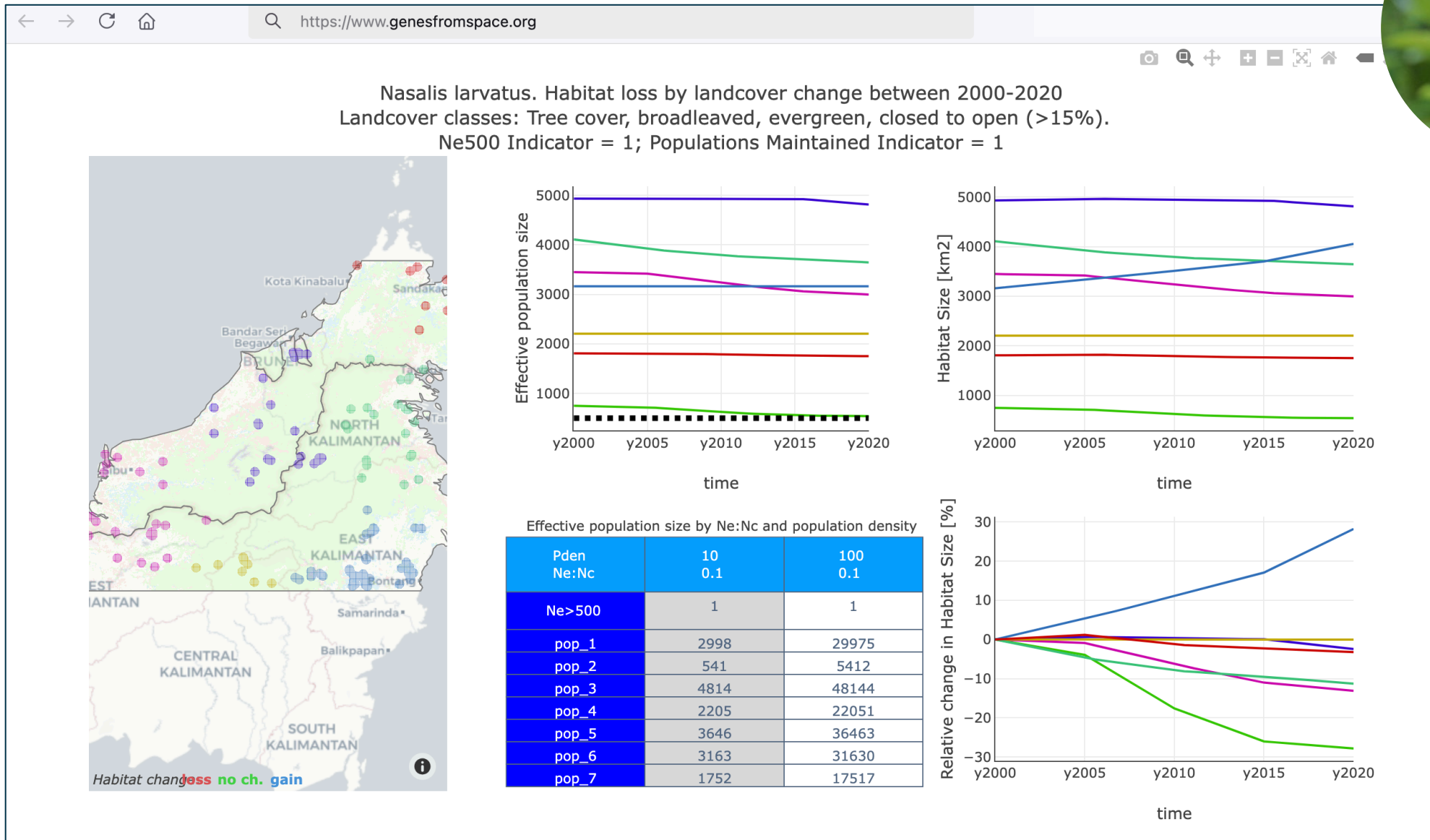
- Name of species**: A text input field containing "Nasalis larvatus".
- Geographic distribution of populations**: A dropdown menu currently showing "→ How to provide species coordinates?".
- How will species observation coordinates be provided?**: Two radio button options: "User-provided" (unselected) and "Retrieved from GBIF" (selected).
- How will the GBIF region of interest be specified?**: Two radio button options: "Draw region of interest on a map" (unselected) and "Select one or more countries from a list" (selected).
- Countries of interest**: A multi-select dropdown menu showing "Malaysia" as the selected country.

→ Open development within **Bon In a Box**

→ Free, available online, in english and spanish

→ Interactive interface, **no programming skills required**

# The monitoring tool



# A collaborative development

→ Tool is currently a prototype

→ Beta testing phase: ~100 participants (researchers & stakeholders), feedback on:

→ **Reliability:** validate with DNA or field data, estimate uncertainty

→ **Ease-of-use:** develop guidelines to define parameters

→ **Usefulness:** output formats usable for reporting





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