Report on the outcomes of a Short-Term Scientific Mission[1]

Action number: CA17108

Grantee name: Sotiris Meletiou

Details of the STSM

Title: Modelling of mosquito abundance and diversity in Cyprus in response to invasive species introductions.

Start and end date: 30/05/2022 to 10/06/2022

Description of the work carried out during the STSM

Description of the activities carried out during the STSM. Any deviations from the initial working plan shall also be described in this section.

During the first stage of my training, the database of all sampling points was preliminary examined to identify which variables are to be selected in accordance with our hypotheses. The main questions were,

1. How the abundance or Presence/Absence of mosquitos was influenced by local abiotic trap conditions recorded by the mean temperature and humidity
2. The study of species abundance within the wet and dry seasons, in addition to range shifts in response to any effect that might be observed.
3. The comparison of the effectiveness in species richness and abundance among the BG and EVS traps.

A deviation from the initial working plan was agreed regarding the plotting of WNV detection as due to time constraints the molecular identification of the virus was not finalized prior the STSM. The training on VecMap took placed as planned in the application **Appendix 1**. Briefly, the plan was implemented as follows:

Day 1: Database cleanup and data manipulation. Identification of tools that will be required (Terra package, QGIS)

Day 2: Research on the implementation of RF and GLM models

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Day 3-4: Vecmap Set up and configuration. Creation of Loops for presence absense data in Rstudio for further use in GLM.

Day 5-6: Terra package training and visualisation of data in QGIS.

Day 7: Finalisation of future plans for cooperation and review of workflow.

For the first stage a data clean-up methodology was applied along with specific conditions to all datapoints (traps). The condition of trap would have to be listed as Perfect; Fan working at full speed uppon collection and no damaged parts. Specimens enlisted as unidentified and extremely damaged were excluded. Following, the examination of the data, resulted in the decision to proceed a Presence/Absence statistical approach as abundance methods significantly rely upon sampling methodology and optimal trap placement for each location. Moreover, for the purpose of studying the distribution of all collected species and in response to possible invasions the presence/absence statistical approaches maximize confidence in our results and significatly reduce the sampling bias mentioned above.

On a second phase, the necessary tools required for the efficient application of our statistical and spatial analysis were decided. Initially, the R studio package Terra was selected, and a three-day training followed with more emphasis on spatial distribution models. Later, QGIS software was used for the initial visualisation of the extracted data (Figure 1). Finally, the Vecmap web component was set up by importing and converting the existing spreadsheet database to an interactive lab and field layouts. Consequently, field sampling variables such as, location, set up & collection time and traptype are directly imported through the supported mobile app. Subsequently, the lab personnel can automatically insert the results of the species identification. During the third and final stage, the two statistical approaches were identified and further studied with regard to their applications on biological data and the background mathematical processes of each model. Random Forest (RF) and Generalized linear models with bootstrapping (GLM) were selected.
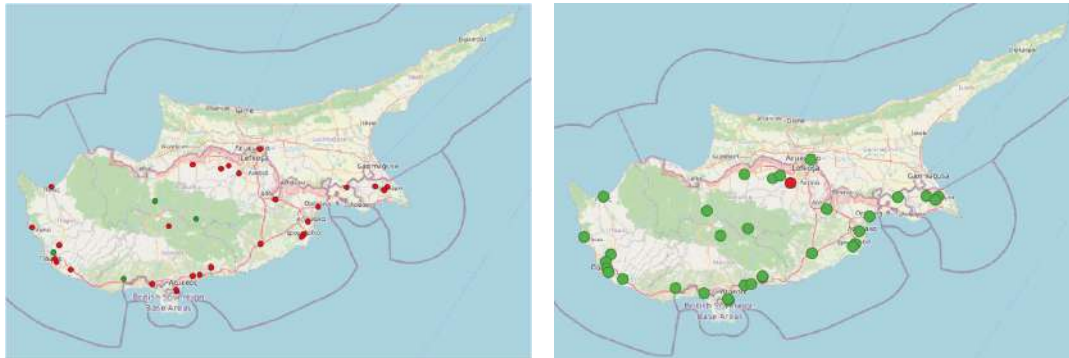

Figure 1: Distribution maps of Culex pipiens(Left) and Culex martinii (right) during dry season (red=present, green= absent)

Description of the STSM main achievements and planned follow-up activities

Description and assessment of whether the STSM achieved its planned goals and expected outcomes, including specific contribution to Action objective and deliverables, or publications resulting from the STSM. Agreed plans for future follow-up collaborations shall also be described in this section.

During this STSM I had the chance to work and collaborate with leading experts in the field of spatial analysis and modelling of disease vectors. As an early career researcher this was very valuable as I had first-level experience in the different approaches to analysis of data with the advantages and disadvantages of each one being identified. I had the chance to expand my statistical analysis tools by using the Terra package in R studio, Vecmap and QGIS. By that an example workflow for analysing field data was developed as in the case of invasive mosquito species distributions. The established methodology and skills acquired in this STSM will aid in the rapid identification and surveillance of any invasive Aedes species reported. As this is an ongoing project any confirmed invasive species will be part of an already established surveillance network. By that the identification of variables that might influence their spread from the initial point of detection will be possible. We have also agreed to a future collaboration plan regarding the further application of more complex models with Avia-GIS as soon as all field data are collected. In conclusion, this collaboration has the potential to be applied and further developed in any future projects regarding mosquito serveilance and control.

Vecmap Set-up and configuration

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Step 1 Project Structure

-Creation of two levels

1. Location

Default level YES

Mobile layout YES

2. Trap collection – Date
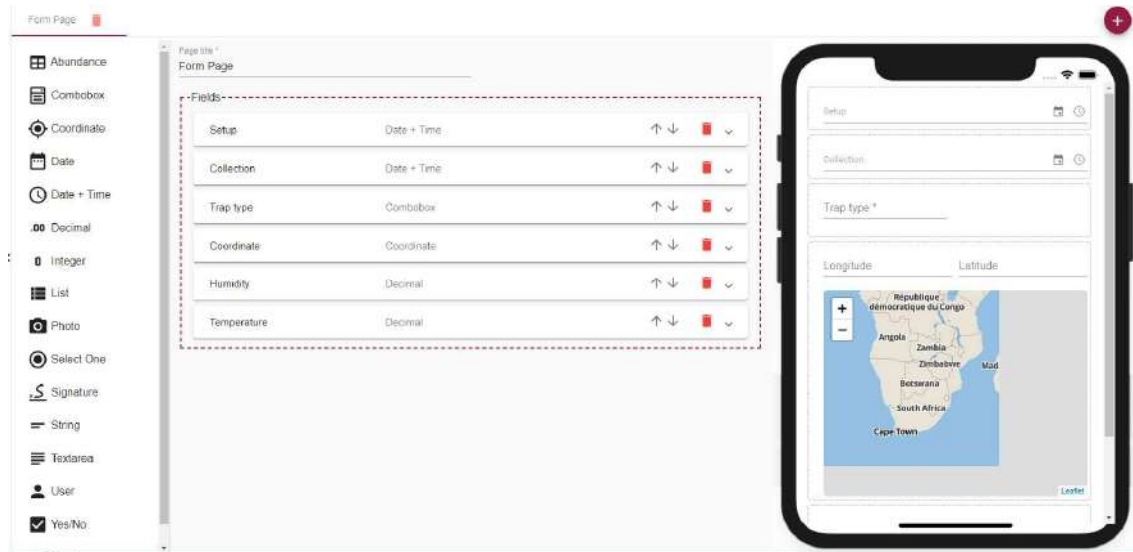

Mobile layout YES

Lab YES

Use assignments on this level YES

Step 2 Creating Layouts

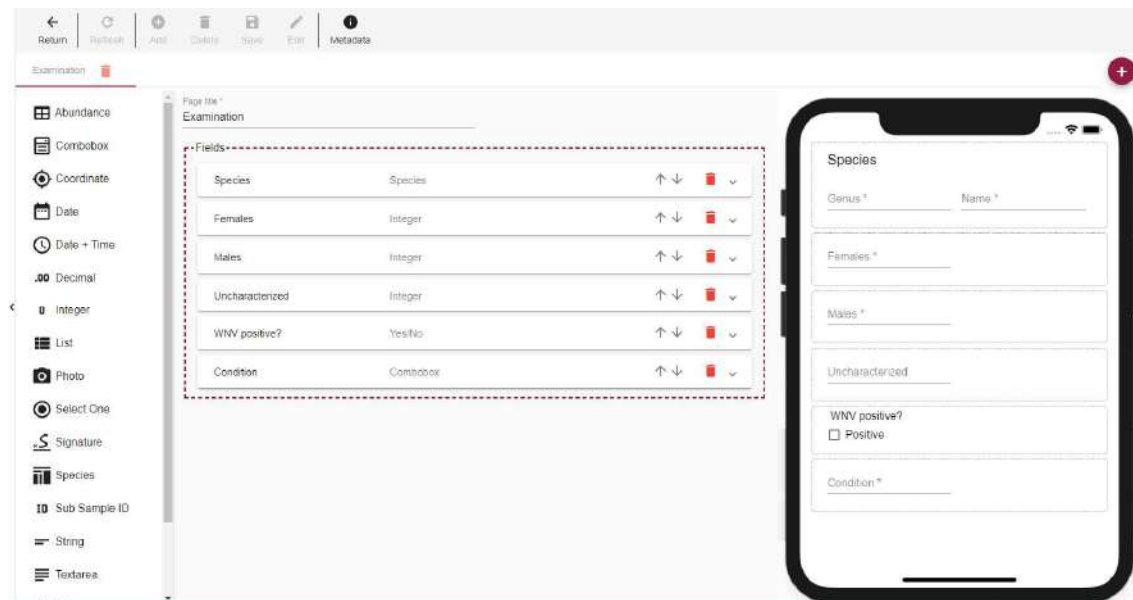Interfaces that **correspond** to each variable in our dataset

For the purposes of this project, we have to create Field and lab layouts

Field

Lab

Step 3 Import our existing database

Data files tab: Upload **.CSV** file

We first must import our first level that will also be the parent record that is going to be linked to level two (dates).

Because of our unique identification codes (ex. BPAR18112021) the trap type can be inferred.
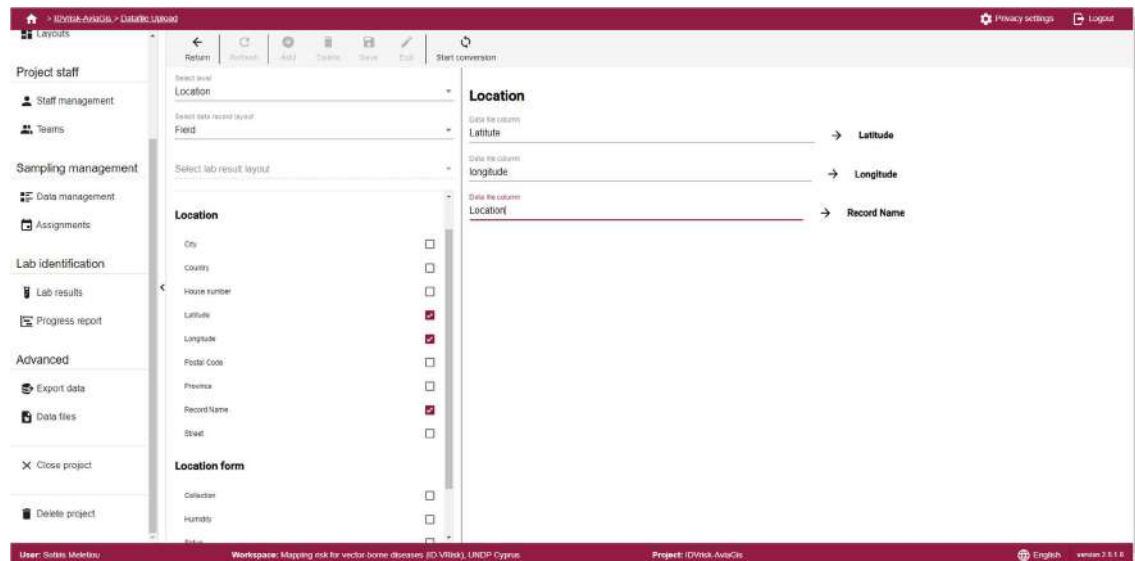
Problem 1:

Going to DataManagement tab you will notice that for each location several rows have been creates as it corresponds to the rows of the file.

You can select everything and then deselect one for each location, After that we have a list of all location.
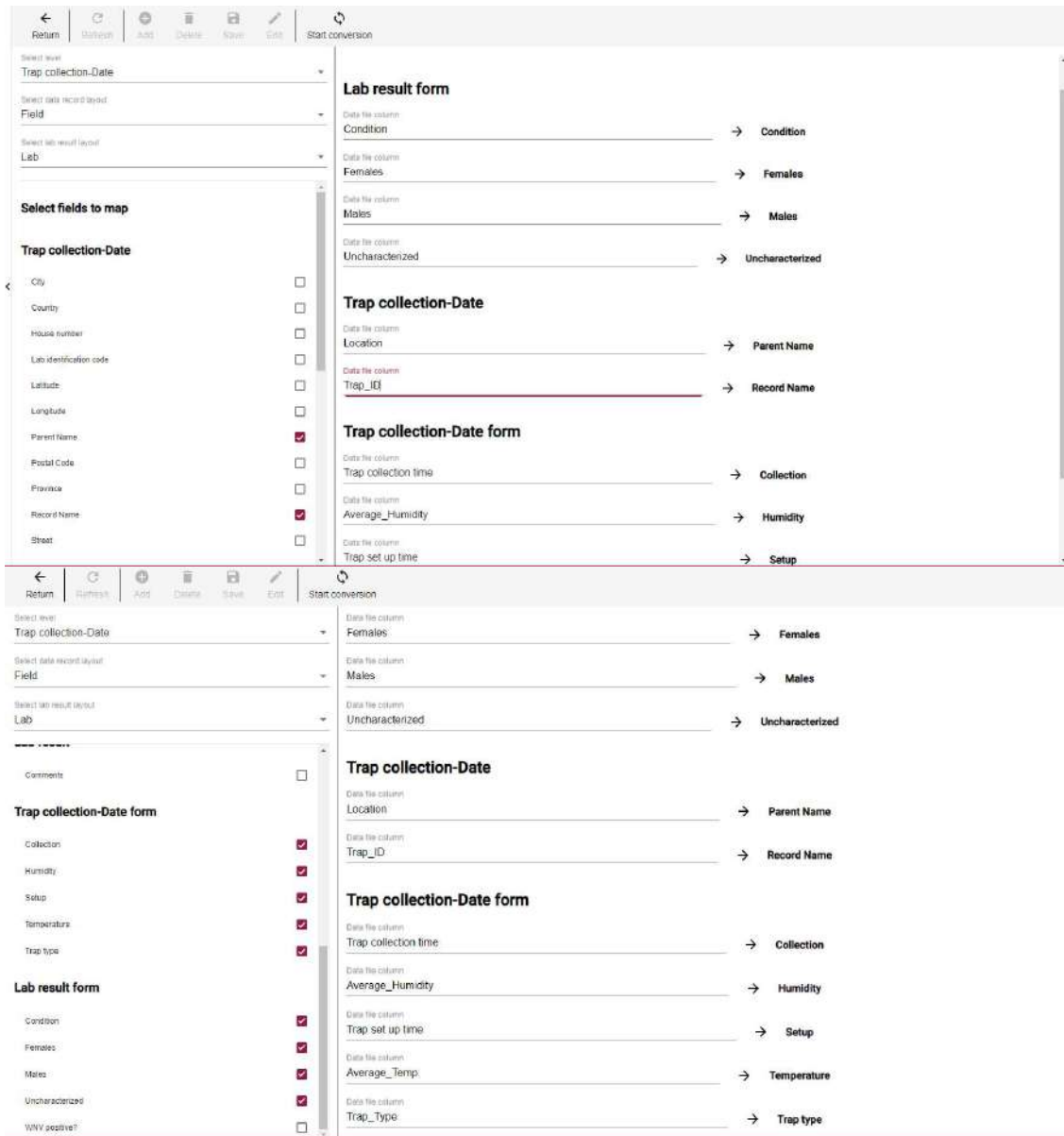
Next step.

Importing everything else (see below)

SOS: **Parent name** option linked the two levels on our preferred variable so it will be **Location**

Record name should be our unique **trap ID**

Click Convert 1

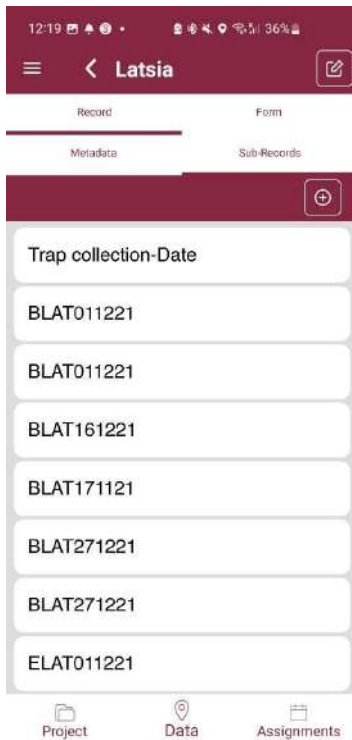**Click convert 2**

Mobile layout
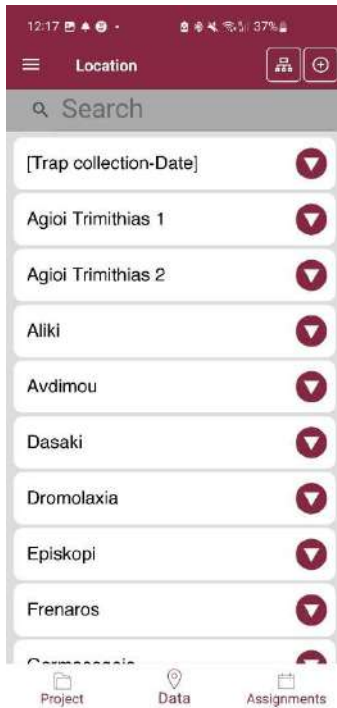
Go to Data tab

Select location level from top right

Press on desired location Name

Click Sub-records

These are all the previous collections made on that Location

Press + in the sub records tab

In the metadata Tab:

Fill Name: Trap ID

Everything else in covered

In the form Tab:

Press Now in the set up section to record set up time

Select trap type

Afterwards you can modify and input from the web component:

- Collection time
- Temperature and humidity
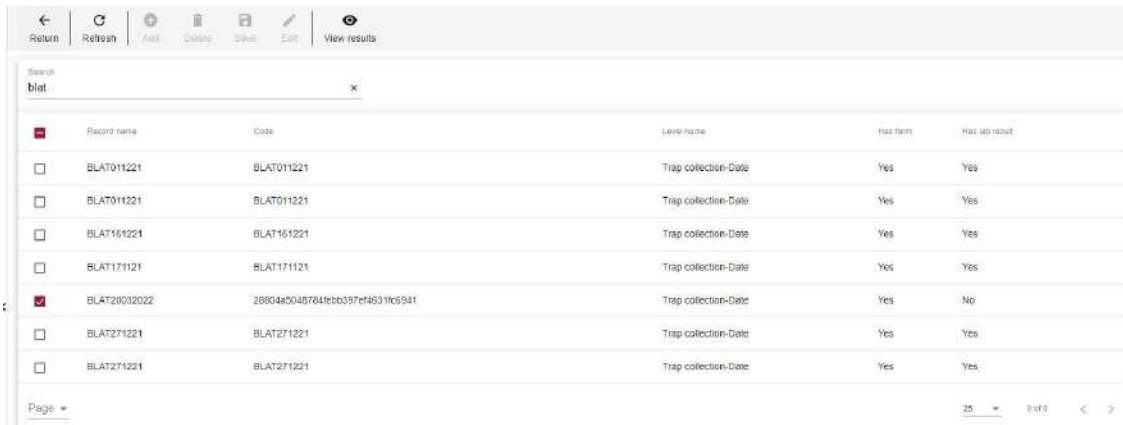
NOTE: Sync after every sampling so the results can be seen on the WEB
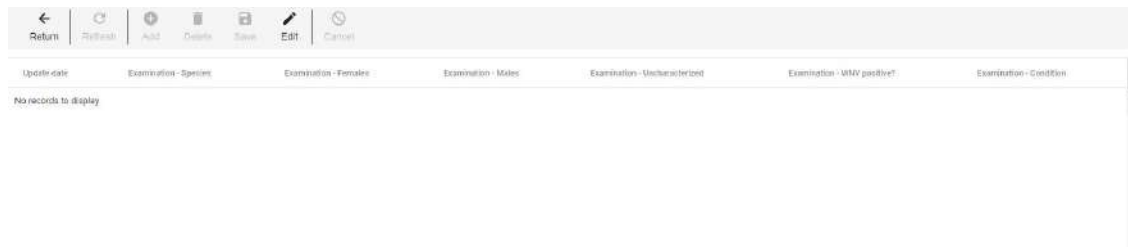
Lab Identification Web component

When a sampling at a point has been inserted in the app it will be automatically transferred (After you synch) to the lab results section in the web component and it will be like this:

You have to search for the name

Press View results:

If no results you can select EDIT and then ADD

Then click save, you can always edit the results afterwards like in the case of unidentified specimens