

Outcome of CoR Meeting:

Confirmation of Status meeting: 12th March 2021

Dan Smith

Committee members present: Julie Hawkins (chair), Tom Oliver

Julie and Tom congratulated Dan on the work to date. The report was well-written, and the work of a high standard. In his writing, Dan might consider being more cautious in his interpretations – this is the case in his discussion of mutualistic interactions. Dan's oral presentation with slides of that work was excellent; so was his ability to answer questions.

We spent some time discussing Dan's future work plan. We explained that an expectation is that students would present a thesis with three solid data chapters. We were concerned that Chapter 4 (phylogeny) was high risk, and if it wasn't possible to deliver something satisfactory Dan's thesis would have just two good data chapters.

The risks associated with Chapter 4 are

- Lack of trait data – Dan explained he might spend a lot of time looking and find that ultimately he only has sufficient trait data for a very thin analysis of traits over a larger taxonomic group or to include more traits he would need to focus on a small group
- Complexity of the trait data, associated challenges in extracting and encoding it
- The steep learning curve for delivering phylogenetic analyses to a high enough standard (training needs; we noted Dan had invested in learning to use BEAST, but there could have been easier methods to pick up that would have been as appropriate – guidance here before the time investment would have been good)

We suggested that Dan rethinks his plans. We had suggestions:

- Is it possible to split current Chapter 3 into two chapters? Perhaps by considering some trait data here without phylogeny? Then the phylogeny chapter would be a pilot study or not needed.
- If there is a big time investment in the exploration of the availability of trait data, could the findings of that survey be written up as an output? i.e. as a review of the availability of trait data (gaps analysis)/as a perspectives piece highlighting research needs for any phylogenetic study of traits.

Dan and his supervisors might consider these suggestions, but ultimately identify other ways forward.

We asked that Dan submit a short report (a couple of pages suggested) outlining his thoughts on future work in one month's time. We would like to review this before confirming Dan's status as PhD student.

Julie Hawkins & Tom Oliver

My Thoughts:

The second chapter “Mosquito Distribution and Disease Risk” modelling can be split quite easily into two thesis chapters, giving overall three data chapters for the PhD overall and one review chapter, which the committee said was perfectly fine for my thesis:

1. Somerset Levels Data Chapter
2. ECDC Distribution Modelling Chapter 1
3. ECDC Distribution Modelling Chapter 2
4. The availability and use of traits

I think this is fine and achievable, and I have enough notes to make a rough start on a review chapter anyway, which would compliment also compliment a small analysis using thes traits in one of the spatial modelling chapters or appended to the Chapter 4 review.

Now just need to determine what to do with the ECDC data:

- What to model (species & predictors)?
- What is novel?
- What is useful to stakeholders?

Spatial Distribution Project Chapters:

Committee reminded me to make sure that easy routes and simple analysis that add value are not overlooked, potentially adding novel results with little more effort in terms of developing new techniques, etc. Particularly that a focus on disease risk is topical and a good theme for the PhD thesis overall.

- 1. What is the risk of West Nile Virus (WNV) transmission in Europe using overlapping niche predictions of both vector and WNV environmental niches?

Marcantonio M, Rizzoli A, Metz M, et al. Identifying the environmental conditions favouring West Nile Virus outbreaks in Europe. *PLoS One*. 2015;10(3):e0121158. Published 2015 Mar 24. doi:10.1371/journal.pone.0121158

The closest resource/paper discussing finding the environmental niche of WNV. Here on a continental and country scale they identified climatic and land variables important or associated with WNV (cases per unit population). Overall study has some merits about identifying the true niche of , but I think we could do better. Especially as the range of data they used concerned just two years of WNV

data. Potentially incorporating this into a larger model that also predicts mosquito occurrence or abundance across a continental scale may give us a better risk map of WNV across Europe.

Overall this would actually be fairly feasible, we could use the methods already mentioned in this paper, ordination and multinomial models, which should be replicable with CORINE and other country wide data being fairly easily accessible for Europe. This in conjunction with our VectorNET data may provide a better alternative to risk mapping the potential for WNV in future climate scenarios etc. Things to think about would be how to incorporate both risk categories of countries (here in this: paper, land use, mean summer temp, rainfall) and the probability of vector presence into a calculation of risk for regions of Europe etc.

- 2. Can we incorporate novel predictors of mosquito distributions using better hydrological models and remote sensing data?

May be interesting if we can leverage any new modelling techniques that focus on ephemeral water duration during peak mosquito breeding months accompanied by relevant temperature and precipitation data. Resolution of these data sources can often be poor and sometimes not account for mosquitoes micro-habitats (just something to bear in mind).

Similarly incorporating known host data and their distributions into SDM's would be interesting, as well as any host associations with habitats that they may share with mosquitoes.

- 3. Will overlapping WNV or RVF mechanistic models with SDM models allow for integration (or at least the comparison) of mechanistic and correlative models.

Potentially complicated and relies upon finding a mechanistic model of WNV or RVF diseases that can be run fairly simply without much tinkering. Similar experiments and comparisons done on sindbis virus below:

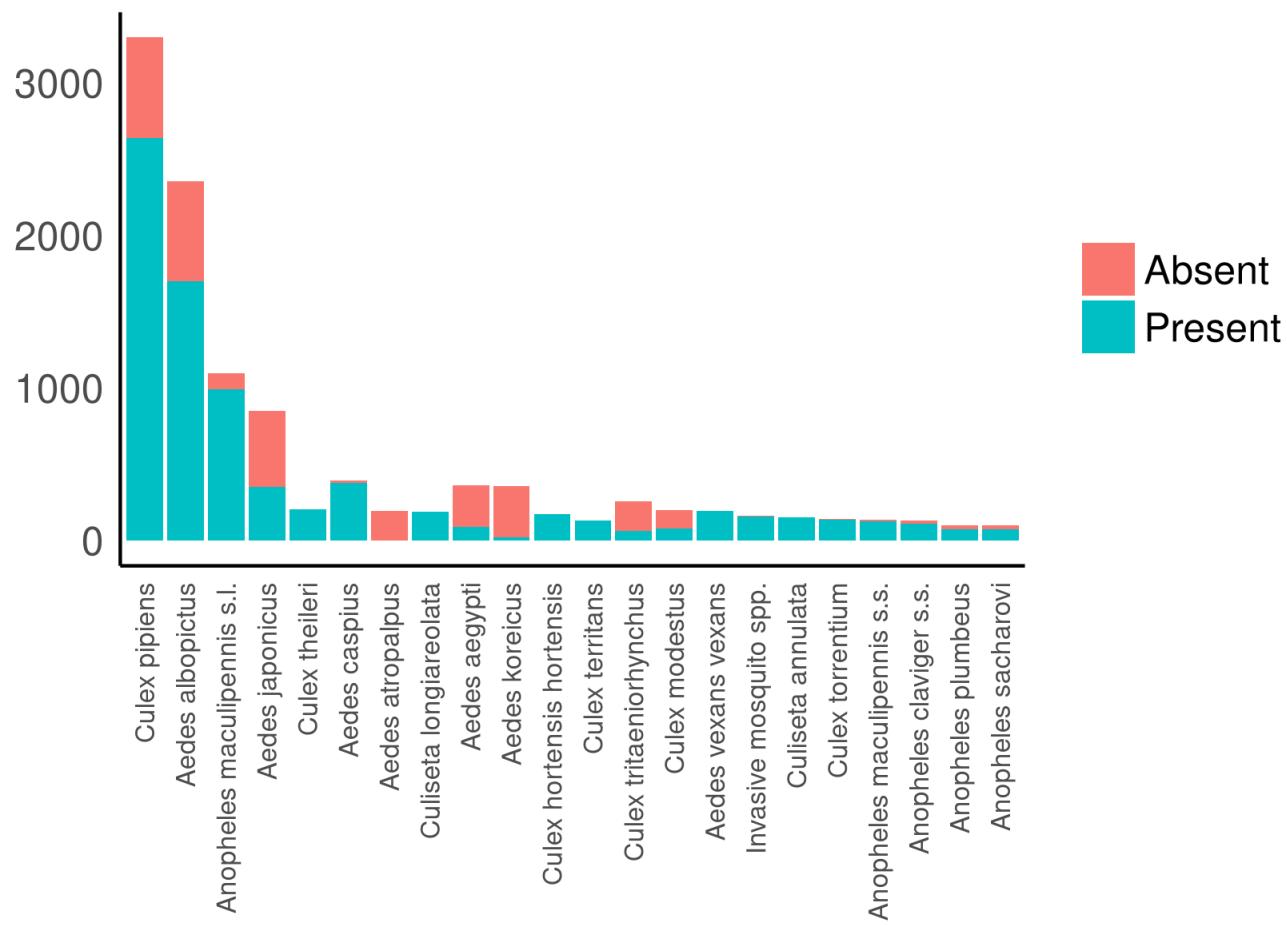
Cheng, Y., Tjaden, N.B., Jaeschke, A. et al. Evaluating the risk for Usutu virus circulation in Europe: comparison of environmental niche models and epidemiological models. *Int J Health Geogr* 17, 35 (2018). <https://doi.org/10.1186/s12942-018-0155-7>

Spatial Distribution Data Overview

Data Availability:

Data Sources	Details	Total Records	Number of Species
GBIF	GBIF search for all mosquito species in the European region since 1970. Must have spatial coordinates and no listed geo-spatial issues. However, only contains species presences, not suitable for many techniques involving traits etc.	3431	51
VectorNet Refined	Refined version of the ECDC mosquito occurrence and abundance data. Contains abundances and absences of many species, though not all species have large samples.	11209	22

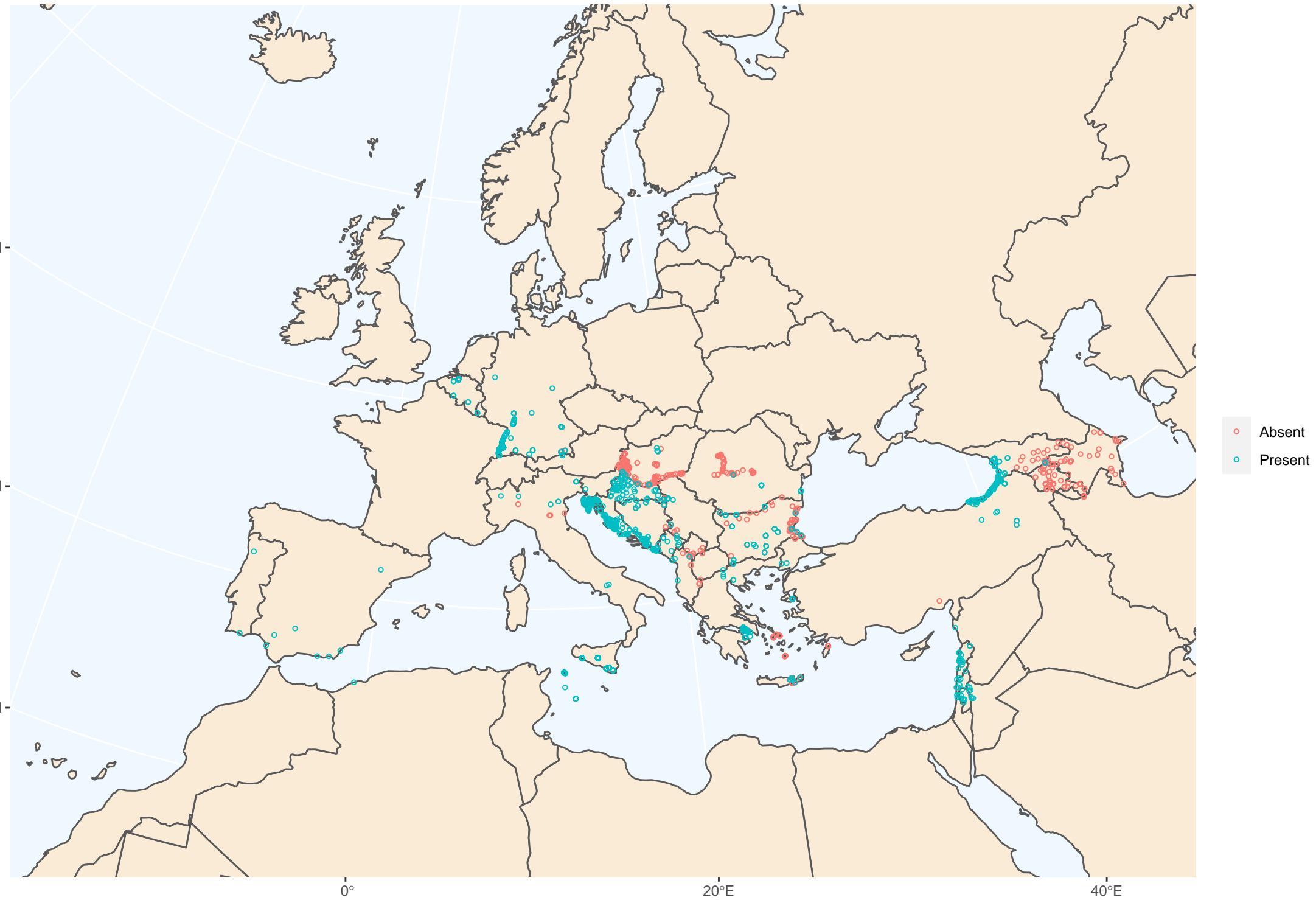
Of all the records in the VectorData set here are the species and their counts of presence and absences in plots:



Of the VectorNet species, these are the following species that have more than 50 absences and presence values in the dataset:

Species	Absent	Present
"Aedes albopictus"	661	1699
"Culex pipiens"	659	2642
"Aedes japonicus"	497	353
"Aedes aegypti"	271	92
"Culex tritaeniorhynchus"	193	63
"Culex modestus"	119	80
"Anopheles maculipennis s.l."	105	993

Aedes albopictus



Culex pipiens



Culex tritaeniorhynchus



Anopheles maculipennis s.l.



Culex modestus



Aedes aegypti



Aedes japonicus

