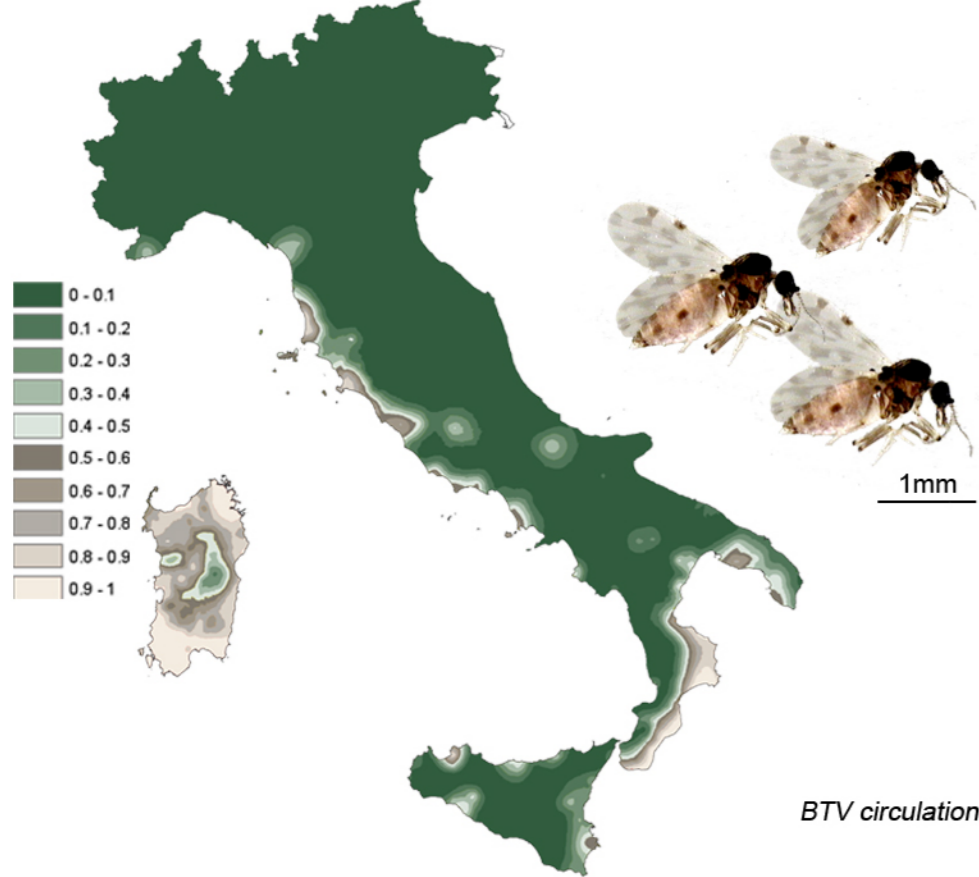# Predicting *Culicoides imicola* populations in space and time using a discrete-time population model

T. Rigot [1], A. Conte [2], M. Goffredo [2], G. Hendrickx [3], E. Ducheyne [3], M. Gilbert [1, 4]

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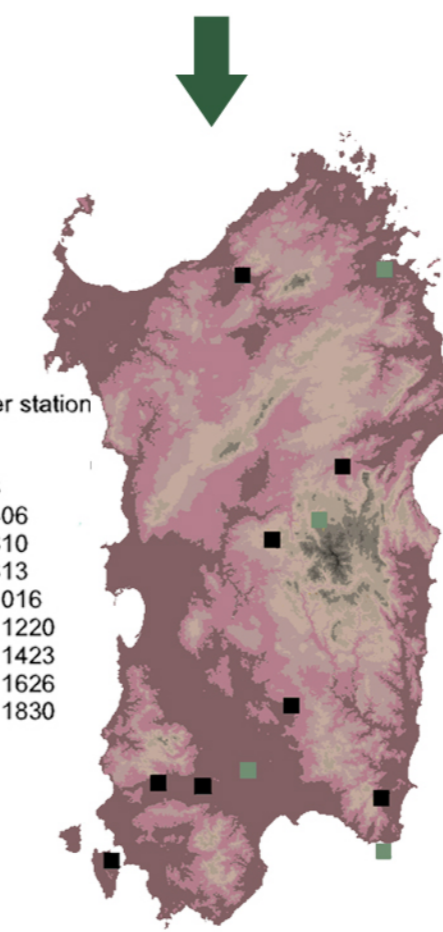
Introduction:

Culicoides imicola is a blood-feeding insect encountered between 35°S and 46° N, from South Africa to South-East Asia. In southern Europe, it is considered to be the main vector of bluetongue disease (BT), a severe, but non-contagious, viral disease affecting domestic and wild ruminants. Over the last 10 years, BT has spread dramatically throughout Europe and the Mediterranean Basin, where six serotypes (BTV-1, 2, 4, 9, 15, 16) spread from southern and south-eastern regions, and one (BTV-8) made a long-distance jump to northern Europe from sub-Saharan Africa. This northward expansion was attributed to global warming, as higher temperatures are associated with higher Culicoides vector competence and also with greater virus replication within the vector.

Understanding how and why vectors distribute and spread in space and time is crucial to understand spatial dynamics of vector-borne pathogens.

Several studies have been working on distribution models of *C. imicola* in Mediterranean countries. Using different types of predictors, statistical approaches and training set, they are difficult to compare even if they provide a good accuracy in space. Most of the time, variables selection occurs during the modelling approach. This leads to spurious correlations and difficulties to interpret some of the variables selected.

Probability of C. imicola presence in Italy
Conte et al. 2010

BTV circulation

Maps of Sardinia and its Dem

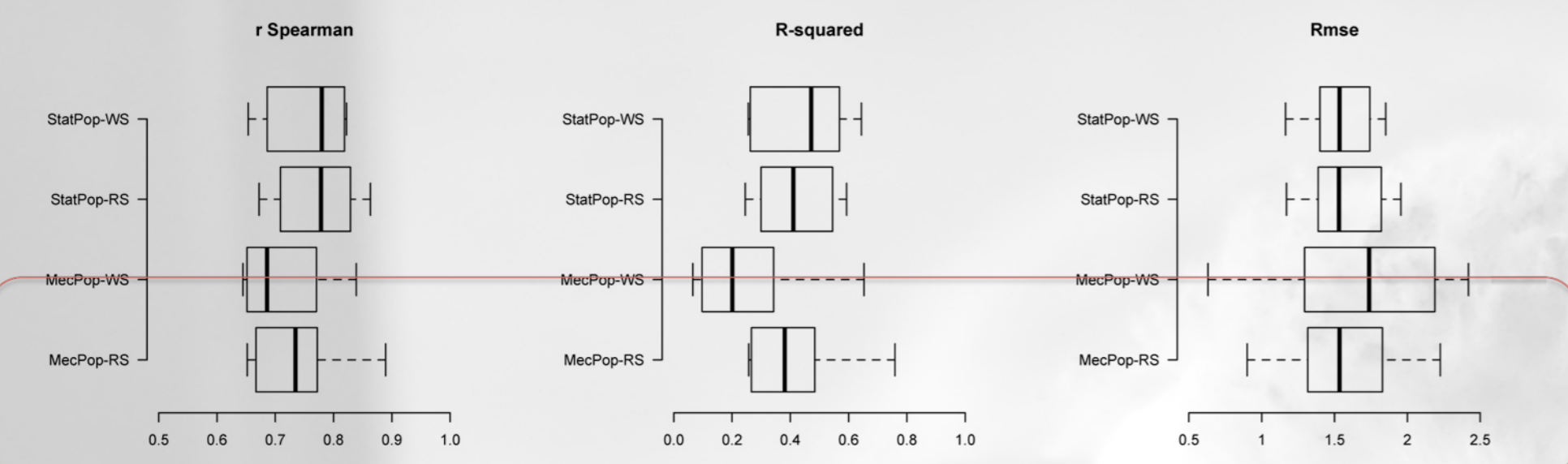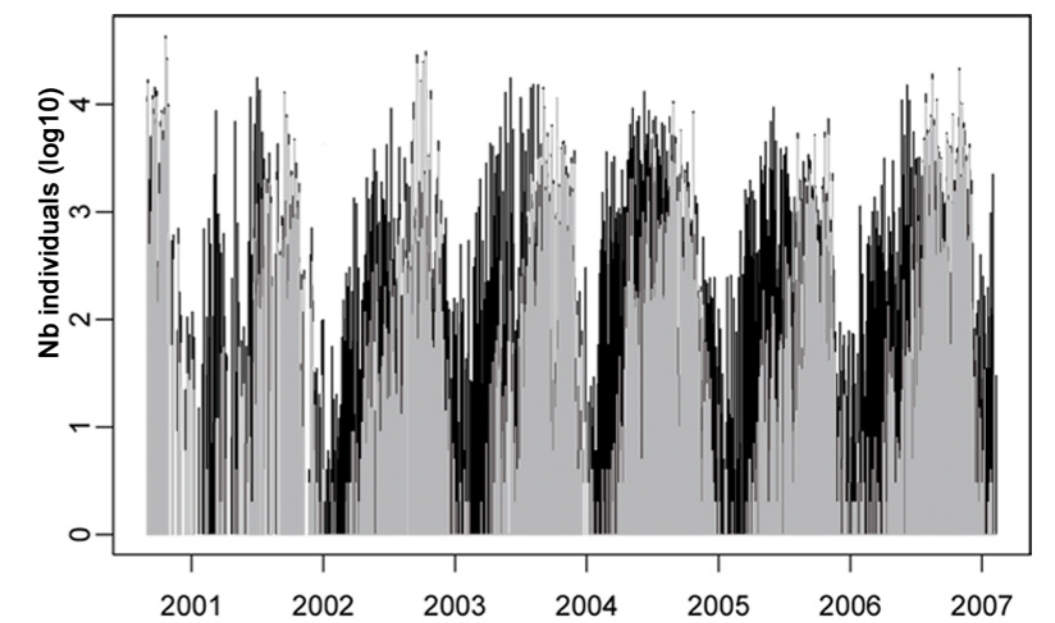Population dynamics of *Culicoides spp.* & *C. imicola*

But:

We decided to build a mechanistic time-dependent and spatially realistic model using *C. imicola* collections achieved in Sardinia during the 2001-2006 vector survey. Our primary aim is to define biological requirements of *C. imicola* populations and their link(s) with RS eco-climatic variables. We secondly aim to simulate the presence/abundance outside stations of collection. In fine, we hope to establish BT risk maps that are biologically coherent with the ecology of its vector.
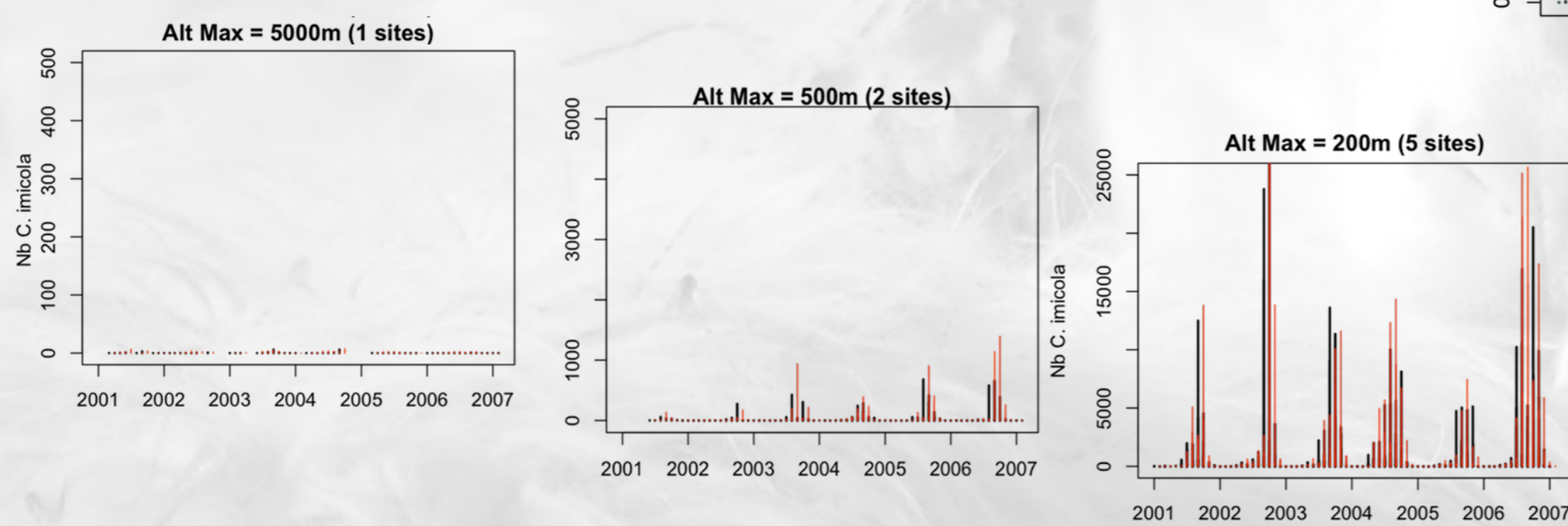
Trap
Weather station

Dem
0 - 203
204 - 406
407 - 610
611 - 813
814 - 1016
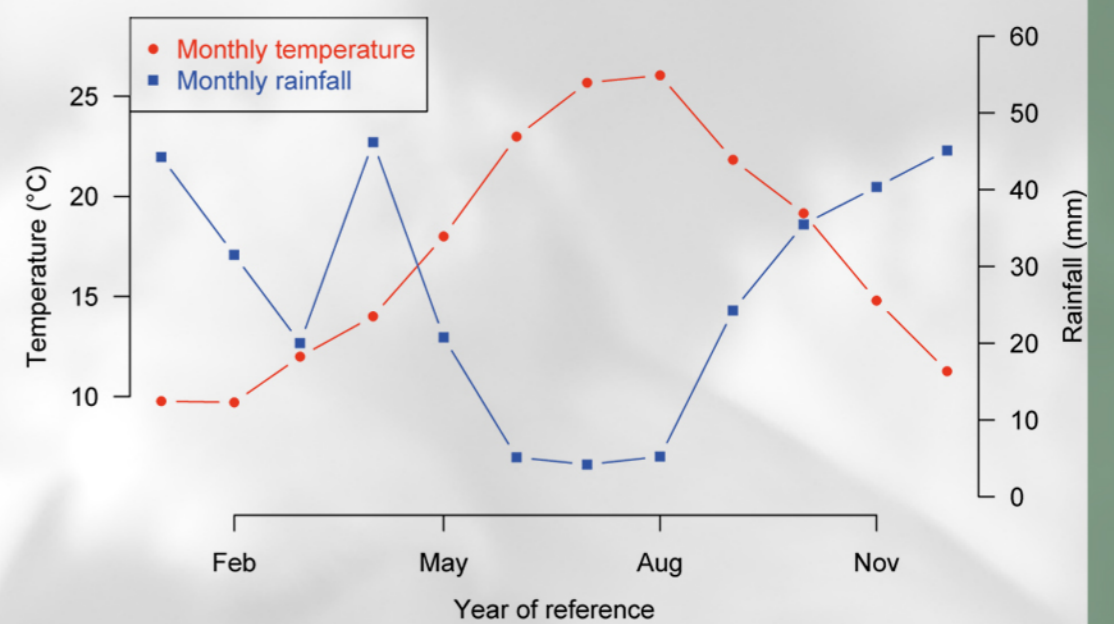1017 - 1220
1221 - 1423
1424 - 1626
1627 - 1830

Result:

Both models, MecPop and StatPop, using RS or WS data, were trained on the whole temporal series (8 sites, 2001-2006) and show similar predictive capacities (see boxplots above). Validations of MecPop in space (various altitudes or Toscana) and in time (training set 2001-2004 / validation 2005-2006) using RS eco-climatic variables (Modis LST and EVI) are respectively presented on the right and below on the left.
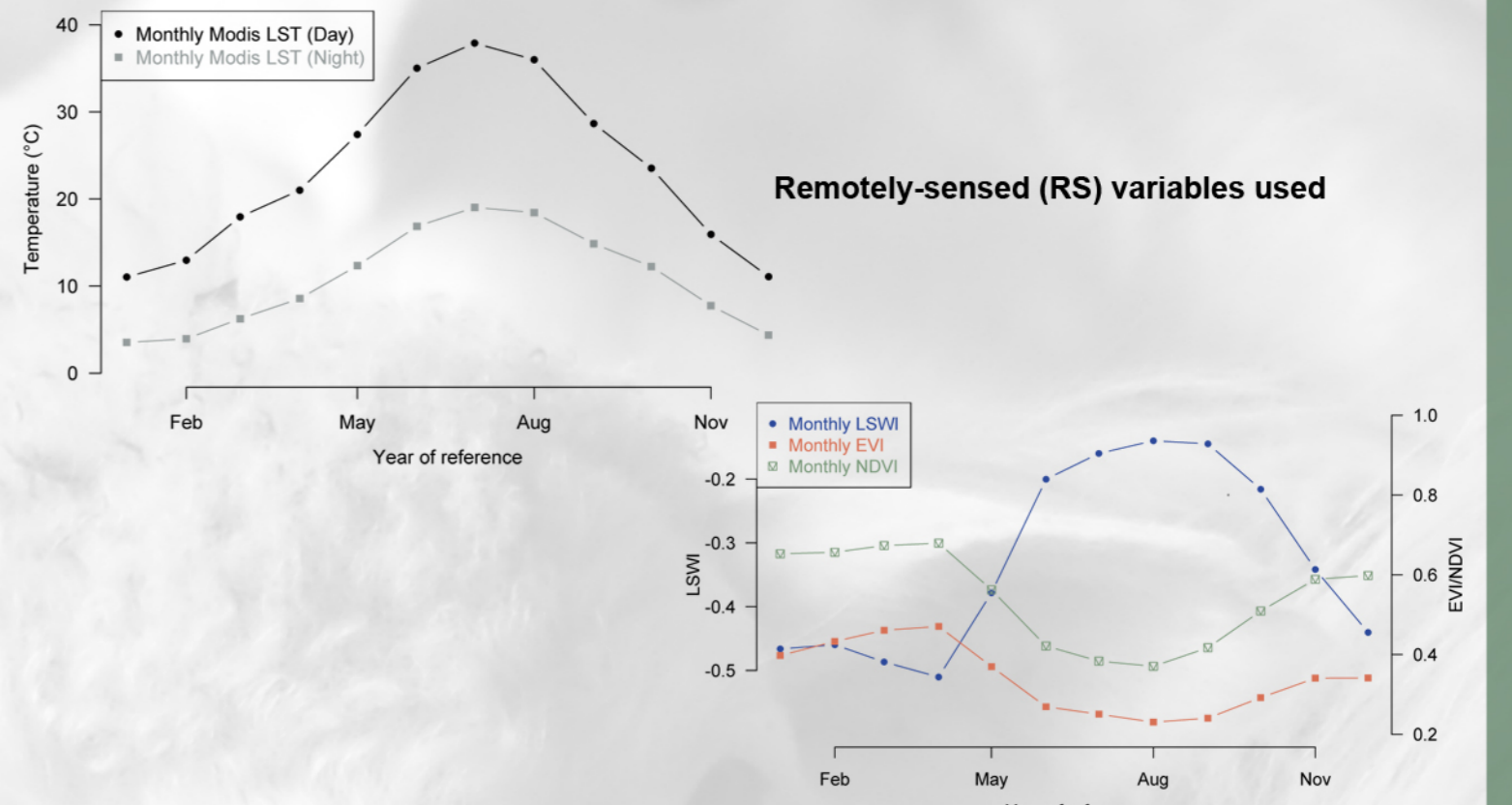
r Spearman

R-squared

Rmse

Coef	Estimate
Modis T	2.75×10^{-3} ***
Modis T²	-9.10×10^{-6} ***
EVI	0.14 ***
Intercept	-20.84 ***

Training Set 2001-2006

Alt Max = 5000m (1 sites)

Alt Max = 500m (2 sites)

Alt Max = 200m (5 sites)

r2=0.71 /corr=0.87 /rmse=1.6

Training set 2001-2004

Validation 2005 - 2006

Validation Toscana 11 sites

r2 = -6.9 /corr=0.44 /rmse=1.9

Methods:

It likes it hot and humid

Weather station (WS) variables used

Monthly temperature
Monthly rainfall

Monthly Modis LST (Day)
Monthly Modis LST (Night)

Remotely-sensed (RS) variables used

Monthly LSW
Monthly EVI
Monthly NDVI

Mechanistic Population growth model

$$N_t = N_{t-1} \cdot e^{r \cdot \Delta t} = N_{t-1} \cdot e^{(n-m) \Delta t}$$

$$n(t) = f(a \cdot \mathrm{var}_1 + b \cdot \mathrm{var}_2 + c)$$

$$m(t) = f(a' \cdot \mathrm{var}_1 + b' \cdot \mathrm{var}_2 + c')$$

$$r_{obs} = \ln(N_t - N_{t-1}) / \Delta t$$

$$r_{obs} = f(a \cdot \mathrm{var}_1 + b \cdot \mathrm{var}_2 + c)$$

Mec Pop

A priori variable selection

vs.

Statistical Population model with quasi poisson noise term

$$N_{s,t} = QuasiPois(\lambda_{s,t})$$

$$\log \lambda_{s,t} = \log N_{s,t-1} + a \cdot \mathrm{var}_1 + b \cdot \mathrm{var} 2 + c$$

Stat Pop

Breaking news

1/ Humans are not spared by *Culicoides* biting midges: among 1250 species encountered all around the world, some really appreciate human blood. Their bites are irritating and this is particularly painful where they act in large number.

2/ Collecting biting midges is very easy when you know where to find them: the use of a UV light-trap during hardly one hour may conduct the entomologist to collect more than 10 000 individuals.

3/ The main limitation encountered during *Culicoides* populations' surveys is the time need to identify them at the level of the genus – because they are numerous – and worst at the level of species. In Belgium for example, on the 44 species encountered, about 20 are easily identifiable using stereomicroscope. Distinctions between the others need to be investigated under optical microscope and in certain cases through genetics.

Conclusion:

Accounting only for Modis LST and EVI, our results showed that the mechanistic model (MecPop) takes into account seasonal activity of *C. imicola* populations. Their preference for hot and humid areas is also supported. In addition the model captures well the changes in population levels as a function of elevation.

Preliminary attempts to try to apply it to Tuscany resulted in a poor fit, with a general tendency to overpredict populations. This suggests that the variables considered in the model should be complemented by other factors that may constrain populations in Tuscany region (e.g. soil characteristics).

Besides the fact that the use of RS data appears - at least statistically - as informative as the use of data gathered by weather stations, the high spatial resolution they offer makes them tools of choice for following steps in our investigations on vectorial disease propagation.

Finally, the statistical model (StatPop) developed here gives also interesting results. We probably will continue to use both methods due to their complementarities to interpret analyzed signals, both biologically and statistically.

Perspective:

To infer emergence patterns of *C. imicola* populations in every area of Sardinia (spatial resolution given by available eco-climatic variables), we still have to simulate and validate the "natural" propagation of the signal in time following the introduction of a given initial population at a given time during their activity season. This approach is currently tested with a monthly resolution. We hope to fine-tune our predictions by disaggregating *C. imicola* population dynamic signals to the finest temporal resolution offered by satellite imagery.