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Bosch, J; Asensio, A; Iglesias, I; de la Torre, A; Muñoz, M.J. (reoyo@inia.es)  
Animal Health Research Centre (CISA-INIA), Valdeolmos, 28130 Madrid

## Introduction



Wild boar is an important reservoir for many diseases shared by both domestic pigs (Classical swine fever, Aujeszky Disease, etc.) and humans (tuberculosis, salmonellosis, brucellosis, etc.). Depending on the type of pig production, the area along the country, in our case Spain, can be delimited and therefore health management at specific regions and provincial level can be achieved. However, in order to carry out surveillance programs of the diseases, the identification of contact areas between pig production and wild boar becomes of high priority to point out the spatial location of the higher risk zones. These sites are very important in the transmission and endemism of these diseases and, in general, in health management.

In shared diseases, the availability of wildlife biodiversity models that consider the species' distribution, density and abundance is of great importance. However, they are often scarce for large-scale studies, so its development becomes of great interest. Some efforts have been carried out to solve the situation for wild boar. Melis et al (2006) evaluated the biogeographical variation in the population density of wild boar in western Eurasia, whereas Oliver and Leus (2008) evaluated its distribution in the Euroasiatic zone. More recently, a suitability map of wild boar has been developed for the Iberian Peninsula (Bosch et al., 2012). Suitable potential habitats where the wild boar might thrive were determined on the basis of selected land uses and assigned specific weights related to the land's ability to supply food and/or shelter to the animals.

The objective of this study is to identify contact zones in the wildlife-livestock interface in order to know the higher risk contact areas between wild boar and free ranging pig farms. The results obtained will permit not only to focus the surveillance sanitary plans at municipal level but also to prioritize the efforts of the health management.

## Material & Methods

Most likely contact areas between wild boar and domestic pigs have been identified using SPATIAL ANALYSIS (ArcGIS 10.0).

And they were defined as those areas that match the highest densities of free ranging pig farms and the highest densities of wild boar: Southwest part of Spain.

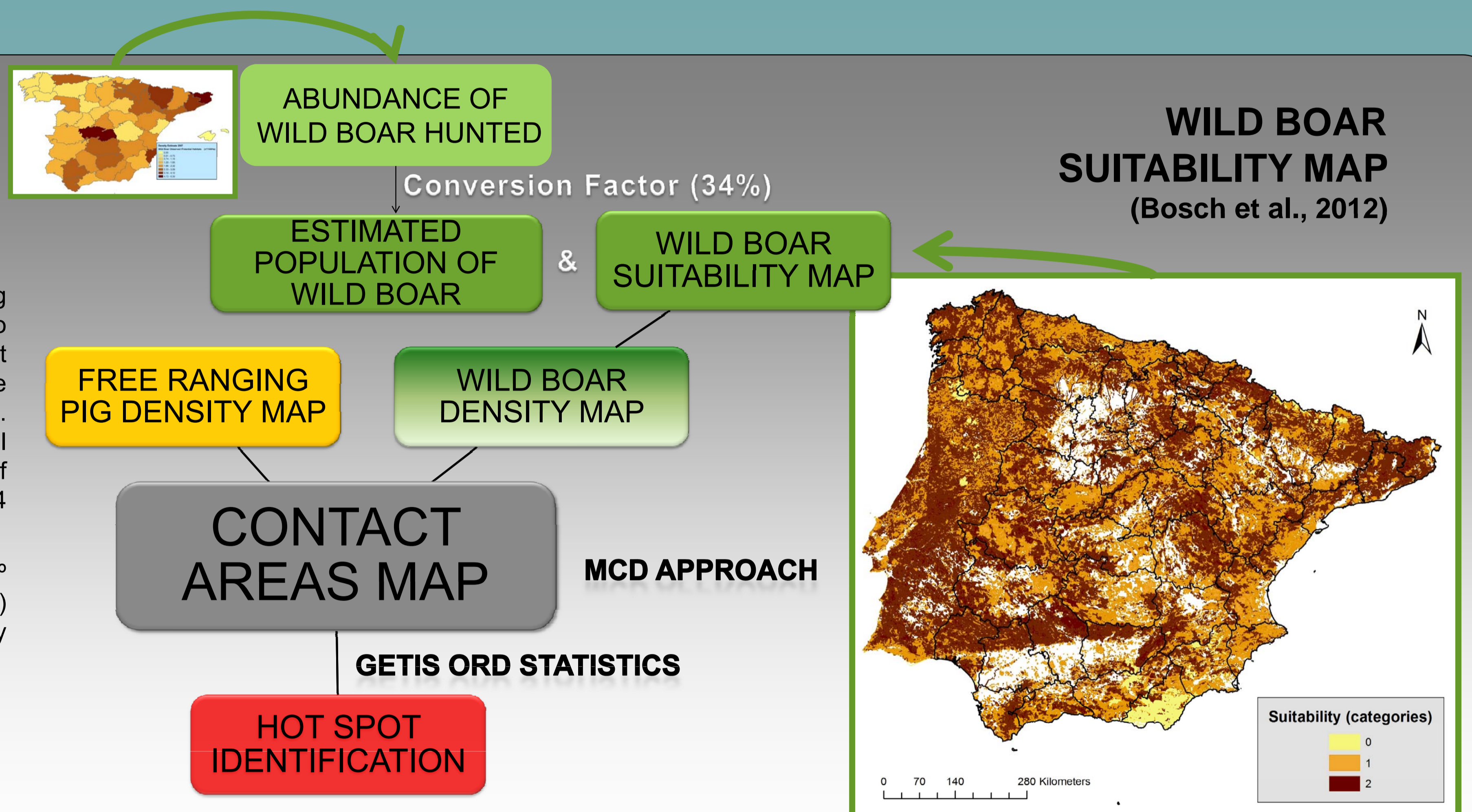
### Input variables:

• WILD LIFE VARIABLE = WILD BOAR DENSITY (n°/Km<sup>2</sup>) was estimated assigning hunting bags, at province level, to potential habitat (food y/or shelter) according to their specific weights, obtaining the "abundance of wild boar hunted" (Bosch et al., 2012). By a hunting conversion factor of 34% (34 of each 100 animal are hunted) "abundance of wild boar hunted" was transformed to "population estimate". This conversion factor was selected by reviewing scientific and technical information and selecting the worst value, ie the existence of a larger number of wild boars, and therefore the highest risk. We obtained a range (0-6.54 animals/Km<sup>2</sup>) of density values in Spain.

• LIVESTOCK VARIABLE = FREE RANGING PIG FARM DENSITY (n° animals/km<sup>2</sup>). It was gathered from the Registration Farms database (REGA) provided by the Ministry of Agriculture, Food and Environment (MAGRAMA). Only farms providing data from 2011 were considered.

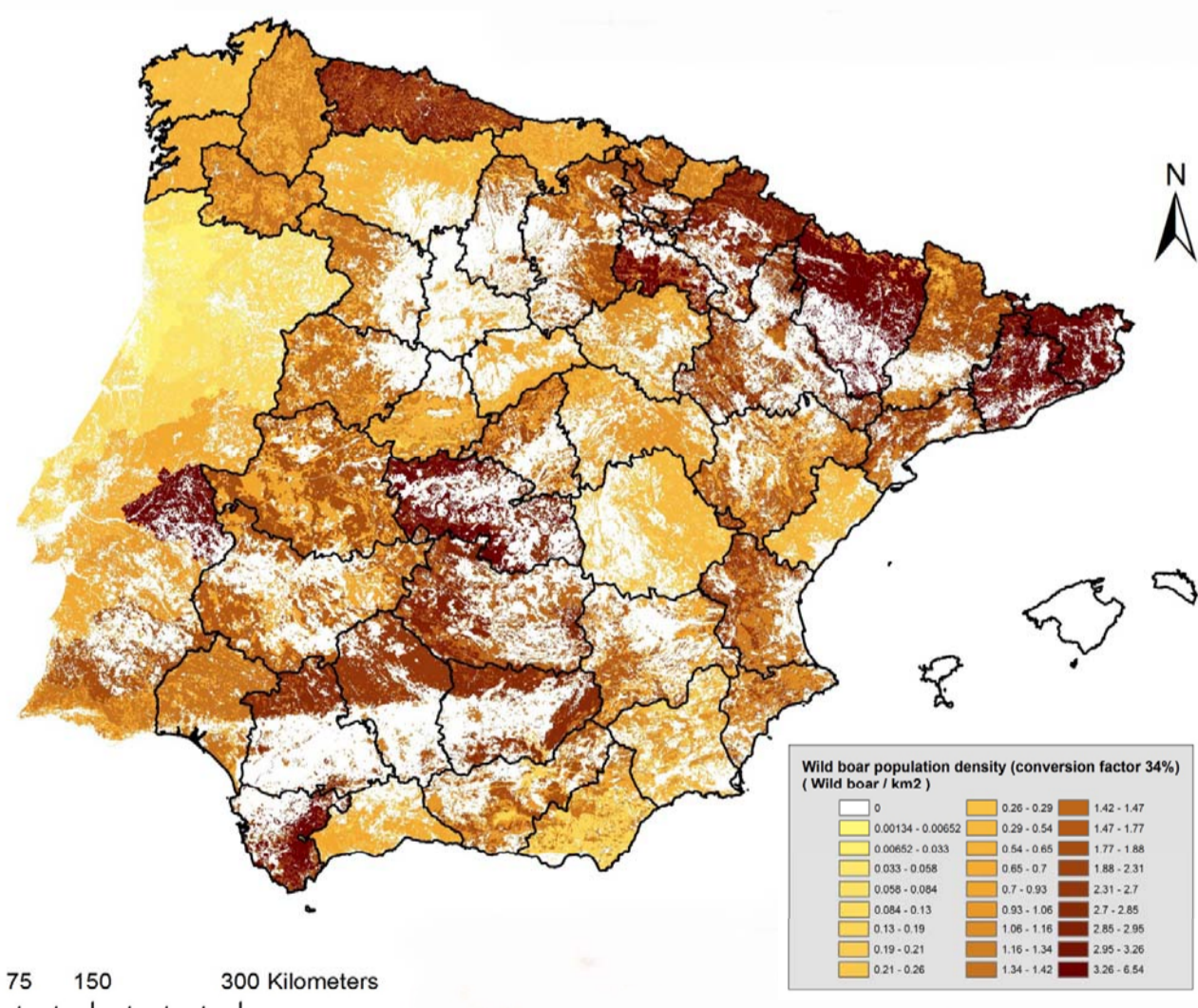
### Model building:

- MODEL INPUTS: Wild boar and domestic pig density maps (spatial resolution 1:100.000).
- CONTACT AREAS MAP: Wild boar and domestic pig density maps were added employing MCD (MultiCriteria Decision).
- SPATIAL AUTOCORRELATION STUDY: Getis-Ord Gi statistic.

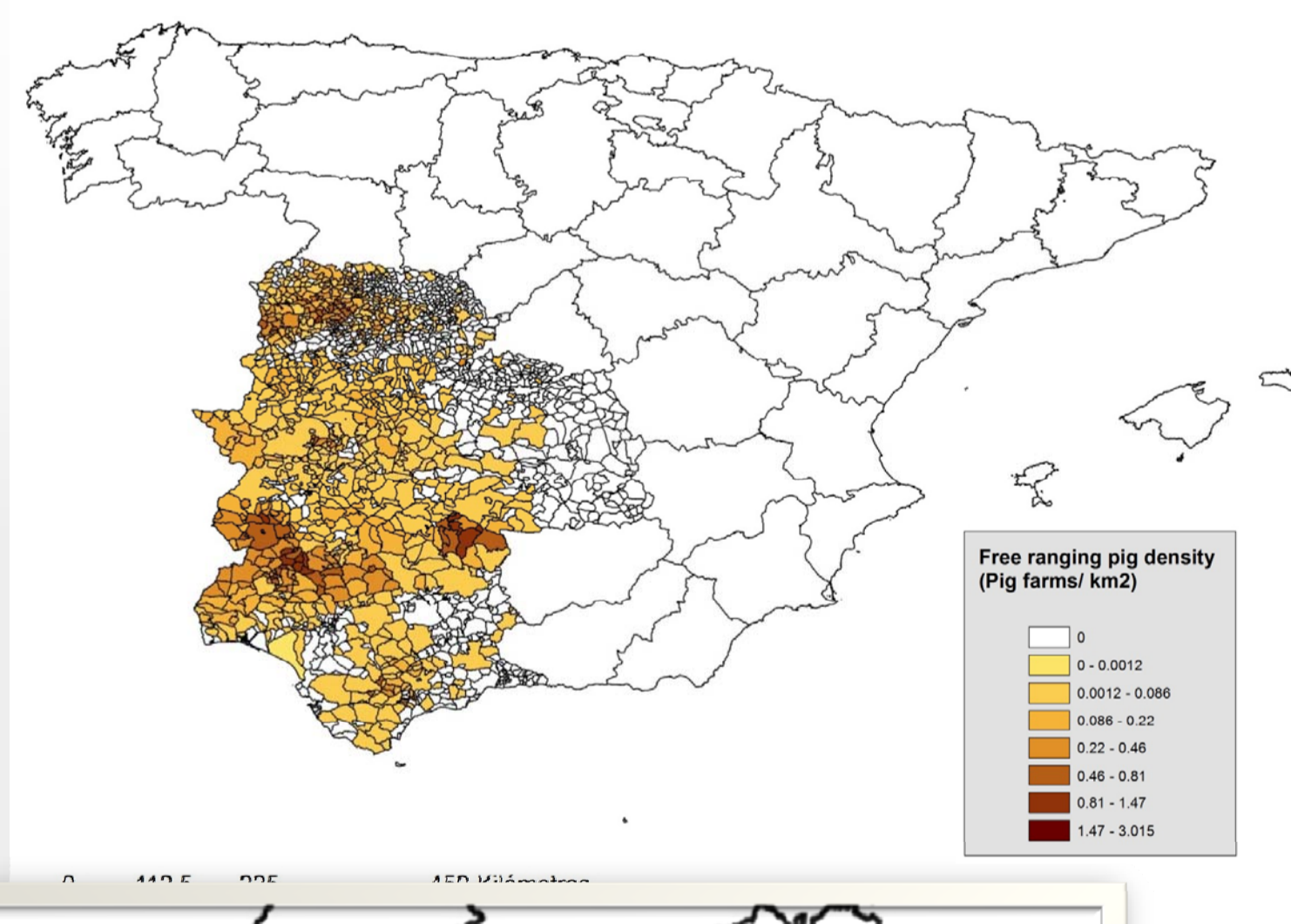


## Result & Discussion

### WILD BOAR DENSITY MAP



### DOMESTIC PIG DENSITY MAP

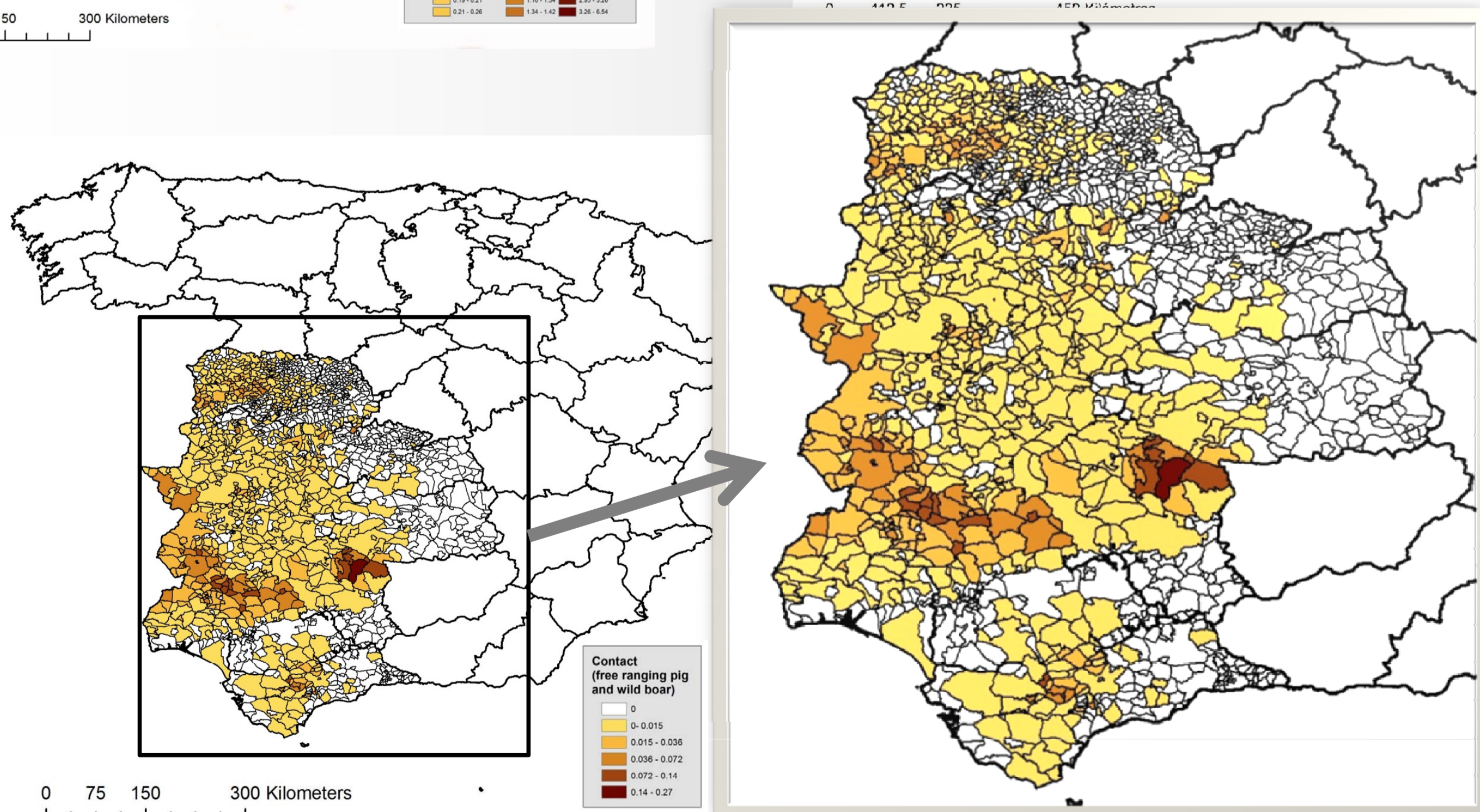


The "densities of free ranging pig farms" was selected as the livestock variable to identify contact areas, because it better describe the local interface between wild boar and pigs than "density of free-ranging pig census".

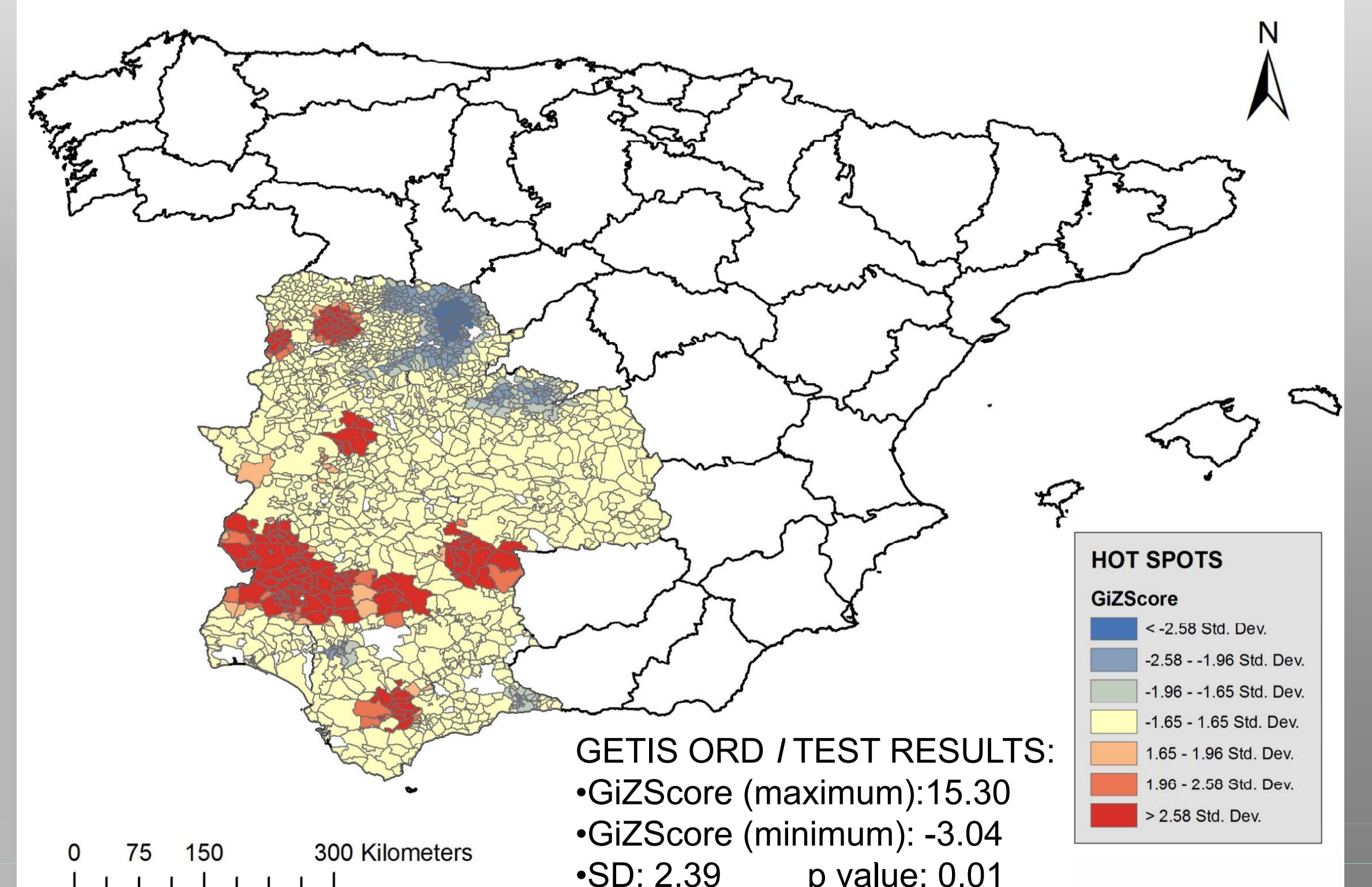
Spatial autocorrelation permit us establish with spatial location the "hot spot" of contact areas. It allowed to identify and prioritize the municipalities for health intervention, surveillance and control purposes.

When wildlife is involved on managing of livestock diseases the development of models of biodiversity is always a necessary tool, mainly when wildlife can act as a risk factor. They would provide significant improvements for modeling the disease.

### CONTACT AREA MAP



### SPATIAL AUTOCORRELATION



## Bibliography

- Bosch, J; Peris, S.; Fonseca, C.; Martinez, M.; De la Torre, A.; Iglesias, I. and Muñoz, M.J. "Distribution, abundance and density of the wild boar, *Sus scrofa* L., on the Iberian Peninsula, based on the CORINE program and hunting statistics". *Folia Zoologica* 61 (2): 138-151 (2012).
- Getis, A., and J.K. Ord, 1992: The analysis of spatial association by use of distance statistics, *Geographical Analysis*, 24, 189-206.
- Melis, C., Szafranska, P. A., Jędrzejewska, B. and Bartoń, K. (2006), Biogeographical variation in the population density of wild boar (*Sus scrofa*) in western Eurasia. *Journal of Biogeography*, 33: 803-811. doi: 10.1111/j.1365-2699.2006.01434.x
- Oliver, W. & Leus, K. 2008. *Sus scrofa*. In: IUCN 2012. IUCN Red List of Threatened Species. Version 2012.2. <www.iucnredlist.org>. Downloaded on 11 March 2013.

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