

Tools (to improve the detection of index cases of known absent diseases) or (to enhance identification of suspects)

Marta Martínez Avilés, Lucy Snow, Gerdien van Schaik, Marisa Peyre, rest of RiskSur consortium, Dirk Pfeiffer, José Manuel Sánchez-Vizcaíno

1890 characters without spaces- there are currently 1186

The correct and fast identification of suspects is a key element for the early detection of notifiable diseases with severe and irreversible consequences. One of the elements that enhances suspect identification results from an intensified surveillance when and where the probability of exposure is estimated to be high. Despite the existence of tools to estimate this probability of exposure, there is a lack of standardisation across diseases and countries. Boundary areas with infected countries are often chosen as the areas with highest probability of exposure in free countries. This way, high risk areas keep being redefined as outbreaks spread throughout the free country, questioning the benefits of a risk-based surveillance. With this work we group the tools to estimate this probability of exposure that were published in a scientific literature review of surveillance systems (Rodríguez-Prieto et al, 2014), classifying them according to data needs and type of analysis (i.e. quantitative, qualitative or semiquantitative). Based on the OIE risk assessment framework, we present tools to estimate the identification of the threat, to assess the release through the identification of transmission pathways for the introduction, and to assess the exposure to the threat. Many of the tools presented are based on spatial analysis and have been mainly applied to vector-borne diseases.

References:

Rodríguez-Prieto V, Vicente-Rubiano M, Sánchez-Matamoros A, Rubio-Guerri C, Melero M, Martínez-López B, Martínez-Avilés M, Hoinville L, Vergne T, Comin A, Schauer B, Dorea F, Pfeiffer DU, Sánchez-Vizcaíno JM. Systematic review of surveillance systems and methods for early detection of exotic, new and re-emerging diseases in animal populations. *Epidemiology and Infection*, 2014, 25 pp, doi: 10.1017/S09 5026881400212X