In the topic of vector-borne diseases it is important to know the spatial distribution of the vector-borne infections and their vectors. In clinician viewpoint it gives information what vector-borne infections may occur on a certain area. From epidemiological aspect it is necessary for disease prevention and control. **Epidemiology is the study of disease in populations and of factors that determine its occurrence; the key word being populations.**

The arthropod vectors are poikilotherm organisms, their life processes are influenced fundamentaly by the ambient environmental temperature. Since the environmental conditions (e.g. temperature) have spatial heterogeneity, it is naturally the geographic distribution of vectors (and borne infection) shows similar heterogeneity over the globe. To demonstrate the spatial distribution of any agent or their vector it is necessary to use some term from epidemiology like incidence and prevalence. **Incidence is the number of new cases that occur in a known population over a specified period of time. Prevalence represents the fraction of existing cases in a population; or the probability that a randomly-choosen animal is diseased.**

To obtain information about the occurence of a certain infection in a population it is necessary collect data from that. In data gathering it is a fundamental question what portion of the population investigated should be, or from how many geographic locations data should be collected. The data collection may be performed occasionaly or systematicaly. In veterinary epidemiology two types of systematic data gathering must be mentioned, monitoring and surveillance. **Monitoring is a systematic, ongoing or repeated, measurement, collection, collation, analysis, interpretation and timely dissemination information of animal health related data without an associated pre-defined plan of (control) action. Surveillance is a systematic, ongoing or repeated, measurement, collection, collation, analysis, interpretation and timely dissemination of animal health related data, essential for describing hazard occurrence and for the planning, implementation, and evaluation of risk mitigation (control) measures.**

Census if all animals in a population are investigated. If a survey is designed well, then a reasonably accurate and acceptable estimate of a variable can be made by examining some of the animals in the relevant population; that is, a sample. When only a well defined subpopulation is sampled, the number of animal should be sampled is obtained by sample size estimation.

In the evaluation of samples the investigator must take into consideration that the diagnostic methods (e.g. serological tests) have certain biases. It means that the diagnostic methods identify true positive samples as negative, and real negative ones as positive. This is misclassification bias of the diagnostic methods, tool. Actually, this property belongs to the qualitative diagnostic procedures. Nevertheless, as in the case of quantitative methods the investigator orders the measured values into categories (e.g. positive, negative) by any threshold, finaly it will produce qualitative results as well. To quantify the misclassification bias the sensitivity and specificity are used. **Sensitivity is the probability that a truly diseased animal will be classified as diseased. Specificity is the probability that a truly non-diseased animal will be classified as non-diseased.** In a well designed epidemiological study for the sample size estimation and prevalence estimation the sensitivity and specificity of the applied diagnostic method must take into consideration.

To get an idea about the spatial distribution of the vector-borne infection, and its vector the methods of spatial epidemiology must be used. In the simplest case the gathered data may be mapped to get quantitative view of spatial distribution. **Disease mapping may be point based, choropleth or isopleth. In the first case the collected data is plotted onto a map with point level. The choropleth map visualize the collected data aggregated on area level (e.g. county, census tract). On isopleth maps based on data of observed locations to the non sampled locations some estimation, prediction made by different smoothing technics.**

Beyond mapping approaches, further spatial ana-

lytical methods are the spatial pattern analysis to get more information about the geographic distribution. From the numerous methods in the veterinary parasitology, epidemiology literature the spatial cluster analysis is one of the most widely used pattern analysis approach. Here **"cluster" is an unusual aggregation, real or perceived, of health events that are grouped together in time and/or space.** The goal of spatial cluster analysis is to identify (if there is) aggregation of health related event in the space (and/or time). Of course one can identify clusters on maps by naked eye, but that approach is suffered from many biases (e.g. zoom level) and lead to erroneous conclusions. The quantitative cluster analysis may be global, local and focused. **By the global methods one can get information about that if there is any cluster in the study region or not, but they can't give information about the location of the cluster(s). To localize the cluster(s) the local clustering methods should be used. By focused clustering methods one can check if around any suggested infection source there is aggregation of health related events (e.g. is there more incidence of malaria close to marshland than farther).**

In the human and veterinary parasitology, epidemiology literature numerous spatial clustering methods are used. In the presented examples of lectures from the global methods the Moran's I was used in the study on LaCrosse virus infection cases in West Virginia, and Cuzick-Edwards' k-nearest neighbour test in the study on *Yersinia pestis* seroprevalence in California coyotes. For the localization of the clusters in both studies the Kulldorff's spatial scan statistic was used. Also Kulldorff's test was used as local clustering method in the study on spatial pattern of human granulocytic ehrlichiosis, bovine hypodermosisand *Plasmodium falciparum*. In the study of West Nile incidences in the US beside Kulldorff's method Local Moran's I was also used localize the clusters.

If any clusters of health related events are identifiable on the study area, then in the next step one can carry out further research on the reason of that spatial aggregation, especially the environmental impacts associated with that pattern.

The associations of occurence of infections or vectors with environmental factors usually analysed by modelling methods of environmental epidemiology. The models allow conclusions to be quantified, what can be the subject of further studies. Another results of these environmental modelling is that based on them it is possible to make predictions on the geographic distribution of vectors, infections. Schematic example of the latter might be if we collect data of infection or vector occurence from fairly large number of locations. For the same points we gather relevant environmental condition data (e.g. climate, land cover, vegetation). Using appropriate statistical model we build up association between these two types of input data (e.g. how depends the tick occurrence on the rainfall, vegetation). To construct the connection between the occurrence and environmental data regression models (e.g. logit, probit) and classification procedures (e.g. neural networks, support vector machine, random forest) are widely used. In the next step we gather environmental data for those points were not involved into the model fitting. Based on this latter data and the fitted model we can predict occurrence probability of infections or vectors for those points where we had only environmental data without occurrence information. Thus, although we had no occurrence information from all points of the study region, finally we get prediction for the whole area of interest.

In the last decade researchers become more and more engaged with changes of geographic distribution of vectors due to the climate change. **The climate change has numerous effects on human or animal health. One of the indirect effects is that, arthropod vectors can colonize new geographic territories where earlier the environment did not satisfy their living and reproduction conditions.** Already numerous examples show changes in spatial distribution of certain vectors, vector-borne diseases. Northern or altitudinal shifts in tick distribution have been observed in Sweden and Canada, and altitudinal shifts have been observed in the Czech Republic. Cutaneous leishmaniasis has been reported in dogs (reservoir hosts) further north in Europe, although

the possibility of previous under-reporting cannot be excluded. Changes in the geographical distribution of the sandfly vector have been reported in southern Europe.

One of the most important question of vector-borne disease distribution changes due to climate change is that, which new infections are expected in the near future. To answer this question in the epidemiological literature some different approaches are proposed. Although there are some attempts to answer the question on qualitative, expert opinion based way, the main direction is the application of statistical modelling to produce quantitative predictions of the newly appearing infections. **Naturally, for the future we may have no observed environmental data. However, for the future there are available climate projection datasets based on climate scenarios, models. These climate projections founded on two components: the global circulation models (GCM) depicting the physical system of the atmosphere; while the emission scenarios (SRES) specifies the amount of green house gas emission.**

In the examples presented in lectures there was mentioned the projected distribution of *Oncomelania hupensis* as the vector of *Schistosoma japonicum* and the projection of Lyme-disease vector distribution based on climate scenarios. While present and past environmental data was used to model the geography distribution of leishmaniosis in Colombia and the spatial pattern of prevalence of malaria in Somalia.