57.028

Comparison of three time series models for predicting campylobacteriosis risk in Georgia, Minnesota and Oregon

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Background: Three time series models (regression, decomposition, and Box-Jenkins Autoregressive Integrated Moving Averages) were applied to national surveillance data for campylobacteriosis with the goal of disease forecasting in three U.S. states.

Methods: Data sets spanned 1998 to 2007 for Minnesota and Oregon, 1999 to 2007 for Georgia. Year 2008 was used to validate model results. Mean absolute percent error, mean square error and coefficient of determination (R2) were the evaluation fit statistics.

Results: Results showed that decomposition best captured the temporal patterns in disease risk. Training dataset R2 values were 72.2, 76.3 and 89.9% and validation year R2 values were 66.2, 52.6 and 79.9% respectively for Georgia, Oregon and Minnesota. All three techniques could be utilized to predict monthly risk of infection for *Campylobacter* sp. However, the decomposition model provided the fastest, most accurate, user-friendly method.

Conclusion: Use of this model can assist public health personnel in predicting epidemics and developing disease intervention strategies.

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57.029

Anticipating the species jump: Surveillance for emerging viral threats

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Emerging infectious diseases (EID) may pose new international security threats because of their potential to inflict harm upon humans, crops, livestock, health infrastructure, and economies. Some viruses pose unique challenges because of their high mutation rates, which enable them to evade host immunity, persist in the environment, and infect new host species. For example, influenza and human immunodeficiency viruses originally infected animals, but subsequent mutations enabled these viruses to ''jump'' to new human hosts. Current disease surveillance efforts rely upon data from clinical specimens — that is, from individuals who are already sick. As a result, little is known about the abundance of viruses that exist in nature but do not (yet) cause human disease. Human populations could be preemptively protected if researchers can learn what events lead to viral species jumping. If researchers can discover common genetic and ecological determinants that precede species jumping, then these determinants may be used to detect viruses teetering on the threshold of human pathogenicity. Knowledge of such determinants may ultimately prove useful to threat analysts and others charged with anticipating the genetically engineered viruses of the future, be they natural or man-made. This paper will report the findings of a thought leaders workshop convened to debate the feasibility of identifying determinants and hypothesize what information and technologies might be needed to make such surveillance possible.

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57.030

The making of a world atlas of infectious diseases

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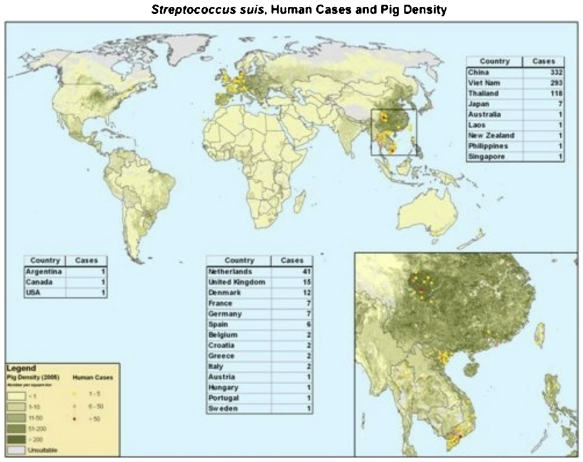
Background: Many infectious diseases are restricted in their geographical range due to climatic conditions, presence of vectors or specific reservoir hosts, local food customs, hygiene, antibiotic use, among others. Currently there is no comprehensive illustrated overview of the geographic spread of infectious diseases and their determinants. Such a compendium of world infectious disease maps is crucial for teaching, research and creating awareness of risk.

Methods: With the collaboration of experts from around the globe we are collecting and making updated maps of more than 100 infectious diseases and their preferred conditions. We do extensive data searches to arrive at the best geospatial data available. Each map will be accompanied by an explanatory text. All our maps are sent out for independent peer review to ensure their quality and accuracy.

Results: The atlas will be published by Wiley-Blackwell, and at a later stage the maps will be updated and made available online under open access.



Streptococcus suis, Human Cases and Pig Density

Conclusion: The printed atlas will be followed up with a web-portal for global infectious disease mapping activities, where all the data will be bundled, visualised and made available to anyone interested, and updated regularly.