Drivers of Infectious Diseases: Connections Matter

Clinician Outreach and Communication Activity (COCA) Call

May 12, 2016

Office of Public Health Preparedness and Response

Division of Emergency Operations

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Objectives

At the conclusion of this session, the participant will be able to:

- **Identify key drivers of zoonotic infectious disease emergence**
- **Describe approaches to identifying risk factors for zoonotic diseases**
- **Describe the difference between disease occurrence mapping and correlation-based disease risk mapping**

Today's Presenter

William B. Karesh, DVM
Executive Vice President, Health & Policy
EcoHealth Alliance

EcoHealth Alliance

Drivers of Infectious Disease: Connections Matter

William B. Karesh, DVM

Executive Vice President for Health and Policy, EcoHealth Alliance

President, OIE Working Group on Wildlife

Co-Chair, Wildlife Health Specialist Group, International Union for the Conservation of Nature

Local conservation.
Global health.

The findings and conclusions in this presentation are those of the author(s) and do not necessarily represent the views of the Centers for Disease Control and Prevention.

Zoonoses

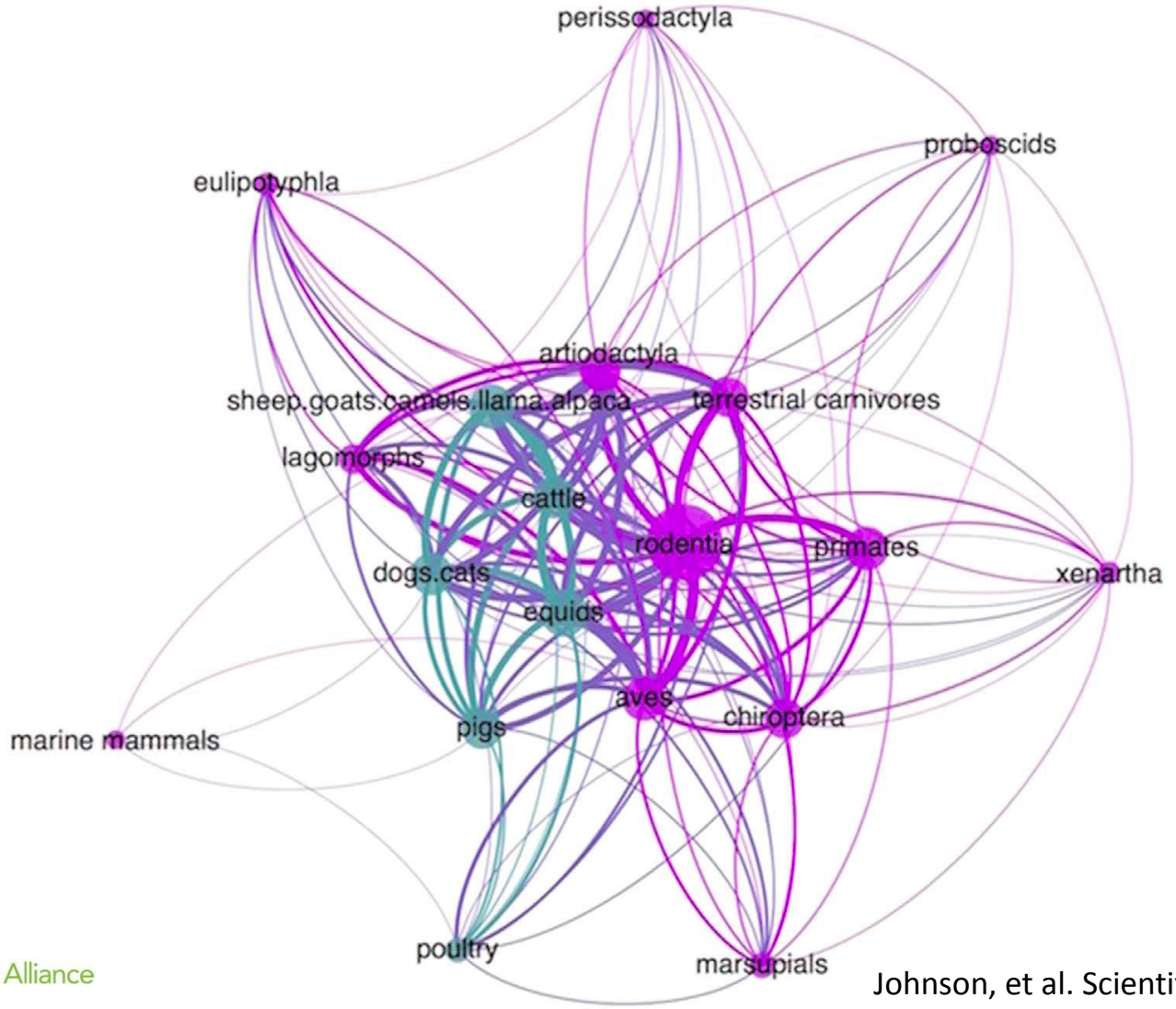
Zoonotic disease organisms include those that are endemic in human populations or enzootic in animal populations with frequent cross-species transmission to people…

…with endemic and enzootic zoonoses causing about a billion cases of illness in people and millions of deaths every year.”

Karesh, et al., The Lancet, Dec 1, 2012

Zoonotic Viral sharing

Green = Domestic Animals Purple = Wild Animals



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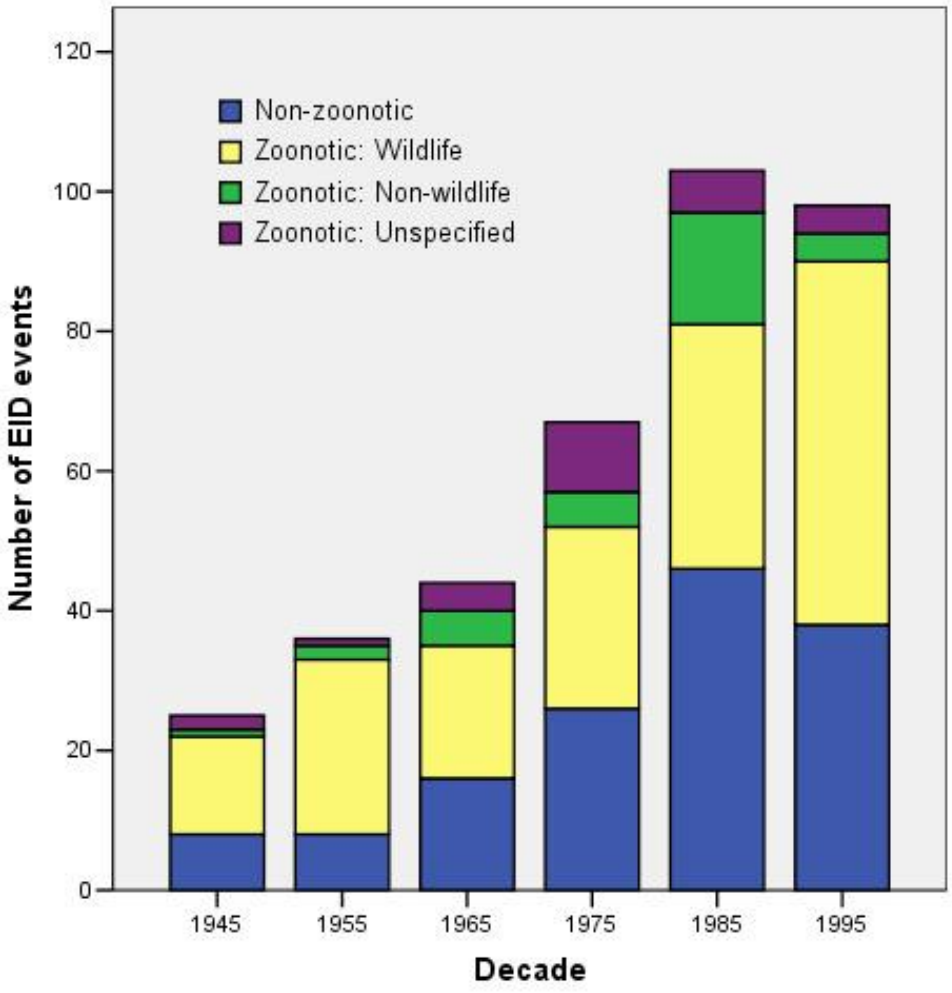
Johnson, et al. Scientific Reports, 2015

Temporal patterns in EID events



- EID events have increased over time, correcting for reporter bias ($GLM_{P,JID}$ F = 86.4, p <0.001, d.f.=57)
- ~5 new EIDs each year
- ~3 new Zoonoses each year
- **Zoonotic EIDs from wildlife** reach highest proportion in recent decade

Jones *et al.* 2008

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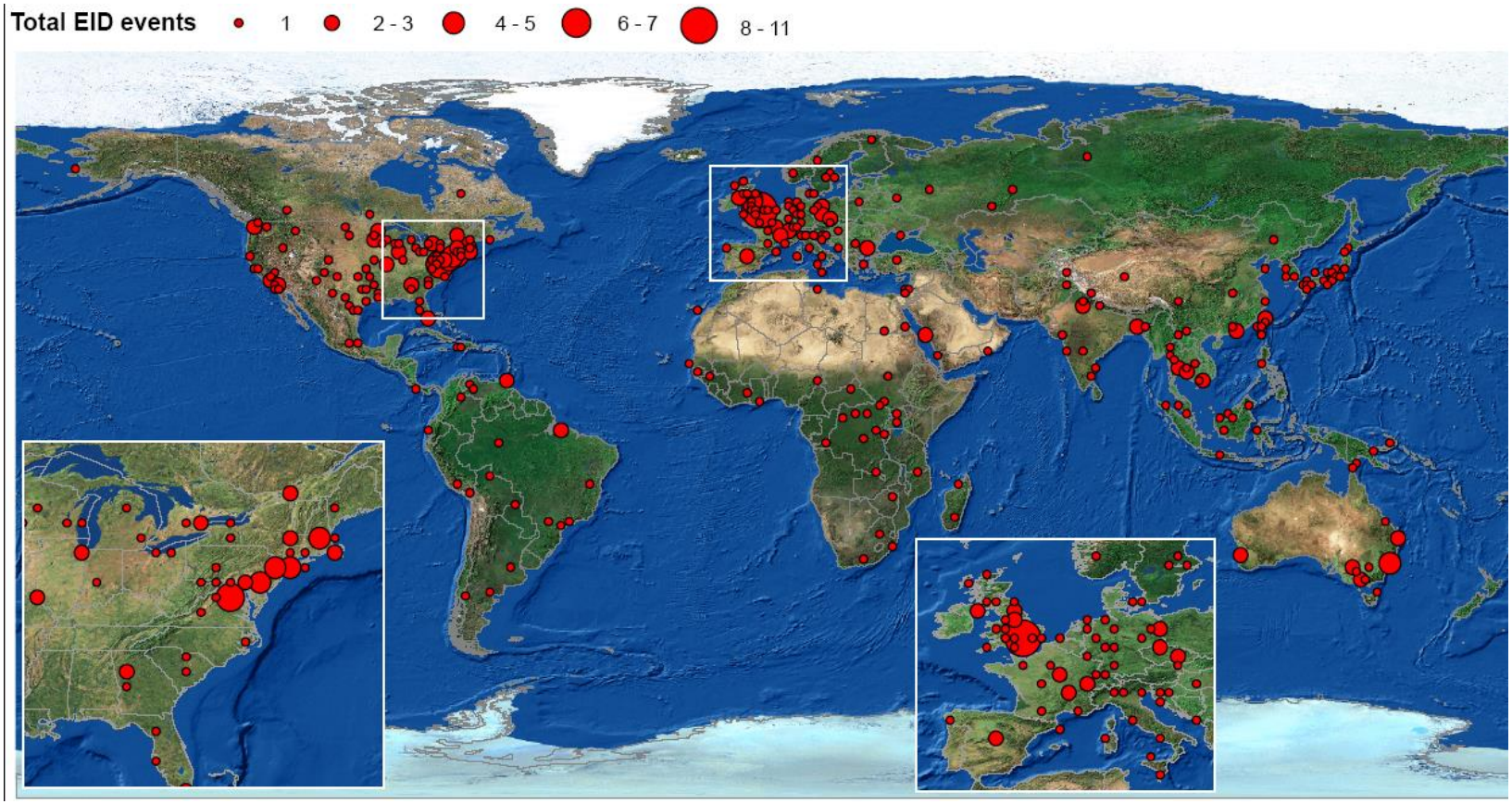
Spatial patterns in EID events



Jones *et al.* 2008

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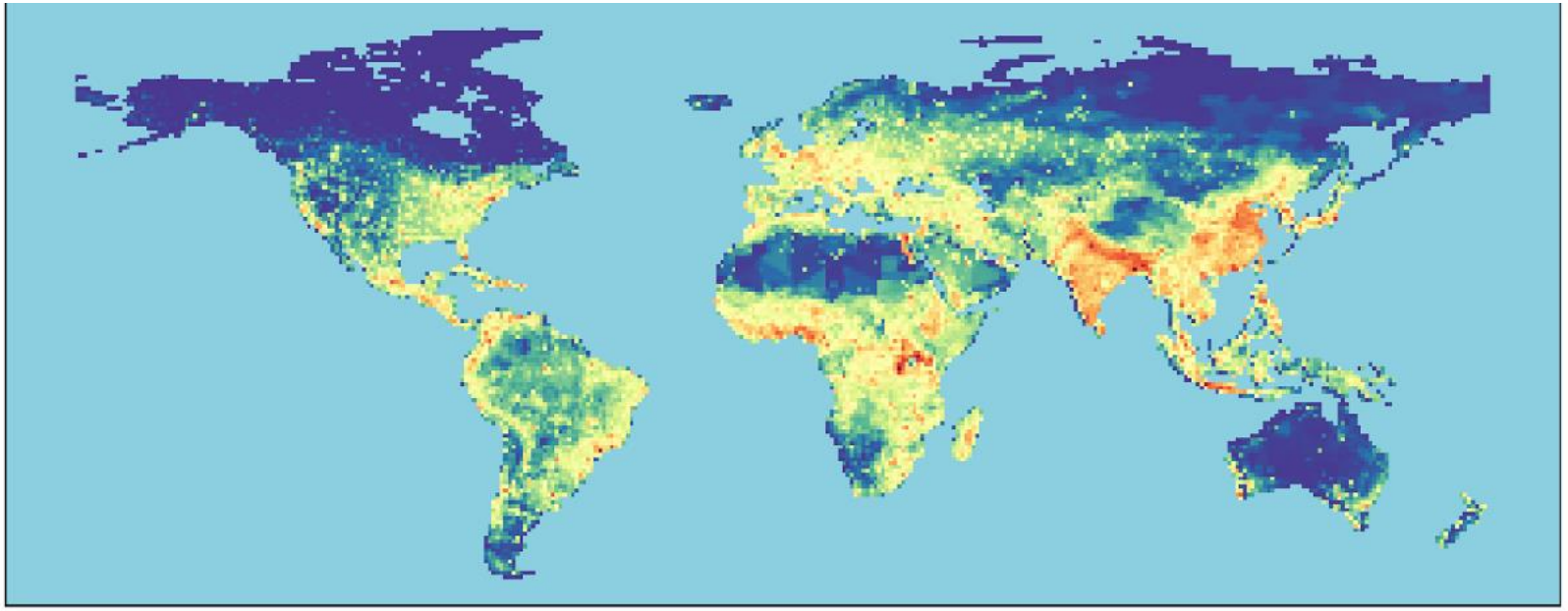
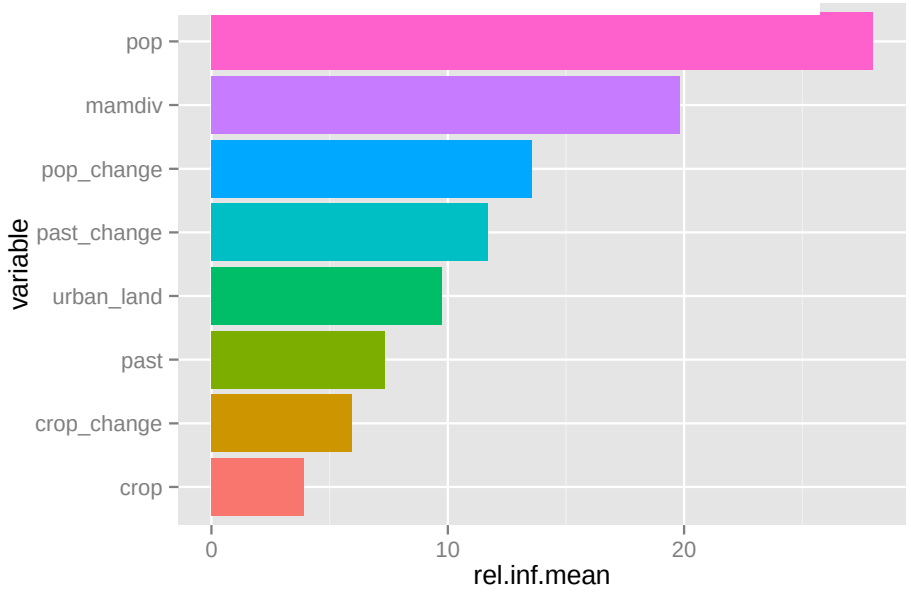
Relative risk of a new zoonotic EID



factors	relative influence (%)	std. dev.
population	27.99	2.99
mammal diversity	19.84	3.30
change: pop	13.54	1.54
change: pasture	11.71	1.30
urban extent	9.77	1.62
…	…	…



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Natural Versus Unnatural

"The emergence of zoonoses, both recent and historical, can be considered as a logical consequence of pathogen ecology and evolution, as microbes exploit new niches and adapt to new hosts…

Although underlying ecological principles that shape how these pathogens survive and change have remained similar, ***people have changed the environment in which these principles operate."***

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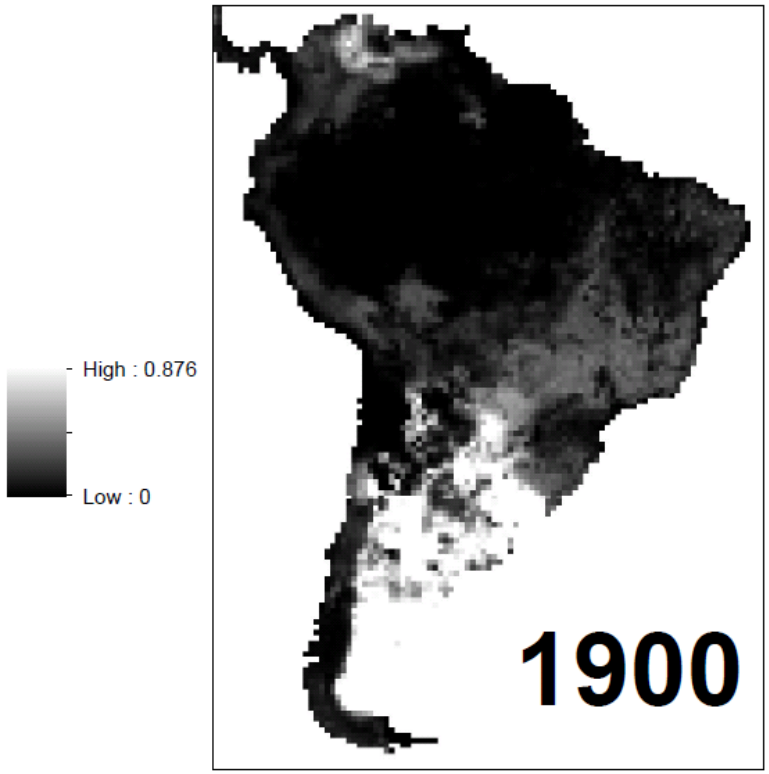
Karesh, et al., The Lancet, Dec 1, 2012

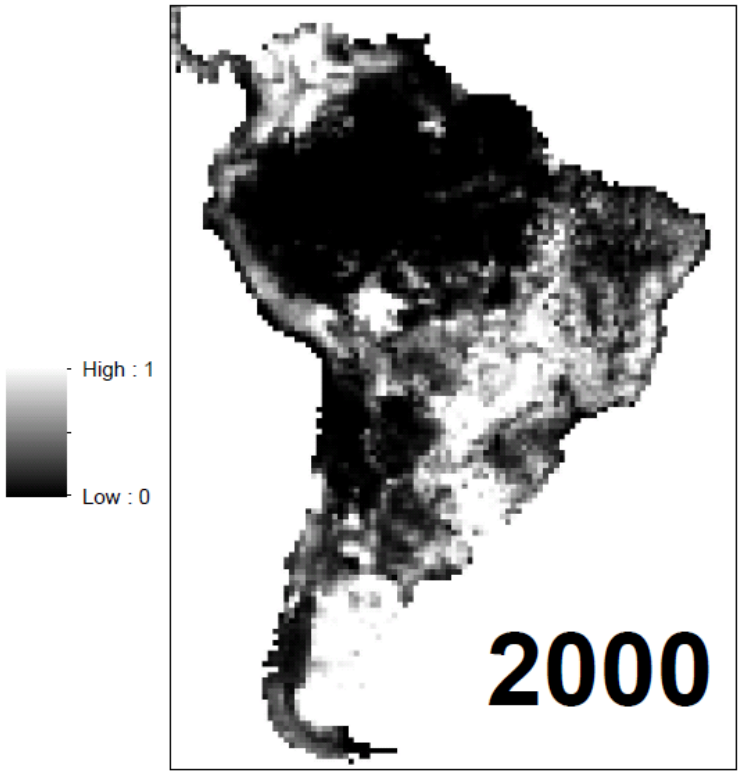
Pasture Data

Source: Ramankutty and Foley, Department of Geography, McGill University

Description: Global historical pasture dataset, available at an annual timescale from 1700 to 2007 and at 0.5 degree resolution.

Proportion of land devoted to pasture, 1900 vs 2000





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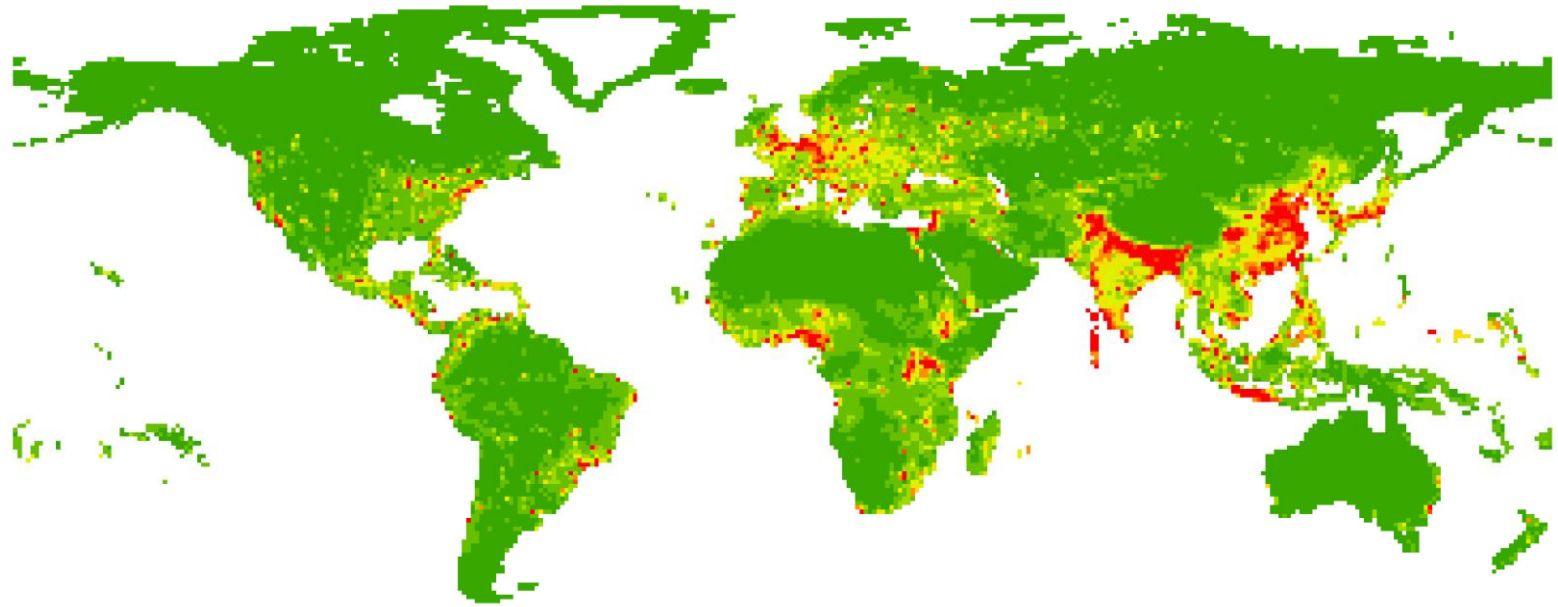
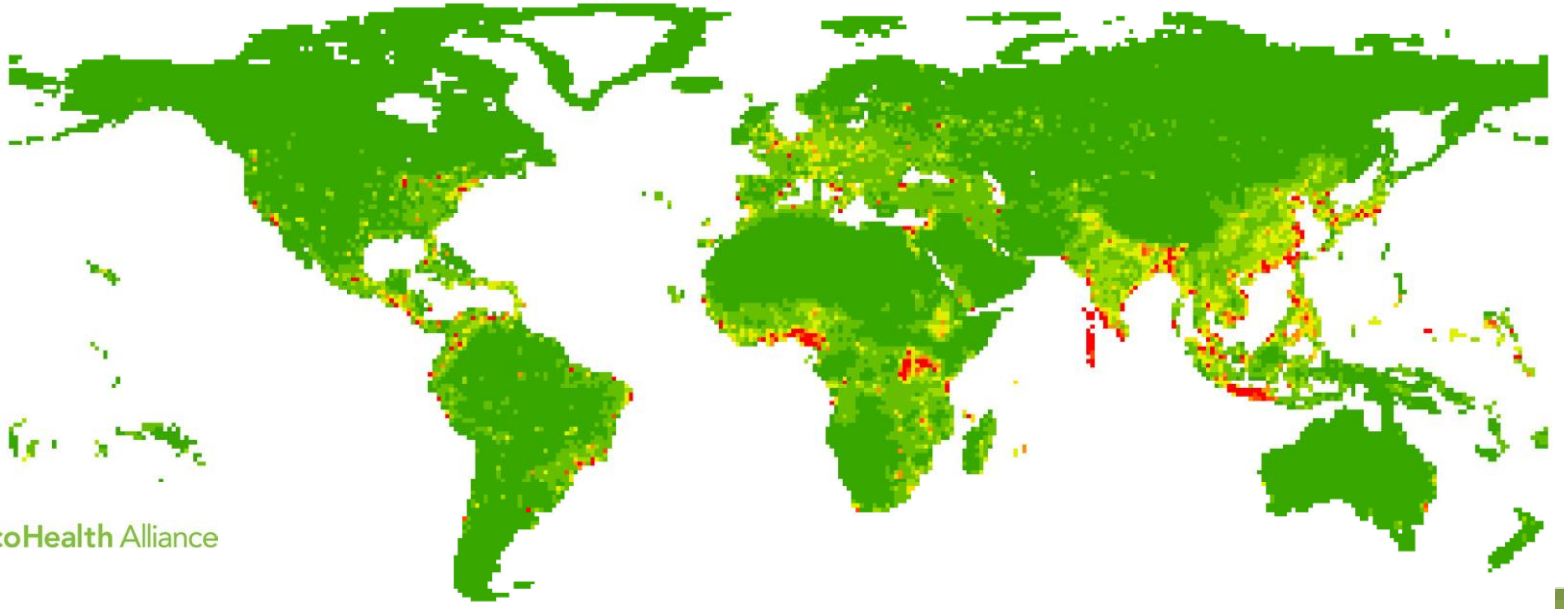
EID Hotspots – Jones 2008 Nature Model



EID Hotspots – New Model with Land Use Change and Livestock



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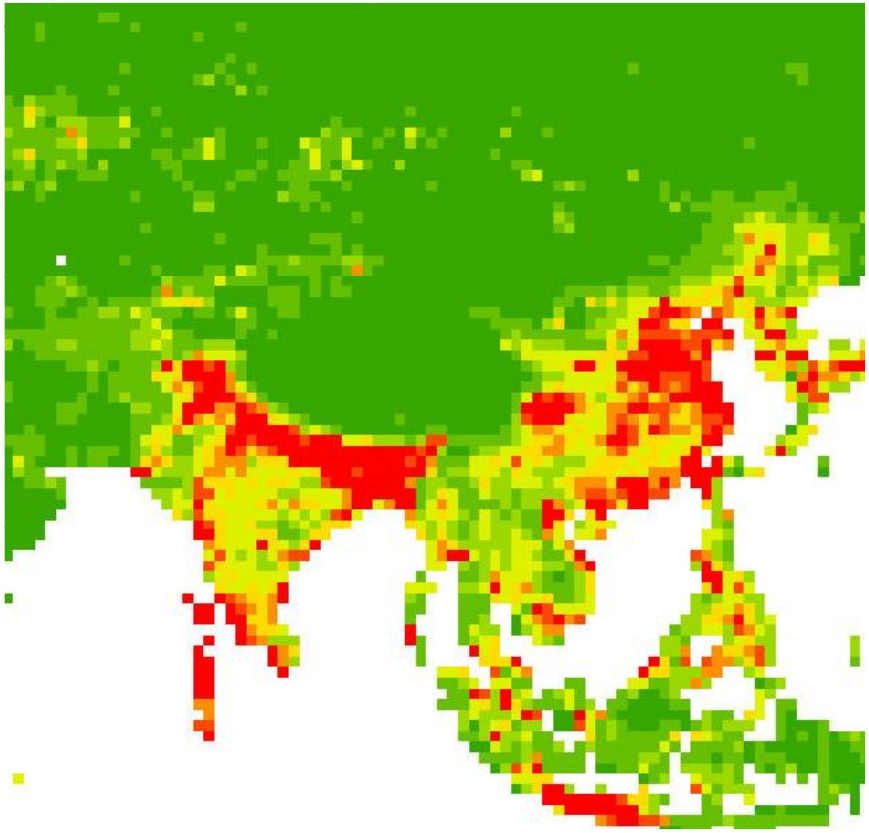
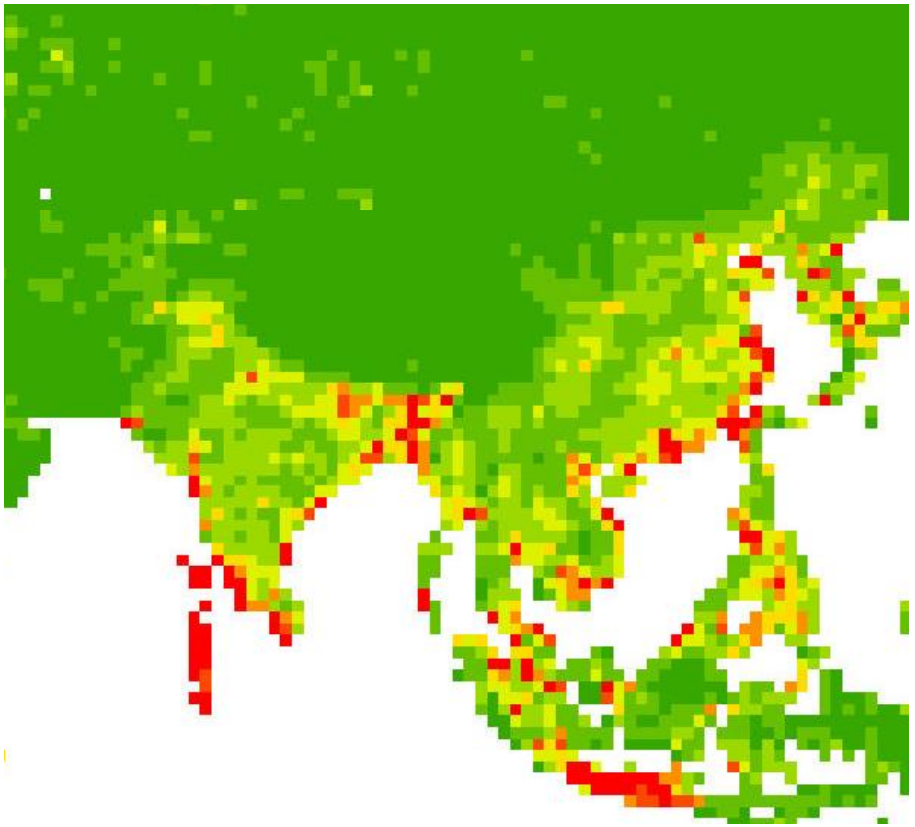
Original v. New Hotspots Model



Original hotspots model (100km)



New hotspots model v2.0 (100km)
Includes anthropogenic activities

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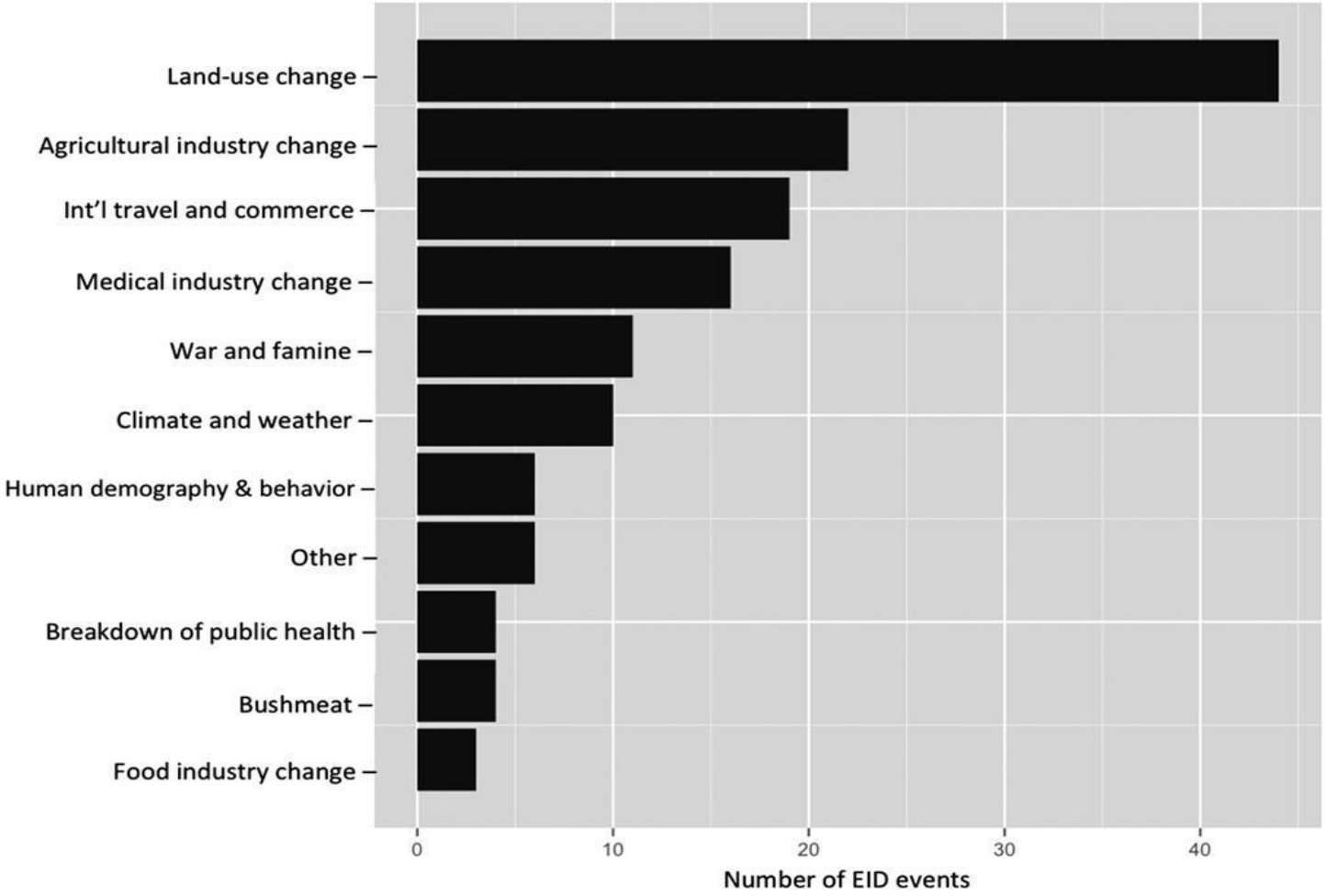
Drivers of Disease Emergence in Humans



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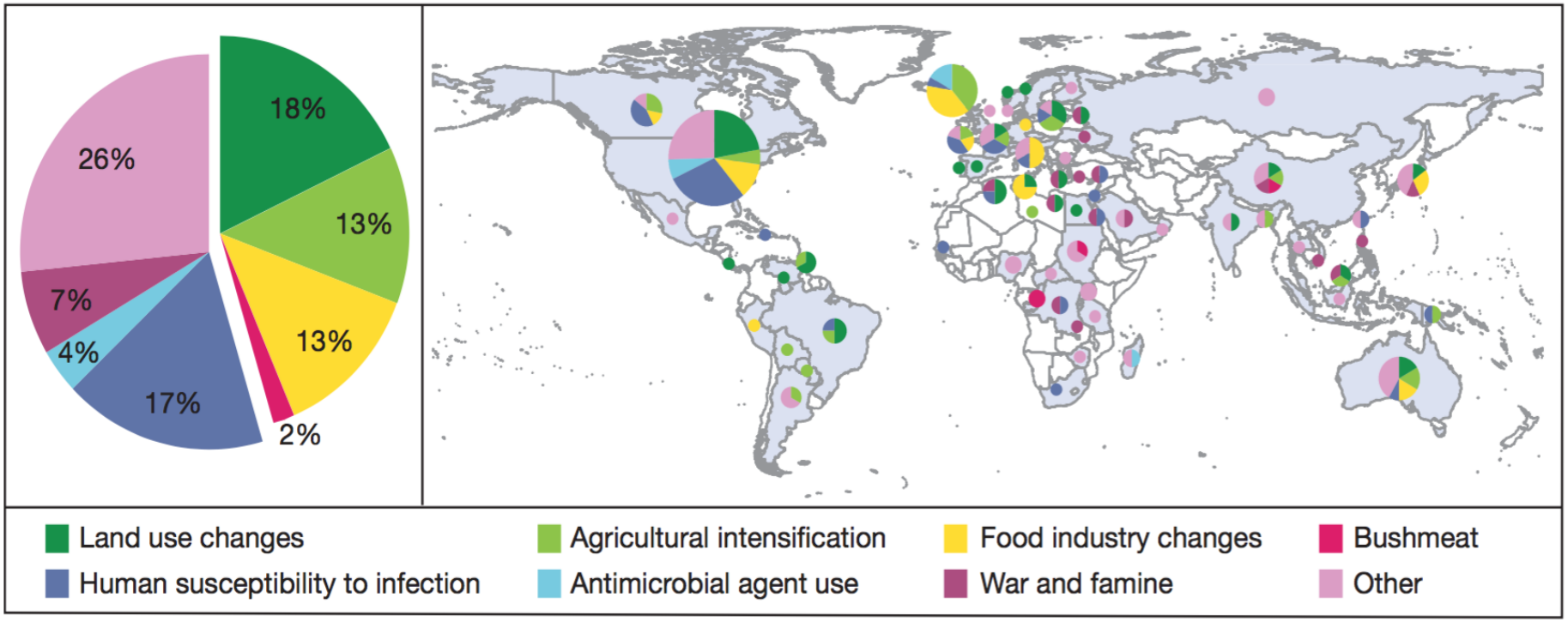
E. Loh et al. 2015. Vector-borne and Zoonotic Diseases 15(7)

Country-Level Drivers of Disease Emergence



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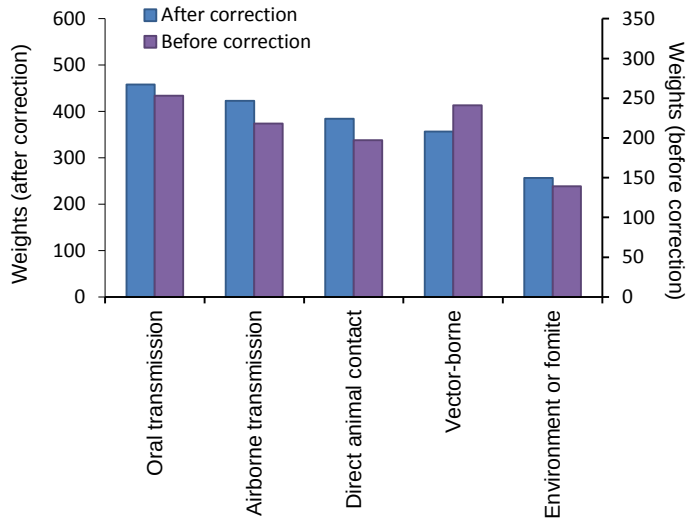
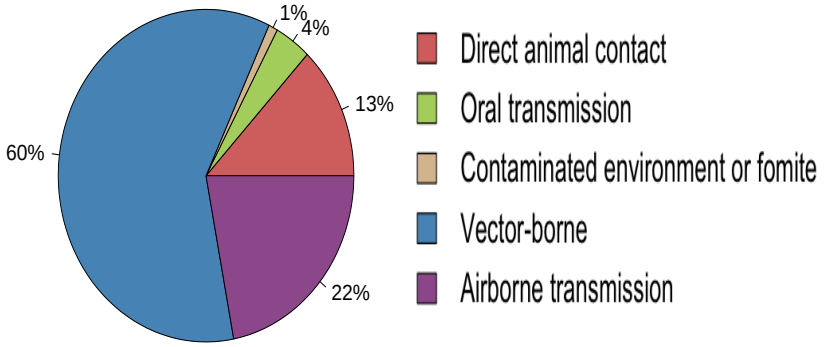
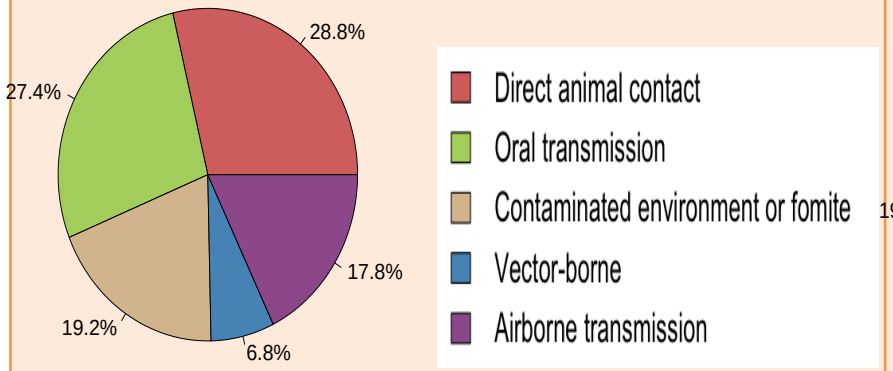
Actionable information to target surveillance and prevention



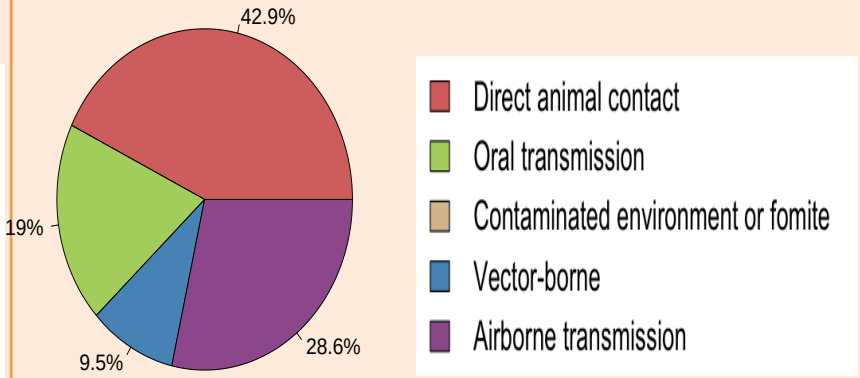
Land use change n= 39



Agricultural industry change n=27



Medical industry change n=11



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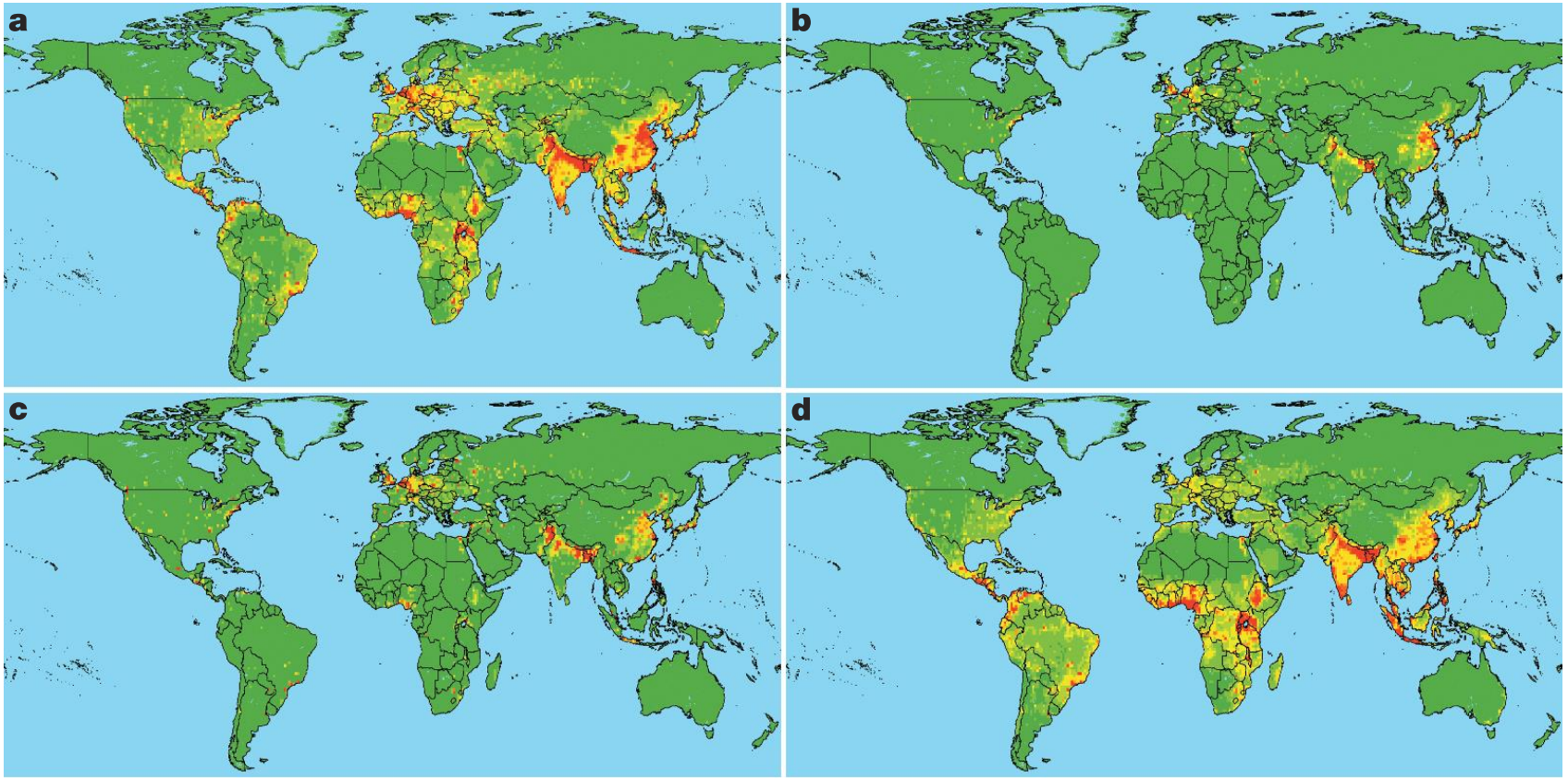
Global Distribution of relative risk of EID events



a) Zoonotic pathogens from wildlife
b) Zoonotic pathogens from domestic animals
c) Drug resistance pathogens
d) Vector-borne pathogens

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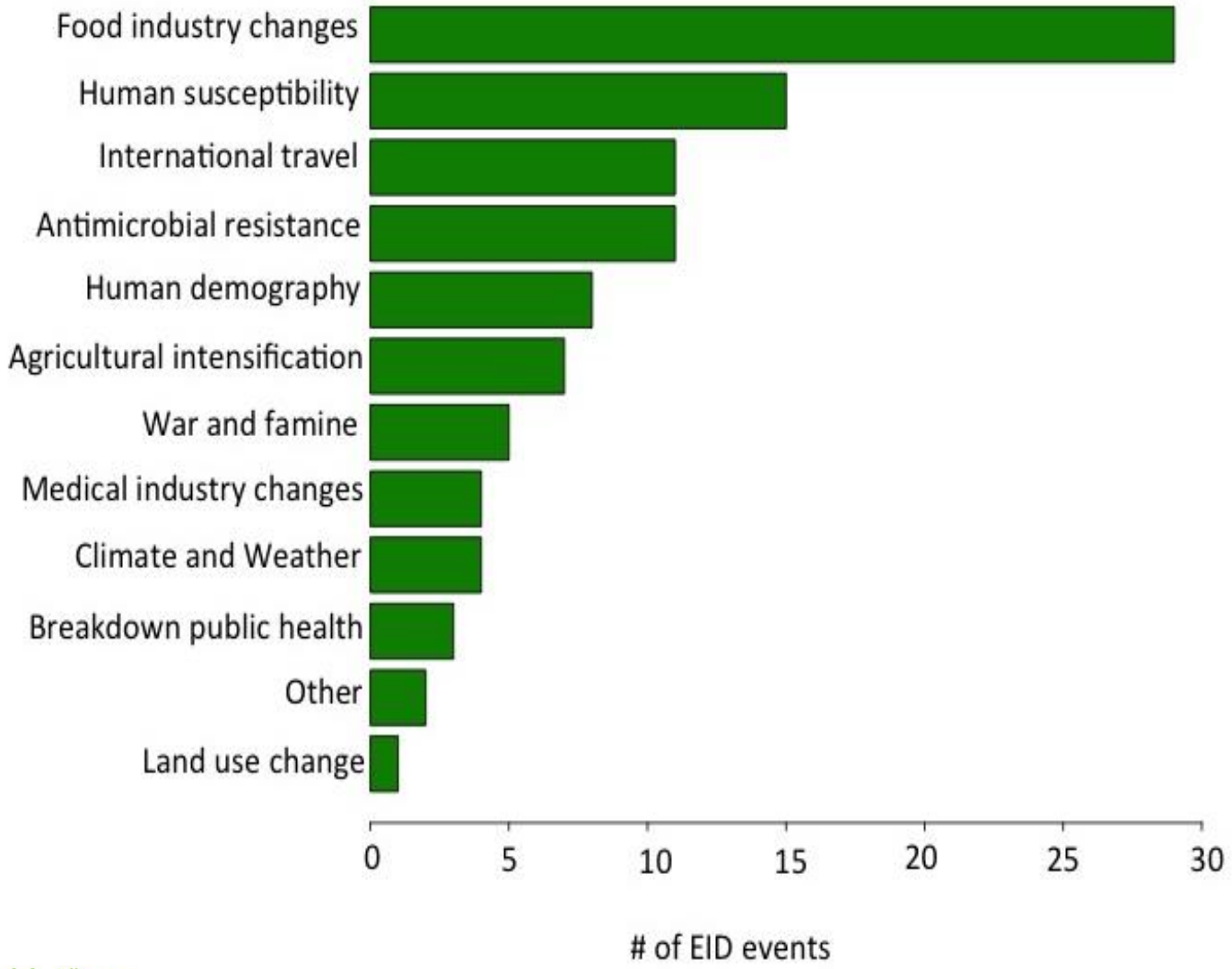
Jones *et al*. *Nature* 2008

Drivers of Foodborne EID events



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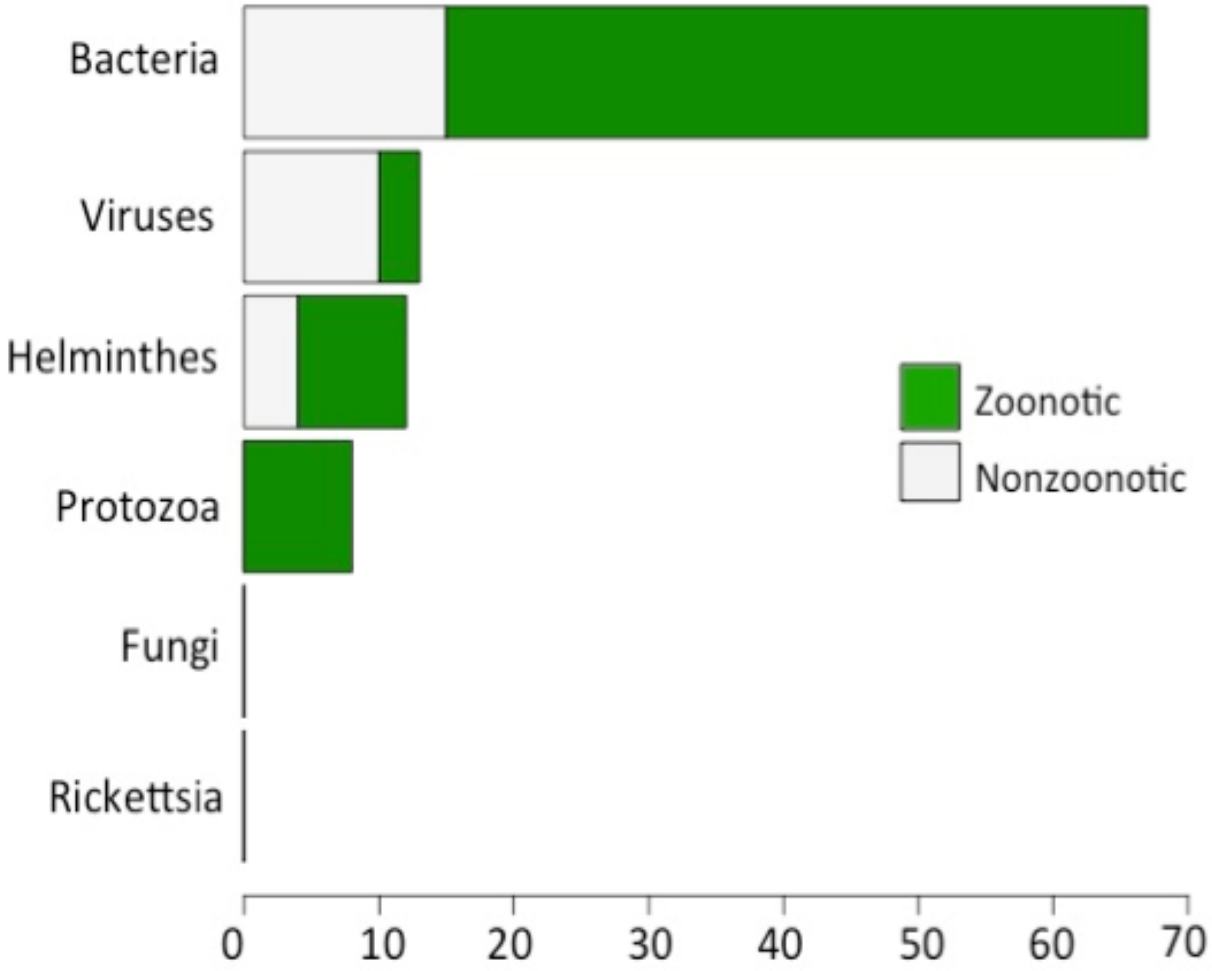
Karesh, et al, IOM Workshop Summary, 2012

Foodborne EID events 1940-2004 (n=100)



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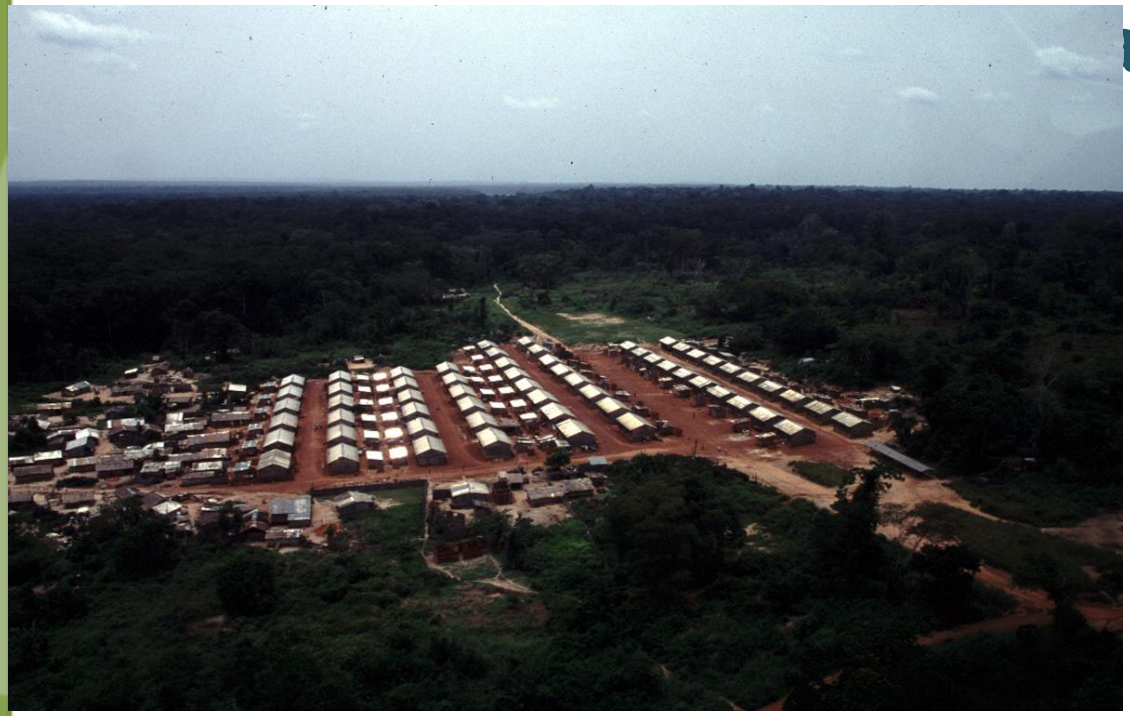
Karesh, et al, IOM Workshop Summary, 2012

A Day in a Food Market



1,000,000,000 Kgs / Year
(Central Africa)

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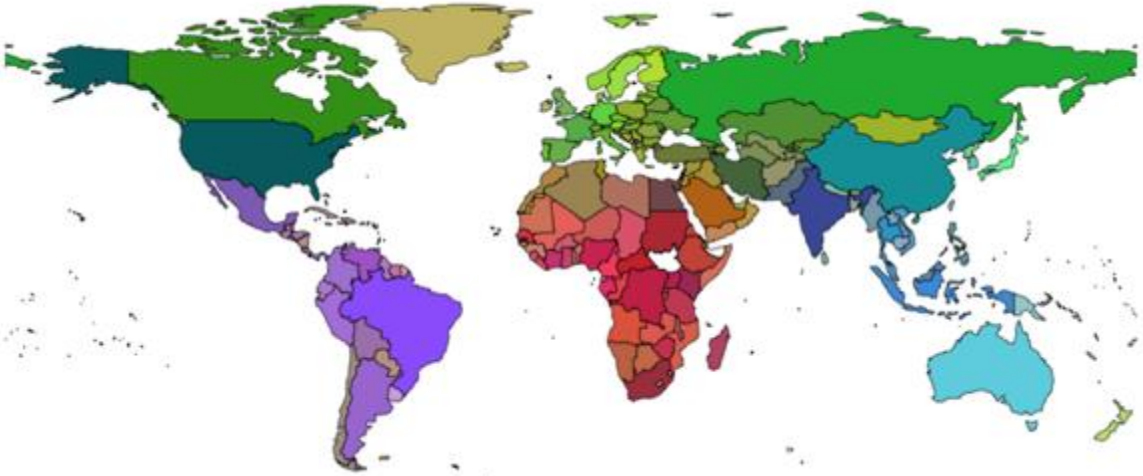
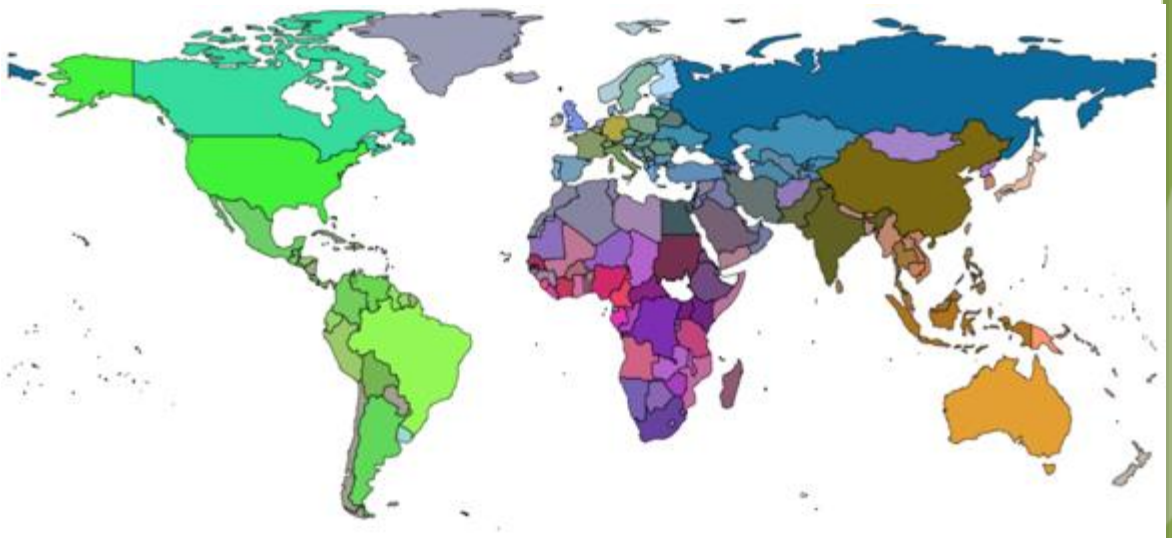
BioGeography of Human Infectious Diseases



Zoonotic disease biogeographic zones

Viral disease biogeographic zones



Based on similarity analysis of zoonotic human infectious disease assemblages at country level.

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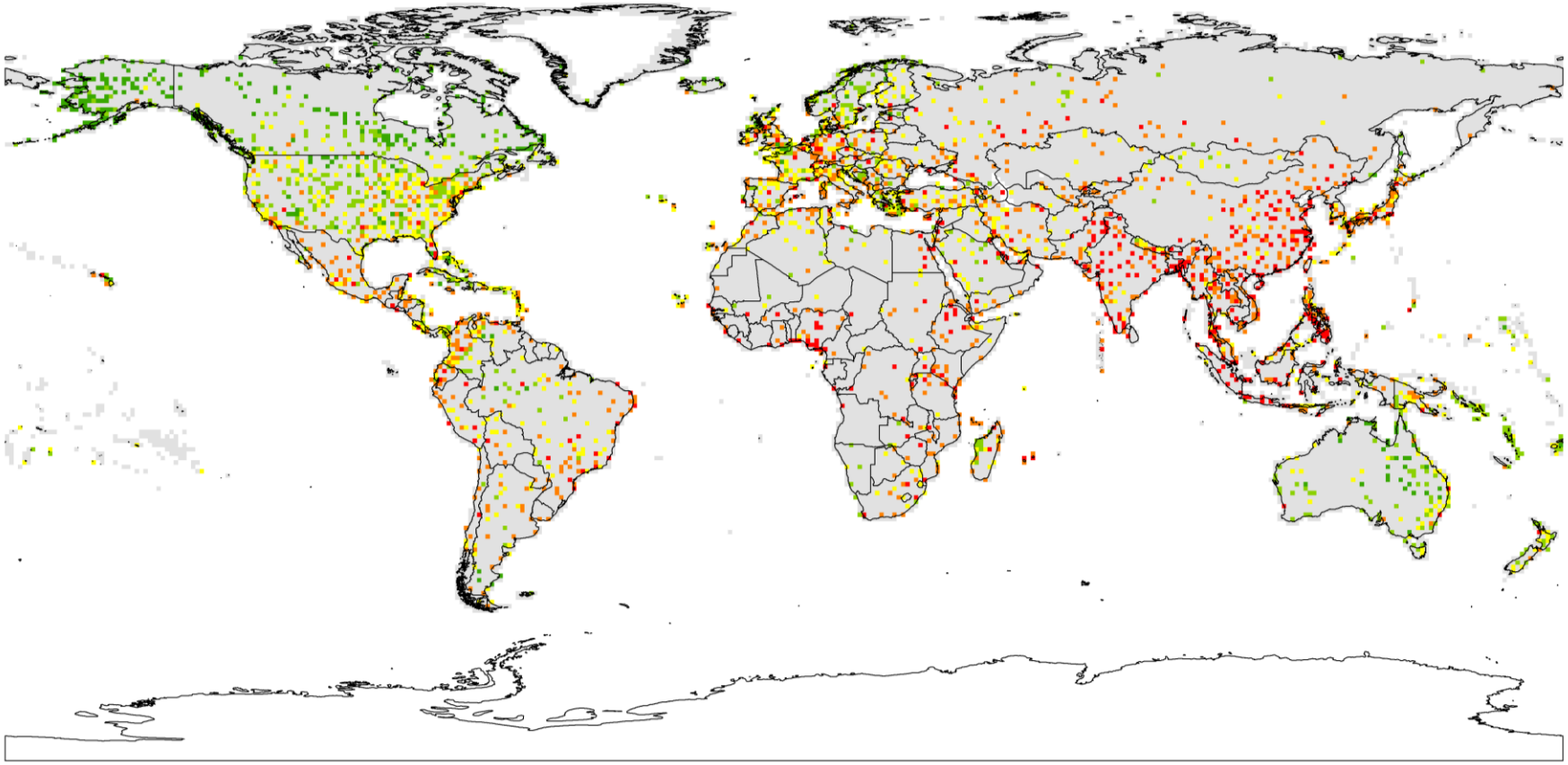
Global vulnerability index

- Calculating index
  - E_i = Jones et al. hotspots
  - C_{ij} = Est. Number of passengers
  - H_i = Healthcare spending per capita
    - i = source of risk
    - j = destination of risk

$$\phi_j = \sum_{all\,i} \frac{C_{ij} \cdot E_i}{H_i}$$

- We then interpolate risk out from airport locations globally
- Using Inverse Distance Weighted interpolation

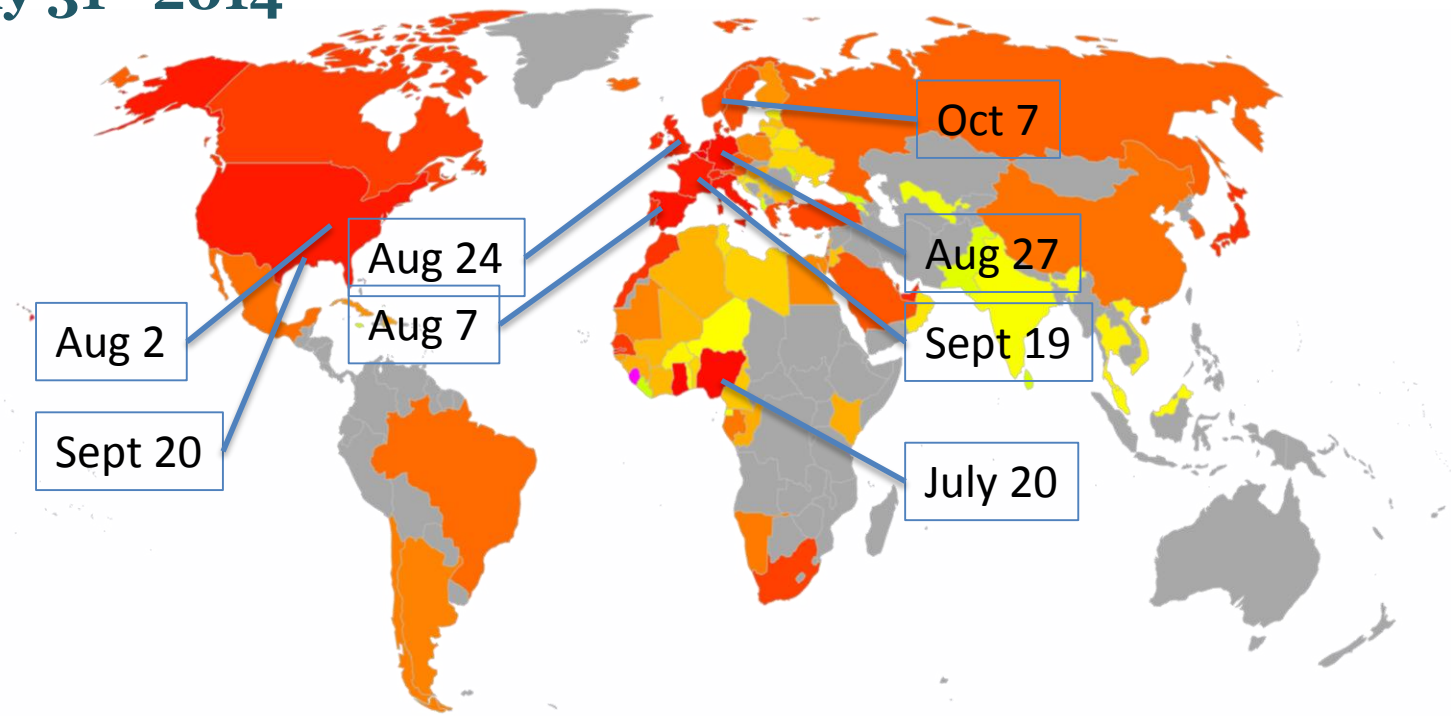
EID risk per airport



Hosseini *et al.* (in review)

Our prediction of which countries were at risk for Ebola spread

July 31st 2014



Red = earliest arrival; Green = last arrival. Grey = countries that can't be reached in 2 legs or less.

There are 10 countries that can be arrived at via direct flights, and 95 that can be reached by flights of two legs or less.

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EcoHealth Alliance HP3 Database

2755 unique mammal-virus associations

768 mammal species

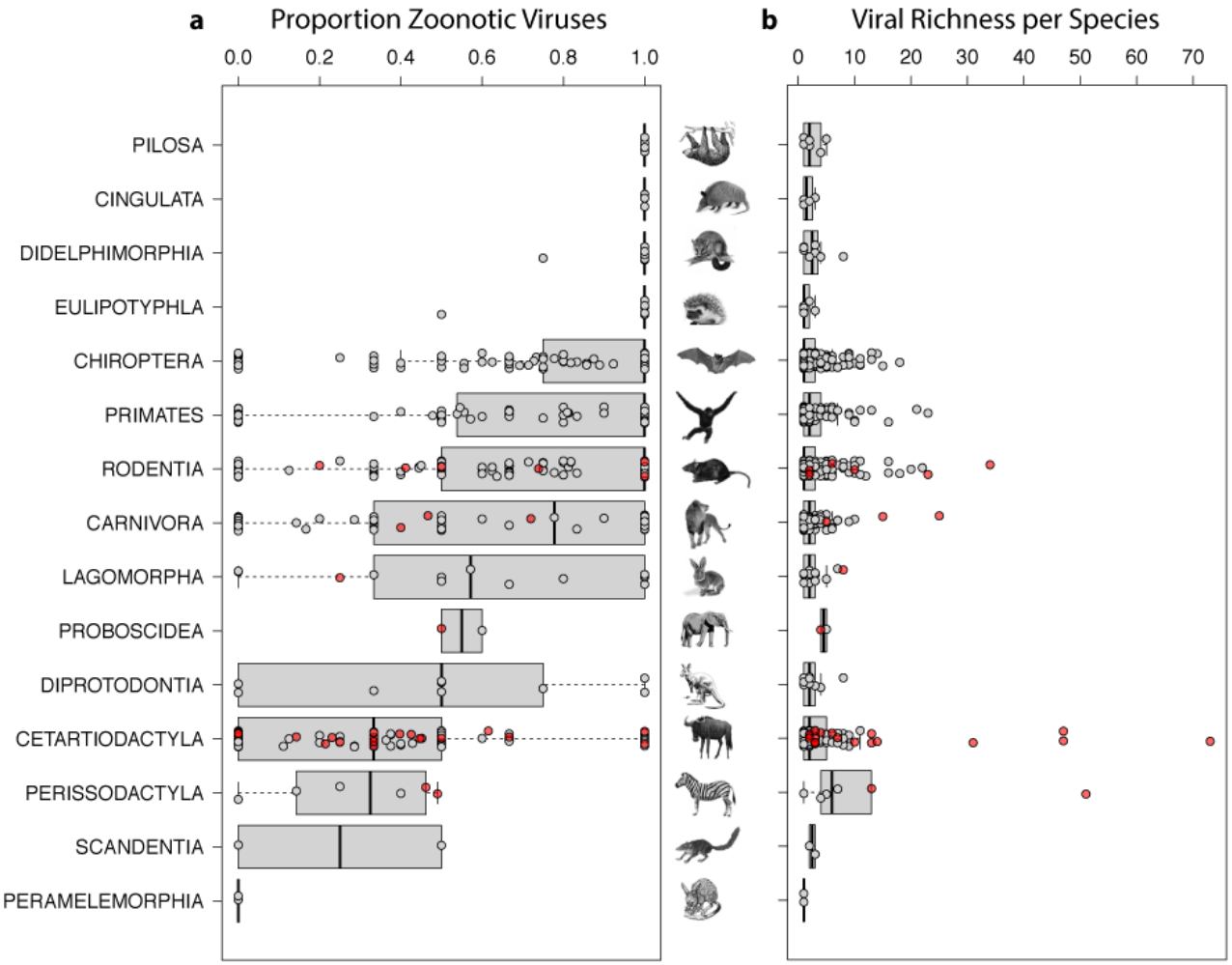
- 374 genera, 80 families, 15 orders

590 ICTV unique viruses found in mammals

- 382 RNA; 208 DNA viruses
- **258** of all these viruses have been detected in humans (44%)
- 93 exclusively human.
- 165 (64%) of human viruses are ‘zoonotic’

Olival et al. *In Revview: NATURE*

Observed viral richness varies little by Order, but proportion of zoonotic viruses does



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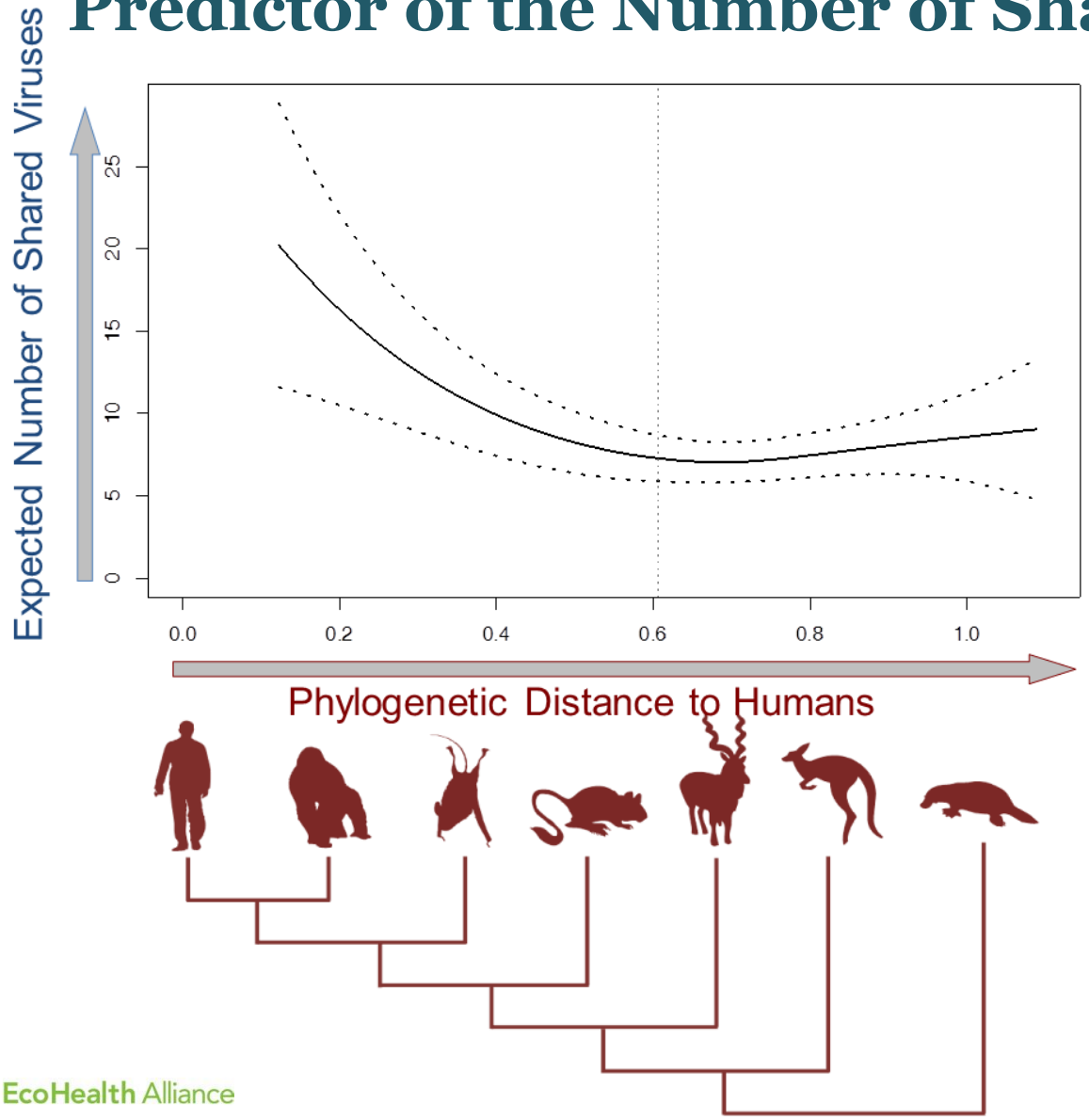
Olival et al. *In Prep*

Phylogenetic Distance to Humans Significant Predictor of the Number of Shared Viruses



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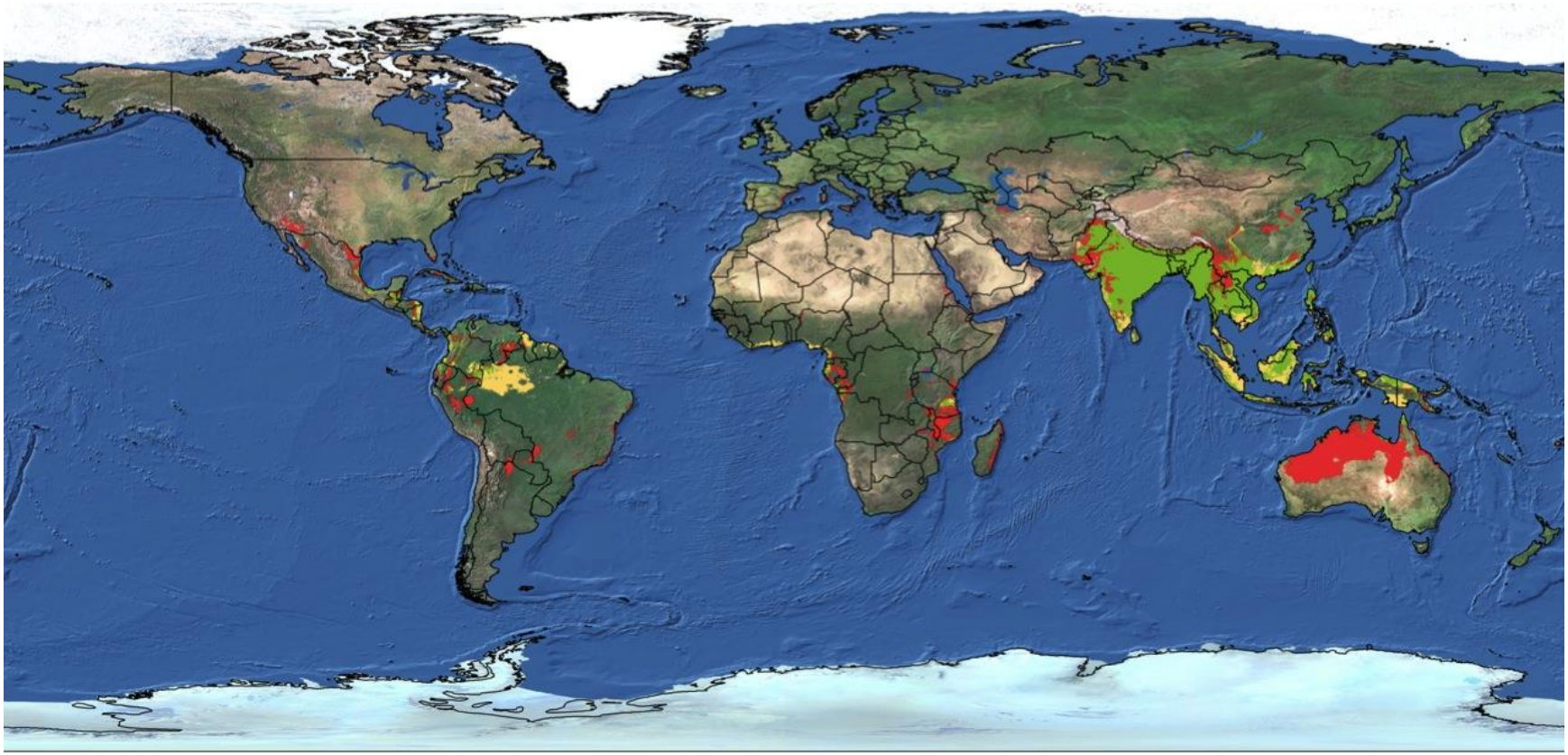
Olival et al. *In Prep*

Climate Change and Emerging Diseases



Future Climate Change Scenario for the distribution of Nipah virus. Year 2050, optimistic scenario (B2). Red areas show new potential areas for virus spread.

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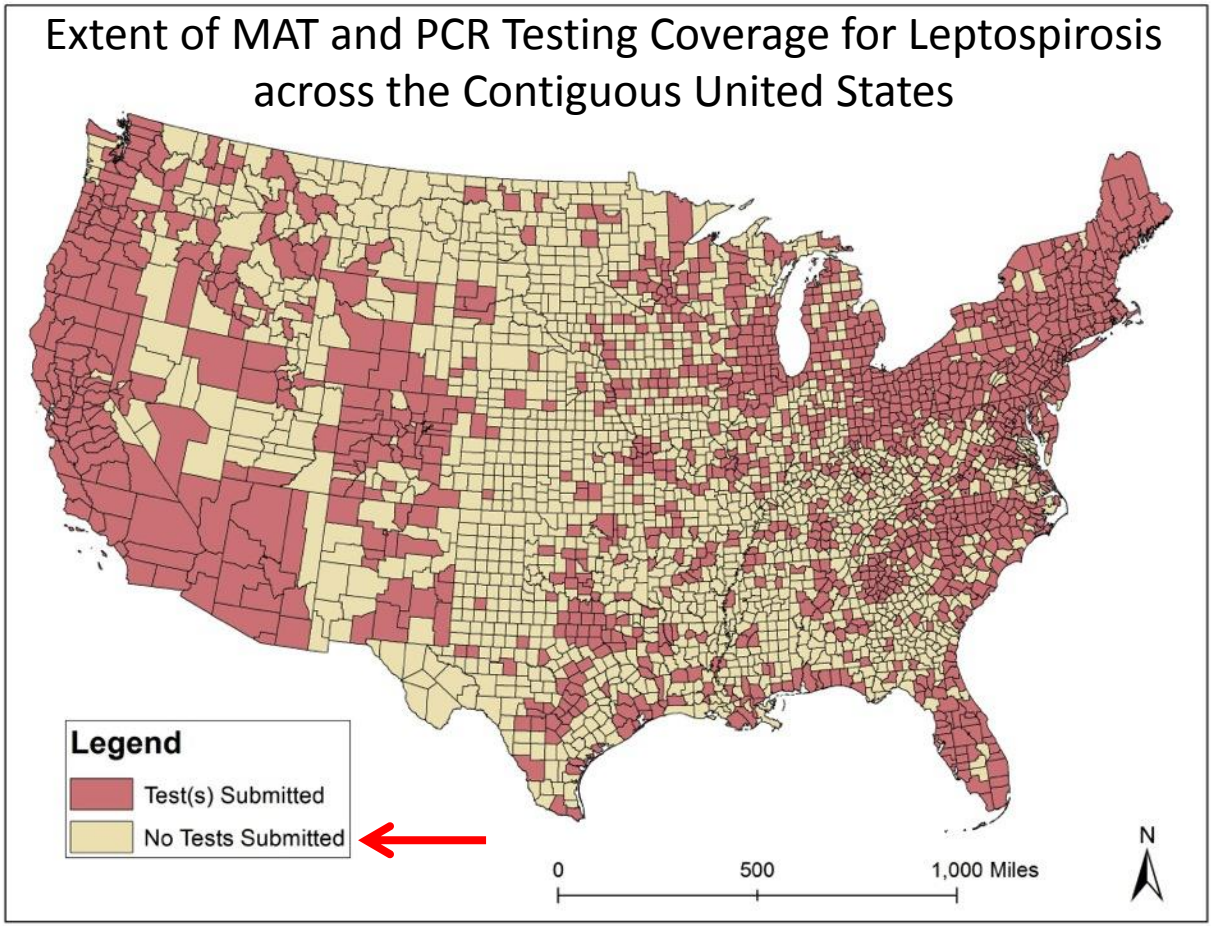
Background on Leptospirosis

- Leptospirosis is a widespread zoonotic disease
  - Can affect a wide variety of domestic animals and wildlife, as well as humans
- Caused by *Leptospira,* an anaerobic spirochete

IDEXX Data Overview



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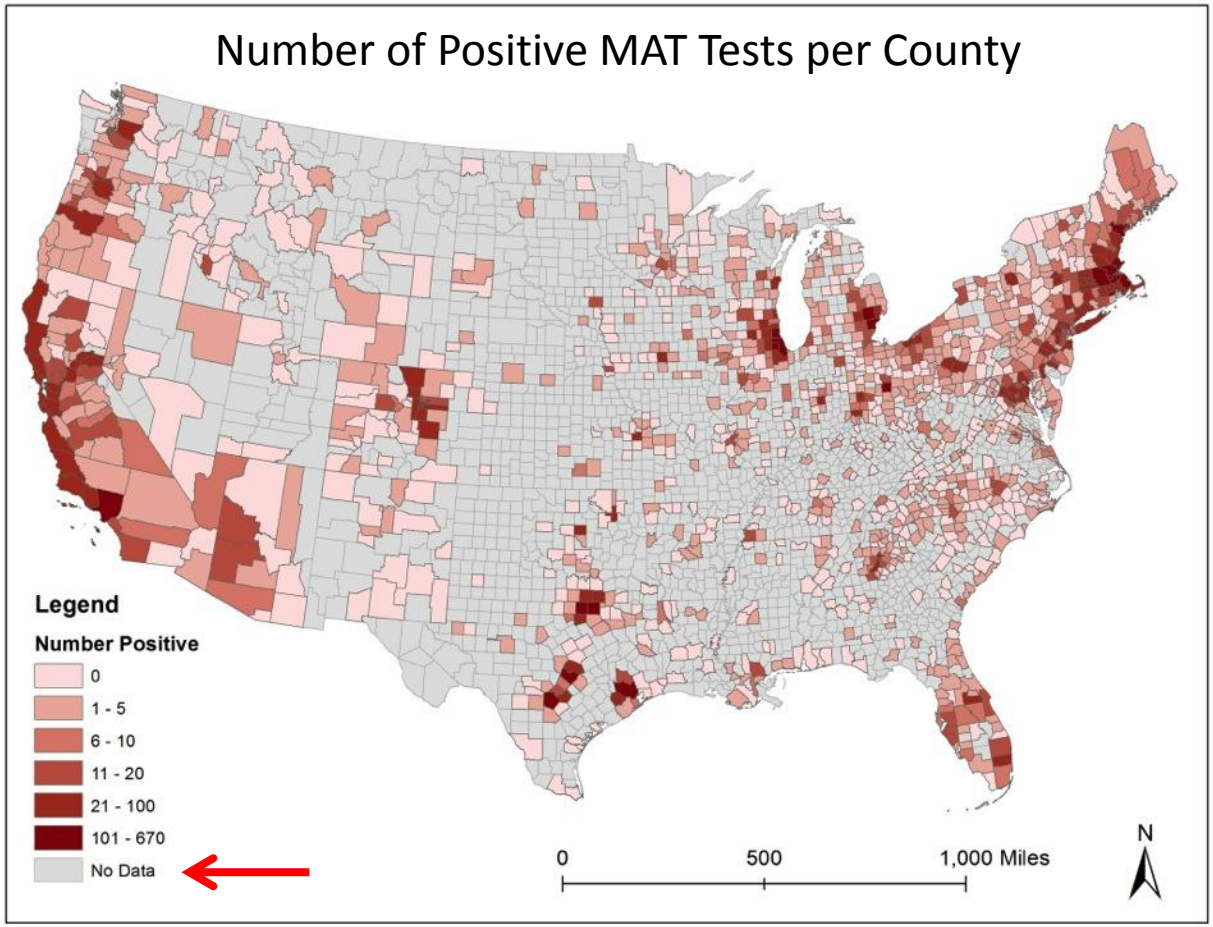
Source: IDEXX Laboratories

MAT Results



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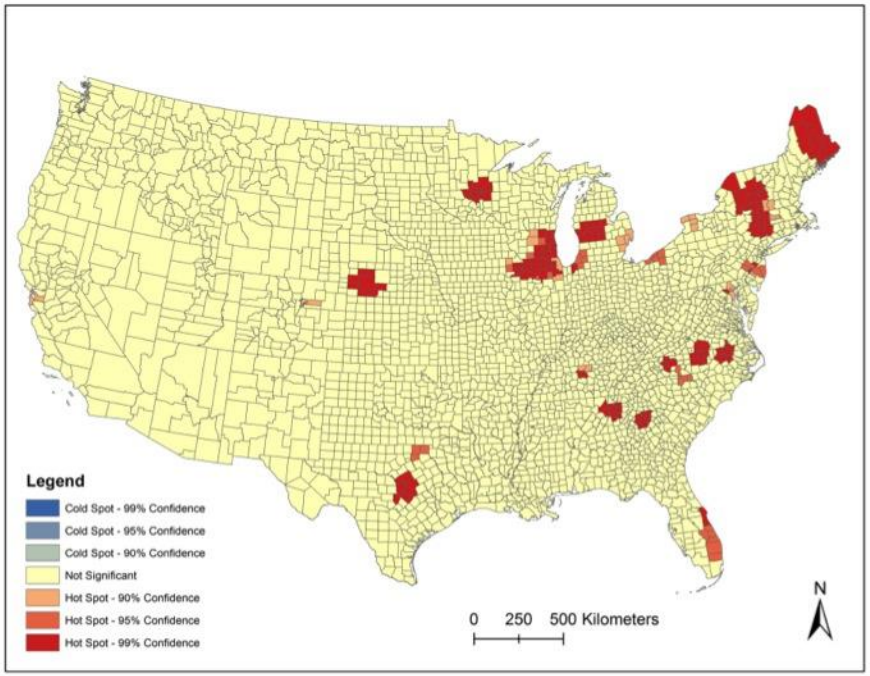
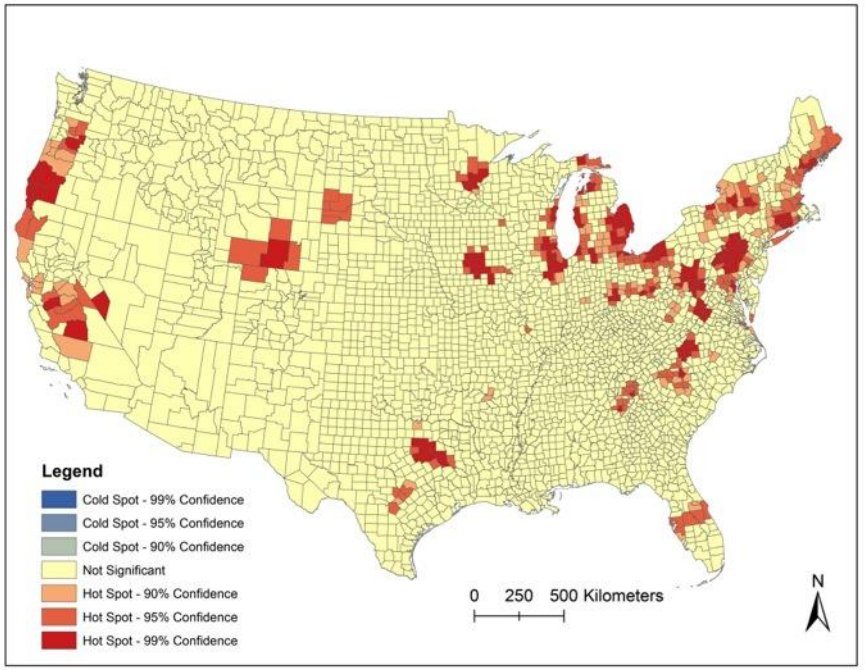
Source: IDEXX Laboratories

Spatial Clusters: Percent of Tests Positive

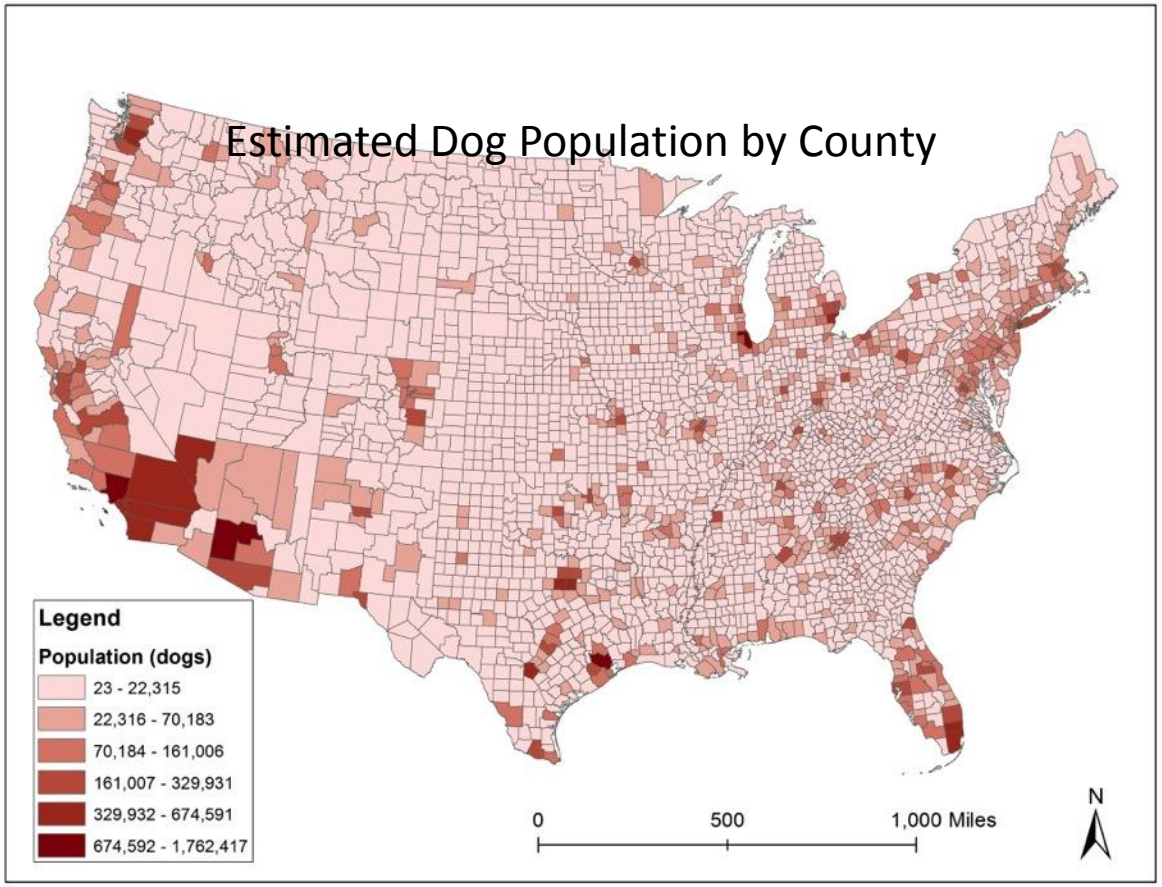
Clusters of Positive PCR Results: Proportion of Positive Results to Total Tests

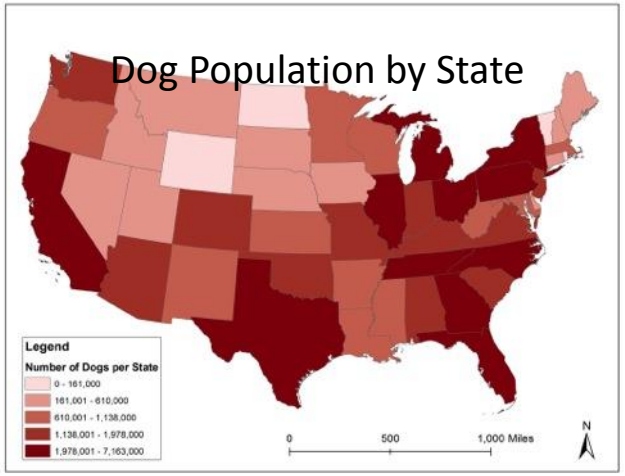


Clusters of Positive MAT Results: Proportion of Positive Results to Total Tests



Dog Population Data



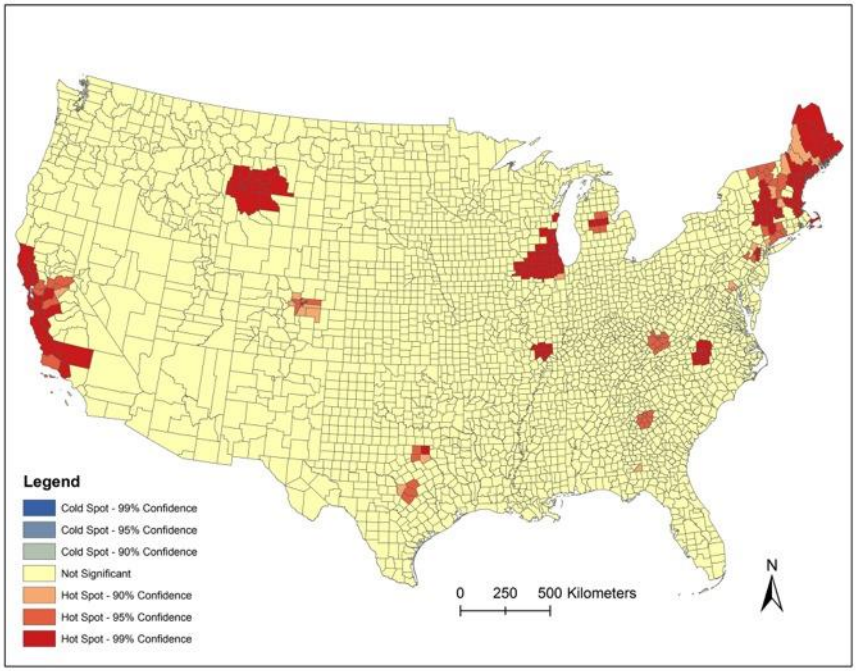


- Used county-level human population census data to estimate population of dogs per county
- Assuming that within each state, dogs are distributed within the state similar to humans

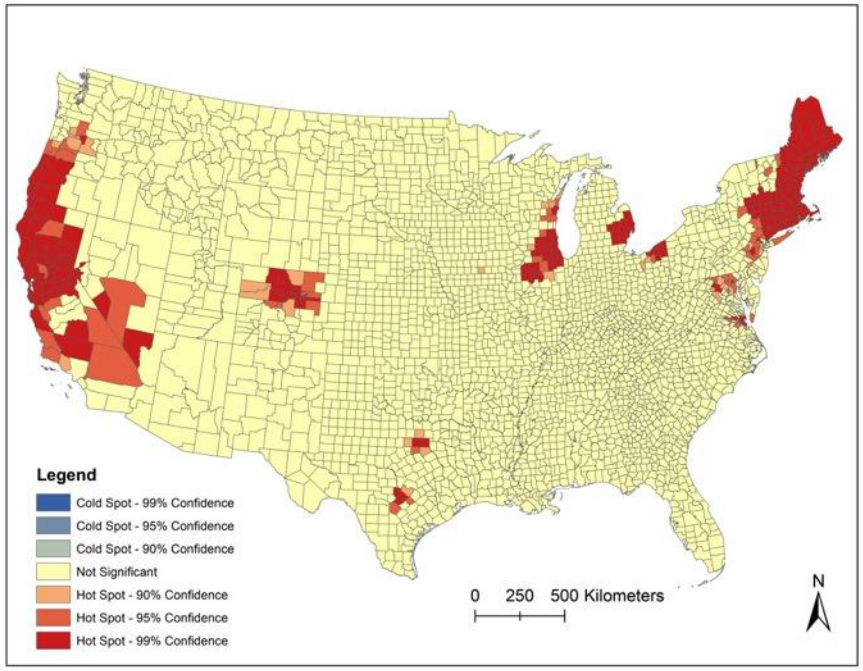
- Human population data from US Census
- State-level data for dogs from AVMA US Pet Demographics Sourcebook 2012

Spatial Clusters: Positive Tests per Estimated County Dog Population

Clusters of Positive PCR Results: Positive Tests per Estimated Dogs



Clusters of Positive MAT Results: Positive Tests per Estimated Dogs



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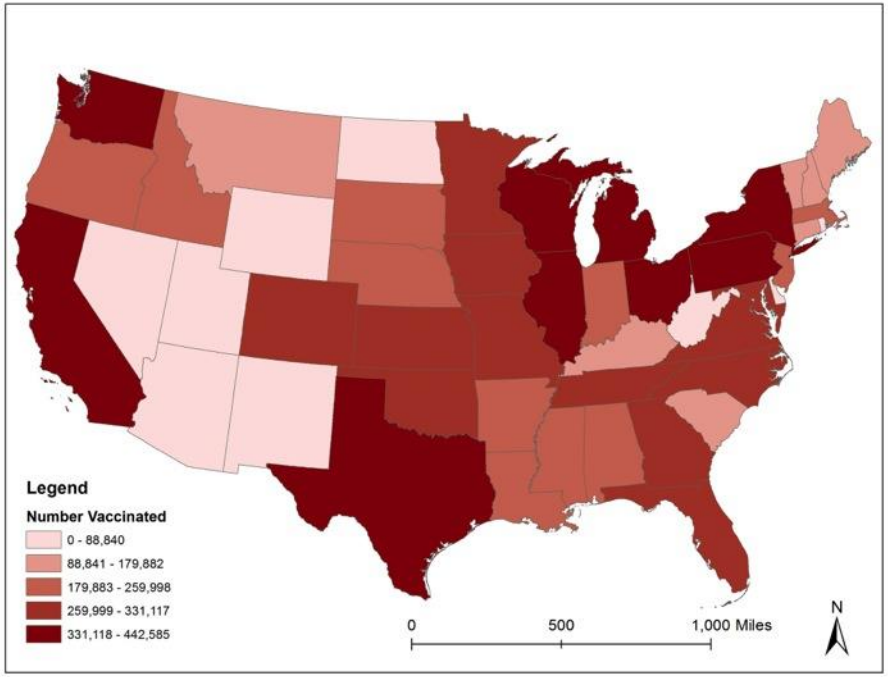
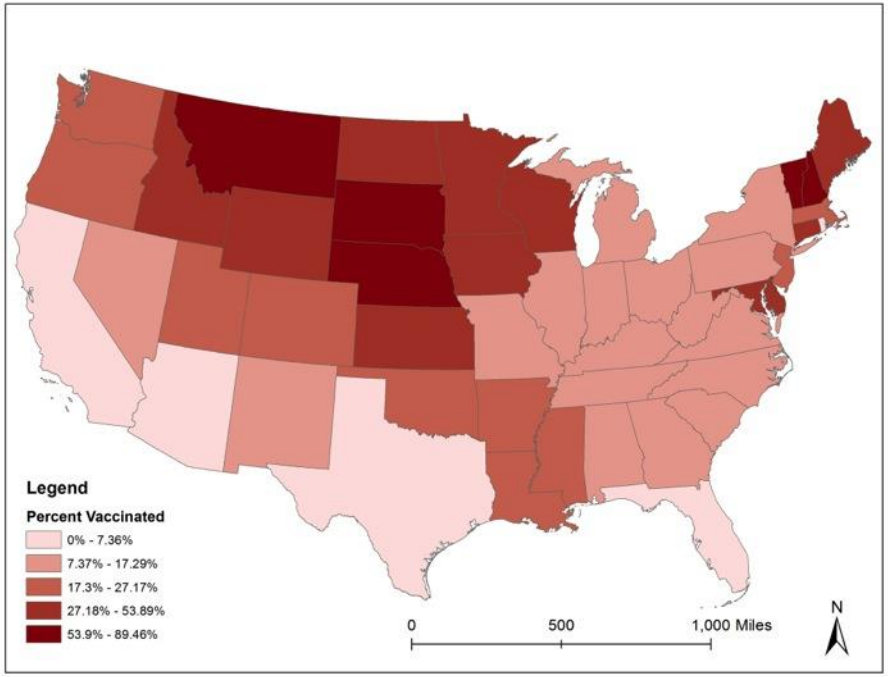
Leptospirosis Vaccination

Number of Dogs Vaccinated per State 2010-2014



Four-Year Vaccination Numbers per Estimated Dog Population by State



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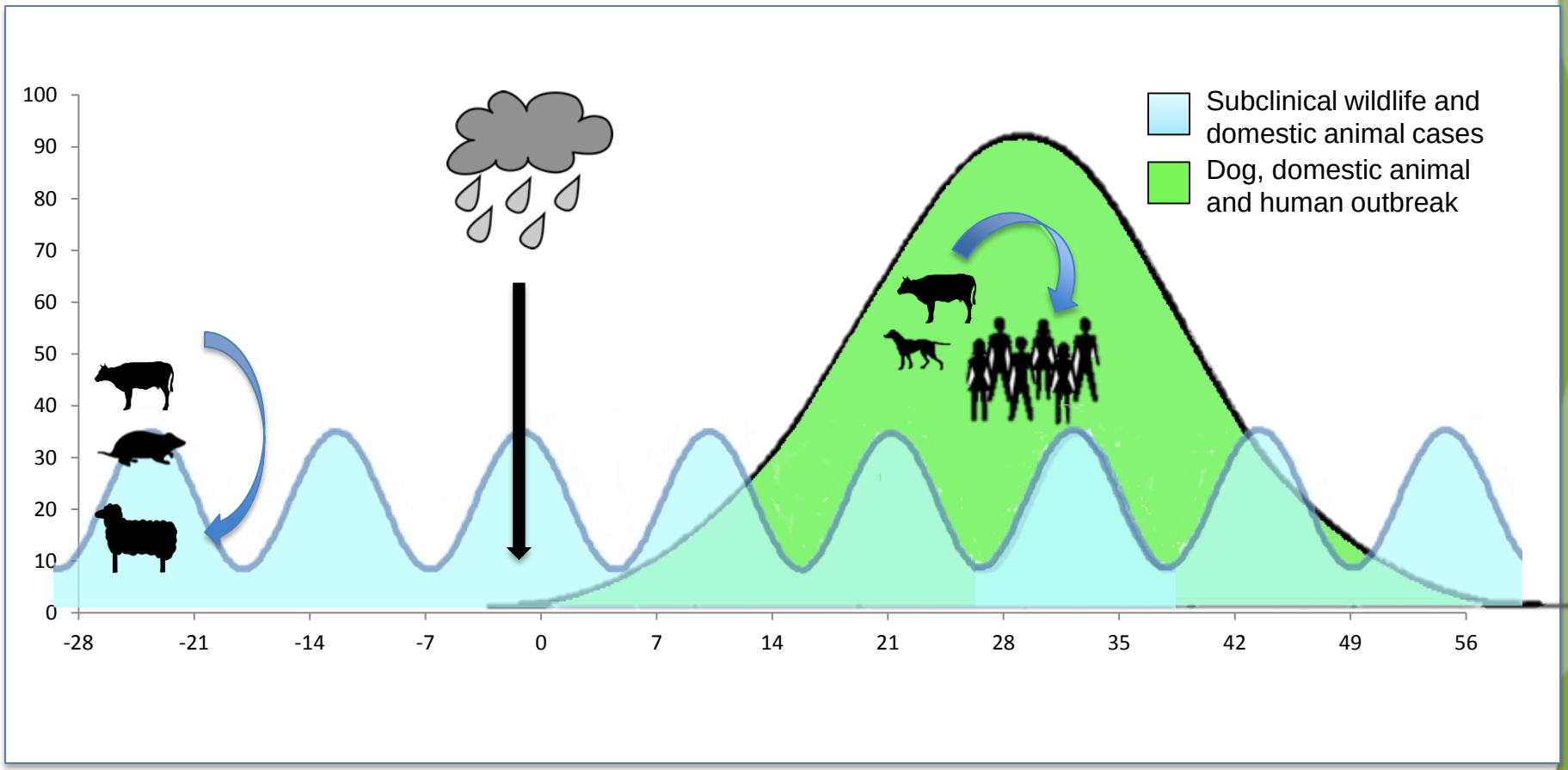
Source: Zoetis Inc.

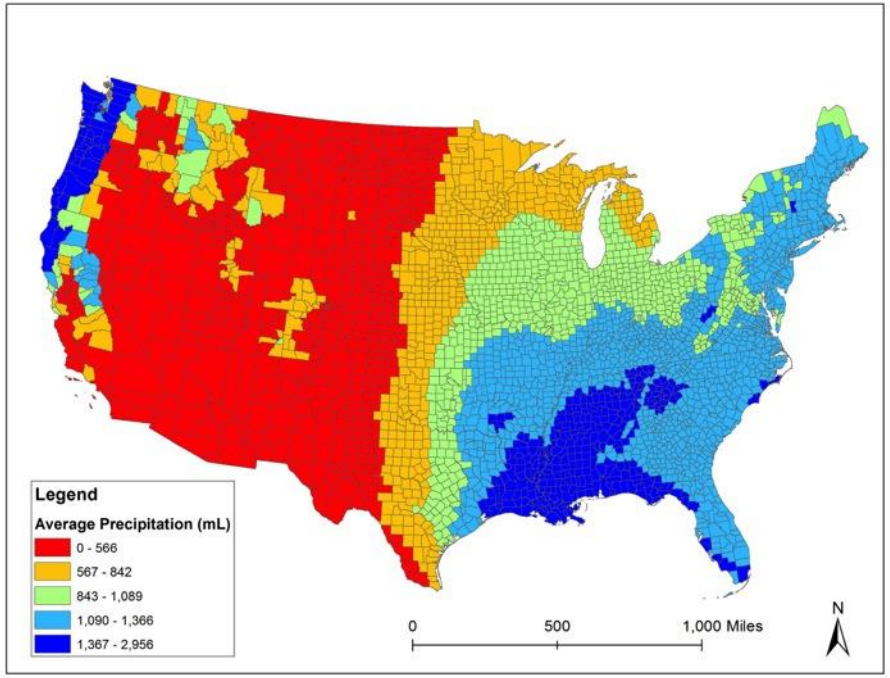
Possible Importance of Rainfall

Determine how other factors could affect transmission and support the ability to predict an outbreak



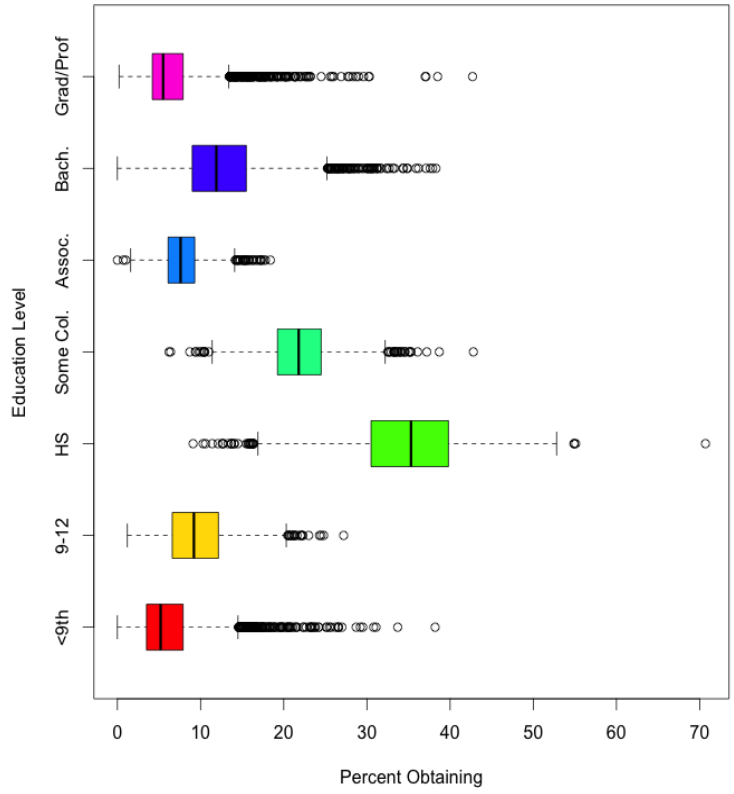
Climatic Variables

- Climate Data
  - Mean Precipitation
  - Mean Temperature
  - Bioclimate Data
    - Represents annual trends, seasonality, and extreme factors (e.g., temperature in coldest month)

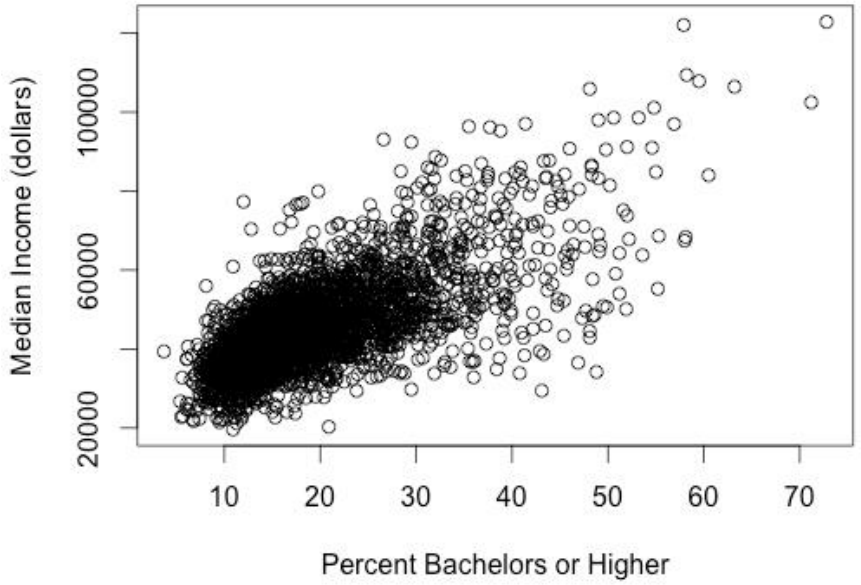


Income and Education Data

Distribution of Education Levels By County



Scatterplot of Income and Education



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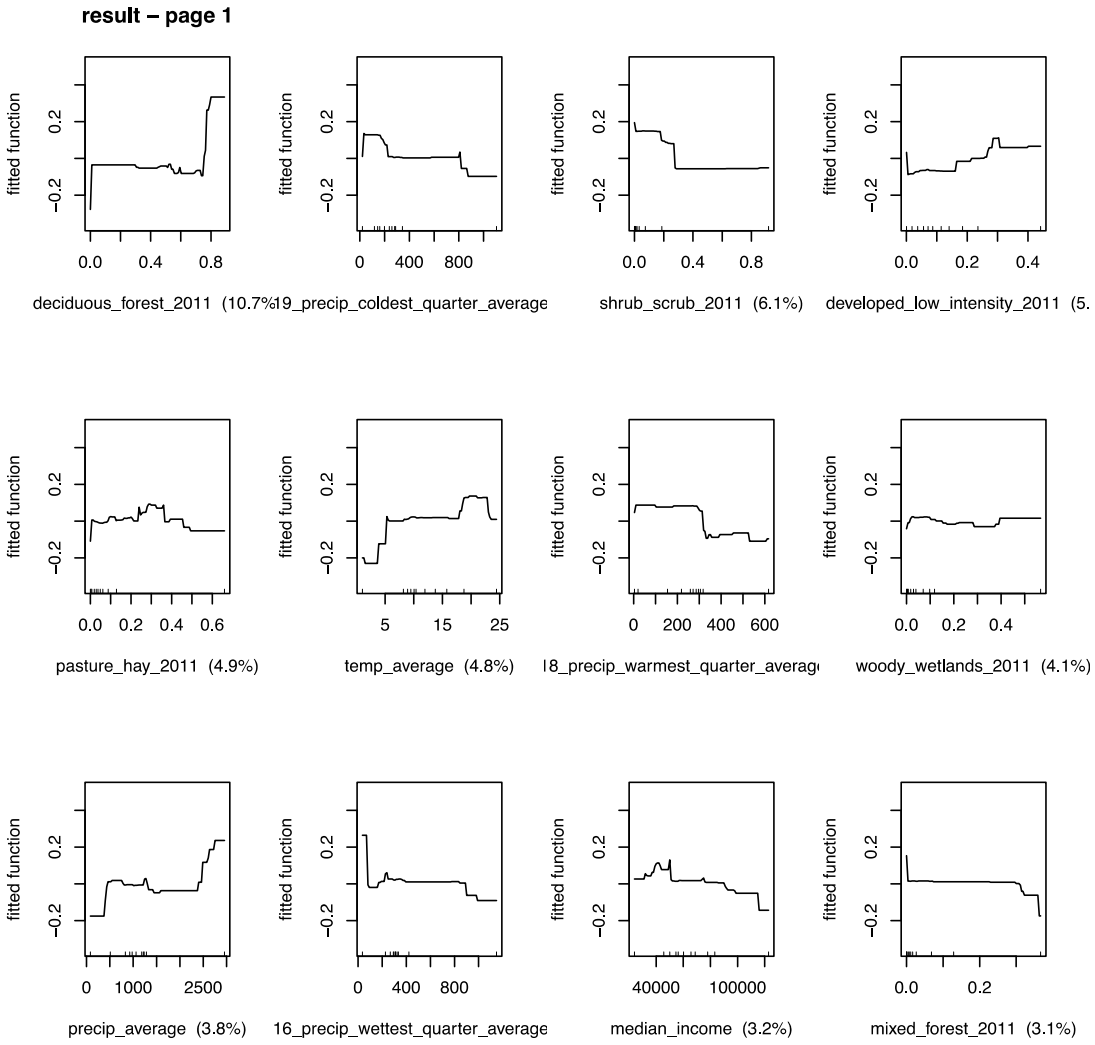
Partial Dependence Plots: MAT Results



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Boosted Regression Tree Results

PCR Model: Top 5 Predictors

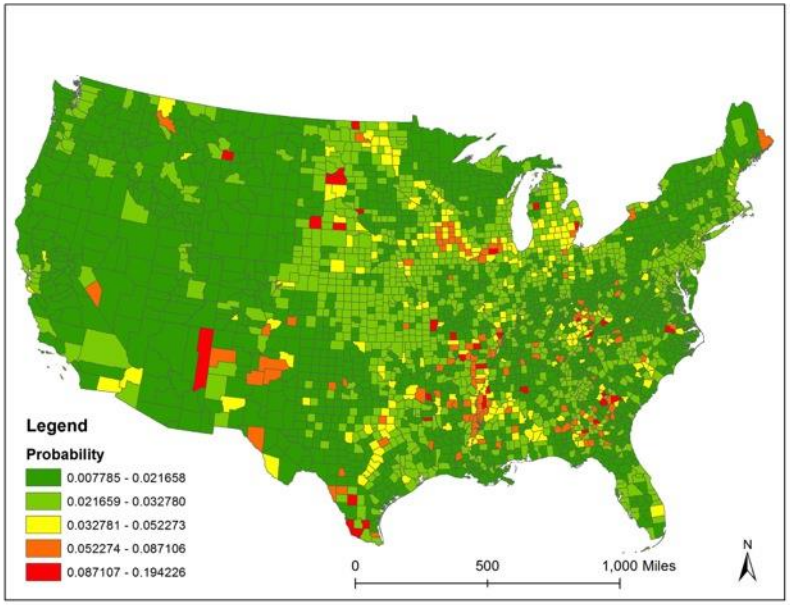
Variable	Relative Influence
Evergreen Forest Cover	12.24919776
Shrub/Scrub Cover	9.887439268
Grassland/ Herbaceous Cover	7.161191081
Developed Open Space Cover	6.195173737
Median Income	5.81007611

MAT Model: Top 5 Predictors

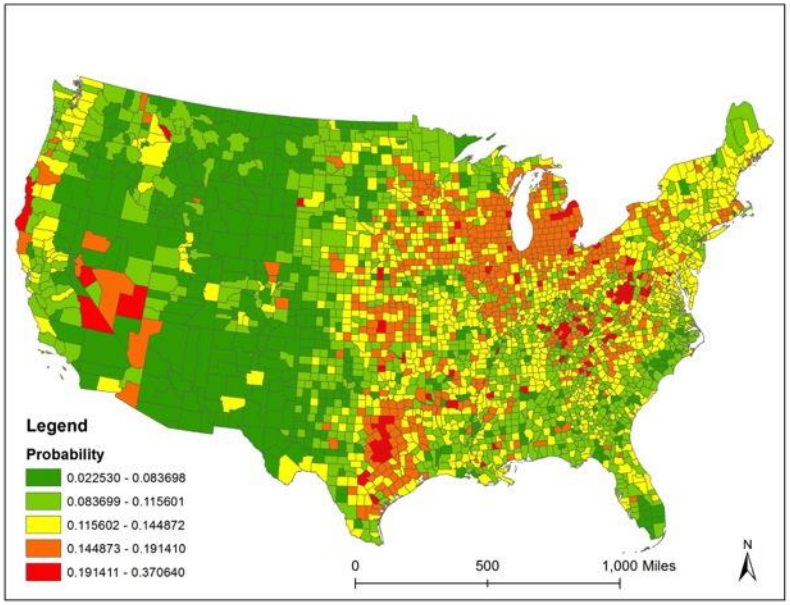
Variable	Relative Influence
Deciduous Forest Cover	10.6624204
Average Precipitation in Coldest Quarter	8.622065784
Shrub/Scrub Cover	6.067515302
Developed Low Intensity Cover	5.785643682
Pasture/Hay Cover	4.897024777

Predictive Modeling Results by County

Inverse Logit Transformed Prediction by County: PCR



Inverse Logit Transformed Prediction by County: MAT



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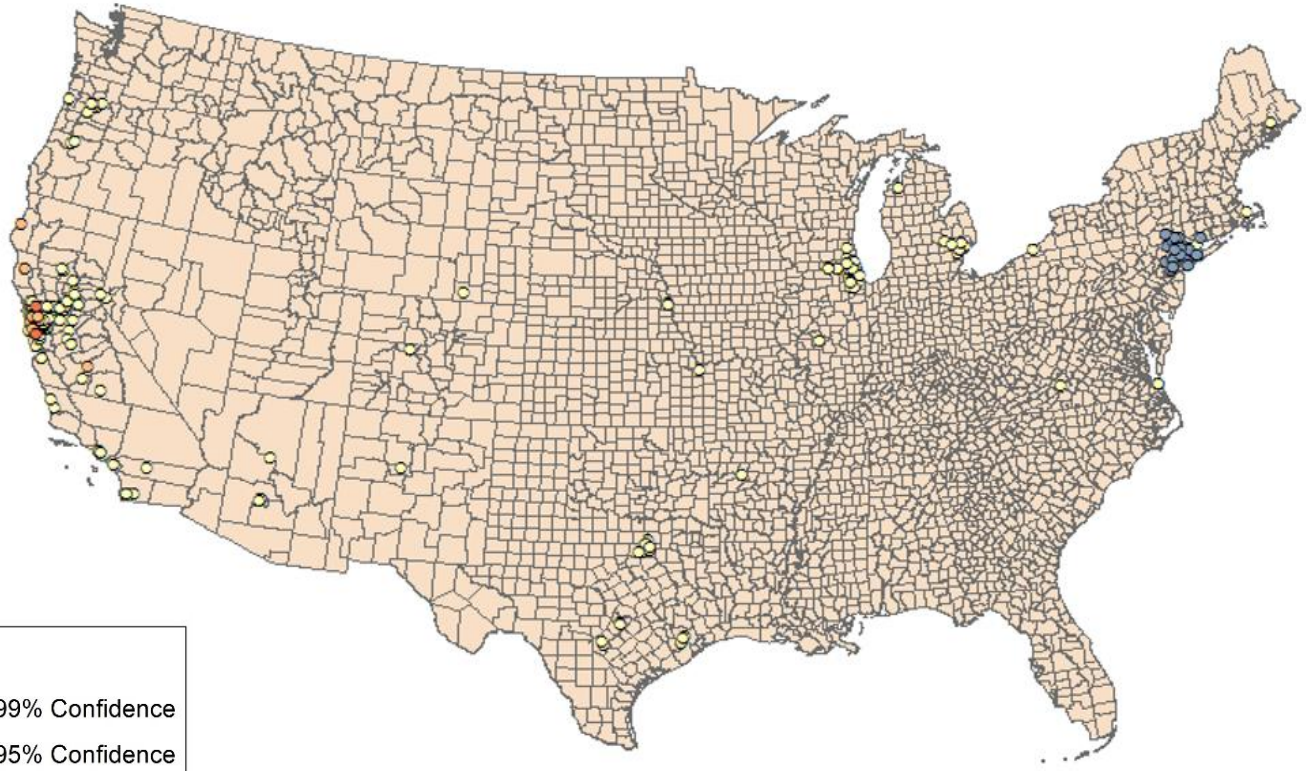
Date: 01/06/00 to 04/06/00



Legend

- Cold Spot - 99% Confidence
- Cold Spot - 95% Confidence
- Cold Spot - 90% Confidence
- Not Significant
- Hot Spot - 90% Confidence
- Hot Spot - 95% Confidence
- Hot Spot - 99% Confidence

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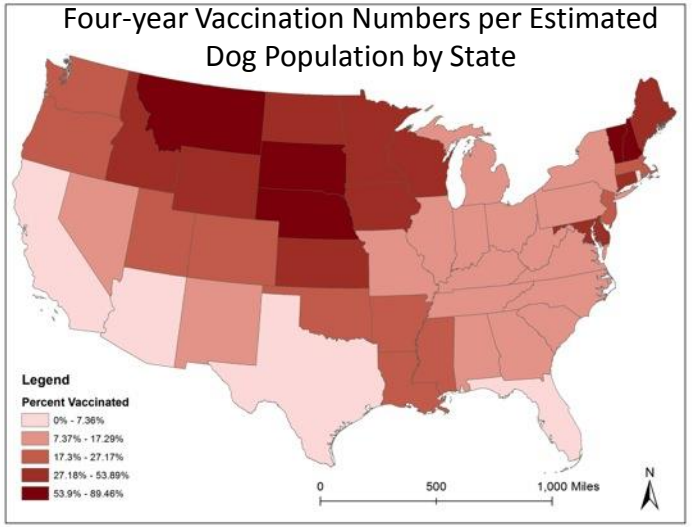
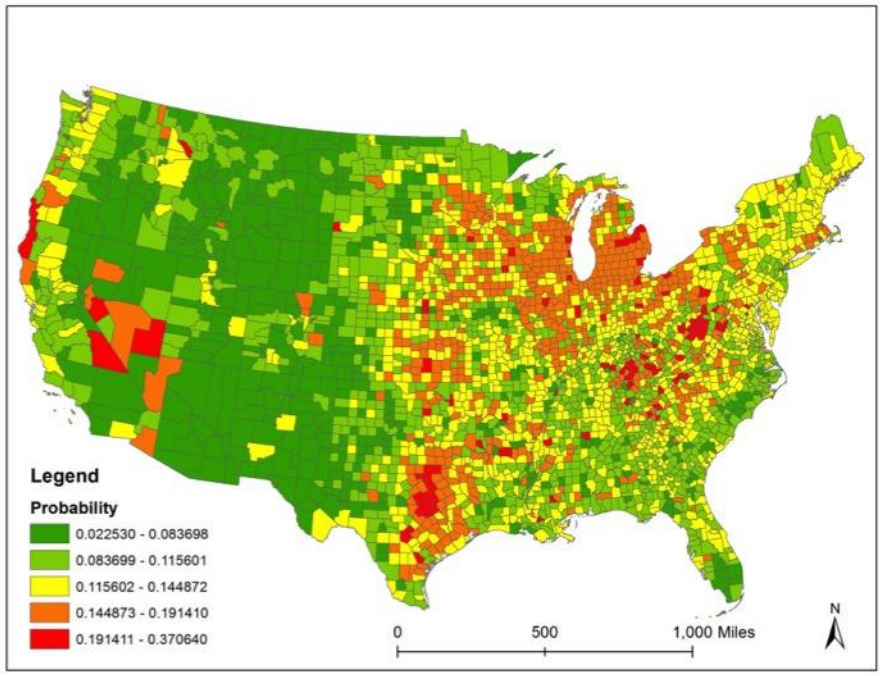
Summary of Final Results: MAT

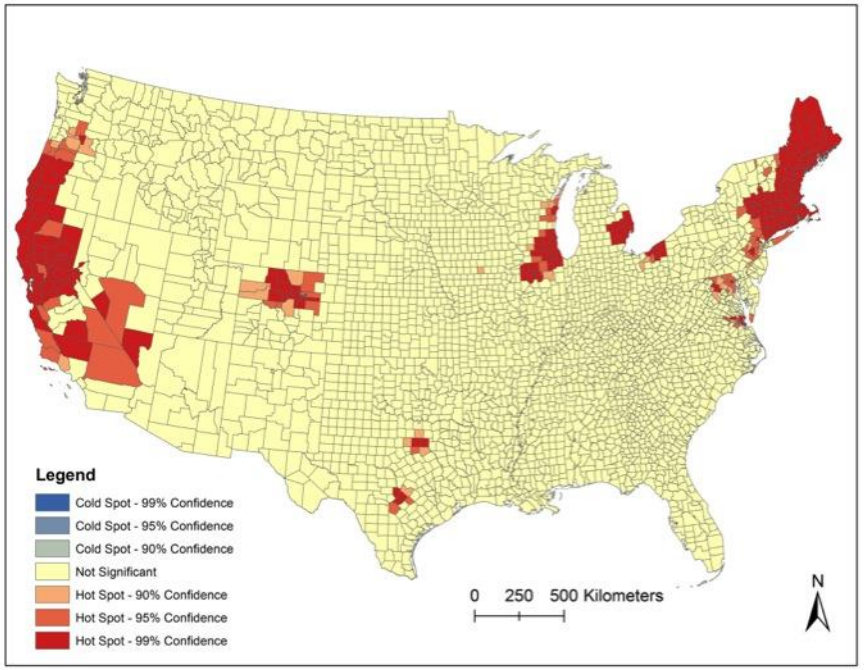
Four-year Vaccination Numbers per Estimated Dog Population by State



Inverse Logit Transformed Prediction by County: MAT



Clusters of Positive MAT Tests Relative to the Estimated County Dog Population



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Drivers of Disease: Connections Matter

William B. Karesh, DVM

Executive Vice President for Health and Policy, EcoHealth Alliance

President, OIE Working Group on Wildlife

Co-Chair, Wildlife Health Specialist Group, International Union for the Conservation of Nature

Local conservation.
Global health.

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  - Listen for the operator to call your name
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