

# *Planning Informed by Epidemiological Simulation: The Geography of Avian Flu in Nigeria*

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# Geospatial Epidemiology Modeling of Zoonotic Diseases

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- Identify current and emerging zoonotic agents
- Identify wildlife reservoirs for human and agricultural animal infection
- Assess the importance of different modes of transmission
  - Waterborne
  - Foodborne
- Predict outbreaks
- Evaluate control strategies
- Effective biosurveillance planning



## Multiple Hosts Model

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Combines the advantages of SEIR-like models:

- exponential epidemic rise, saturation, and fall in well-mixed compartments
- rapid to compute
- easy to match to empirical data

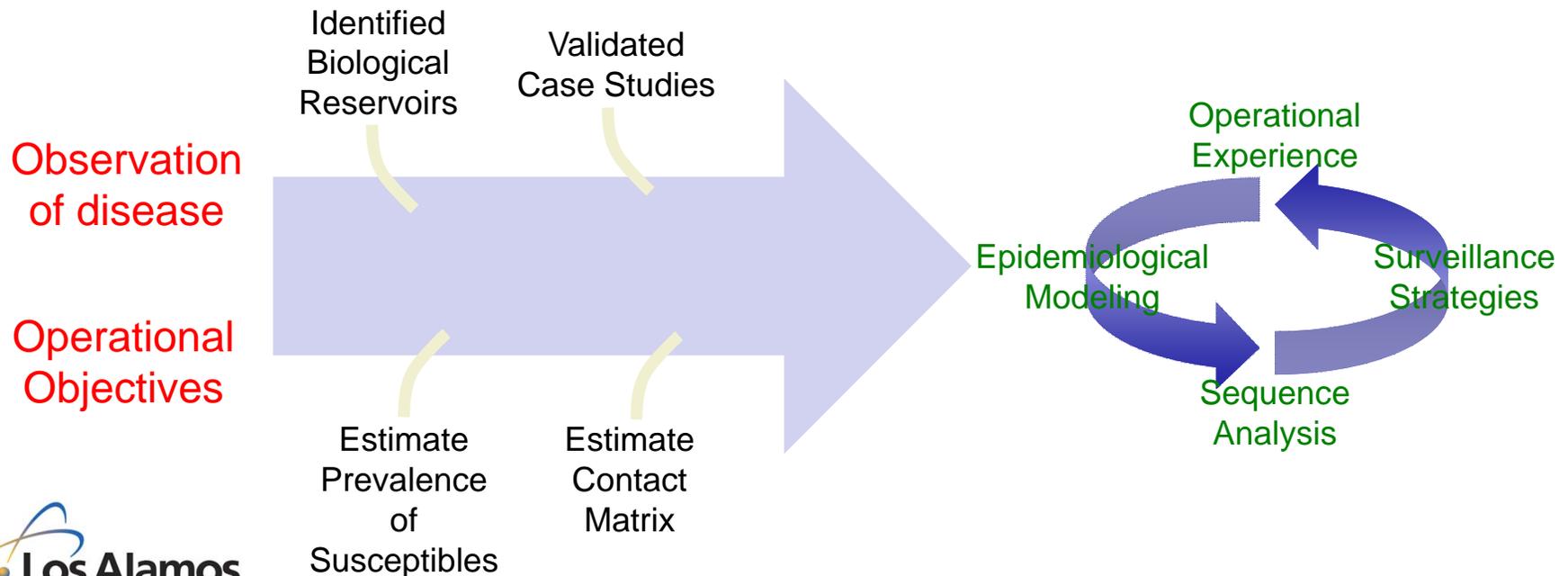
with the advantages of agent-based models at larger scales:

- flexible and explicit rule-based mitigations
- realism (transferability)
- multi-host, with arbitrary transmissibility and susceptibility matrices between hosts
- **Geography for surveillance**



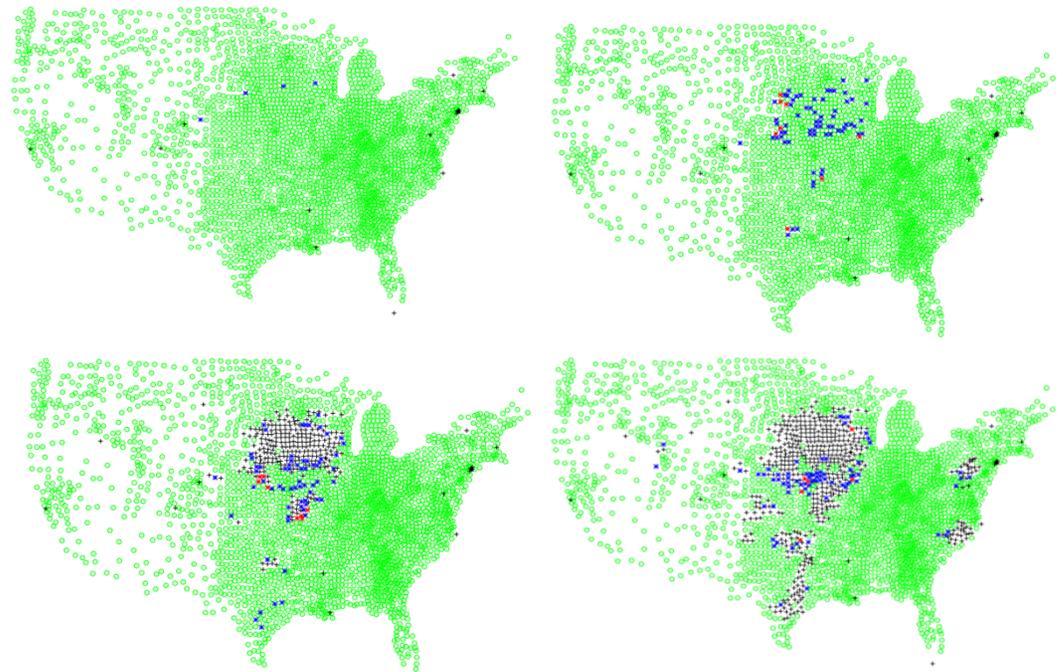
# Extending our multi-species epidemiological simulation tool

**Case Study: Nigeria H5N1 avian influenza outbreak, 2006**  
**Start with avian influenza model from U.S. studies**  
**Update with information from Nigeria**  
**Model viral spread and evaluate effect on operations**



# Multi-Scale Simulation of Zoonotic Epidemics - MuSE

- **Severity of epidemic depends on reaching dense areas in the Midwest**
- **Control Methods**
  - Faster response time in implementing movement restriction
  - Better surveillance in certain counties
  - Faster culling and quarantine response
  - Vaccination



**Time Series of Severe Rinderpest Epidemic In the U.S.**

Manore C., B. H. McMahon, J.M. Fair\*, J. M. Hyman, M. Brown, and M. LaBute. 2011. Disease Properties, Geography, and Mitigation Strategies in a Simulation Spread of Rinderpest Across the United States. *Veterinary Research*. 42:55-64

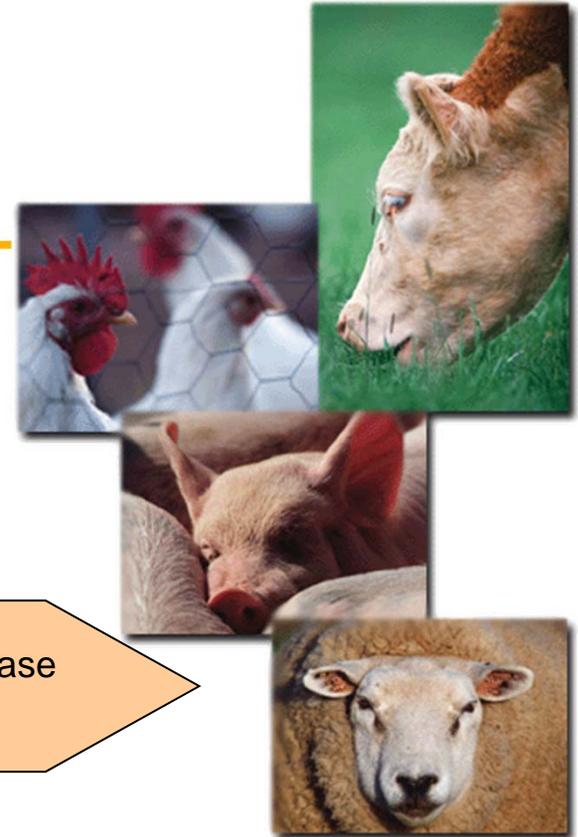
# Input parameters

## Model parameters for animal disease model.

- Transmission rate
- Infected animals that progress to symptoms
- Infected animals that die
- Infected animals that are culled
- Vaccination policy
- Culling rate
- Disease stage time
- Recovery time
- Inter-state movement control efficacy
- Quarantine policy
- Susceptibility

Validation and parameterization critical for both animal and human epidemiology model. Case studies are integral to both model development and validation.

Similar to human disease model parameters



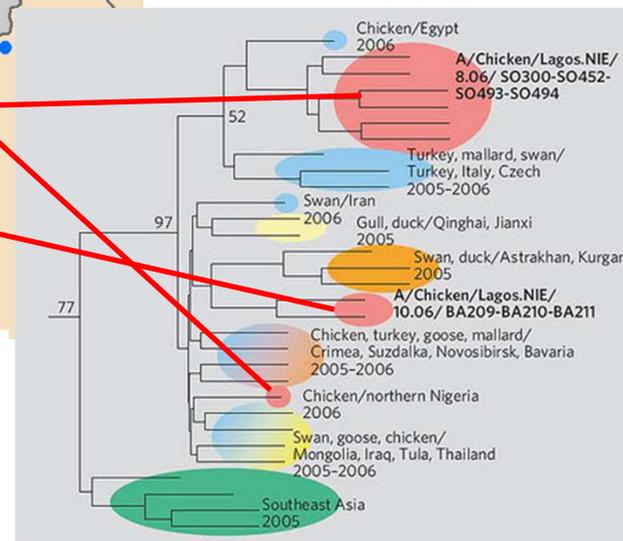
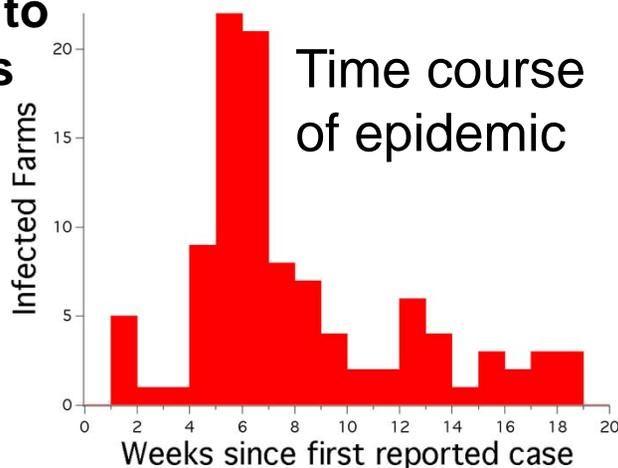
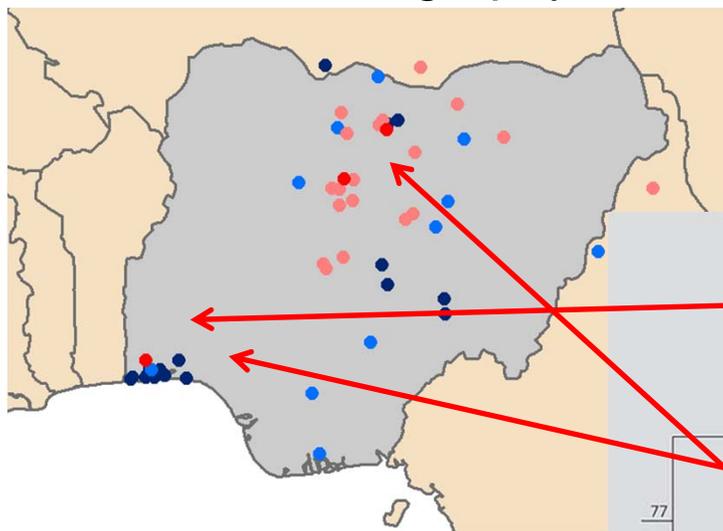
### Completed Diseases

- Cattle and Sheep Diseases
- Foot-and-Mouth Disease
- Rinderpest
- Rift-Valley Fever
- Brucellosis
- Tularemia
- Nipah Virus
- Classical Swine Fever
- Poultry Diseases
- Highly Pathogenic Avian Influenza
- Newcastle Disease Virus

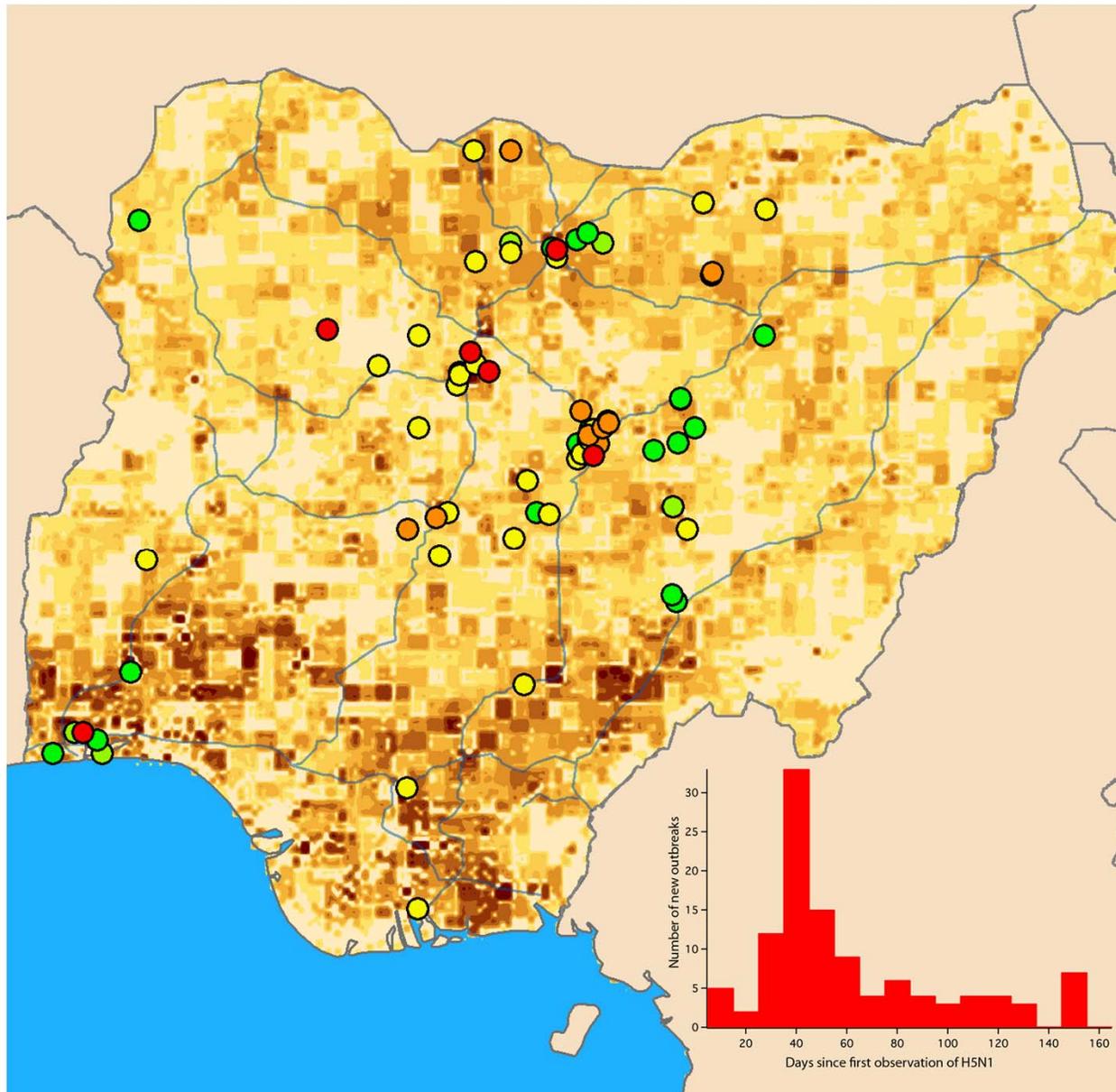
# Nigeria – Biogeography of an outbreak

- Nigerian AI outbreak in 2006 has been well – studied, allowing comparison with simulation output.
- Positive cases: 248
- Depopulated birds: 1,500,000
- Biogeography points to multiple introductions

## Geography

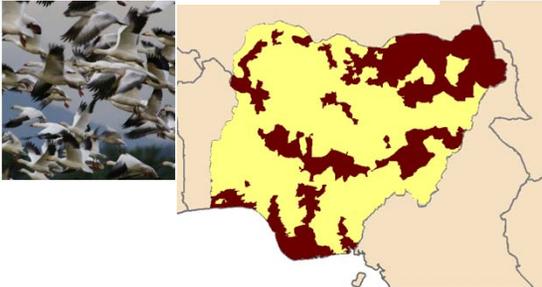


## Sequence Data

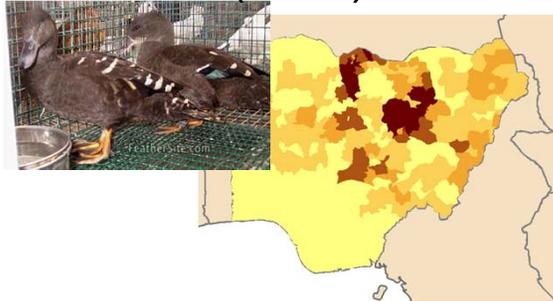


# Needed Inputs for Multi-host Epidemiology Model

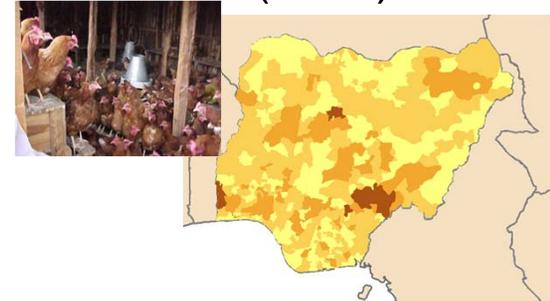
## Wild Birds (FAO)



## Ducks (FAO)



## Chickens (FAO)



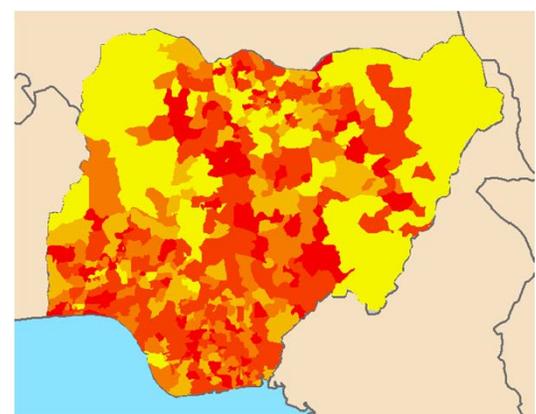
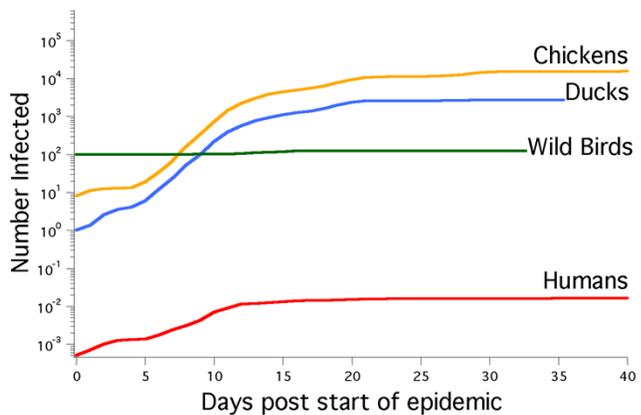
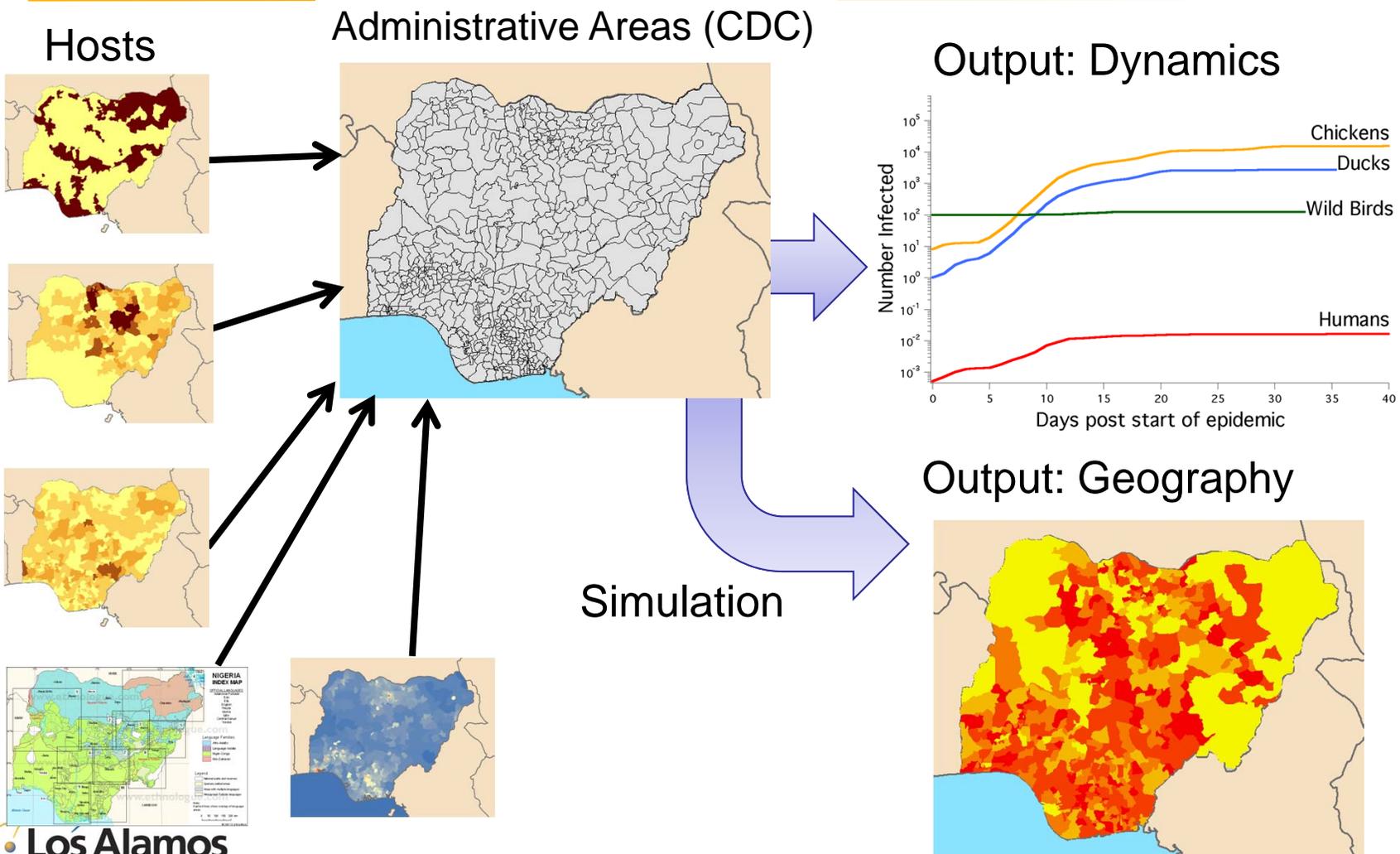
## People (UN, ESRI)



In addition to distribution of hosts, we need:

- Transmission vectors
- Susceptibility vectors
- Approximate long range transmission parameters
- Control measures and mitigative efficacies

# Multihost epidemiological model

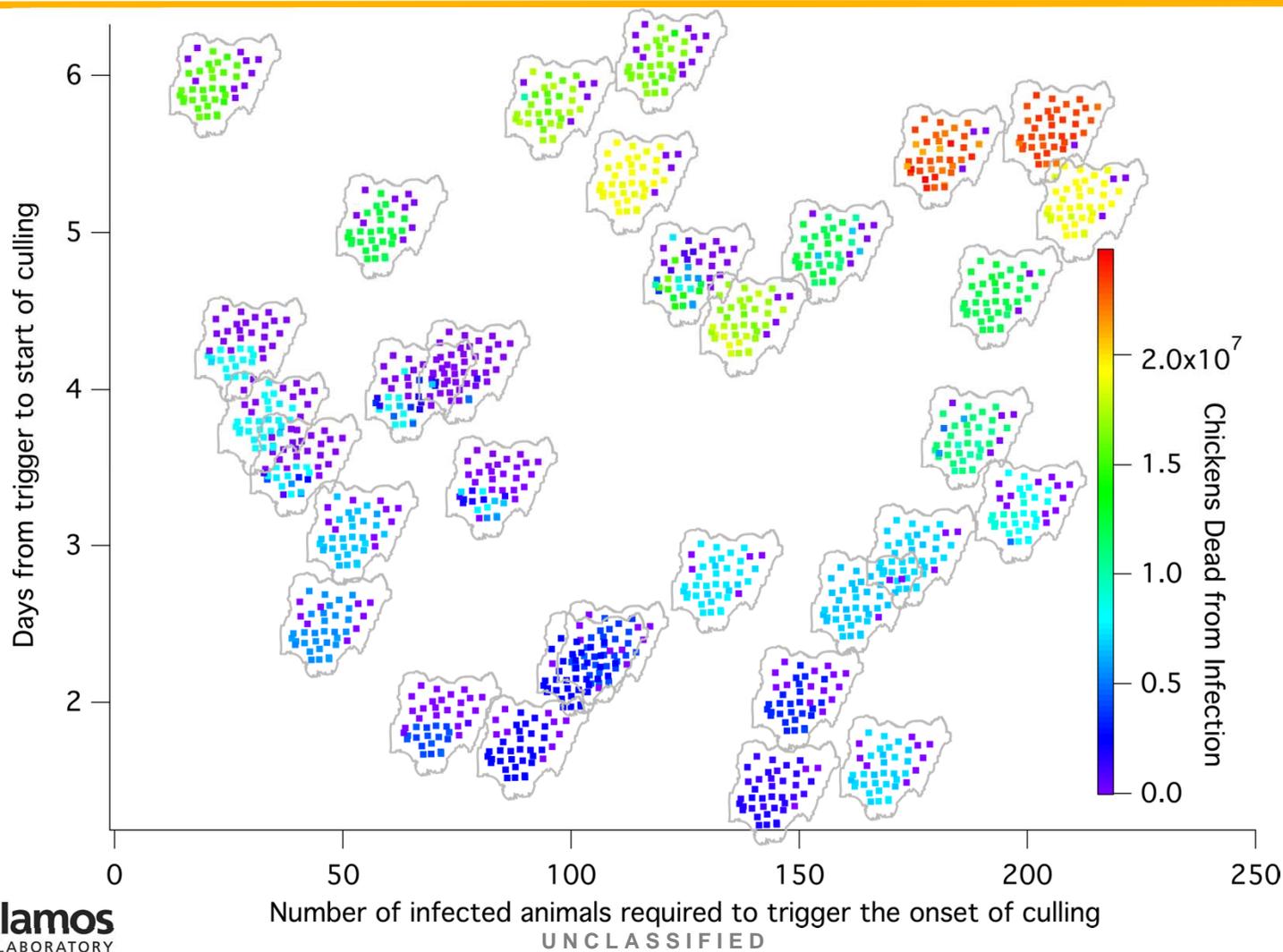


# Regions of Nigeria

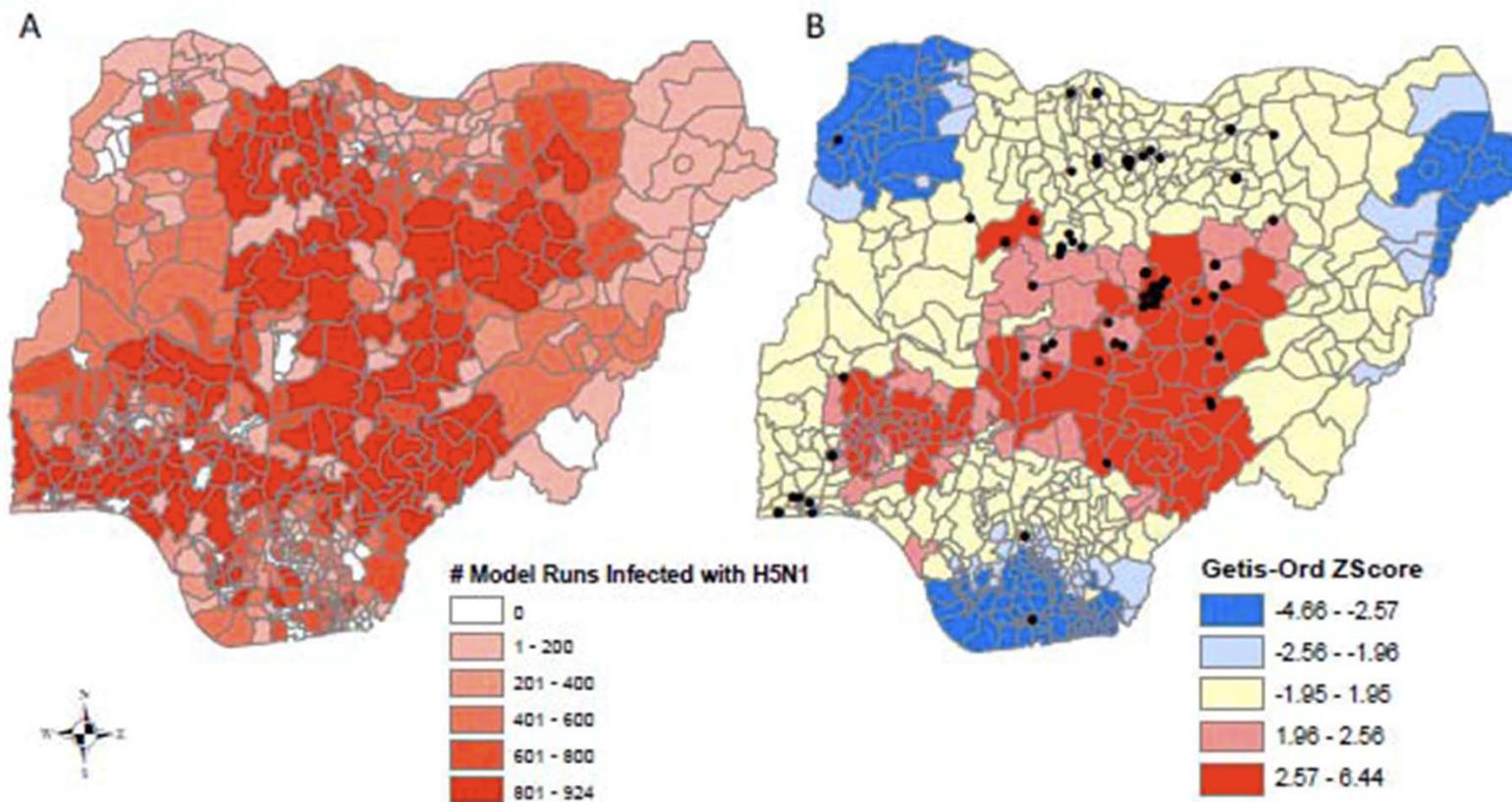
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# Experimental Design Results

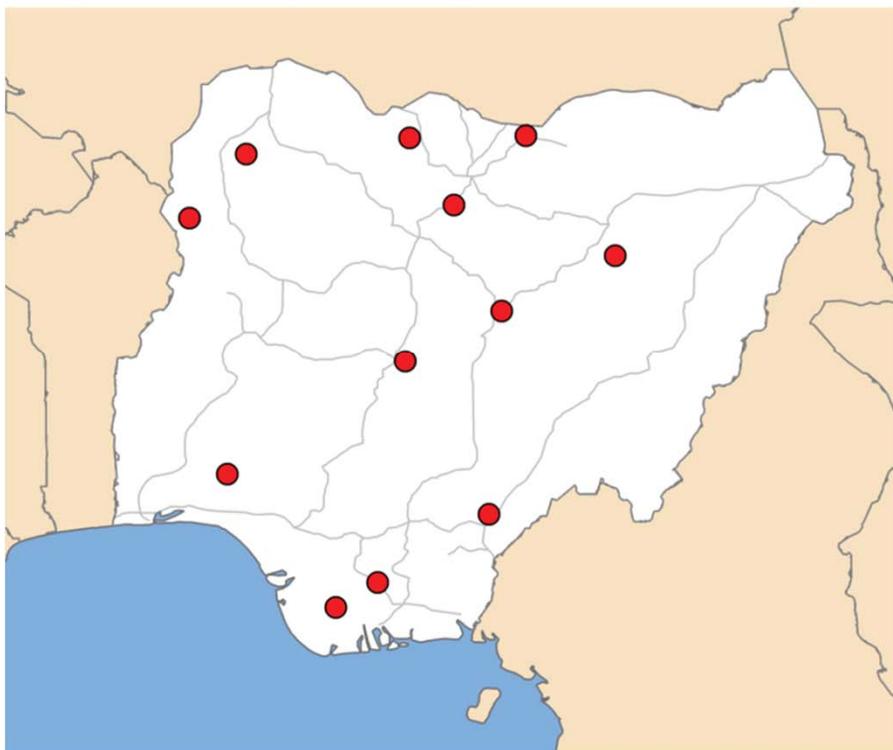


# Simulation Results



# Optimizing for Biosurveillance

a. Optimized for probability of detection

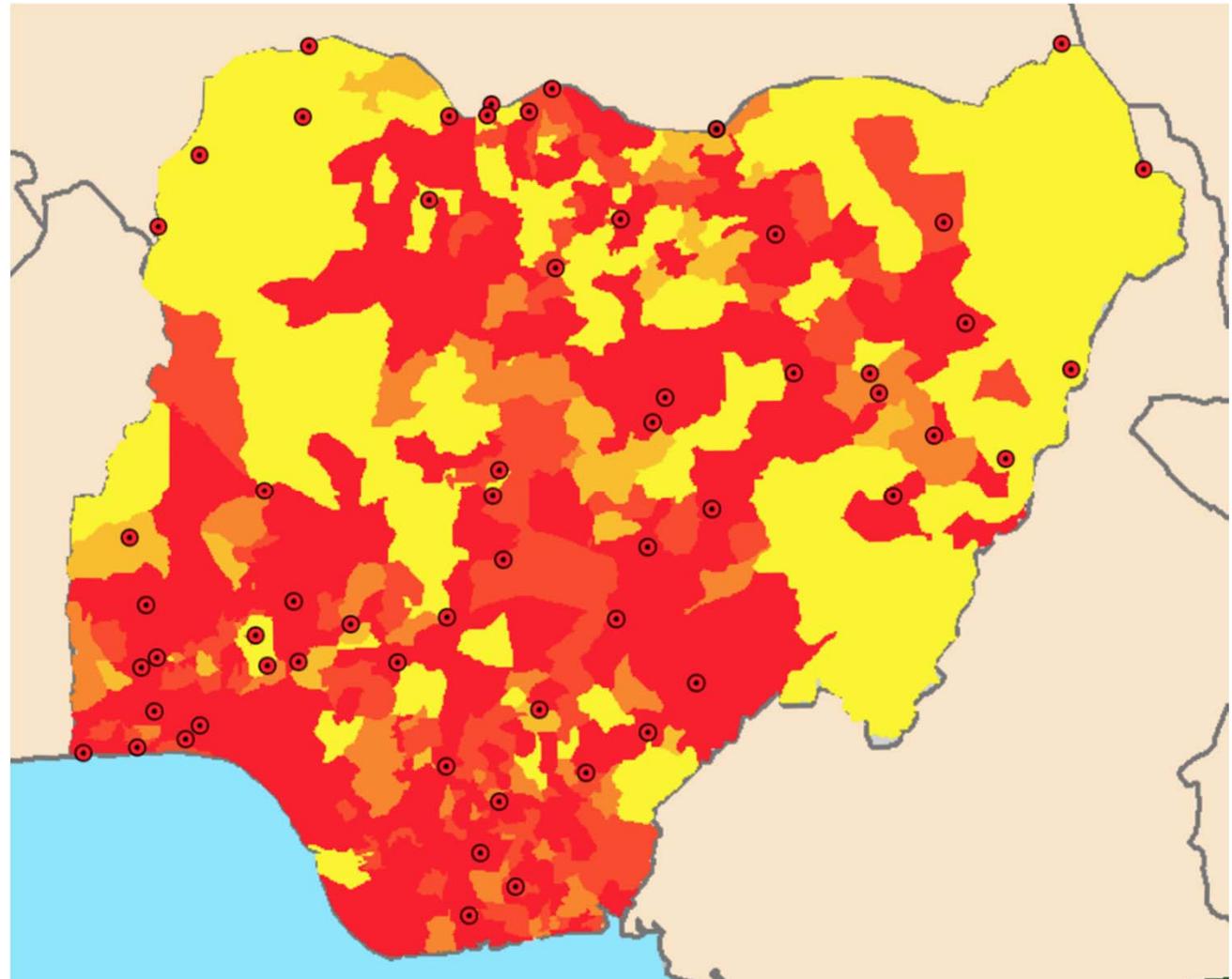


b. Optimized for speed of detection



# Building a Biosurveillance Architecture

- Overall epidemic consequence vs. location of start of epidemic (red indicates higher consequence).
- Markers indicate current surveillance points operated by the Nigerian government.



# Gaps and Needs

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- Incentives for reporting animal infections due to extensive and uncertain economic consequences
- Rapid, real-time genotyping
- High throughput laboratory capabilities
- Making the connection to the facts on the ground more literal and exact
- Spatial-temporal metadata = smart data
- Completion of spatial-temporal analysis



# Acknowledgments

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Mac Brown, Leslie Moore, Dennis Powell, Benjamin McMahon, Montiago LaBute, James Hyman, Ariel Rivas, Mary Greene, Mark Jankowski, Joel Berendzen, and Jason Loeppky.