

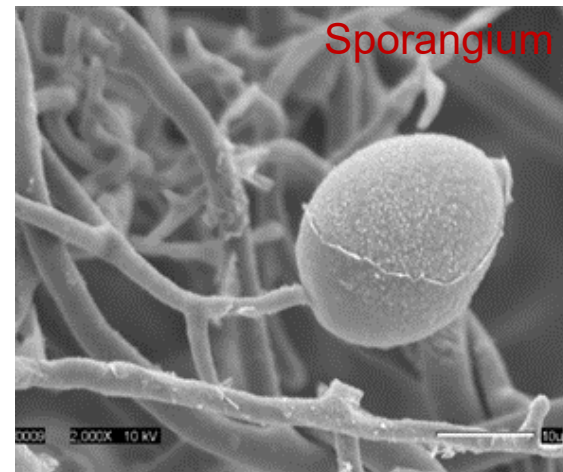
Assessing the Risk of Cucurbit Downy Mildew Outbreak in the Eastern United States

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Cucurbit Downy Mildew (*Pseudoperonospora cubensis*)

- Global distribution
 - World-wide; where cucurbits are found
 - Warm and humid weather
- Status of CDM in the U.S.
 - Mainly in eastern region
 - Resurgence on cucumber since 2004
 - California since 2007
- Control options
 - No resistant cultivars
 - Reliance on fungicides
 - Prediction and forecasting important



Seasonal Spread of Cucurbit Downy Mildew in the Eastern U.S.



- Disease exhibits annual extinction and recolonization cycles
- Determine risk of disease outbreak at landscape level:
 1. Bayesian modeling of time to disease outbreak
 2. Joint modeling of time to disease outbreak and epidemic duration

1. Bayesian Modeling CDM Risk in eastern US

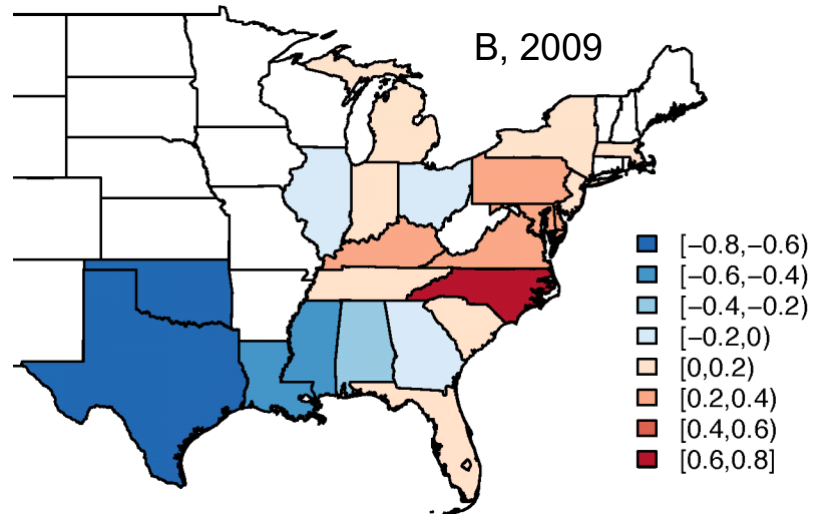
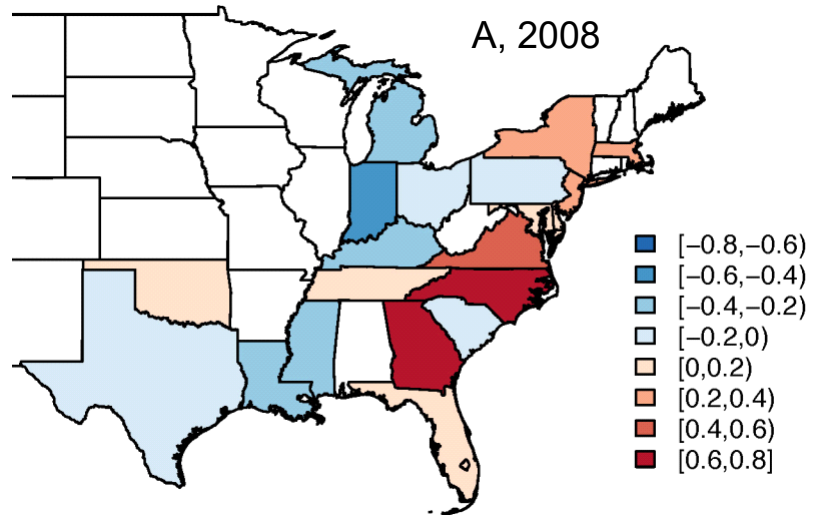
- Hierarchical Bayesian model
 - Combines survival, spatial and Bayesian approaches

$$\left\{ \begin{array}{l} \text{Data model: } \rho_{ij}^{\rho-1} \exp(\boldsymbol{\beta}^T \cdot \mathbf{X}_{ij} + \mathbf{W}_i) \\ \text{Process model: } \mathbf{W} | \lambda \sim \text{CAR}(\lambda); \lambda = 1/\sigma^2 \\ \text{Parameter model: } \boldsymbol{\beta} \rightarrow \text{flat prior } (0 \text{ to } \infty) \\ \rho, \lambda \rightarrow \text{gamma prior } (1, 10^4) \end{array} \right.$$

Year	Model	DIC	Δ DIC
2008	No frailty	2,537	23
	Unstructured	2,520	7
	Structured	2,513	--
2009	No frailty	2,428	18
	Unstructured	2,417	7
	Structured	2,410	--

- Models implemented in WinBUGS using MCMC methods
 - Data (time to disease outbreak) from disease monitoring network
 - Standard survival analysis model (no random effects)
 - Frailty model: structured or unstructured random effects
- Best model selection
 - DIC and Δ DIC
 - Frailty model with structured random effects

Risk of Disease Outbreak: Hierarchical Bayesian Frailty Model



- High risk of disease in North Carolina, Virginia
- Cluster of low disease risk around the Great Lakes in 2008 and 2009
- Cluster of low disease risk in southern states; TX, MS, LA, AL
- Disease control: states in the mid-Atlantic region

2. Joint Modeling of Time to Disease Outbreak and Epidemic Duration

- Rationale: Time to disease outbreak is associated with epidemic duration; Goal: understand the nature of association of these two components on disease risk
- Joint Bayesian hierarchical model with spatial random effects
 - Parametric Weibull model for time to disease outbreak: $h(t_{ji}|x_{1ij}) = \rho t_{ij}^{\rho-1} \exp(x'_{1ij}\beta_1 + \phi_{1i})$
 - Zero-truncated Poisson distribution for epidemic duration:

$$p(y_{ij}|\lambda_{ij}) = \begin{cases} 0, & \text{if } y_{ij} = 0 \\ \frac{\lambda_{ij}^{y_{ij}} \exp(-\lambda_{ij})}{y_{ij}!(1-\exp(-\lambda_{ij}))}, & \text{if } y_{ij} = 1, 2, \dots \end{cases}$$

- Process model: 4 competing model; Spatial: **GMCAR** and **UniCAR**; Non-spatial: **IndNormal** and **MvNorm**)
- Parameter model: prior distributions for all parameters specified
- Best model identified using: DIC, LOOIC

Model Performance and Risk Assessment

- Model performance

- GMCAR had the smallest DIC and LOOIC
- GMCAR selected as process model

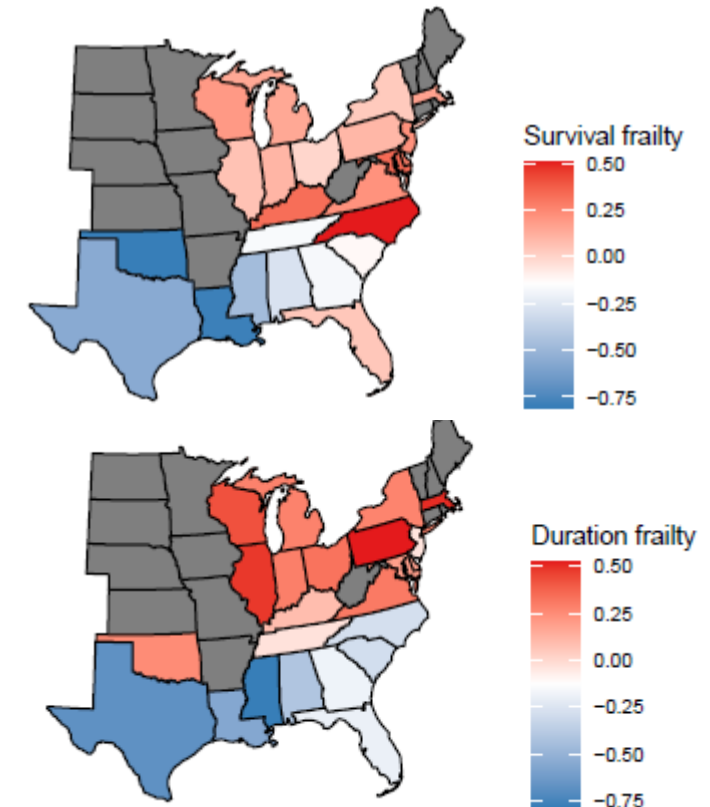
	GMCAR	UniCAR	MvNorm	IndNorm
p_D	33.3	35.6	38.9	38.0
DIC	3677	3678	3678	3679
LOOIC	3756	3760	3762	3766

- Risk of CDM (2009)

- High risk in states along the mid-Atlantic region (NY, PA, NC)
- High risk along the great lakes region (MI, OH)
- Low risk in southwest US (TX, MS, LA)

- Implications for monitoring and control

- Immediate control in high risk states
- Disease monitoring should concentrate in high risk area
- Use network analysis to identify high risk locations



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