

MODELING CHOLERA EPIDEMICS ON HISPANIOLA

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Mentor: Grant Brown, Ph.D.

Acknowledgments

- Grant Brown, Ph.D.
- Gideon Zamba, Ph.D.
- Monica Ahrens
- The ISIB Cohort
- National Heart Lung and Blood Institute (NHLBI) HL131467

Discussion

- Spread of Disease across nations
- Impact of Rainfall
- Impact of Elevation
- Direction of Public Health Resources

Presentation Outline

- Introduction and Cholera Basics
- Compartmental Models
- ABSEIR and Approximate Bayesian Computation
- Two-Location Model
- Full, Provincial Model
- Results
- Discussion
- Acknowledgments
- Citations

Introduction and Cholera Basics

- 2010 Earthquake and subsequent outbreak
- Bacterium, *Vibrio cholerae*, transmission
- Public Health infrastructure
- PAHO



Compartmental Models

Basic SEIR Compartmental Model Diagram



Where:

- S = Susceptible
- E = Exposed
- I = Infectious
- R = Removed

$$S_{t+1} = S_t - E_t^*$$

$$E_{t+1} = E_t + E_t^* - I_t^*$$

$$I_{t+1} = I_t + I_t^* - R_t^*$$

$$R_{t+1} = R_t + R_t^*$$

Other important elements:

$$\beta, \lambda, \gamma, B_{00}$$

CITATIONS

Lekone PE and Finkenstädt, BF (2006): Statistical Inference in a Stochastic Epidemic SEIR Model with Control Intervention: Ebola as a Case Study. *Biometrics* 62:1170-1177.

King et al (2008): Inapparent Infections and cholera dynamics. *Nature* 454, 877-880.

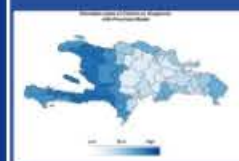
Grant Brown (2016). ABSEIR: Posterior Approximation to Fully Bayesian Spatial SEIR Models using the C++ Actor Framework. R package v 1.2.3.

Results

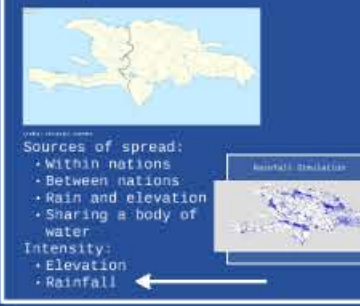
Interpretation	Parameter	Mean	SD	95% LB	95% UB
HTI Intercept	Beta_SE_1	-8.99E+00	1.24E+00	-1.11E+01	-6.40E+00
DR Intercept	Beta_SE_2	-2.93E+00	2.62E-01	-3.41E+00	-2.45E+00
Mean Elev.	Beta_SE_3	-1.45E+00	2.11E-01	-1.86E+00	-1.04E+00
Max Elev.	Beta_SE_4	5.05E-01	7.90E-02	3.55E-01	6.68E-01
Min Elev.	Beta_SE_5	-3.69E+00	7.31E-01	-4.89E+00	-2.30E+00
Elev IQR	Beta_SE_6	8.88E-01	1.83E-01	5.59E-01	1.27E+00
Rainfall	Beta_SE_7	1.63E+00	6.16E-01	3.53E-01	2.68E+00
Rainfall*ElevQR	Beta_SE_8	2.15E+00	1.97E-01	1.76E+00	2.52E+00
Rainfall*minElev	Beta_SE_9	1.95E+00	1.75E+00	-1.93E+00	4.59E+00
DR Contact	rho_1	1.33E-02	3.71E-03	7.42E-03	2.21E-02
HTI Contact	rho_2	2.19E-02	8.85E-03	4.31E-03	3.81E-02
National	rho_3	1.68E-03	8.56E-04	2.65E-04	3.32E-03
WaterBdr	rho_4	7.52E-06	4.89E-06	5.73E-07	1.80E-05
Rain	rho_5	7.16E-03	3.08E-03	1.66E-03	1.28E-02
Rain*water	rho_6	6.25E-03	3.33E-03	5.75E-04	1.34E-02
Latent time	gamma_EI	7.34E+00	5.53E-01	6.31E+00	8.47E+00
Infectious time	gamma_IR	4.91E-01	1.60E-02	4.64E-01	5.24E-01
Prop. Reported	report_fraction	9.61E-01	7.52E-03	9.45E-01	9.75E-01

Model	Terminating Epsilon
Two Location	1.97*10 ⁰
Full Provincial	7.85*10 ⁰

Provincial Visualization



Full, Provincial Model



Two-Location Visualization



Two-Location Model



ABSEIR

```

Spatial Epidemic Modeling
Sampling Parameters
Model Components
Data
Exposure
Distance
Transition
Initial Values
  
```

Approximate Bayesian Computation

- Bayesian method: Rubin ('84)
- Bypass likelihood
- Parameter Priors
- Simulate
 - Compare with Data
 - Evaluate with Distance Metric
- Approximate Posterior with Accepted Simulations

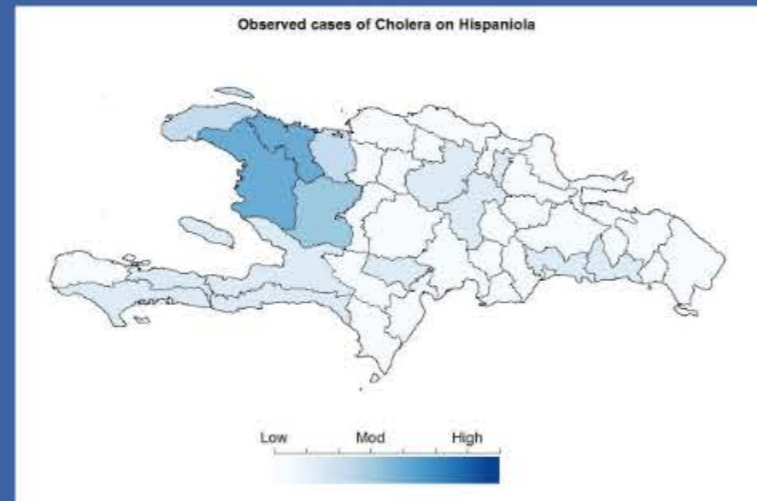
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Introduction and Cholera Basics

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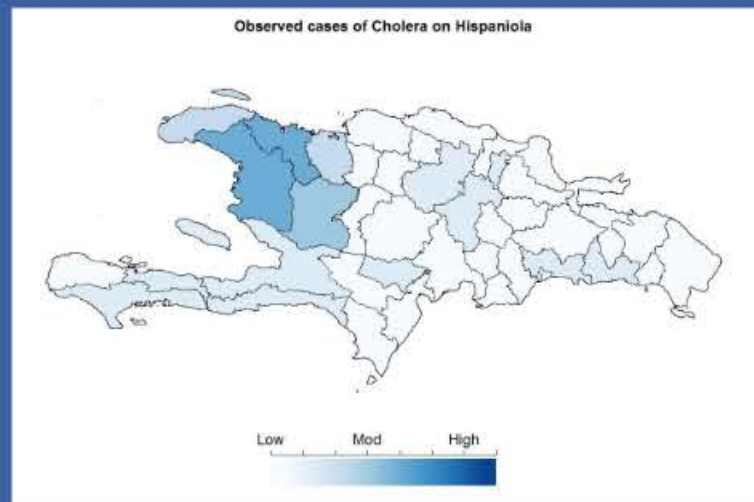
Visualizing the Outbreak



Introduction and Cholera Basics

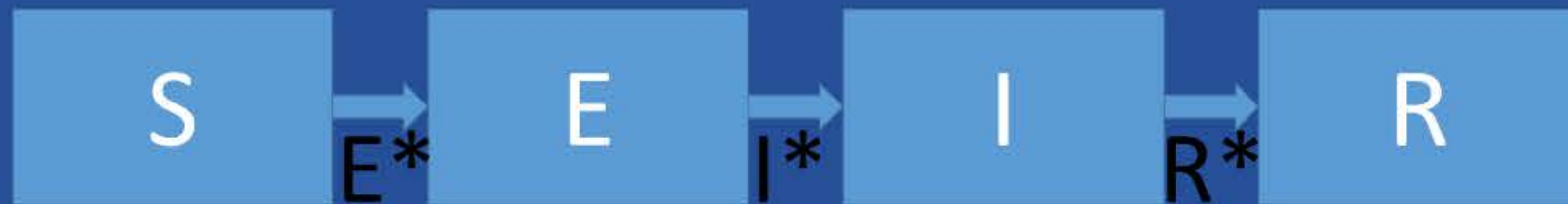
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Visualizing the Outbreak



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$$R_{i+1} = R_i + R_i^*$$

Other important elements:

$$\beta, 1/\gamma, R_0$$



Approximate Bayesian Computation

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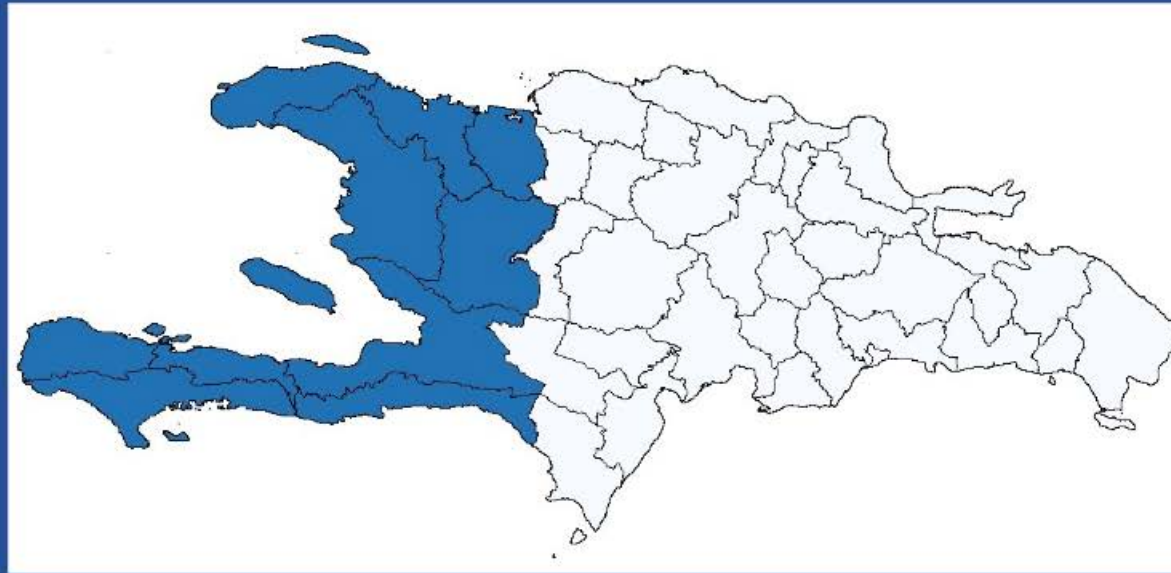
ABSEIR

```
sampling_control = SamplingControl(seed = 123123,  
                                   n_cores = 14,  
                                   algorithm = "Beaumont2009",  
                                   params = list(batch_size = 10000,  
                                                epochs = 1e6,  
                                                max_batches = 500,  
                                                shrinkage=0.99,  
                                                multivariate_perturbation=FALSE,  
                                                keep_compartments=TRUE,  
                                                init_batch_size=250000))  
  
print(system.time(SEIR.results <- spatialSEIRModel(data_model,  
                                                    exposureModel,  
                                                    reinfection_model,  
                                                    distanceModel,  
                                                    transition_priors,  
                                                    initial_values,  
                                                    sampling_control,  
                                                    samples=200,  
                                                    verbose=2)))  
  
save(SEIR.results, file = "laggedModelResults.rda")
```

- Spatial Epidemic Modeling
- Sampling Parameters
- Model Components
 - Data
 - Exposure
 - Distance
 - Transition
 - Initial Values



Two-Location Model



- Contact Between DR and Haiti
- Temporal Basis:
 - Spline with 6 df
 - Annual, Biannual Outbreaks
 - Separate Basis for DR and Haiti



Full, Provincial Model



Credit: Wikimedia Commons

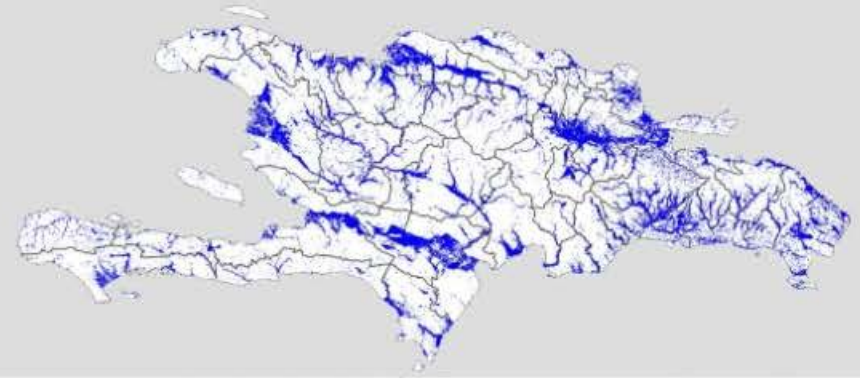
Sources of spread:

- Within nations
- Between nations
- Rain and elevation
- Sharing a body of water

Intensity:

- Elevation
- Rainfall

Rainfall Simulation



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