Effects of Climate Change on Valley Fever: A Markov Model in R

Mathematical Epidemiology Research Group

I. Bibayoff, A. Galindo, R. Genova, M. Maquelin, S. Prioty, M. Reyes, C. Rice, M. Willis C. Zuniga
Faculty Advisor: Omayra Ortega

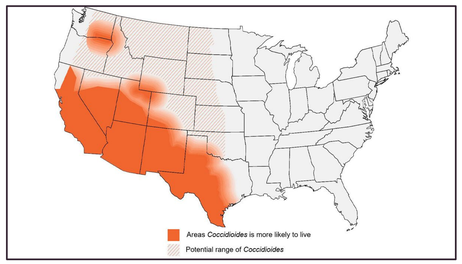
SONOMA STATE UNIVERSITY
MCNAIR SCHOLARS PROGRAM

Background

Valley Fever (coccidiomycosis) is a fungal illness with flu-like symptoms that is endemic to California's central valley and other dry areas in the southwestern United States. As valley fever incidents increase, there is a higher total amount of severe cases. Due to the nature of the fungus, infection rates depend only on environmental factors like climate.

Infection occurs when a victim inhales the spores. Blue-collar workers are some of the most susceptible to Valley Fever. Many areas with large agricultural industries, and even building operations within arid regions of the southwest, have some of the highest conditions for susceptibility to Valley Fever due to exposure to dust and fungi.

We are looking at the way that climate change is affecting the spread of valley fever using a Markov Chain model for Valley Fever to describe the probability of transitioning between different states related to the disease.



Methods

We take our initial Markov Chain models of Valley Fever infection and include aspects of climate that affect Valley Fever the most: temperature and precipitation. So instead of changing the state space from $X_t = S, I, R, D$ we keep the disease compartments the same, but make the transition law at time t,

$$P(X_t + 1 | X_t, T_t, P_t)$$

depend on weather, where T_t is temperature and P_t is precipitation.

- R & RStudio
- Markovchain, PRISM, & CoSMoS R packages

Model

Transition matrix for our model :

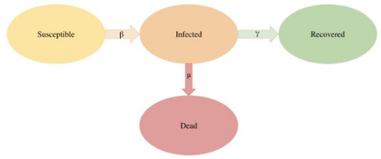


Figure 2: Model 1

$$\begin{bmatrix} 1-\beta & 0 & 0 & 0 \\ \beta & 1-\gamma-\mu & 0 & 0 \\ 0 & \gamma & 1 & 0 \\ 0 & \mu & 0 & 1 \end{bmatrix}$$

Parameters	Meaning	Min	Max
β	Susceptible to Infected	5.23×10^{-5} [5] [8] [20]	2.23×10^{-4} [5]
γ	Infected to Recovered	0.1667 [5]	0.3333 [5]
μ	Infected to Dead	1.62×10^{-4} [8]	4.45×10^{-4} [8]

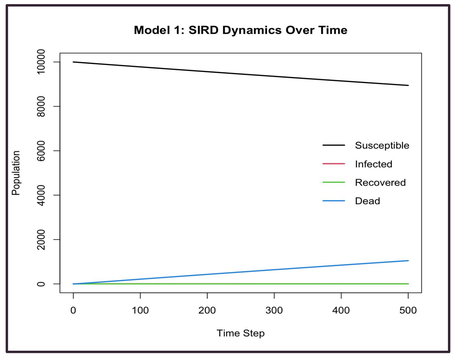
Table 1: Parameters for the 1st model

Model 1 of 3, is our simplest version. We did not include different severities of illness, disseminated versus acute, it is all just "infected."
Our parameters were found by meta analysis, using recently puublised papers to amass different statistics.

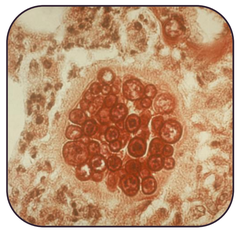
Results

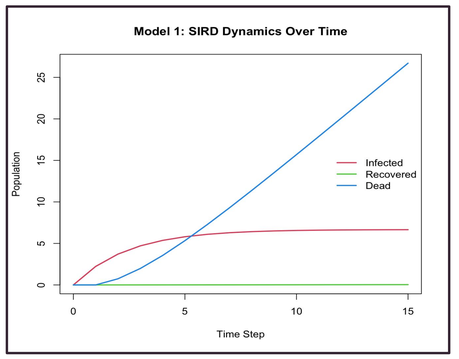
- Simulated three Markov chain formulations of Valley Fever progression and visualized the resulting state distributions over time.
- The resulting trajectories from our R code illustrate how individuals transition through disease states under the specified parameterizations. The trajectories provide a basis for when we compare the structural differences between the models.
- In particular, these simulations highlight how increasing model complexity alters the temporal dynamics of infection, recovery, and disease progression.

Discussion









In this work, we shifted from a standard compartmental epidemic framework into a climate-driven, non-stationary stochastic system. This has meaningful implications for how our results are interpreted scientifically, predictively, and in a policy context.

This will allow for simulations that account for various weather conditions, which could help to provide insight into early warning systems. The additional benefit to the addition of climate driven circumstances as we can gain further insight into what the sources of variation on our model are.

Acknowledgements

We want to thank the SSU Center for Environmental Inquiry (CEI) for their generous funding of our research through the Norwick Fund. We additionally want to thank our many supporters at Sonoma State University's various organizations including: MESA, McNair Scholars, and the Mathematics & Statistics Department.