Comparison Table of Epidemic Models for Spatial Heterogeneity

Anton Antonov,
<u>System Modeling at GitHub/antononcube</u>
2021-03-08

Tasks / Modeling approach	Variables	Spatial structure parameters	Spatial effect modeling mechanism	Additional model features	Model analysis and investigation

Multi-site extension by graph (Antonov, [AA1])	Discrete in space, continuous in time	• Population sizes for each site.
		• Contingency table of traveling patterns between graph nodes.
		• Different at each site:
		  • Death rates
		  • Incubation periods
		  • Infectious periods
		• Model specific choice of population types that travel. (Can travel or are allowed to.)
			• The migrant populations produce new "birth-like" equation terms.
			• The new-comers at a given site become part of site's population.
				• Uses System Dynamics perspective.
				• It is assumed that sites can be become empty.
				• Persons are interchangeable — person's site origin does not matter.
				• Chain-able model-transformations. E.g.
				  1. Modify SEIR with air-travel patterns only of Susceptible and Recovered populations.
				  2. Modify the obtained model with land-travel patterns for all populations.
				• ***Works adequately if the time step is small.*** *(E.g. a day for COVID-19 simulations.)*
					• Demonstrating the algorithm using a:
					  • Trivial graph
					  • Grid graph
					  • Random graph

Multi-patch SEIR (Lloyd & May, [LM1])	Discrete in space, continuous in time	• Population sizes at each patch. • Contact rates between patches. • Universal death rate, average latent disease period, and average infectious period.	• Region-to-region mingling terms are used. • The mingling parameters are given as a matrix of contact rates.	• Simple, yet general approach.	• SEIR model based analysis. • Stability and bifurcation analysis. • Forced seasonalities.
Multi-region mobility incorporation into SIR (Sattenspiel & Dietz, [SD1])	Discrete in space, continuous in time	• Population sizes for each region. • Fractions of travelers for each patch. • Probability to go from patch i to patch j. • Per capita return rate for travelers from patch i at patch j. • A list of matrices for the proportion of contacts in region k between a susceptible from region i and an infective from region j. • Average number of contacts per person for each patch.	• Region-to-region mingling terms are used. • Multiple mingling parameters. (See left cell.)	• Markov chain perspective on traveling. • Travelers do not "forget their home." • No death rate, average latent disease period, and average infectious period are included in the model.	• Taking the model to different extreme cases in order to do mathematical analysis. • SIR model based analysis. • Application to real-life Measles modeling.
By Partial Differential Equations (PDEs), (Kot [MK1], Wu [JW1])	Continuous in space, continuous in time.	• The continuous distribution of the population in space and its growth in time. • Diffusion coefficients population motion. • Relevant death rates, contact rates, incubation period, etc.	• PDEs of reaction-diffusion type.	• Assumes populations migrate according to Fick's laws of diffusion.	• Derivation of the model • Application to real-life Rabies and West Nile virus modeling.

References

[AA1] Anton Antonov, "Scaling of Epidemiology Models with Multi-site Compartments", (2020), SystemModeling at GitHub/antononcube.

[MK1] Kot, M.: Elements of Mathematical Ecology. Cambridge University Press, Cambridge (2001).

[LM1] Lloyd, A., and May, R.M.: Spatial heterogeneity in epidemic models. J. Theor. Biol. 179, 1–11 (1996).

[SD1] Sattenspiel, L. and Dietz, K.: A structured epidemic model incorporating geographic mobility among regions. Math. Bios. 128, 71–91 (1995).

[JW1] Jianhong Wu, "Spatial Structure: Partial Differential Equations Models", in Mathematical Epidemiology, Springer, 2008.