

PDE Group Homework # 13

2.

Both Yellow	Some Yellow	Both Red
“We leveraged a compartmental SEIRD model that incorporates the spatial spread of the disease with inhomogeneous diffusion terms” (pg 2)	Assuming recovered patients are immune	Brownian motion
$n(x,t) = s(x,t)+e(x,t)+i(x,t)+r(x,t)$	Birth rate alpha	Allee effect (depensation)
Homogeneous Neumann boundary conditions	We set $\alpha=0$ and $mieu=0$	Asymptomatic recovery rate, contact rate, infected mortality rate, different diffusion parameters
Symptomatic contact rate	“Spatial movement over a large population is described by an inhomogeneous random walk” (though we considered a homogeneous random walk, I think)	Gaussian circular functions
Parameter estimation is difficult/not viable...but we can measure death rate relatively easily	We assume B_i and B_e to be equal (this makes it equivalent to our case)	Finite-element spatial discretization
Fitting model to a system of exclusively time-dependent ODEs		Backward-Euler method for time integration
Errors in mortality data could be due to		Assessing goodness through R^2 and root

unknown transmission rates		mean squared error (RMSE)
“Importance of qualitative agreement to test novel modeling approaches”		Recursive simulations to match data, use the R^2 coefficient and the RMSE to assess the goodness of fit.
Despite simplifications in model, model still shows “good qualitative agreement with reality”		Model the escalation of lockdown restrictions
		Distinction between symptomatic and asymptomatic individuals
		Maintenance of restrictions vs relaxation of the lockdown everywhere incorporated into model
		Impact of geographical features

3. Pick three of the red items highlighted that seem interesting to your group, and look those up. As your answer, for this question, write what you learned about those three things. Depending on the items you picked, you may not fully understand them, even after reading about them, which is OK. Please cite sources you used to research your three red items.

Allee Effect:

- Usually defined in terms of biological reproduction. A textbook online we found described the Allee effect as “occur[ing] when dwindling population levels lead, in turn, to increasingly diminished reproduction, despite the lack of intraspecific competition” (Salisbury 61). With respect to COVID, this means that the disease spreads more slowly in sparsely populated areas. When applying the Allee effect to an actual biological model it is important to find the critical threshold value, below which we see the population (or COVID cases) decaying. Allee effects are widely varied based on the population under consideration. They can be based on non-cooperative behaviors or cooperative behavior; they are also either component (single component of a species, such as offspring survival) or demographic (overall population) (Angulo et al).

Assessing Goodness through R² and Root Mean Squared Error (RMSE):

- Since this model is trying both to simulate existing data and to predict the future trajectory of the data, part of determining the goodness/accuracy of the model is seeing how well the existing data fits with the data predicted by the model. Thus, both R-squared and RMSE are ways of assessing this fit.
- Both are dependent on two sums of squares: the Sum of Squares Total (SST)—which “measures how far the data are from the mean”—and the Sum of Squares Error (SSE), which “measures how far the data are from the model’s predicted values” (Grace-Martin). Grace-Martin writes that “different combinations of these two values provide different information about how the regression model compares to the mean model.”
- R-squared is given by the difference of SST and SSE divided by SST $\rightarrow |SST-SSE|/SST$. The difference of SST and SSE tells us “the improvement in prediction from the regression model” in comparison to the data. The scale is from zero to one, where one indicates a perfect fit and zero indicates that “the proposed model does not improve prediction.”
- RMSE is the “square root of the variance of the residuals” and indicates “how close the observed data points are to the model’s predicted values. Whereas R-squared is a relative measure of fit, RMSE is an absolute measure of fit... RMSE can be interpreted as the standard deviation of the unexplained variance.” If RMSE is smaller, the fit is better. Additionally, if the model’s central purpose is prediction, RMSE is “the most important criterion.”

Gaussian Circular Functions:

- In one dimension, the Gaussian function is the [probability density function](#) of the [normal distribution](#). The circular Gaussian function is this in two dimensions for uncorrelated variables x and y . The values of the circular distribution are angles between 0 and 2π most commonly. These distributions can be continuous or discrete.
- $$f(x, y) = \frac{1}{2\pi\sigma^2} e^{-[(x-\mu_x)^2 + (y-\mu_y)^2]/2\sigma^2}.$$
- Circular Gaussian functions have equal standard deviation for each variable, as opposed to elliptic Gaussian distribution.
- The paper used Gaussian circular functions to find different population numbers, centered at the latitude and longitudinal coordinates (x and y in the distribution). This makes sense because we want a range of spatial population values across the distribution. In other words, we don’t just want to randomly pick initial subpopulation locations, we instead want them to be placed on an actual distribution that we can analyze across the entire population.

4. Answer the following questions about your paper. Each response should be a few sentences.

(a) What research question is being addressed?

- How can SEIRD mathematical models based on PDEs be used to describe the spatio-temporal spread of the COVID-19 pandemic, and how can this model based on Italy be used to model the spread in other global regions?

(b) What were the methods/tools used to address the research question?

- They use a “compartmental SEIRD model that incorporates the spatial spread of the disease with inhomogeneous diffusion terms” (2). The diffusion terms describe the movement of people and vary depending on population density.
- The model includes variables for the total living population (sum of susceptible, exposed, infected, and recovered), the birth rate, incubation period, and asymptomatic/symptomatic contact rates.
- They use homogeneous neumann boundary conditions to mimic isolation of the given region (3).
- They iteratively refine recursive simulations of the 5 main equations (rate of change of each subpopulation) to match the data.
- Diffusion parameters based on population density

(c) What is one main finding of the paper?

One important finding of the paper is that lockdown measures should be put in place for longer periods of time in areas that are high-population, high-density in order to control the spread of COVID-19. This is a significant finding, as many areas and their respective leaders have conflicting ideas on implementing restrictions.

(d) How the paper is related to the SIR model with diffusion that we studied in our class (for the fox rabies case study). What is the same, what is different ?

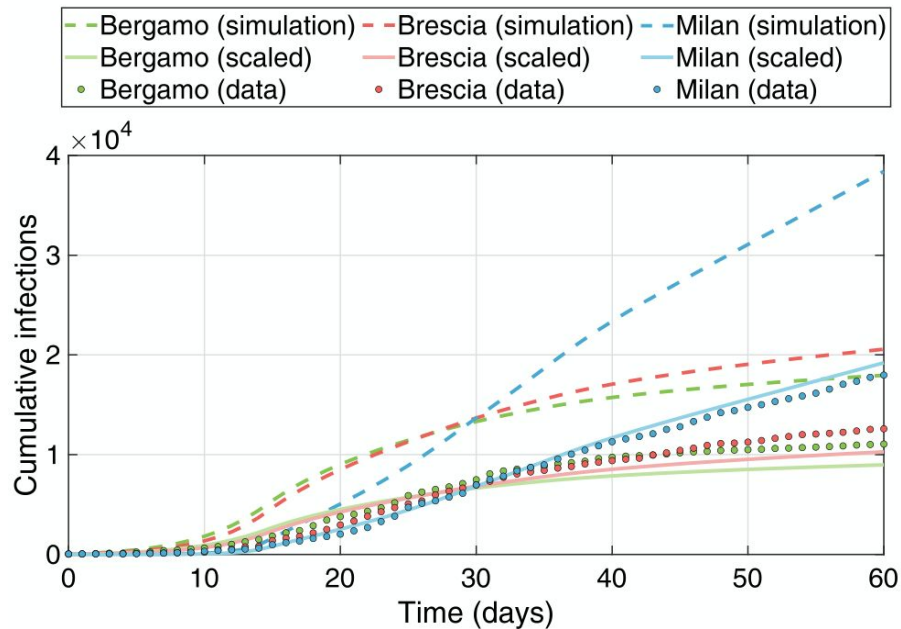
Where we considered only S (susceptible individuals), I (infected individuals), and R (recovered or dead individuals), this model also adds E (exposed individuals) and distinguishes recovered and dead individuals into two variables, R and D. They use multiple inhomogeneous diffusion parameters, while we had only one homogeneous diffusion parameter. They had a diffusion parameter for each population group, while we assumed that the movement of all foxes was random (single diffusion parameter). These diffusion terms were population-dependent instead of being the same across the entire region.

They also added many different parameters, besides just the changes concerning diffusion, to include in the initial PDEs. They added a birth rate, a death rate (not due to COVID-19), the inverse of the incubation period (as we didn't consider incubation in our model!), and the asymptomatic recovery rate (as we didn't consider asymptomatic individuals!). An important difference is that in our model, we assumed that once a fox was infected they died.

In order to match the model to the data set, the paper ran simulations recursively to refine the parameters. We did not even begin to do this in class, as it took a whole video to just analyze the contagion parameter!

This paper also approached the idea of implementing varying degrees of restrictions in order to see how they would impact the number of infections. Foxes probably wouldn't listen to government mandates!

(e) Include at least one key graph from the paper, and describe what is going in the graph.



This graph shows the number of infections over time in three different regions in Italy, starting from day 0 → February 26, 2020 to day 60 → April 26, 2020. The dotted lines represent the reported infections, the dashed lines represent the data predicted by the simulation, and the solid line represents the reported infections scaled to “match the order of magnitude of the reported infectious data.” This graph is highly significant, as it clearly shows the differences between the simulated model and the actual data to suggest visually the accuracy of the model.

Sources:

- Alexander Salisbury, “MATHEMATICAL MODELS IN POPULATION DYNAMICS”, Division of Natural Sciences New College of Florida, 2011 <https://core.ac.uk/download/pdf/141995076.pdf>
- Angulo et al, “Review: Allee effects in social species,” Journal of Animal Ecology, 2017, <https://besjournals.onlinelibrary.wiley.com/doi/full/10.1111/1365-2656.12759>

- Karen Grace-Martin, “Assessing the Fit of Regression Models,” *The Analysis Factor*,
”<https://www.theanalysisfactor.com/assessing-the-fit-of-regression-models/>
- <https://archive.lib.msu.edu/crcmath/math/math/g/g087.htm>
- <https://mathworld.wolfram.com/GaussianFunction.html>