

# Informing Policy via Dynamic Models: Cholera in Haiti [1]

Jesse Wheeler   Edward Ionides (Advisor)

2023-03-07

# Advantages of Statistical Modeling

- Nonlinear-dynamic statistical models have proven to be a useful tool for modeling infectious disease outbreaks (TODO: CITE)
- Most common examples are SIR models and their various extensions.
- This class of models enable the modeling of scientifically meaningful latent variables, prediction of the future state of the outbreak, and modeling the potential effects of interventions (such as vaccinations) [2]
- Despite their utility, there exist many cautionary warnings against the use of these types of models [3–6].
- Current standards for model based inference do not adequately address these valid concerns.

# Topics

We try to address common shortcomings in non-linear dynamic modeling for policy inference. Topics we consider include:

- The use of *benchmarks*
- Fitting meta-population models
- Reproducibility and *Extendability*

We begin by providing a brief description of the class of models being considered and the methods used to calibrate the models to observed incidence counts.

# Partially Observed Markov Processes

- The models we focus on are partially observed Markov process (POMP) models.

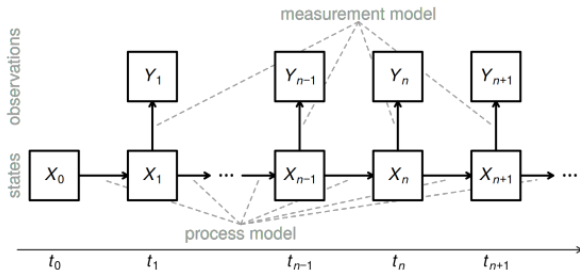


Figure 1: Credit: [7]

# POMP Models

- 1 Parameter vector  $\theta$  that indexes the model
- 2 One step transition density:  $f_{X_n|X_{n-1}}(x_n|x_{n-1}; \theta)$ .
- 3 Measurement Model:  $f_{Y_n|X_n}(y_n|x_n; \theta)$ .
- 4 Initial density:  $f_{X_0}(x_0; \theta)$

We limit ourselves to the case when we can only simulate from (2), and call this the *plug-and-play* property.

This framework allows us to consider arbitrary dynamic models; our limitations are our scientific creativity and the information available in the data.

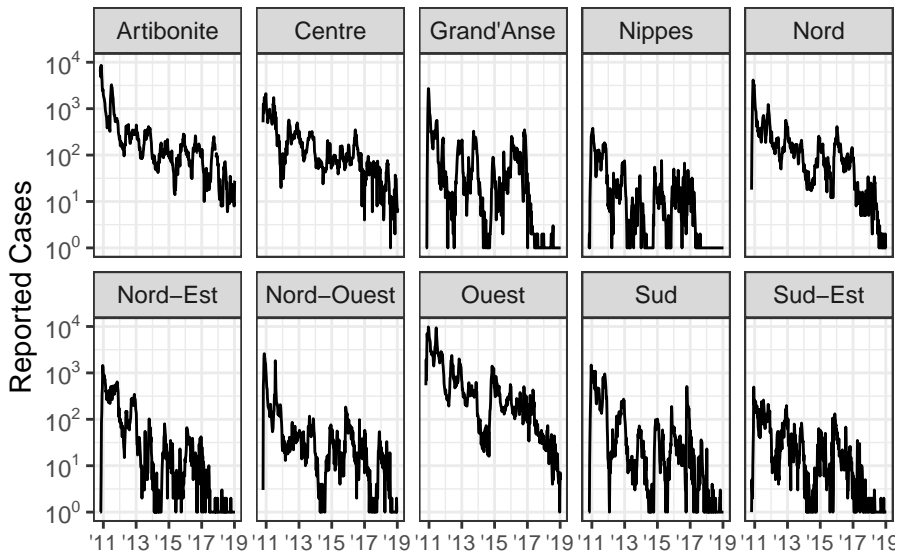
# Cholera in Haiti

- We consider the 2010-2019 cholera outbreak in Haiti.
- Cholera was introduced to Haiti in 2010 following the devastating earthquake of the same year.
- Although some new cases have been detected, there were no recorded cholera cases in Haiti between February, 2019 and September 2022 [8].

# Data



# Department Specific Data





# Models

- We build on the study by Lee et. al (2020), in which expert teams independently built non-linear models to describe cholera dynamics.

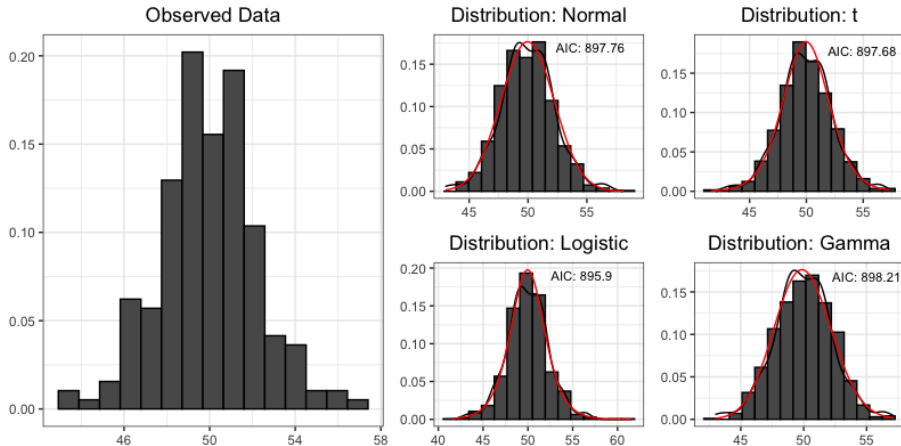
	Model 1	Model 2	Model 3
Type	Stochastic	Deterministic	Stochastic
Spatial Model	No	Yes	Yes
Structure	SEIAR	SEIARW	SIARW
Fitting Method	IF2 [9]	Trajectory Matching	IBPF [10]

- The inability of the original models to predict the long absence of cases (2019-2022) has led to some discussion [11–14].

# Common workflow

- In our literature review of papers that model cholera in Haiti, nearly all papers had a workflow similar to the following:
  - Propose one (or more) models for the disease system
  - Calibrate model parameters and pick final model based on some criteria (visually, posterior predictive checks, AIC, etc.)
  - Use final model to make inference on the system and make policy suggestions.
- Missing from this common workflow are comparisons to models outside of the paper and quantitative descriptions on the goodness-of-fit.
- The primary form of model validation is often visual comparisons to observed data.

# Example: Common Workflow



## Example: Common Workflow

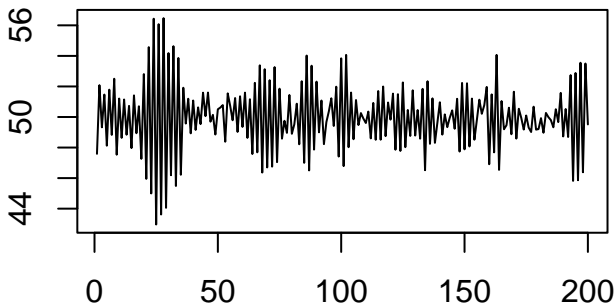
Using the common workflow, we may pick the Logistic model as a valid description of our data and use this model to make inference on the data.

Unfortunately, none of the proposed models are a good description of the data, and each provides a relatively weak prediction of future observations.

Each model is missing an important feature of the data: time dependence between observations.

## Example: Continued...

An ARMA(1, 0) model has AIC value 541.23 (compared to the AIC of the logistic model: 895.5).



# Benchmarking

- Comparisons across models only informs us about the relative goodness-of-fit of each model.
- Visual comparisons can be misleading and cross-validation is not a viable approach to validating dynamic models.
- To calibrate relative measures of fit, it is useful to compare against a model with a well-understood statistical ability to fit to data. We call such a model a *benchmark*. In other areas, this could include linear / logistic regression or even an iid model.
- A log-linear Gaussian ARMA model makes a good benchmark for epidemiological models [15].
- We compare to a log-ARMA model using log-likelihoods due to its statistical properties.

# Benchmarking (continued...)

Some additional considerations for benchmarking:

- Not every model needs to beat a benchmark: suitable benchmarks are typically designed to maximize their predictive ability, whereas POMP models provide a valuable mechanistic description of the system in question.
- Benchmarks can be beneficial when developing models at differing spatial scales (where direct comparison between models is meaningless) by comparing models to their respective benchmarks and assessing their respective advantages and shortcomings.

	Model 1 (p)	Model 2 (p)	Model 3 (p)
Wheeler et al	-2731.3 (15)	-21957.3 (6)	-17850.4 (35)
Lee et al	-3030.9 (20)	-29367.4 (6)	-31840.8 (29)
Log-ARMA(2,1)	-2803.7 (4)	-18027.0 (40)	-18027.0 (40)

## Section 1

# Model Fitting



# Models 1 and 2

- Model 2 is deterministic and consequently the easiest to fit. We did simple trajectory matching using the spatPomp package in R.
- Model 1 is stochastic, spatially aggregated. We used the iterated filtering method to estimate model parameters [9].
- Iterated filtering is a likelihood based approach to estimating model parameters for a plug-and-play POMP model.
- Iterated filtering was originally used to fit Model 3 [2], which is both stochastic and has a meta-population structure.

# Model 3

- IF is based on particle filters (PF) [16] and scales poorly to meta-population models.
- Rebeschini and Van Handel [17] proposed the block particle filter (BPF) and provided some theoretical support for many scenarios.
- Recently developed iterated block particle filters (IBPF) [10] build on the BPF algorithm and it has similar theoretical properties [18].
- We use the IBPF to fit Model 3 to the spatially explicit department data.

# Reproducibility and Extendability

- Reproducibility implies that the same results can be obtained at a later date.
- In statistics, this often means setting a random seed and providing your data and code along with your submission.
- Large projects, however, may make code hard to read or difficult for someone else to run.
- A higher standard of reproducibility is that someone who was not directly involved in your initial project should be able to run and understand your code with limited effort.
- This higher standard is particularly difficult given potential updates to software over time.
- *Extendability* is the idea that it should not be excessively burdensome for someone else to try a small modification to your analysis (such as a model modification or a change to a figure).
- Scientific results are only trustworthy to the extent that they can be critically questioned, and an extendable analysis should facilitate such

# Tools

- The use of *dynamic documents*, like Sweave or knitr, which allow for the integration of  $\text{\LaTeX}$  and the code used to generate results.
- Virtual environments can be used so that the same version of R / Python and each of the packages used during the analysis can be loaded and used at a later date.
- R packages and Python libraries can also be built in the context of a data analysis project. This can be useful even if the only purpose of the package is for the problem at hand, since the package can contain data, code, and documentation.

# References I

- [1] WHEELER, J., ROSENGART, A., ZHUOXUN, J., TAN, K., TREUTLE, N. and IONIDES, E. L. (Submitted, 2023). Informing policy via dynamic models: Cholera in Haiti. *arXiv:2301.08979*.
- [2] LEE, E. C., CHAO, D. L., LEMAITRE, J. C., MATRAJT, L., PASETTO, D., PEREZ-SAEZ, J., FINGER, F., RINALDO, A., SUGIMOTO, J. D., HALLO-RAN, M. E., LONGINI, I. M., TERNIER, R., VISSIERES, K., AZMAN, A. S., LESSLER, J. and IVERS, L. C. (2020). Achieving coordinated national immunity and cholera elimination in Haiti through vaccination: A modelling study. *The Lancet Global Health* **8** e1081–9.
- [3] BEHREND, M.-G. A. H., Matthew R. AND Basáñez. (2020). Modelling for policy: The five principles of the neglected tropical diseases modelling consortium. *PLOS Neglected Tropical Diseases* **14** 1–17.
- [4] SALTELLI, A., BAMMER, G., BRUNO, I., CHARTERS, E., DI FIORE, M., DIDIER, E., NELSON ESPELAND, W., KAY, J., LO PIANO, S., MAYO, D., et al. (2020). Five ways to ensure that models serve society: A manifesto.

# References II

- [5] IOANNIDIS, J. P., CRIPPS, S. and TANNER, M. A. (2020). Forecasting for COVID-19 has failed. *International Journal of Forecasting*.
- [6] GANUSOV, V. V. (2016). Strong inference in mathematical modeling: A method for robust science in the twenty-first century. *Frontiers in Microbiology* **7** 1131.
- [7] KING, I., A. (2022). Short course on simulation-based inference for epidemiological dynamics. *Summer Institute in Statistics and Modeling in Infectious Diseases (SISMID)*.
- [8] TREVISIN, C., LEMAITRE, J. C., MARI, L., PASETTO, D., GATTO, M. and RINALDO, A. (2022). Epidemicity of cholera spread and the fate of infection control measures. *Journal of the Royal Society Interface* **19** 20210844.
- [9] IONIDES, E. L., NGUYEN, D., ATCHADÉ, Y., STOEVI, S. and KING, A. A. (2015). Inference for dynamic and latent variable models via iterated, perturbed Bayes maps. *pnas* **112** 719--724.

# References III

- [10] IONIDES, E. L., NING, N. and WHEELER, J. (2022). An iterated block particle filter for inference on coupled dynamic systems with shared and unit-specific parameters.
- [11] FRANCOIS, J. (2020). Cholera remains a public health threat in haiti. *The Lancet Global Health* **8** e984.
- [12] REBAUDET, S., GAUDART, J. and PIARROUX, R. (2020). Cholera in haiti. *The Lancet global health* **8** e1468.
- [13] HENRYS, J. H., LEREBOURS, G., ACHILLE, M. A., MOISE, K. and RAC-CURT, C. (2020). Cholera in haiti. *The Lancet Global Health* **8** e1469.
- [14] LEE, E. C., TERNIER, R., LESSLER, J., AZMAN, A. S. and IVERS, L. C. (2020). Cholera in haiti—authors' reply. *The Lancet Global Health* **8** e1470–1.
- [15] HE, D., IONIDES, E. L. and KING, A. A. (2010). Plug-and-play inference for disease dynamics: Measles in large and small towns as a case study. *jsrj* **7** 271–83.

## References IV

- [16] ARULAMPALAM, M. S., MASKELL, S., GORDON, N. and CLAPP, T. (2002). A tutorial on particle filters for online nonlinear, non-Gaussian Bayesian tracking. *tsp* **50** 174–88.
- [17] REBESCHINI, P. and HANDEL, R. van. (2015). Can local particle filters beat the curse of dimensionality? *The Annals of Applied Probability* **25** 2809–66.
- [18] NING, N. and IONIDES, E. L. (2021). Iterated block particle filter for high-dimensional parameter learning: Beating the curse of dimensionality.
- [19] GENTLEMAN, R. and TEMPLE LANG, D. (2007). Statistical analyses and reproducible research. *Journal of Computational and Graphical Statistics* **16** 1–23.