HMS 581 Final Project

Modeling Measles in New York & Vermont

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Abstract. We model the spread of the measles pathogen in New York and Vermont from **START_DATE** to **END_DATE** using an SIR model. Our model has been augmented from a basic SIR model to incorporate annual seasonality, births and deaths, and a multi-year seasonality term for the strength of the strain of the pathogen. To optimize and fit our model, we adapted to python, the R implementation of particle MCMC provided to us.

1. Introduction and Model Augmentations

The standard SIR model tracks the portion of or total number of people from the population which are

1.1. Seasonality.

1.2. Birth Deaths.

1.3. Pathogen Strength (Multi-year oscilations).

2. Model Fitting and Results

TODO: Sumarize pMCMC and present plots

3. Conclusion

TODO: summarize, discuss possible future work

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Appendix A. Best Fit Statistics

TODO: make a table of best fit parameters

Appendix B. Code

TODO: Link to the github page with the code