

Marissa Renardy

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EDUCATION

The Ohio State University

PhD, Mathematics

May 2018 | Columbus, OH

Virginia Tech

BS/MS, Mathematics

May 2013 | Blacksburg, VA

SELECTED PUBLICATIONS

- M Renardy et al. Global sensitivity analysis of biological multi-scale models. *Current Opinion in Biomedical Engineering*. 2019; 11: 109–116.
- M Renardy et al. Data-driven model validation across dimensions. *Bulletin of Mathematical Biology*. 2019; 81(6): 1853–1866.
- M Renardy & D Kirschner. Evaluating vaccination strategies for tuberculosis in endemic and non-endemic settings. *Journal of Theoretical Biology*. 2019; 469: 1–11.
- J Gallaher et al. Methods for determining key components in a mathematical model for tumor-immune dynamics in multiple myeloma. *Journal of Theoretical Biology*. 2018; 458: 31–46.
- M Renardy et al. Parameter uncertainty quantification using surrogate models applied to a spatial model of yeast mating polarization. *PLoS Computational Biology*. 2018; 14(5): e1006181.

OBJECTIVE

I am seeking part-time consulting work as a mathematical modeler and/or data analyst.

ACADEMIC APPOINTMENTS

May 2018 – present Postdoctoral Research Fellow

Kirschner Lab, University of Michigan, Ann Arbor, MI

SKILLS

- Mathematical and computational modeling
- Parameter identifiability
- Parameter sensitivity
- Parameter estimation
- Data analysis
- Ordinary differential equations
- Partial differential equations
- Agent-based modeling
- MATLAB
- R

RESEARCH

Epidemiology of tuberculosis and COVID-19

I have combined a network modeling framework with synthetic population datasets to realistically model disease spread at the county level. I am currently applying this framework to study tuberculosis (TB) in Arkansas and to study COVID-19 dynamics in Washtenaw County, MI. I have also developed and analyzed age-structured PDE models to study TB at the national level for the United States and Cambodia. We utilized this model to evaluate and optimize age-targeted vaccination strategies for theoretical pre- and post-exposure vaccines.

Data analysis of tuberculosis granulomas

I applied data analysis methods including machine learning, correlation analysis, and topological data analysis to understand and classify tuberculosis granulomas based on their temporal and spatial characteristics. I applied these analyses to a database of simulated granulomas as well as to experimental immunohistochemistry (IHC) images of granulomas in non-human primates.

Tumor-immune interactions in multiple myeloma

I worked as part of an interdisciplinary team of mathematicians, clinicians, and immunologists worked to build and parameterize a model of tumor-immune interactions in multiple myeloma. My primary role in this work was to apply parameter sensitivity analysis to help identify the key components of the model, which could potentially serve as future treatment targets.

Parameter uncertainty quantification

I have applied parameter sensitivity and identifiability analysis in various contexts, ranging from cell biology to within-host disease dynamics to epidemiology. Recently, I have been developing a framework to perform structural identifiability analysis for PDE models.

LEADERSHIP ROLES

- Society for Mathematical Biology, *Co-Chair of Membership* (2019 – present)
- Association for Women in Mathematics, *Student Chapter Founder and President* (2015 – 2018)