

Pepperdine University
Pepperdine Digital Commons

Summer Undergraduate Research in Biology Program

Seaver College

Summer 7-21-2022

Modeling How Tamiflu Treatment Affects the Immune Response to Influenza in PhysiCell

Melanie Sadecki Drake University

Courtney Davis Pepperdine University

Follow this and additional works at: https://digitalcommons.pepperdine.edu/surb

Recommended Citation

Sadecki, Melanie and Davis, Courtney, "Modeling How Tamiflu Treatment Affects the Immune Response to Influenza in PhysiCell" (2022). Pepperdine University, *Summer Undergraduate Research in Biology Program.* Paper 14.

https://digitalcommons.pepperdine.edu/surb/14

This Research Poster is brought to you for free and open access by the Seaver College at Pepperdine Digital Commons. It has been accepted for inclusion in Summer Undergraduate Research in Biology Program by an authorized administrator of Pepperdine Digital Commons. For more information, please contact bailey.berry@pepperdine.edu.

Response to Influenza in PhysiCell

OP

peripheral





Modeling How Tamiflu Treatment Affects the Immune Melanie Sadecki, Drake University and Mentor: Dr. Courtney Davis, Pepperdine University

Introduction

Influenza presents a major public health issue, and complications result in about 114,000 hospitalizations and 20,000 deaths each year in the U.S. [1]. The best way to avoid serious flu complications is to get the annual flu vaccine. Once infected, treatments are limited and include antiviral drugs like Tamiflu (oseltamivir phosphate). Tamiflu inhibits neuraminidase to prevent viral secretion by infected cells.

This study aims to adapt a PhysiCell computational model of the immune response to influenza within the body to investigate the effects of antiviral treatment on various immune/disease metrics. PhysiCell is a multiscale agentbased model that tracks both viral replication inside cells and individual immune cell interactions within lung tissue. This project adds new treatment functionality to the PhysiCell Tissue Immune Submodel and allows for investigation of the behavior of neuraminidase inhibition on multiple aspects of the immune response. Through modeling we can gain crucial insights to better understand the dynamics of immune-drug interactions during a viral infection.





Influenza:

- Enveloped RNA virus
- Surface proteins: hemagglutinin and neuraminidase (HxNx)
- Causes respiratory symptoms
- Tamiflu is a neuraminidase inhibitor, preventing influenza viral release from infected cells
- [1]

PhysiCell:

- Agent-based, multi-scale, spatial computational model of host tissue
- High performance computing, written in C++ and XML
- Open source and continuously enhanced:
- 2018: Cancer model [3]
- 2020: COVID-19 model with immune submodel [4]
- 2021: Influenza tissue immune submodel [5]

PhysiCell Tissue Immune Submodel [4]



Biological questions:

We investigate the relationships between the antiviral treatment Tamiflu, influenza virus, and the immune system, such as:

- How does the presence or absence of treatment impact influenza virusimmune interactions and outcomes?
- 1. How well does Tamiflu control infection at different doses and administration times, such as upon exposure and once symptomatic?



Pharmacokinetic modeling of Tamiflu

Metabolism

OP central

Pharmacokinetics (PK): movement of drugs through the body • We employ a 7-compartment model of PK dynamics of Tamiflu [5] • Oseltamivir phosphate (OP) is the ingested form of Tamiflu, which is then converted to the active form oseltamivir carboxylate (OC)

Ingestion



Model OC concentrations are converted to appropriate PhysiCell units (moles/ μ m³), exported to a .bin file, and read into PhysiCell.

PhysiCell code and parameters

Code implementing the effect of Tamiflu on viral release in relation to its IC₅₀ value.

(pCell->phenotype.molecular.internalized_total_substrates[vtest_external]*Vvoxel>8e3 && PhysiCell_globals.current_time>pCell->custom_data["eclipse_time"]) double treatment_concentration = pCell->nearest_density_vector()[treatment]; if(treatment concentration>0) pCell->phenotype.secretion.secretion_rates[vtest_external] = parameters.doubles("kRel")*(1-(treatment_concentration/(tIC50+treatment_concentration))); // std::cout<< (1-(treatment concentration/(tIC50+treatment concentration))) << std::endl</pre>

e-l Interferon		
amm. cytokine kine		
mph node/		
DC		
+		

nterferon	
m. cytokine	Dtreatment
ph node	λ treatment
DC	TRo

Parameter	Description	Value
Dtreatment	Diffusion rate of Tamiflu	420
∖ treatment	Decay rate of Tamiflu	1.7 x 10 ⁻³
TRo	Initial concentration of Oseltamivir Carboxylate (OC)	1.2 x 10 ⁻²¹
tIC50	IC₅o value of Tamiflu	7.77 x 10 ⁻²³

Acknowledgements

This research was funded by the National Science Foundation REU-Site Grant DBI-1950350 and the Natural Science Division of Pepperdine University. We thank Adrianne Jenner, Morgan Craig, Amber Smith, Penelope Morel, and the entire Tissue Immune Response Subteam for code, inspiration, and insights for this project. In addition, we thank Paul Macklin, Michael Getz, Yafei Wang, Randy Heiland and the whole PhysiCell COVID-19 Tissue Simulator team.

References

- [1] McClellan K, Perry C. Drugs 61(2): 263-283 (2001)
- [2] Centers for Disease Control and Prevention website (21 Sept. 2021) [3]Ghaffarizadeh A et al. PLoS Computational Biology 14: e1005991 (2018) [4]Getz M et al. Iterative community-driven development of a SARS-CoV-2 tissue simulator. bioRxiv preprint (Nov. 2020)
- [5] Jenner A et al. Unpublished (2021)
- [6] Gibiansky L et al. Journal of Pharmacokinetics and Pharmacodynamics 42: 225-236 (2015) [7] Hawles M et al. Molecular Pharmaceutics 15: 1534-1547 (2018)
- [8] Jullien V et al. Antimicrobial Agents and Chemotherapy 55(9): 4183-4187 (2011)
- [9] Widmer N et al. Clinical Pharmacokinetics 49: 741–765 (2010)

Drug action



Units	Ref
µm²/min	[7]
1/min	[8]
moles/µm³	[9]
moles/µm³	[9]







Initiating Tamiflu treatment earlier results in shorter infection time, whereas dose amount does not substantially affect infection length.

Conclusions and Future Directions

- We built antiviral treatment functionality into a computational immune model that can be generalized to other RNA viruses.
- Tamiflu shortens infection time compared to infection time without treatment.'
- Administering treatment earlier shortens infection. When Tamiflu treatment begins at day two, effectiveness does not depend heavily

Future directions:

on dosage.

- Include different subtypes of influenza virus, particularly those causing pandemic versus seasonal influenza.
- Model other antiviral drug mechanisms of action such as viral replication or viral entry.
- Adapt the model to analyze the effects of simultaneous drug treatment.