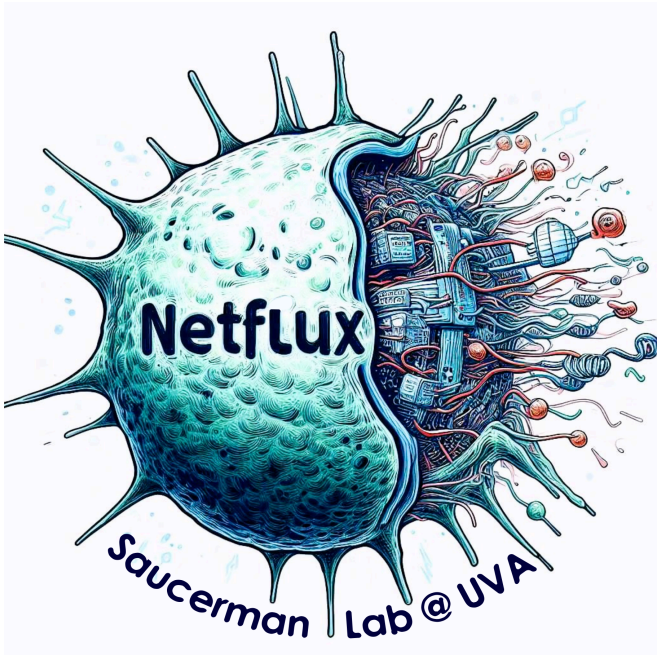


3rd Netflux and Logic-based Network Biology Conference

January 8, 2025, 1-5 pm EST on Zoom

Keynote speaker: Réka Albert (Penn State), Distinguished Professor of Physics and Biology

Short talks and lightning talks from students with a wide range of biological applications and approaches for logic-based network modeling

Live demos of Netflux and Cell Collective tools for user-friendly modeling of biological networks

Program Committee:

Kwang-Hyun Cho (Korea Advanced Institute of Science and Technology), Shannon Flanary (U. Minnesota), Tomas Helikar (U. Nebraska), Will Richardson (U. Arkansas), Kyoko Yoshida (U. Minnesota)

For info: meeting chair Jeff Saucerman, jsaucerman@virginia.edu

Registration, Abstract Submission, and Agenda:
https://tinyurl.com/netflux2025

Student Workshop at UVA Jan 10:

https://tinyurl.com/netfluxstudent

Registration

Registration form: https://forms.gle/Gc6eFjicAmEqj6xa9

Abstract Submission

Abstract submission form: CLOSED 12/13

Agenda (tentative)

1:00 pm Jeff Saucerman (U. Virginia), Meeting introduction

1:10 pm Alex Clark (U. Virginia), Tutorial on Netflux (w. 5 min questions)

1:30 pm Tomas Helikar (U. Nebraska), Tutorial on Cell Collective (w. 5 min questions)

1:50 pm 10 min break

2:00 pm Session 1 (moderator: Alice Luanpaisanon, Malcolm O'Malley)

Short talks (12 min + 3 min questions each)

Kyoko Yoshida (U. Minnesota), Cell signaling applications in pregnancy biomechanics

Johane H. Bracamonte, Lionel Watkins, Betty Pat, Louis J. Dell'Italia, Jeffrey J. Saucerman, Jeffrey W. Holmes (U. Alabama Birmingham), Bayesian analysis of the drivers of volume overload-induced hypertrophy using logic-based network models

Najme Khorasani, Haibo Ni, Eleonora Grandi (UC Davis), Computational modeling of cardiac fibroblast signaling reveals a key role for Ca2+ in regulating atrial fibrillation-associated fibrosis

Lightning talks (4 min + 1 min questions each)

Lavie Ngo, Antonio Abbate, Stefano Toldo, Jeff Saucerman (U. Virginia), Computational Model Predicts Mechanisms of LRP1-mediated Cardioprotection

2:50 pm 10 min break

3:00 pm Session 2 (moderator: Bryce Murillo, Sophia Kerns)

Short talks (12 min + 3 min questions each)

Ana Estrada (Fairfield U.) and Jay Humphrey (Yale U.), Multi-cell, multiscale model of inflammation-driven aortic growth and remodeling

Amir Mahar, Philip Stauffer, Vito Quaranta, Leonard Harris (U. Arkansas), Computational modeling of ER-Mitochondrial Ca2+ transfer and metabolic dysregulation in BRAF- mutant melanoma cells

Lightning talks (4 min + 1 min questions each)

Annika Sama, Kaitlyn Wintruba, Jeff Saucerman (U. Virginia), Predicting Network Mechanisms of Negative Regulators of Cardiomyocyte Proliferation

Ishaan Shah, Tanya Cruz, Delaney Fisher, Richard Price (U. Virginia), Computational Modeling of Astrocyte Signaling Pathways and AI-Driven Therapeutic Target Prediction for Cerebral Cavernous Malformations

Sophia Kerns, Antonio Abbate, Stefano Toldo, Jeff Saucerman (U. Virginia), Network Model Predicts Anti-Inflammatory Mechanisms of Colchicine

3:45 10 min break

3:55 **Keynote: Réka Albert (Penn State)**, Automated model refinement using perturbation experiments, (40 min + 5 min questions; moderator Jeff Saucerman)

4:45 Wrapup: Jeff Saucerman

Technical issues connecting or sharing your talk? Email Kaitlyn, npw7gn@virginia.edu and Jamie, jsaquing@virginia.edu

New to Netflux and interested in learning how to use it? Attend the Student Workshop on Modeling Biological Networks with Netflux at UVA, Jan 10. https://tinyurl.com/netfluxstudent

Resources

Netflux software for user-friendly modeling of biological networks

https://github.com/saucermanlab/Netflux

Video introduction and tutorials for Netflux

https://www.youtube.com/watch?v=tU2gU8d5hvQ&list=PLTbDE7ZQfKy-ijd5ZrCQJ7eB-NSCQKIBi

61 publications Using Netflux or Logic-Based Differential Equations

https://docs.google.com/document/d/1FjzbdYM3lyIlpgx0t4mQ6_zQETJ1MS2QQAgsE_rX1Fo/edit?usp=sharing

COLOTMOTO consortium for logic-based modeling

The CoLoMoTo Consortium | CoLoMoTo

Cell Collective (collaborative web-based platform for network modeling, including logical, metabolic, and kinetic models; contains 300+ models)

https://cellcollective.org