

Home > Sessions > Hierarchical Models for Omics Data

M14: Hierarchical **Models for Omics** Data

Wed. March 8, 8:00 a.m. — 10:24 a.m. **PST**

Room 206

Sponsoring Units: DBIO

Chair: Mihaela Sardiu, University of Kansas Medical Center

Session Type:

Search by author, title, or number



- 001 Growing a network via oscillations on nodes
- 002 Mechanisms of mammalian drug resistance acquired during long-term evolution
- 003 Specificity, cooperativity, synergy, and mechanisms of splice-modifying drugs
- 004 Experimental quantification of model identifiability and information loss due to distortions in fluorescence microscopy and image processing
- 005 Computational agent-based modelling reveals the role of tumour microenvironment on the success of combination chemotherapy/immunotherapy to treat glioblastoma
- 006 Using the Finite State Projection based Fisher Information Matrix to optimize single-cell experiment designs under different combinations of discrete stochastic models and measurement errors
- 007 Live imaging of gut-associated innate immune cell motion
- 008 Identifying the transition genes and state specific gene regulation from single-cell transcriptome data with spliceJAC
- 009 Analytical model for vaccination protocols that optimally produce broadly neutralizing antibodies
- 010 A model for how T cellmediated autoimmunity can be triggered by persistent viral infections
- 011 Optimal design of cocktail boosters to elicit a polyclonal response against related viral strains

012 Stochastic modeling for

studying the effects of BET inhibitors on the modulation of P-TEFb levels

Optimal design of cocktail boosters to elicit a polyclonal response against related viral strains

Wed. March 8, 10:00 a.m. — 10:12 a.m. PST Room 206

Immune escape from previous antibody responses by variants of a pathogen is a common threat from frequently mutating viruses, like influenza or SARS-CoV2. A recently developed strategy for epidemic control of the latter is the administration of a cocktail vaccine booster made of ancestral strain and omicron strain (1:1), which has already undergone clinical trials and has been approved in some countries. By exploiting a mapping of models describing the evolutionary dynamics of B cells during affinity maturation to a simple quantum mechanical analog, we investigate the optimal antigen composition of the cocktail vaccine in order to best exploit immune memory generated by previous encounters of related pathogen strains.

Presented By

Federica Ferretti (MIT)

Authors

- Federica Ferretti (MIT)
- Arup K Chakraborty (MIT)
- Mehran Kardar (Massachusetts Institute of Technology MIT)

Registration **Schedule**

Attendees & Presenters Travel & Hotels

Exhibits

About

Scientific Sessions

Become an APS Member Renew Membership

Join an APS Unit

Update Contact Information

Donate to APS

Press

Reserve an Exhibitor Booth Sponsor the March Meeting Learn About the In-Person Meeting Learn About the Virtual Meeting Job Expo

American Physical Society 1 Physics Ellipse College Park, MD 20740-3844 301.209.3200



(O,

[2]





