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Vás pozývajú na 135. prednášku v rámci Kuželových seminárov:

dr. Fereydoun Hormozdiari

Department of Biochemistry and Molecular Medicine,
University of California Davis, School of Medicine, USA

COMPUTATIONAL AND AI MODELS FOR ANALYZING NON-CODING REGIONS AND CELL-FREE RNA IN CANCER DETECTION

ktorá sa uskutoční **24. septembra 2025** (streda) o **16:30**
v miestnosti **CH1-222** Prírodovedeckej fakulty UK

<http://www.naturaoz.org/seminare.html>
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Hostiteľ: Tomáš Vinař, FMFI

Fereydoun Hormozdiari, PhD.

Dr. Fereydoun Hormozdiari, an associate professor at the University of California, Davis (UC-Davis), leads a lab focused on computational biology and genomics. He holds a BSc in Computer Engineering from Sharif University of Technology, and MSc and PhD degrees in Computing Science from Simon Fraser University, where his doctoral thesis earned him the Governor General Academic Medal. Dr. Hormozdiari's significant contributions have been recognized with the Solan Research Award and the NSF CAREER Award. He has also played a key role in influential consortiums such as the 1000 Genomes Project and the Great Ape Genome Project. His current research focuses on developing computational algorithms and designing machine learning and AI approaches to study human health and diseases, with a particular emphasis on autism and cancer.



Synopsis of the talk

Recent advances in cancer genomics have highlighted the crucial roles of non-coding regions and cell-free RNA (cfRNA) in cancer development and non-invasive diagnostics. I will first present our approach for analyzing the impact of non-coding structural variants on genome organization and their impact on diseases such as cancer. Next, I will introduce a computational framework for identifying non-coding cis-regulatory driver elements associated with gene dysregulation using tissue-matched enhancer-gene maps. We show that somatic mutations in these regulatory elements can disrupt transcription factor binding, leading to oncogene activation and tumor suppressor silencing, underscoring the functional significance of distal non-coding regions in cancer. I will then describe an AI-based model for cfRNA analysis in liquid biopsies. Our multi-task variational autoencoder achieves high sensitivity and specificity in detecting non-small cell lung cancer using serum-derived orphan non-coding RNAs. Together, these studies demonstrate how advanced computational methods and AI can decode the regulatory landscape of cancer and accelerate the development of cfRNA-based diagnostics.

Selected publications:

- Momen-Roknabadi A, Karimzadeh M, Chen NC, Cavazos TB, Wang J, Ku J, Degtiar A, Krishnan A, Hernandez M, Gebala M, Huang A, Chen S, Nguyen D, Lam T, Hanna R, Fish L, Smith AJ, Sekhon S, Yen J, Gregg J, Li H, **Hormozdiari F**, Behsaz B, Hartwig A, Goodarzi H, Schwartzberg L, Alipanahi B. (2025). Detection of Early-Stage Colorectal Cancer Using Cell-Free oncRNA Biomarkers and Artificial Intelligence. *Clin Cancer Res.* 31(15): 3229-3238.
- Karimzadeh M, Momen-Roknabadi A, Cavazos TB, Fang Y, Chen NC, Multhaup M, Yen J, Ku J, Wang J, Zhao X, Murzynowski P, Wang K, Hanna R, Huang A, Corti D, Nguyen D, Lam T, Kilinc S, Arensdorf P, Chau KH, Hartwig A, Fish L, Li H, Behsaz B, Elemento O, Zou J, **Hormozdiari F**, Alipanahi B, Goodarzi H. (2025). Deep generative AI models analyzing circulating orphan non-coding RNAs enable detection of early-stage lung cancer. *Nat Commun.* 15(1):10090.
- Tomkova M, Tomek J, Chow J, McPherson JD, Segal DJ, **Hormozdiari F**. (2023). Dr.Nod: computational framework for discovery of regulatory non-coding drivers in tissue-matched distal regulatory elements. *Nucleic Acids Res.* 51(4):e23.
- Denti L, Khorsand P, Bonizzoni P, **Hormozdiari F**, Chikhi R. (2023). SVDSS: structural variation discovery in hard-to-call genomic regions using sample-specific strings from accurate long reads. *Nat Methods* 20(4):550-558.
- Chow JC, Zhou R, **Hormozdiari F**. (2022). MAGI-MS: multiple seed-centric module discovery. *Bioinform Adv.* 2(1): vbac025.