

# POZVÁNKA na SEMINÁŘ

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## Biomarker discovery and precision oncology through sparsity-inducing methods

**Abstrakt:** Tumor heterogeneity plays a critical role in cancer progression and therapy resistance, hindering the effectiveness of therapeutic approaches and disease management. Emerging biomedical technologies, particularly those generating omics data (e.g., genomics, transcriptomics, proteomics), now allow us to investigate the molecular entities that govern tumor heterogeneity and could serve as candidates for disease biomarkers and therapeutic targets. Omics data are high-dimensional, with the number of features greatly outnumbering the number of observations. This calls for the need to develop statistical and machine-learning methods to translate vast amounts of data into meaningful biological solutions. Such approaches have the potential to enhance diagnosis, prognosis, survival rates, and overall quality of life for cancer patients. In this presentation, I will discuss strategies for extracting relevant information from high-dimensional transcriptomics data. This will include topics such as model regularization for feature selection, network discovery, and patient classification, illustrated with examples of application in glioma, the most common brain tumor in adults.

K účasti jsou zváni jak členové katedry, tak všichni učitelé, vědečtí pracovníci a studenti, kteří mají o problematiku zájem.

Aktuální program sledujte na [webových stránkách katedry](#), [Facebooku](#) či [Instagramu](#).

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