PRP@CERIC Seminar

AREA Science Park – Research Institute for Technological Innovation

"Mining Biological Intelligence From Cells: a Network-Based Approach"*

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PROGRAM

10:00 – 11:30	**Seminar** at the Padriciano Campus, Conference Hall, Building C -102
12:00 – 12:30	**Visit to ICGEB**, Padriciano Campus
12:30 – 13:30	Lunch at the campus canteen
13:40 – 15:00	**Visit to LAGE and the data center**, Basovizza Campus

*ABSTRACT

Despite the widening range of high-throughput platforms and exponential growth of data volumes, the discovery of disease drivers and biomarker validation remain challenging tasks. We proposed tackling cancer heterogeneity and data dimensionality via a sensitive and robust network approach to the pathway analysis. It transforms the original omics space into a pathway dimension which is both more compact and relevant to the underlying biology. The new coordinates can then be used in downstream analyses. The method proved superior to various alternative algorithms in terms of 1) applicability to different data types, 2) reproducibility across datasets, and 3) ability to explain patient response. The method discovered predictors valid both in vitro and for patients treated with same drug[1]. Similarly, we applied the approach to finding novel cancer driver genes[2]. Due to scarcity of mutation patterns, such drivers were poorly detectable via mutation frequency but could be discovered by accounting for co-occurrence in tumor genomes. The ability to identify previously unnoticed candidate drivers emerged from combining individual genomic context with a pathway and network perspective. The discovered drivers were shown to have low error rates, informative on cancer outcome, and related to cancer biology domains poorly covered by previous analyses.
I will present our web resources for network-assisted exploration of omics data, EviNet and EviMark[3,4] as well as latest results from both the method development and application to biological problems[5].

1. Franco M, Jeggari A, ... Alexeyenko A **(2019)** Prediction of response to anti-cancer drugs becomes robust via network integration of molecular data. **Scientific Reports,**

2. Petrov I, Alexeyenko A **(2022)** Individualized discovery of rare cancer drivers in global network context. **eLife.**

3. Jeggari A. ... Alexeyenko A **(2019)** EviNet: a web platform for network enrichment analysis with flexible definition of gene sets. **Nucleic Acids Res**.

4. Petrov I, Alexeyenko A **(2022)** EviCor: interactive web platform for exploration of molecular features and response to anti-cancer drugs. **J Mol Biol.**

5. Alexeyenko A, Brustugun OT, Eide IJZ, Gencheva R, ... Ekman S **(2022)** Plasma RNA profiling unveils transcriptional signatures associated with resistance to osimertinib in EGFR T790M positive non-small cell lung cancer patients. **Translational Lung Cancer Research**.

** **BIOGRAPHY**:

Andrey Alexeyenko is an associate professor at Karolinska Institutet, Stockholm, specializing in bioinformatics, biostatistics, and systems biology. He develops computational methods and tools for integration and analysis of heterogeneous large-scale datasets in the context of global cellular networks. The methodology is applied to systematic data analysis and interpretation across diverse biomedical and clinical projects.