

Il seminario/Gli sviluppi delle tecnologie computazionali nella lotta al cancro

Scritto da Red.

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Friday
February 26, 2021
15:00 (CET)

**Computational and
Quantitative Biology
Lecture Series**

The seminar will be held on line using TEAMS. Please register at <https://bit.ly/334UovJ>
You will receive an invite with the link to the seminar.

Supporting machine learning with biological knowledge to extract insight from omics data

Modern technologies allow us to profile in high detail biomedical samples at fast decreasing costs. New technologies are opening new data modalities, in particular to measure at the single cell level. Prior knowledge, and biological networks in particular, are useful to integrate this data and distill mechanistic insight. This can help to interpret the result of machine learning or statistical analysis, as well as generate input features for these methods. Towards this end, we have developed a number of tools that range from a meta-resource of biological knowledge (Omnipath) to methods to infer pathway and transcription factor activities (PROGENy and DoRothEA, respectively) from gene expression and subsequently infer causal paths among them (CARNIVAL). To tools to infer logic models from phosphoproteomic and phenotypic data (CellKit and PHORENAS). We have recently adapted these tools to single-cell data. I will illustrate their utility in cases of biomedical relevance, in particular to improve our understanding of cancer and to develop novel therapeutic opportunities. As main application I will discuss our work analysing, as a model for personalized medicine, large pharmaco-genomic screenings in cell lines. I will also present the DREAM challenges, a crowdsourcing effort to accelerate machine learning in biomedical research.

Julio Saez-Rodriguez is Professor of Medical Bioinformatics and Data Analysis at the Faculty of Medicine of Heidelberg University, director of the Institute for Computational Biomedicine, group leader of the EMBL-Heidelberg University Molecular Medicine Partnership Unit, a member of the Heidelberg ELIS Unit, and a co-director of the DREAM challenges. He holds a PhD (2007) in Chemical Engineering. He was a postdoctoral fellow at Harvard Medical School and MIT (2007-2010), group leader at EMBL EBI, Cambridge (2010-2015), and professor of Computational Biomedicine at RWTH Aachen (2015-2018). His research focuses on computational methods to understand and treat the deregulation of cellular networks in disease (www.saezlab.org).

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ARIANO IRPINO – Gli sviluppi delle tecnologie computazionali nella lotta al cancro e la messa a punto di possibilità terapeutiche innovative saranno il fulcro dell'intervento di Julio Saez Rodriguez al prossimo seminario Unina, sponsorizzato da Biogen. Obiettivo plausibile grazie al "profiling" sempre più dettagliato dei campioni biomedici della malattia e grazie alla disponibilità di nuove metodiche come i sequenziamenti a livello di singole cellule. "Come principale applicazione – ha anticipato il direttore dell'Istituto di Biomedicina Computazionale dell'Università di Heidelberg - parlerò del nostro lavoro, analizzando un largo insieme di screening farmacogenomici nelle linee cellulari utilizzate come modelli per la medicina personalizzata".

Nel corso del seminario saranno inoltre presentati i 'Dream challenges', un tentativo di crowdsourcing per accelerare l'uso dell'intelligenza artificiale nella ricerca biomedica.

Il convegno punta anche a fare il punto sulle conoscenze pregresse e sui diversi strumenti sviluppati ad Heidelberg. Dalla meta risorsa di conoscenze biologiche (Omnipath) ai metodi finalizzati alla inferenza di pathway e di attività dei fattori trascrizionali (rispettivamente Progeny e DoRothEA).

La partecipazione a tutti gli eventi è prevista in versione on-line previa registrazione.