

Friday
December 16, 2020
15:00 (GMT+1)

Computational and Quantitative Biology Lecture Series

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

Signature reversion and other computational strategies for identifying drug repositioning opportunities

Given the high attrition rates, substantial costs and slow pace of new drug discovery and development, repurposing of 'old' drugs to treat both common and rare diseases is increasingly becoming an attractive proposition because it involves the use of de-risked compounds, with potentially lower overall development costs and shorter development timelines. Various data-driven and experimental approaches have been suggested for the identification of repurposable drug candidates; however, there are also major technological and regulatory challenges that need to be addressed. We will explore computational approaches used for drug repurposing (also known as drug repositioning), discuss the challenges faced by the computational biology community on this regard and innovative ways by which these challenges could be addressed to help realize the full potential of drug repurposing.

Francesco Iorio is a Research Group Leader in Computational Biology at the Human Technopole (Milan, Italy) where he is establishing a research group in Computational Pharmacogenomics and Therapeutic Target Discovery. He has been awarded a joint EMBL – European Bioinformatics Institute (EBI) and the Wellcome Sanger Institute (WSI) post-doctoral (ESPOD) fellowship. Following this, He worked as senior bioinformatician at EBI and currently leads the Cancer Dependency Map Analytics team at the WSI.



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