
Ottava Giornata della Ricerca della Svizzera Italiana

Venerdì 9 marzo 2018

Modulo per la sottomissione abstract ricerca di LABORATORIO

Titolo (massimo **15 parole**)

OmicsNet: Integration of Multi-Omics Data using Path Analysis in Multilayer Networks

Autori (cognome e iniziali, es: Grassi L.)

Akhmedov M., Arribas A., Montemanni R., Bertoni F. and Kwee I.

Affiliazioni (ospedale o istituto, servizio o reparto, indirizzo, es: Ospedale Regionale di Lugano, Servizio di angiologia, Lugano)

Università della Svizzera italiana, Institute of Oncology Research, Bellinzona; Dalle Molle Institute for Artificial Intelligence Research, SUPSI, Manno; Oncology Institute of Southern Switzerland, Bellinzona; Swiss Institute of Bioinformatics, Lausanne; BigOmics Analytics, Bellinzona.

Testo (massimo **250 parole**, preferibilmente in italiano (accettato anche in inglese), suddiviso in Introduzione, *Metodi, Risultati, Conclusioni e Finanziamento*)

Integrative analysis of heterogeneous omics data is essential to obtain a comprehensive overview of otherwise fragmented information and to better understand dysregulated biological pathways leading to a specific condition. One of the major challenges in systems biology is to develop computational methods for the integration of multi-omics data of heterogeneous types. We propose OmicsNet that uses a multilayer network for the integration and analysis of multi-omics data.

Each layer of the multilayer network represents a certain data type: input layers correspond to genotype features and the output layer corresponds to phenotypes, while intermediate layers may represent genesets or biological concepts to facilitate functional interpretation of the data. OmicsNet calculates the highest coefficient paths in multilayer network from each genomic feature to the phenotype by computing an integrated score along the paths. These paths may indicate plausible signalling cascades caused by perturbed genotype features leading to a particular phenotype response.

In biological examples, with typically five or more layers and hundreds of thousands of variables, our method successfully identifies genomic and functional modules that are related with the phenotype. We illustrate application of OmicsNet in the functional analysis, biomarker discovery and drug response prediction in personalized medicine using multi-omics data.

We believe our method will be significant contribution to available methods for multi-omics integration and be a starting point for a new class of integration algorithms based on multilayer graphs and path analysis.

Financial support: SNFS 205321-147138/1 (MA). Disclosure: A patent on the method has been filed as IPTO 102017000125434.

Visto superiore (prego indicare Nome e Cognome del superiore)

Francesco Bertoni



Criteri per sottomissione Abstract:

NO Case report

NO Abstract senza nessun risultato

VISTO da un superiore

Invio Abstract