MultiOmics Network Embedding for SubType Analysis

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Biological systems are complex entities whose behavior emerges from an enormous number of reactions taking place within and among different internal molecular districts. The dissection and the modeling of the entities and the interactions constituting these interactions are essential in biological processes behind normal and pathological conditions as well as the perturbations induced by the exposure to external molecules like drugs. The recent explosion of omics data fueled the creation of diverse systems biology models. The majority of these are focused on the representation of interactions taking place in single molecular districts and have been successfully used to perform sample stratification, especially in cancer disease. Despite the usefulness proven by these models, they still did not reach the level of complexity needed to distinguish different biological conditions.

One step forward in this direction is the creation of multi-omics models capturing the dynamics taking place within and between omics layers. This latter approach needs powerful modeling strategies and is still an open research field. We propose the application of a powerful AI technique based on graph embedding for the creation of a system that, starting from multi-omics measurements, is able to model and generate knowledge about multi-omics interactions.

Here we present a novel approach implemented as an R package named MultiOmics Network Embedding for-SubType Analysis (MoNETA) for the identification of relevant multi omics relationships between biological samples. This approach has been applied in the identification of different cancer subtypes using multi omics data form the The Cancer Genome Atlas (TCGA) and the Clinical Proteomic Tumor Analysis Consortium (CP-TAC) datasets. MoNETA will be freely available as an R package at https://github.com/BioinfoUninaScala/MoNETA.

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