

# CLUSTER ANALYSIS OF CANCER METABOLIC NETWORK ENSEMBLES

Ichcha Manipur<sup>1</sup>, Iliara Granata<sup>1</sup>, Lucia Maddalena<sup>1</sup>  
and Mario R. Guarracino<sup>2</sup>

<sup>1</sup> High-Performance Computing and Networking Institute, Consiglio Nazionale delle Ricerche, (e-mail: [ichcha.manipur@icar.cnr.it](mailto:ichcha.manipur@icar.cnr.it), [ilaria.granata@icar.cnr.it](mailto:ilaria.granata@icar.cnr.it), [lucia.maddalena@cnr.it](mailto:lucia.maddalena@cnr.it))

<sup>2</sup> Department of Economics and Law, University of Cassino and Southern Lazio, (e-mail: [mario.guarracino@unicas.it](mailto:mario.guarracino@unicas.it))

**ABSTRACT:** Biological networks are representative of the diverse molecular interactions that occur within cells. They model protein-protein interactions, gene regulation, and metabolic pathways. Among these, metabolic networks are of great interest, as they directly influence all physiological processes. Exploration of biochemical pathways using multigraph representation is essential in understanding complex regulatory mechanisms. We present a cluster analysis on tissue-specific metabolic networks for three primary tumor types: breast, lung, and kidney cancer. The metabolic networks integrate genome-scale metabolic models with gene expression data. We empirically proved that network clustering could characterize groups of patients in multiple conditions to explore and characterize the metabolic landscape of tumors.

**KEYWORDS:** biological network ensembles, network summarization, networks clustering.

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