

CEMiTool: Coexpression Modules Identification Tool

Pedro de Sá Tavares Russo¹, Gustavo Rodrigues Ferreira¹, Lucas Cardozo¹,
Matheus Carvalho Bürger¹, Raúl Arias-carrasco², Sandra Regina Maruyama¹,
Thiago Dominguez Crespo Hirata¹, Diógenes Saulo Lima¹, Fernando Marcon
Passos¹, Kiyoshi Ferreira Fukutani¹, Melissa Lever¹, João Santana Silva¹, Vinicius
Maracaja Coutinho², Helder Takashi Imoto Nakaya³

1 USP

2 UNIVERSIDAD MAYOR

Abstract

The analysis of co-expression gene modules can help uncover the mechanisms underlying diseases and infection. We present a fast and easy-to-use Bioconductor package named CEMiTool that unifies the discovery and the analysis of co-expression modules. Using the same real datasets, we demonstrate that CEMiTool outperforms existing tools, and provides unique results in a user-friendly html report with high quality graphs. Among its features, our tool evaluates whether modules contain genes that are over-represented by specific pathways or that are altered in a specific sample group, as well as integrate transcriptomic data with interactome information, identifying potential hubs on each network. We successfully applied CEMiTool to over 1,000 transcriptome datasets, and to a new RNA-seq dataset of patients infected with Leishmania, revealing novel insights of the disease's physiopathology.

Funding: FAPESP