GECNAV description

GECNAV (Gene Expression-based CNA Validator) is a Python 3.7 software package that validates CNAs using gene and miRNA expression data from the TCGA PanCanAtlas (https://gdc.cancer.gov/about-data/publications/PanCan-CellOfOrigin). Low quality samples and metastatic samples are filtered out. CNA validation is based on comparing the CNA status of a given gene in a given patient to expression of this gene in this patient relative to the median expression of this gene across all patients. miRNA genes are also included into the verification process. The pipeline can be executed fully automatically in less than one hour on a modern PC (Linux, Windows or MacOS).

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Roles: concept, pipeline, supervision

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A detailed description of pipeline steps can be found in the file GECNAV pipeline.pdf

Instructions for executing the code can be found in the file Instructions.txt