TCGA matchmaker – SRS

Software requirement specification

V. 1.1

For: TCGA matchmaker

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1. Introduction

This is a tool that checks if a gene expression profile can be matched to different cancer samples from TCGA. The purpose is to investigate if a cancel sample has recurring features in other cancerous tissues as well. This would help in recycling therapies and understand cancer development.

<https://www.cancer.gov/about-nci/organization/ccg/research/structural-genomics/tcga>

1. Overall description

Input: Two files: Gene expression profiles for a number of genes. One input file contains a singular cancerous tissue sample. The other input file contains gene expression levels of various cancer tissues (annotated).

Output: TCGA samples that are associated (matched) with the input gene expression profile based on criteria for matching. (In which other types of cancer are genes upregulated?)

1. Requirements

Input data format for gene expression: text file with two columns gene symbol and gene expression. The file can be in txt. or .cvs format.