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 a cancer sample from TCGA

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

1. Overall description

Input: Gene expression profile for a number of genes

Output: TCGA samples that are associated (matched) with the input gene expression profile based on criteria for matching.

1. Requirements

Input data format for gene expression: text file with two columns gene symbol and gene expression