Instructions

Make sure the packages pracma, MSBVAR and tseries are installed.

Install the package SpliceNet_1.0.tar.gz

Sample data 1: Expressions of EGFR, CD44 and CEACAM1 isoforms in Lung Adenocarcinoma (LUAD) matched samples

- Sample-Normal-Exon-Expression-Matrix.txt
- Sample-Cancer-Exon-Expression-Matrix.txt

Sample data 2: Expressions of 44 genes involves in non-small cell lung cancer pathway from Lung Squamous Cell Carcinoma (LUSC) samples.

- LUSC-25-Samples.txt
- LUSC-50-Samples.txt
- LUSC-100-Samples.txt
- LUSC-200-Samples.txt
- LUSC-225-Samples.txt

Usage 1: For isoform specific gene co-expression networks

SpliceNet(<Input File>,<Output File>, α)

Input: Exon expression matrix (header not required)

<Isoform ID>	<Exon coordinates>	<Sample 1>	<Sample 2>	..	<Sample M>
NM_138578	chr20:30309458-30310152:-	46.41502115	91.31948375	..	52.15802836
NM_138578	chr20:30310421-30310657:-	0	3.849126456	..	16.23299434
NM_001001389	chr11:35198122-35198288:+	1.667866662	5.905634996	..	9.867583853
NM_001001389	chr11:35201821-35201955:+	2.515107276	7.844003443	..	14.1972565
NM_001001389	chr11:35208379-35208448:+	2.863275549	8.951956772	..	17.63405843
NM_001001389	chr11:35211382-35211613:+	2.568751767	8.832367975	..	15.36543055
NM_001001389	chr11:35219668-35219794:+	2.807808781	4.290396186	..	7.396610234
NM_001001389	chr11:35222629-35222743:+	0.93101028	2.623243357	..	8.780771213

Alpha (α): Significance level of the test

Output 1: Dependency matrix file

I-Matrix	NM_138578	NM_001001389
NM_138578	1	0
NM_001001389	0	1

Output 2: Dependency *p-value* matrix file

I-Matrix	NM_138578	NM_001001389
NM_138578	0.0027	0.22
NM_001001389	0.22	0.046

Usage 2: Differential network

SpliceNetDN(<NormalNet>,<CancerNet>)

Input: Networks generated using SpliceNet() function.

Output: Differential edges

<Isoform 1>	<Isoform 2>	<Normal>	<Cancer>
NM_138578	NM_001001389	0	1