PSFC: a guide to common rule settings

Here we explore two algorithms used for signal flow calculation on biological pathways, with published results. We show how to implement those algorithms in PSFC by applying appropriate rules.

Preset1: PSF algorithm default

The following options are applied in a previously published Pathway Signal Flow algorithm [1]

Node data type

Node data is in the form of fold change values – the ratios of absolute expression values between the studied condition and the reference.

Simple rules

The network should contain two edge types: e.g. activation and inhibition, with the following rules:

EdgeTypes config file:	Rule config file:
`activation  *` `inhibition  /`	`*      source * target` `/      1/source * target`

Multiple input and output edge rules

The signal is split according to relative fold change values of multiple source nodes.

Signal split rule: *Proportional*
Split signal on: *Incoming edges*

The signals coming from multiple sources are added to each other to generate the signal at the target node:
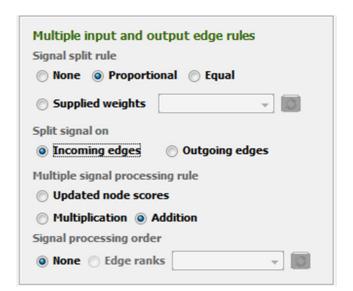
**Multiple signal
processing rule:**   *Addition*

The order of edges does not matter:
**Signal processing
order:**   *None*

Loops:

The **loops** option is set to "*Ignore feedback loops in a pathway*".

Preset2: Pathway scoring application

The following options are applied in a previously published Pathway Scoring Application algorithm [2].

Node data type

Node data is in the form of rank scores: the ranks of nodes are computed from gene expression and methylation data as described in [2].

Simple rules

The network should contain two edge types: e. g. activation and inhibition, with the following rules:

EdgeTypes config file:	Rule config file:
`activation   +` `inhibition   -`	`+      target + source` `-      target - source`

Multiple input and output edge rules

The signal is from a single source node is split according to relative fold change values of multiple target nodes.

Signal split rule: *Proportional*
Split signal on: *Outgoing edges*

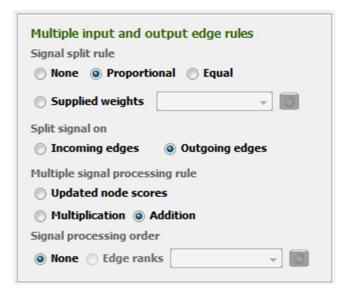The signals coming from multiple sources are added to each other to generate the signal at the target node:

Multiple signal
processing rule: *Addition*

The order of edges does not matter:
Signal processing
order: *None*

Loops:

The **loops** option is set to *"Iterate until convergence"*. The **"convergence threshold"** and **"Max number of iterations"** may be chosen arbitrarily.

References

1. Arakelyan A, Aslanyan L, Boyajyan A. **High-throughput Gene Expression Analysis Concepts and Applications.** Sequence and Genome Analysis II – Bacteria, Viruses and Metabolic Pathways. *iConcept Press,* 2013. ISBN: 978-1-480254-14-5.

2. Isik Z1, Ersahin T, Atalay V, Aykanat C, Cetin-Atalay R. **A signal transduction score flow algorithm for cyclic cellular pathway analysis, which combines transcriptome and ChIP-seq data.** *Mol Biosyst* 2012, 8(12):3224-31.