

Percentage of Pathway covered by PFM

Pathways	$\ Sw\ _1$ regularization		$\ Sw\ _2$ Regularization					
	SPMFA for ALL data samples		SPMFA for ALL data samples		SPMFA for STEADY STATE data samples		SPMFA for TIME COURSE data samples	
	1 st	2 nd	1 st	2 nd	1 st	2 nd	1 st	2 nd
	SPMF ⁽¹¹⁾	SPMF ⁽¹¹⁾	SPMF ⁽¹²⁾	SPMF ⁽¹²⁾	SPMF ⁽¹²⁾	SPMF ⁽¹²⁾	SPMF ⁽¹²⁾	SPMF ⁽¹²⁾
inositol pyrophosphates biosynthesis	100.0	0.0	0.0	100.0	100.0	0.0	0.0	100.0
Pyruvate	0.0	50.0	0.0	100.0	100.0	0.0	0.0	100.0
Glycolysis	30.8	38.5	38.5	38.5	38.5	53.9	30.8	38.5
Glyoxylate cycle	22.2	66.7	22.2	55.6	33.3	11.1	22.2	55.6
TCA cycle	8.3	75.0	25.0	25.0	16.7	41.7	33.3	25.0
transport_cyt_mit	7.1	50.0	28.6	28.6	7.1	50.0	35.7	35.7
Acetaldehyde	0.0	0.0	33.3	33.3	0.0	66.7	0.0	33.3
Glyoxylate cycle peroxisome	25.0	25.0	25.0	25.0	25.0	50.0	25.0	25.0
Acetyl-Coa mitochondrion	66.7	66.7	0.0	0.0	66.7	0.0	0.0	0.0
1,3--D-glucan biosynthesis	100.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
Acetyl-Coa mitochondrion	50.0	50.0	0.0	0.0	50.0	0.0	0.0	0.0
Pyruvate mitochondrion	0.0	0.0	66.7	0.0	0.0	0.0	66.7	0.0
Oxidative phosphorylation	12.5	62.5	12.5	12.5	0.0	0.0	12.5	12.5
methylglyoxal degradation V	0.0	33.3	33.3	0.0	33.3	0.0	33.3	0.0
PPP	0.0	27.3	18.2	9.1	0.0	9.1	27.3	9.1
2-methylcitrate cycle I	0.0	0.0	0.0	0.0	50.0	50.0	0.0	0.0
Glycolysis-up	0.0	0.0	0.0	50.0	0.0	0.0	0.0	50.0
amino acids per	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0
amino acid	0.0	23.1	0.0	0.0	0.0	23.1	7.7	0.0
Acetaldehyde mitochondrion	0.0	33.3	0.0	0.0	0.0	33.3	0.0	0.0
transport_cyt_per	0.0	25.0	0.0	0.0	0.0	0.0	0.0	0.0