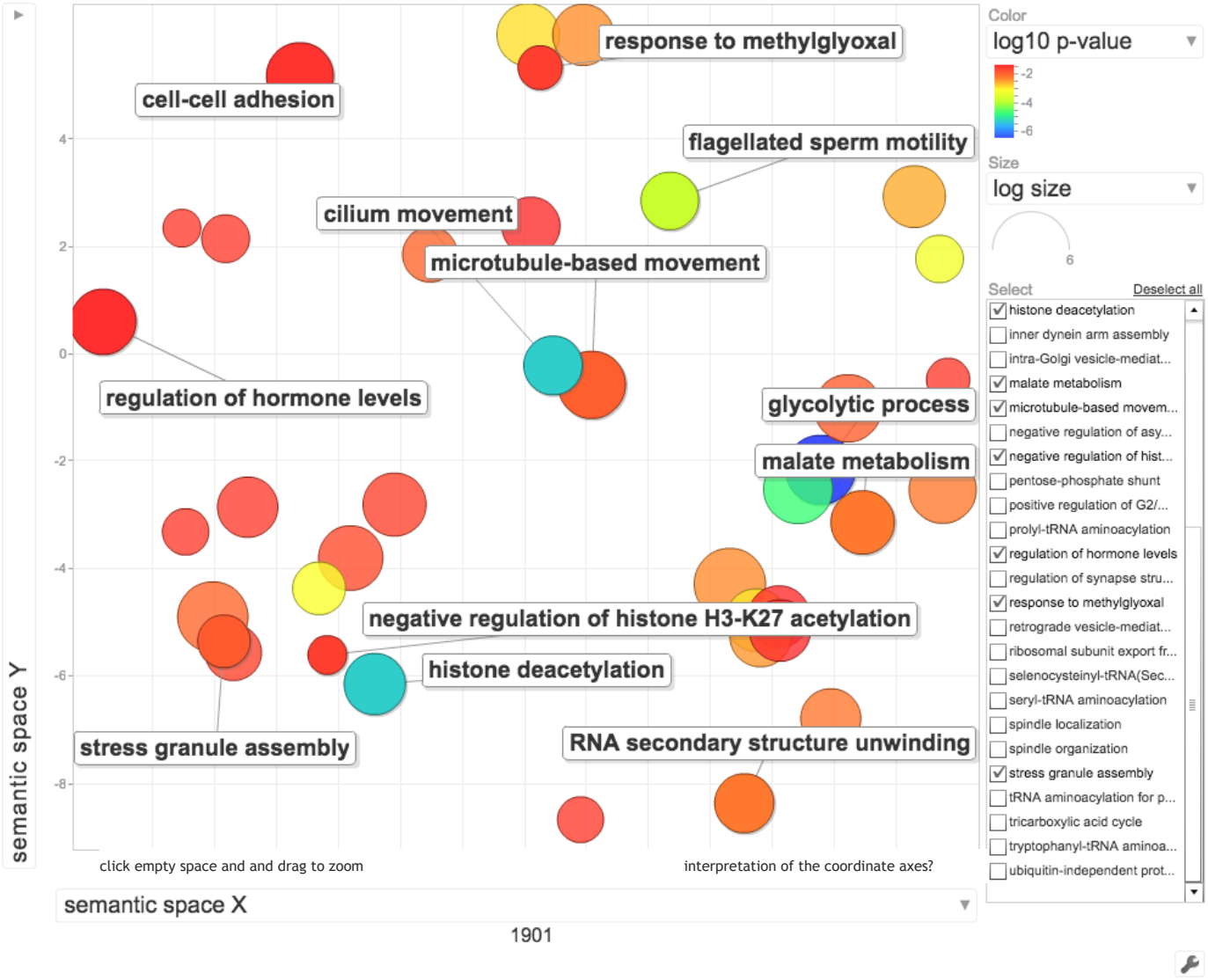
response to methylglyoxal
cell-cell adhesion
flagellated sperm motility
cilium movement
microtubule-based movement
regulation of hormone levels
glycolytic process
malate metabolism
negative regulation of histone H3-K27 acetylation
histone deacetylation
stress granule assembly
RNA secondary structure unwinding
semantic space Y
semantic space X
1901
click empty space and and drag to zoom
interpretation of the coordinate axes?
Color
log10 p-value
-2
-4
-6
Size
log size
6
Select
Deselect all
histone deacetylation
inner dynein arm assembly
intra-Golgi vesicle-mediat...
malate metabolism
microtubule-based movem...
negative regulation of asy...
negative regulation of hist...
pentose-phosphate shunt
positive regulation of G2/...
prolyl-tRNA aminoacylation
regulation of hormone levels
regulation of synapse stru...
response to methylglyoxal
retrograde vesicle-mediat...
ribosomal subunit export fr...
selenocysteinyl-tRNA(Sec...
seryl-tRNA aminoacylation
spindle localization
spindle organization
stress granule assembly
tRNA aminoacylation for p...
tricarboxylic acid cycle
tryptophanyl-tRNA aminoa...
ubiquitin-independent prot...

GO:0006433	prolyl-tRNA aminoacylation	0.052 %	-1.3710	0.62	0.60
GO:0006434	seryl-tRNA aminoacylation	0.053 %	-2.3846	0.62	0.60
GO:0006436	tryptophanyl-tRNA aminoacylation	0.054 %	-1.3710	0.62	0.60
GO:0007409	axonogenesis	0.118 %	-1.6990	0.66	0.61
GO:0021873	forebrain neuroblast division	0.002 %	-1.5440	0.80	0.63
GO:0006094	gluconeogenesis	0.262 %	-2.1770	0.75	0.65
GO:0007018	microtubule-based movement	0.287 %	-1.8687	0.69	0.70
GO:0006099	tricarboxylic acid cycle	0.469 %	-4.6799	0.68	0.73
GO:0051653	spindle localization	0.020 %	-1.3710	0.73	0.74
GO:0006418	tRNA aminoacylation for protein translation	1.099 %	-2.3232	0.56	0.75
GO:0007051	spindle organization	0.083 %	-1.6142	0.58	0.77
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	0.047 %	-2.3401	0.88	0.77
GO:0006098	pentose-phosphate shunt	0.287 %	-1.9078	0.66	0.80

Run Cytoscape in Java web start

Download Cytoscape XGMML file for offline use

Export data to text table (CSV) Make R script for plotting treemaps

Frequent keywords within your set of GO terms:

metabolism anabolic linked modifications single-organism oxoacid g2 ribose cooh coo- 3-hydroxyl modification ribonucleoside transform h3-k27 compound diadenosine g2/m glycolysis individual reactions repetition metabolic organic biopolymer carried rna-protein aminoacylation commits morphological nucleoside keto rco- sugar coenzymes h3k27 chemical k27 self-propelled cx(h2o)y disaggregate architecture rnp level beta-d-ribofuranose purine biochemical alteration acetylation nucleobase low condition esterified self-renewing phases substances monosaccharides carbohydrates microtubule-based tricarboxylic successive macromolecule nucleobase-containing those pathways proceed process cellular macromolecules peptidyl-lysine

Keywords that correlate with the value you provided alongside GO terms:

respiration 2-oxoglutarate carbohydrate nad(p isocitrate amount krebs triphosphate flagellum power confined reduction processes citrate effectively acetyl-coenzyme animals ends succinyl-coa pairs eukaryotes begins embden-meyerhof-parnas again enter citric embryonic anaerobic ethanol undergoes concomitant fad motility beating embden-meyerhof carboxylic enzymatic nad(p)h generate glycolytic coenzyme plants nad completely mitochondria indirectly modification fumarate atp histones self-propelled universal various acetyl-coa successive products electrons coenzymes completing glycolysis thus muscle oxaloacetate nearly provides stored modifed cilium skeletal produced see interconversion transformations aerobic fadh2 phosphorylation energy succinate combines

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