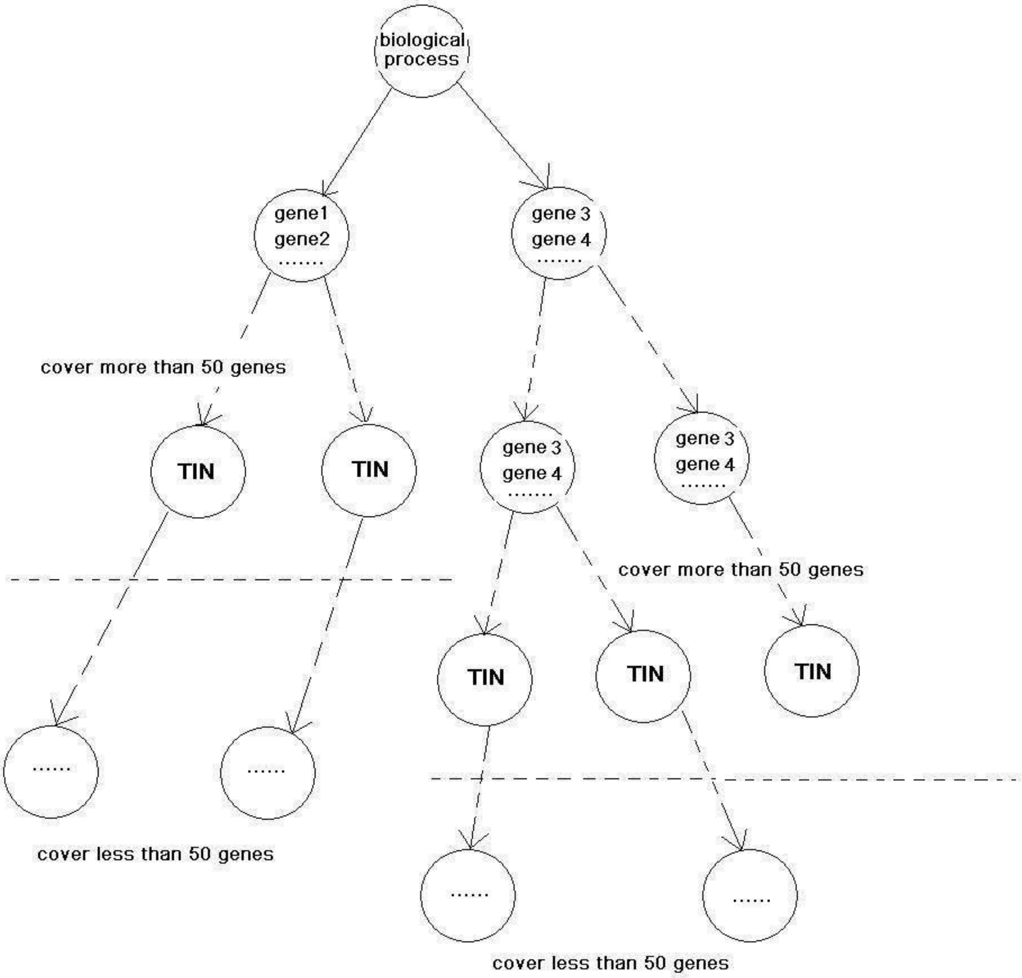

Sketch of TIN: A Directed Acyclic Graph (DAG) structured tree (A example of "biological process"). Each node may cover several or many genes, and Terminal Informative Nodes (TINs) locate in the bottom layer covering more than 50 genes.

31 TINs in cellular component	
GO term	**Function description**
GO:0009505	cellulose and pectin-containing cell wall
GO:0030120	vesicle coat
GO:0022627	cytosolic small ribosomal subunit
GO:0044432	endoplasmic reticulum part
GO:0044431	Golgi apparatus part
GO:0005777	peroxisome
GO:0005743	mitochondrial inner membrane
GO:0044455	mitochondrial membrane part
GO:0031969	chloroplast membrane
GO:0009570	chloroplast stroma
GO:0009543	chloroplast thylakoid lumen
GO:0009535	chloroplast thylakoid membrane
GO:0010287	plastoglobule
GO:0015934	large ribosomal subunit
GO:0000313	organellar ribosome
GO:0005774	vacuolar membrane
GO:0005635	nuclear envelope
GO:0005732	small nucleolar ribonucleoprotein complex
GO:0005667	transcription factor complex
GO:0009523	photosystem II
GO:0000786	nucleosome
GO:0005875	microtubule associated complex
GO:0031968	organelle outer membrane
GO:0000502	proteasome complex
GO:0000151	ubiquitin ligase complex
GO:0005834	heterotrimeric G-protein complex
GO:0031225	anchored to membrane
GO:0016021	integral to membrane
GO:0016469	proton-transporting two-sector ATPase complex
GO:0008287	protein serine/threonine phosphatase complex
GO:0048046	apoplast

82 TINs in molecular function	
GO term	**Function description**
GO:0004601	peroxidase activity
GO:0030246	carbohydrate binding
GO:0050662	coenzyme binding
GO:0005509	calcium ion binding
GO:0005507	copper ion binding
GO:0005506	iron ion binding
GO:0008270	zinc ion binding
GO:0008289	lipid binding
GO:0030533	triplet codon-amino acid adaptor activity
GO:0003700	transcription factor activity
GO:0003723	RNA binding
GO:0003743	translation initiation factor activity
GO:0005524	ATP binding
GO:0005525	GTP binding
GO:0019825	oxygen binding
GO:0005516	calmodulin binding
GO:0003779	actin binding
GO:0031072	heat shock protein binding
GO:0046983	protein dimerization activity
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity
GO:0051082	unfolded protein binding
GO:0046906	tetrapyrrole binding
GO:0008026	ATP-dependent helicase activity
GO:0015662	ATPase activity\, coupled to transmembrane movement of ions\, phosphorylative mechanism
GO:0019829	cation-transporting ATPase activity
GO:0016811	hydrolase activity\, acting on carbon-nitrogen (but not peptide) bonds\, in linear amides
GO:0030599	pectinesterase activity
GO:0004620	phospholipase activity

To be continued on next page

GO term	Function description
GO:0004521	**endoribonuclease activity**
GO:0004527	**exonuclease activity**
GO:0008081	**phosphoric diester hydrolase activity**
GO:0003993	**acid phosphatase activity**
GO:0015071	**protein phosphatase type 2C activity**
GO:0016790	**thiolester hydrolase activity**
GO:0004650	**polygalacturonase activity**
GO:0004843	**ubiquitin-specific protease activity**
GO:0004194	**pepsin A activity**
GO:0004289	**subtilase activity**
GO:0004185	**serine carboxypeptidase activity**
GO:0008237	**metallopeptidase activity**
GO:0003755	**peptidyl-prolyl cis-trans isomerase activity**
GO:0004842	**ubiquitin-protein ligase activity**
GO:0004812	**aminoacyl-tRNA ligase activity**
GO:0016831	**carboxy-lyase activity**
GO:0016836	**hydro-lyase activity**
GO:0030508	**thiol-disulfide exchange intermediate activity**
GO:0009055	**electron carrier activity**
GO:0004497	**monooxygenase activity**
GO:0016616	**oxidoreductase activity\, acting on the CH-OH group of donors\, NAD or NADP as acceptor**
GO:0016651	**oxidoreductase activity\, acting on NADH or NADPH**
GO:0016706	**oxidoreductase activity\, acting on paired donors\, with incorporation or reduction of molecular oxygen\, 2-oxoglutarate as one donor\, and incorporation of one atom each of oxygen into both donors**
GO:0016667	**oxidoreductase activity\, acting on sulfur group of donors**
GO:0016620	**oxidoreductase activity\, acting on the aldehyde or oxo group of donors\, NAD or NADP as acceptor**
GO:0016627	**oxidoreductase activity\, acting on the CH-CH group of donors**
GO:0008080	**N-acetyltransferase activity**

To be continued on next page

GO term	Function description
GO:0004364	**glutathione transferase activity**
GO:0035251	**UDP-glucosyltransferase activity**
GO:0016763	**transferase activity\, transferring pentosyl groups**
GO:0008483	**transaminase activity**
GO:0008757	**S-adenosylmethionine-dependent methyltransferase activity**
GO:0004702	**receptor signaling protein serine/threonine kinase activity**
GO:0004712	**protein serine/threonine/tyrosine kinase activity**
GO:0003899	**DNA-directed RNA polymerase activity**
GO:0008047	**enzyme activator activity**
GO:0046910	**pectinesterase inhibitor activity**
GO:0030414	**protease inhibitor activity**
GO:0005083	**small GTPase regulator activity**
GO:0004888	**transmembrane receptor activity**
GO:0000156	**two-component response regulator activity**
GO:0003777	**microtubule motor activity**
GO:0045735	**nutrient reservoir activity**
GO:0003735	**structural constituent of ribosome**
GO:0016563	**transcription activator activity**
GO:0005351	**sugar\:hydrogen ion symporter activity**
GO:0015103	**inorganic anion transmembrane transporter activity**
GO:0005261	**cation channel activity**
GO:0015082	**di-\, tri-valent inorganic cation transmembrane transporter activity**
GO:0005451	**monovalent cation\:proton antiporter activity**
GO:0015294	**solute\:cation symporter activity**
GO:0005244	**voltage-gated ion channel activity**
GO:0046915	**transition metal ion transmembrane transporter activity**
GO:0015932	**nucleobase\, nucleoside\, nucleotide and nucleic acid transmembrane transporter activity**

125 TINs in biological process	
GO term	**Function description**
GO:0045934	negative regulation of nucleobase\, nucleoside\, nucleotide and nucleic acid metabolic process
GO:0051093	negative regulation of developmental process
GO:0048585	negative regulation of response to stimulus
GO:0048522	positive regulation of cellular process
GO:0051726	regulation of cell cycle
GO:0006355	regulation of transcription\, DNA-dependent
GO:0009966	regulation of signal transduction
GO:0009909	regulation of flower development
GO:0035195	miRNA-mediated gene silencing
GO:0051239	regulation of multicellular organismal process
GO:0031347	regulation of defense response
GO:0045454	cell redox homeostasis
GO:0030005	cellular di-\, tri-valent inorganic cation homeostasis
GO:0009825	multidimensional cell growth
GO:0009826	unidimensional cell growth
GO:0050790	regulation of catalytic activity
GO:0031668	cellular response to extracellular stimulus
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway
GO:0009738	abscisic acid mediated signaling
GO:0009873	ethylene mediated signaling pathway
GO:0007264	small GTPase mediated signal transduction
GO:0007126	meiosis
GO:0012501	programmed cell death
GO:0000904	cellular morphogenesis during differentiation
GO:0051301	cell division
GO:0006334	nucleosome assembly
GO:0043623	cellular protein complex assembly
GO:0006413	translational initiation
GO:0007018	microtubule-based movement
GO:0048193	Golgi vesicle transport
GO:0006605	protein targeting

To be continued on next page

GO term	Function description
GO:0006839	**mitochondrial transport**
GO:0006913	**nucleocytoplasmic transport**
GO:0045045	**secretory pathway**
GO:0009832	**cellulose and pectin-containing cell wall biogenesis**
GO:0042545	**cell wall modification**
GO:0016044	**membrane organization and biogenesis**
GO:0016568	**chromatin modification**
GO:0030036	**actin cytoskeleton organization and biogenesis**
GO:0009658	**chloroplast organization and biogenesis**
GO:0000154	**rRNA modification**
GO:0010026	**trichome differentiation**
GO:0010053	**root epidermal cell differentiation**
GO:0006096	**glycolysis**
GO:0009073	**aromatic amino acid family biosynthetic process**
GO:0006418	**tRNA aminoacylation for protein translation**
GO:0009066	**aspartate family amino acid metabolic process**
GO:0000096	**sulfur amino acid metabolic process**
GO:0006576	**biogenic amine metabolic process**
GO:0009813	**flavonoid biosynthetic process**
GO:0009108	**coenzyme biosynthetic process**
GO:0006779	**porphyrin biosynthetic process**
GO:0042446	**hormone biosynthetic process**
GO:0015986	**ATP synthesis coupled proton transport**
GO:0006633	**fatty acid biosynthetic process**
GO:0046148	**pigment biosynthetic process**
GO:0006414	**translational elongation**
GO:0042364	**water-soluble vitamin biosynthetic process**
GO:0044242	**cellular lipid catabolic process**
GO:0006511	**ubiquitin-dependent protein catabolic process**
GO:0016114	**terpenoid biosynthetic process**
GO:0008654	**phospholipid biosynthetic process**
GO:0008202	**steroid metabolic process**
GO:0009250	**glucan biosynthetic process**

To be continued on next page

GO term	Function description
GO:0006486	protein amino acid glycosylation
GO:0006457	protein folding
GO:0006468	protein amino acid phosphorylation
GO:0016567	protein ubiquitination
GO:0006733	oxidoreduction coenzyme metabolic process
GO:0015994	chlorophyll metabolic process
GO:0006310	DNA recombination
GO:0006281	DNA repair
GO:0006261	DNA-dependent DNA replication
GO:0006397	mRNA processing
GO:0008380	RNA splicing
GO:0043414	biopolymer methylation
GO:0016311	dephosphorylation
GO:0033554	cellular response to stress
GO:0007568	aging
GO:0048438	floral whorl development
GO:0048437	floral organ development
GO:0048507	meristem development
GO:0009793	embryonic development ending in seed dormancy
GO:0009553	embryo sac development
GO:0009555	pollen development
GO:0003002	regionalization
GO:0009640	photomorphogenesis
GO:0017038	protein import
GO:0006865	amino acid transport
GO:0008643	carbohydrate transport
GO:0006855	multidrug transport
GO:0009926	auxin polar transport
GO:0006820	anion transport
GO:0006813	potassium ion transport
GO:0000041	transition metal ion transport
GO:0006869	lipid transport
GO:0006857	oligopeptide transport

To be continued on next page

GO term	Function description
GO:0009814	**defense response\, incompatible interaction**
GO:0006118	**electron transport**
GO:0015980	**energy derivation by oxidation of organic compounds**
GO:0019684	**photosynthesis\, light reaction**
GO:0005984	**disaccharide metabolic process**
GO:0009856	**pollination**
GO:0042742	**defense response to bacterium**
GO:0050832	**defense response to fungus**
GO:0009624	**response to nematode**
GO:0019953	**sexual reproduction**
GO:0009651	**response to salt stress**
GO:0009642	**response to light intensity**
GO:0009411	**response to UV**
GO:0009409	**response to cold**
GO:0009408	**response to heat**
GO:0009414	**response to water deprivation**
GO:0009733	**response to auxin stimulus**
GO:0009735	**response to cytokinin stimulus**
GO:0009739	**response to gibberellin stimulus**
GO:0010038	**response to metal ion**
GO:0009753	**response to jasmonic acid stimulus**
GO:0009743	**response to carbohydrate stimulus**
GO:0006979	**response to oxidative stress**
GO:0009751	**response to salicylic acid stimulus**
GO:0009636	**response to toxin**
GO:0042594	**response to starvation**
GO:0009611	**response to wounding**
GO:0007623	**circadian rhythm**