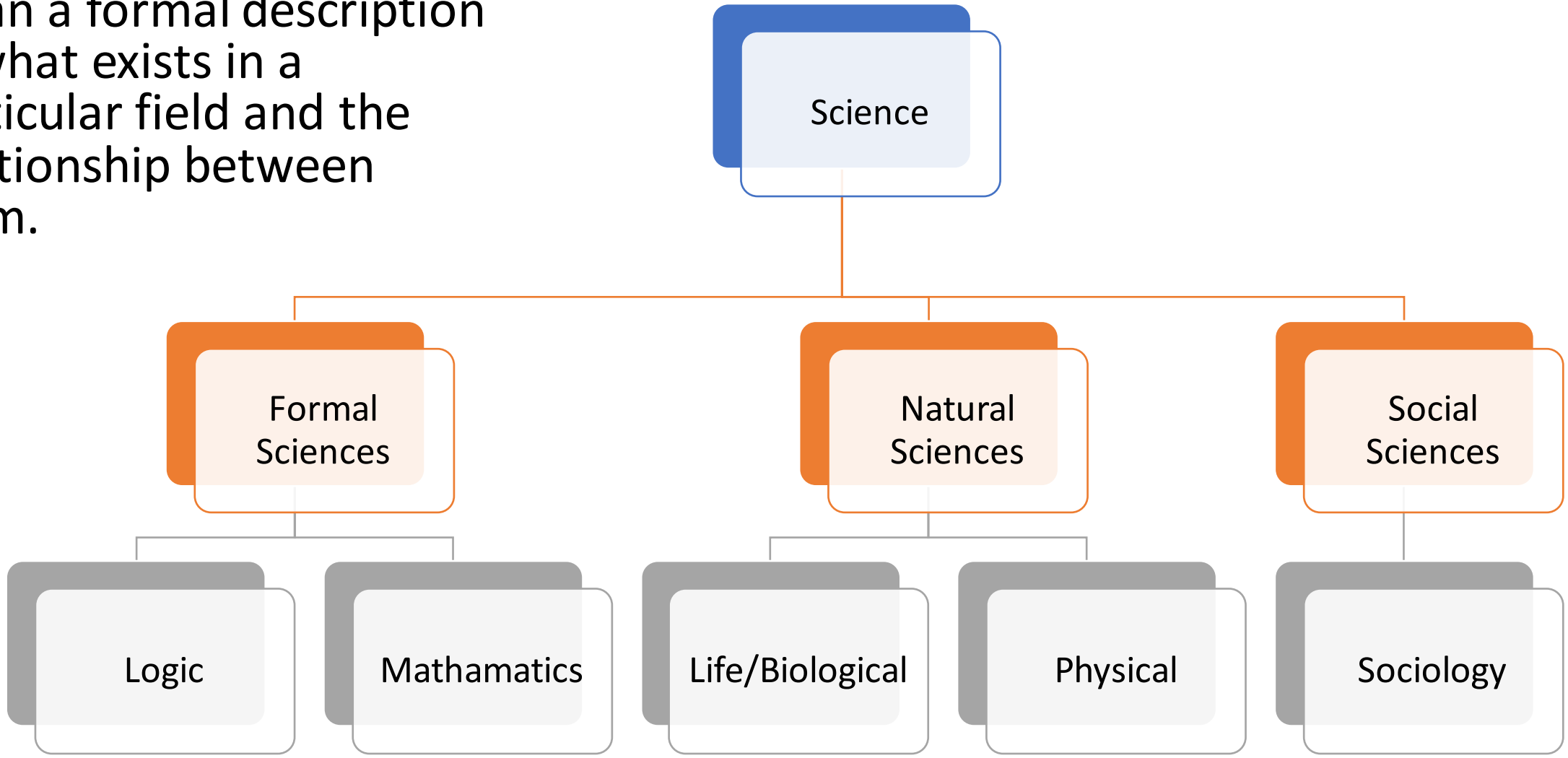
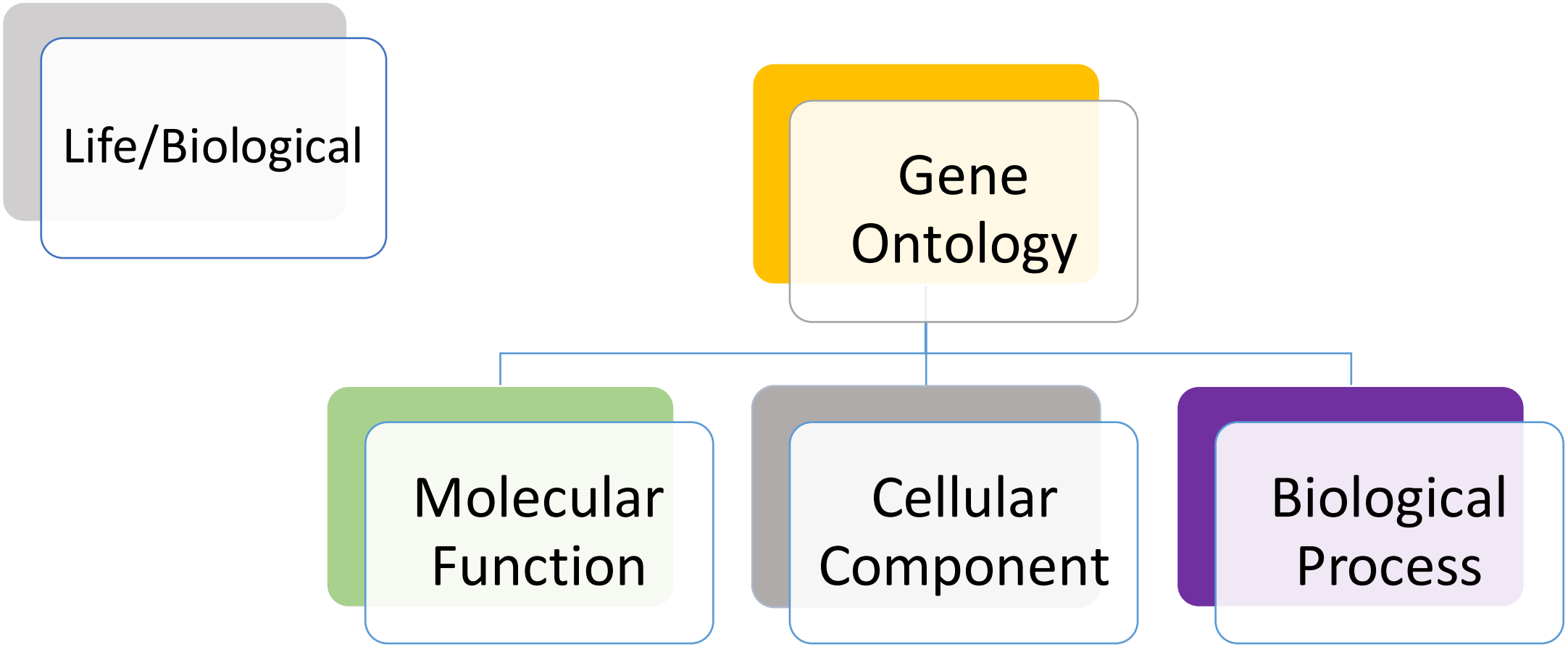
GO terms, EC numbers and enrichment analysis

For our purposes when we talk about ontology we mean a formal description of what exists in a particular field and the relationship between them.

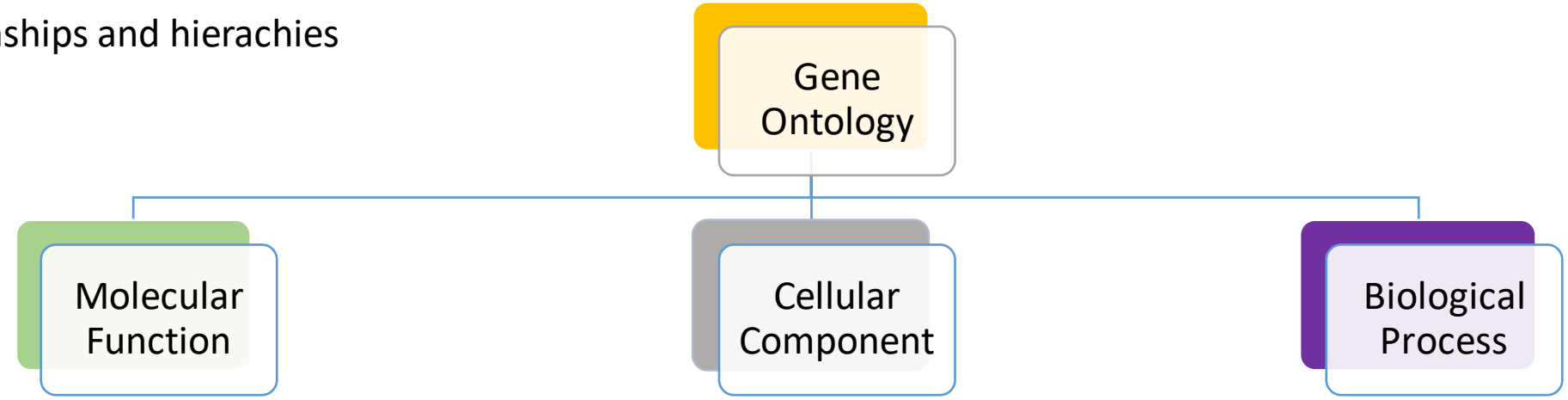




The gene ontology describes the knowledge of biological sciences and divides this knowledge up into three broad categories

http://geneontology.org/docs/ontology-documentation/

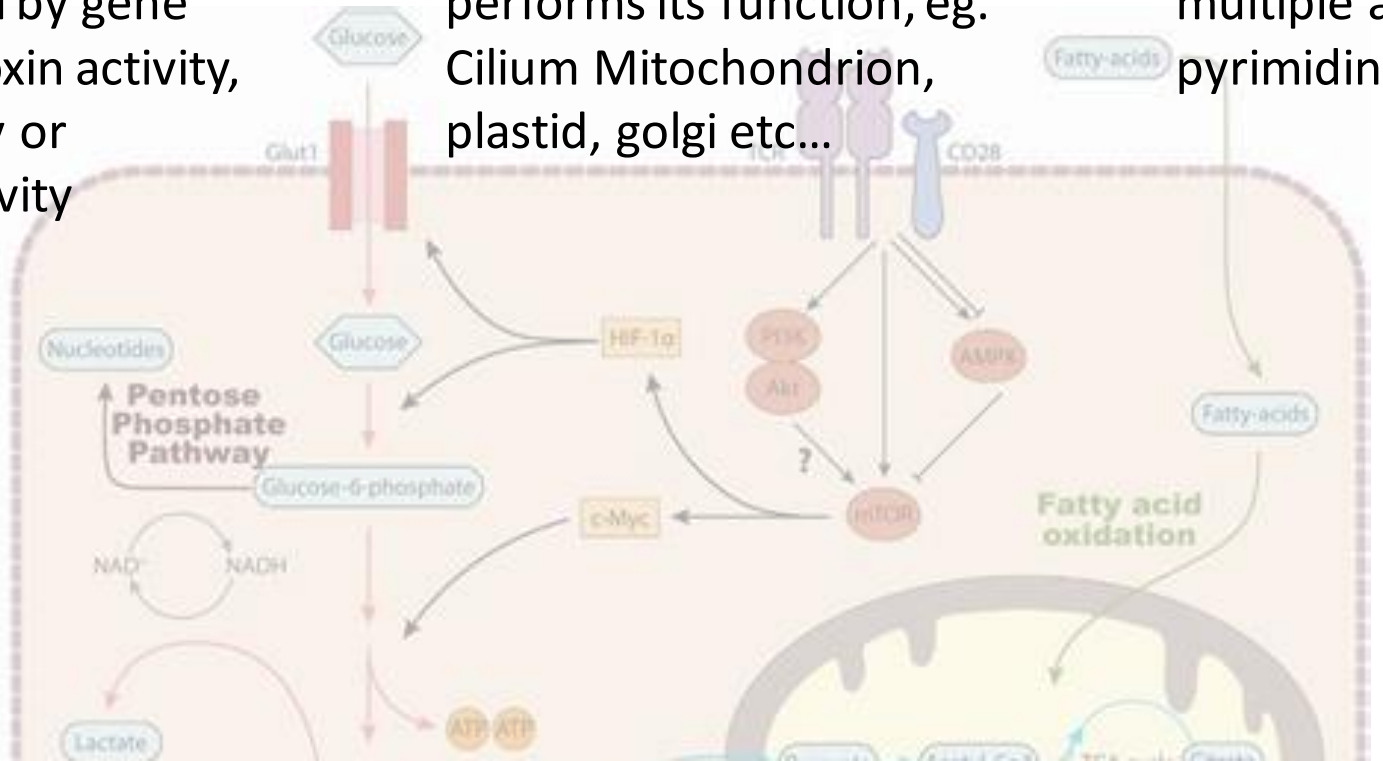
** relationships and hierachies



Activites at the molecular level performed by gene products, eg. Toxin activity, catalytic activity or transporter activity

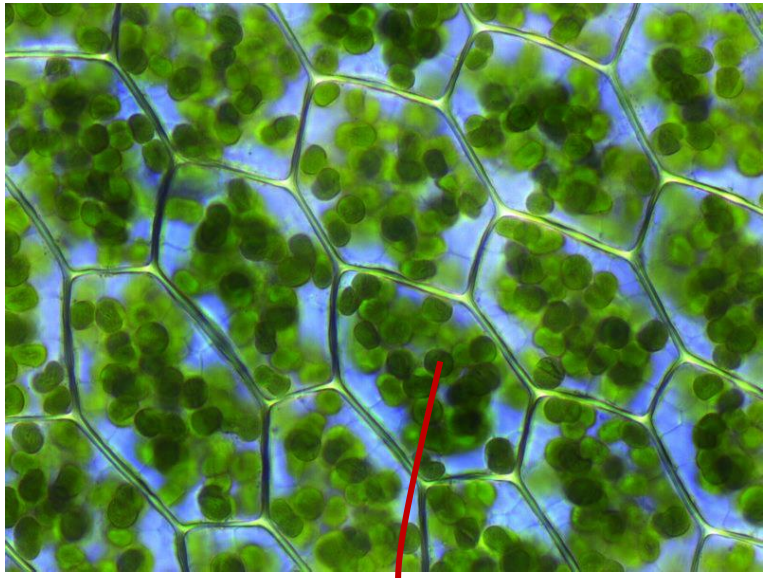
Where a gene product performs its function, eg. Cilium Mitochondrion, plastid, golgi etc…

Proceses accomplished by multiple activities, eg. pyrimidine biosynthesis

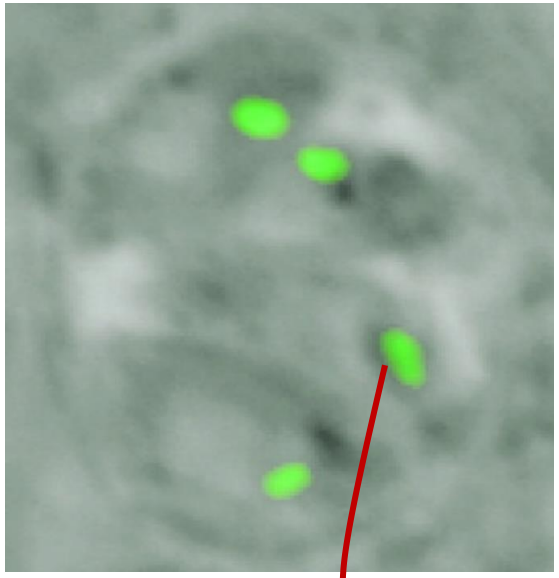


Why is GO ontology useful?

Cyanelle



Chloroplast



Apicoplast

GO:0009536 plastid

http://amigo.geneontology.org/amigo/term/GO:0009536#display-lineage-tab

Enzyme commission numbers:

systematic and logical nomenclature for enzymes

Numbers of composed of 4 digits:

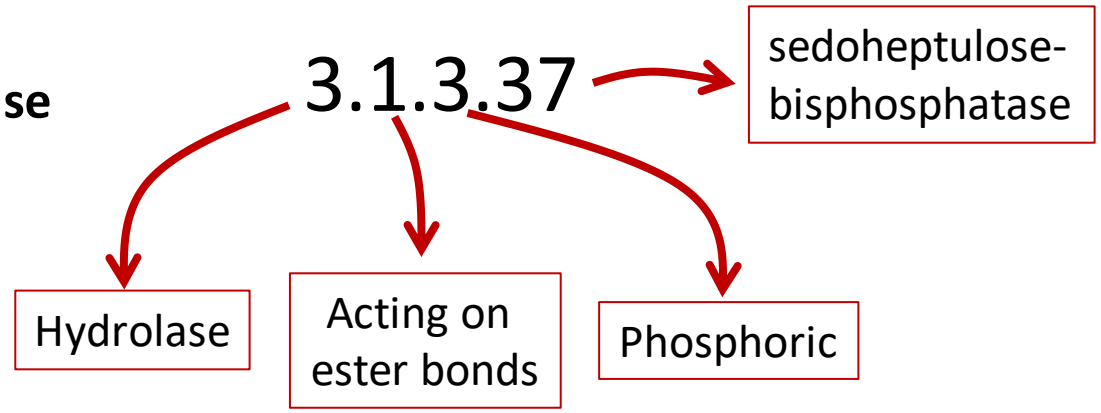
(i) the first number shows to which of the six main divisions (classes) the enzyme belongs,

(ii) the second figure indicates the subclass,

(iii) the third figure gives the sub-subclass,

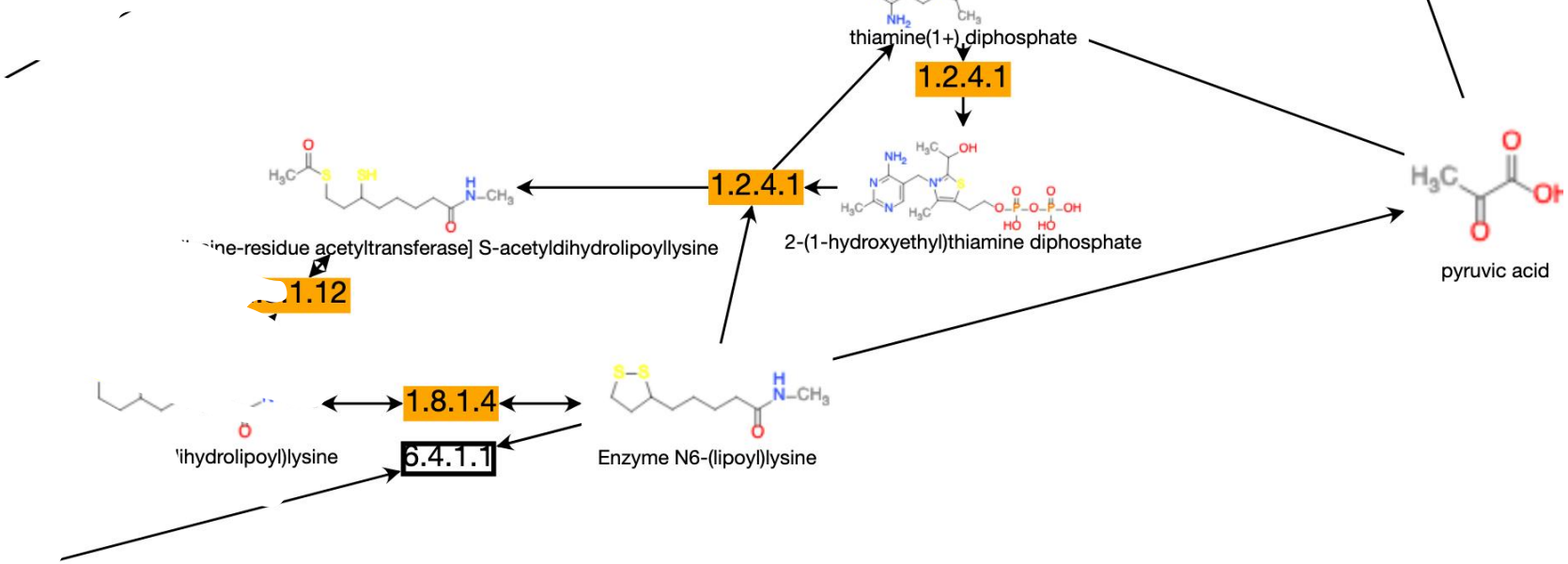
(iv) the fourth figure is the serial number of the enzyme in its sub-subclass.

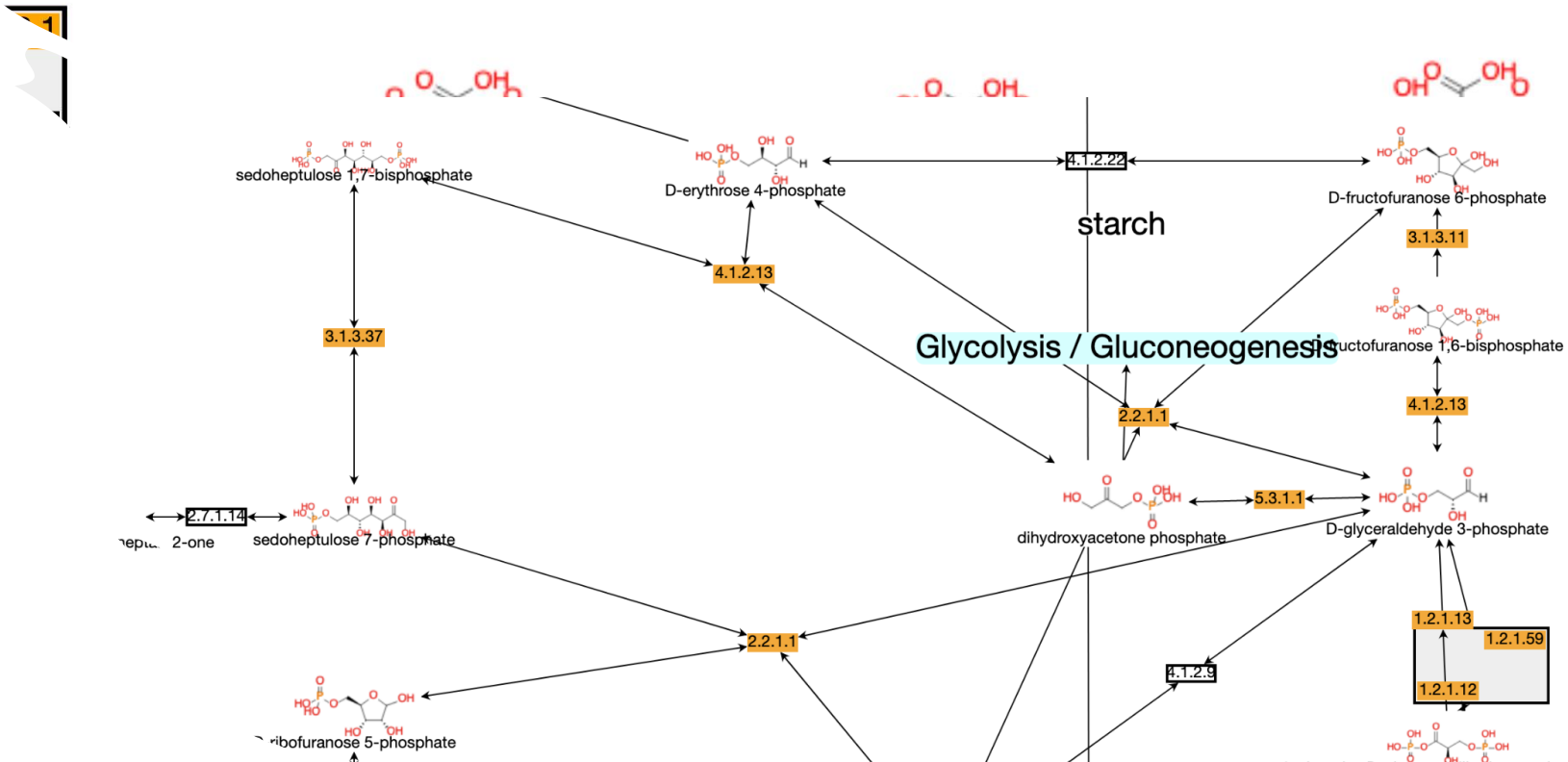
Example**: sedoheptulose-1,7-bisphosphatase**



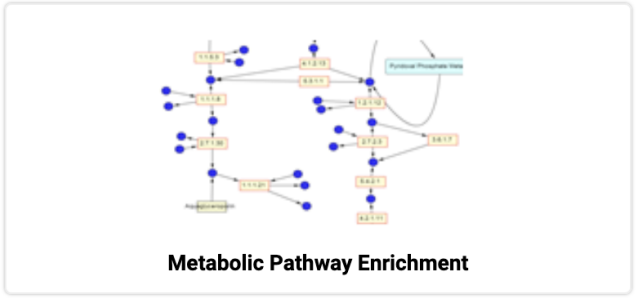
https://www.qmul.ac.uk/sbcs/iubmb/enzyme/

EC numbers can be used to link genes to pathways

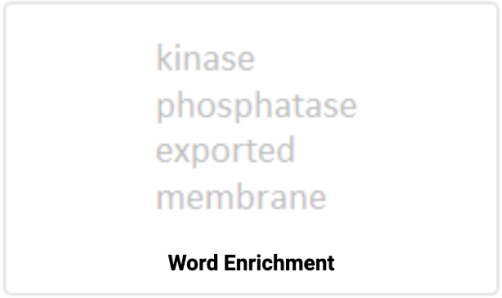




Gene Ontology Enrichment



Metabolic Pathway Enrichment



Word Enrichment

EC numbers and GO terms can be used in enrichment analysis!

- For example: Does my list of genes have an over-representation of specific GO terms compared to the rest of the genome?

- A standard enrichment method is Fisher's exact test which is a statistical test used when analyzing contingency tables. Typically used when you have a small sample size. But when you are doing enrichment analysis on a list of genes with the backgroung being the whole genome, your sample size is not small. As a results the P- value you get from a Fisher's exact test might be misleading.

- With a small sample size the a P-value of less than 0.05 is considered significant (5% chance of being wrong/random). But if you are doing an enrichment analysis with all genes in the genome then each gene can be considered a test so your chances of a type one error becomes higher. As a result you have to correct for this which can be done in different ways including Benjamini-Hochberg false discovery rate (FDR) or Bonferroni adjusted p-value

GO ID	GO Term	Genes in the bkgd with this term	Genes in your result with this term	Percent of bkgd genes in your result	Fold enrichment	Odds ratio	P-value	Benjamini	Bonferroni
GO:0004252	serine-type endopeptidase activity	363	18	5.0	7.44	10.12	1.47e-11	1.28e-9	1.28e-9
GO:0017171	serine hydrolase activity	388	18	4.6	6.96	9.41	4.45e-11	1.29e-9	3.87e-9
GO:0008236	serine-type peptidase activity	388	18	4.6	6.96	9.41	4.45e-11	1.29e-9	3.87e-9
GO:0004175	endopeptidase activity	497	18	3.6	5.43	7.19	2.46e-9	5.36e-8	2.14e-7
GO:0070011	peptidase activity, acting on L-amino acid peptides	659	20	3.0	4.55	6.13	5.60e-9	9.74e-8	4.87e-7
GO:0008233	peptidase activity	667	20	3.0	4.50	6.05	6.88e-9	9.98e-8	5.99e-7
GO:0004866	endopeptidase inhibitor activity	53	7	13.2	19.81	25.08	5.21e-8	6.47e-7	4.53e-6
GO:0061135	endopeptidase regulator activity	55	7	12.7	19.09	24.03	6.78e-8	7.38e-7	5.90e-6
GO:0030414	peptidase inhibitor activity	58	7	12.1	18.10	22.61	9.90e-8	9.57e-7	8.61e-6