

Gene Ontology解析

Shuji Shigenobu

重信 秀治

基礎生物学研究所
生物機能解析センター



What is Gene Ontology (GO)?

- ▶ GO project describes gene products from all organisms using a consistent and computable language.
- ▶ GO produces sets of explicitly defined, structured vocabularies in both a computer- and human-readable manner.
- ▶ 3 categories
 - ▶ Biological processes
 - ▶ Molecular functions
 - ▶ Cellular components
- ▶ 2 components
 - ▶ Ontology: term definition terms and the structured relationships between them
 - ▶ Associations between gene products and the GO terms.

Two components of GO

- ▶ Ontology
- ▶ Gene associations

Gene Ontology Consortium

Search GO data

Search for terms and gene products...

Search

Ontology

[Filter classes](#)

[Download ontology](#)

Gene Ontology: the framework for the model of biology. The GO defines concepts/classes used to describe gene function, and relationships between these concepts. It classifies functions along three aspects:

molecular function

molecular activities of gene products

cellular component

where gene products are active

biological process

pathways and larger processes made up of the activities of multiple gene products.

[more](#)

Annotations

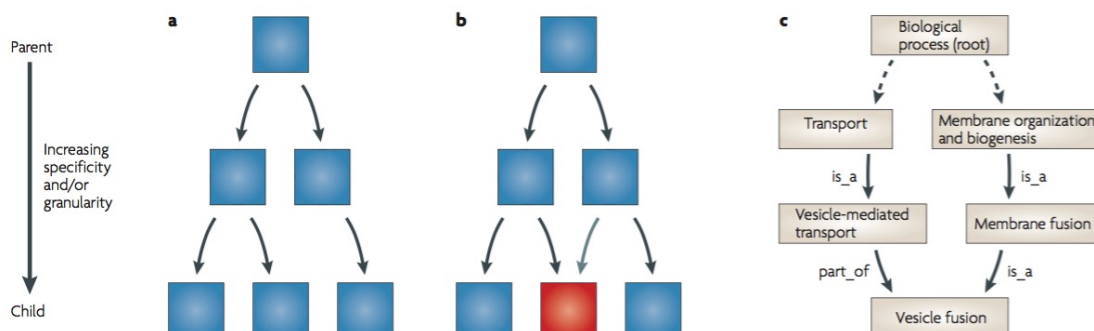
[Download annotations](#) (standard files)

[Filter and download](#) (customizable files <100k lines)

GO annotations: the model of biology. Annotations are statements describing the functions of specific genes, using concepts in the Gene Ontology. The simplest and most common annotation links one gene to one function, e.g. FZD4 + Wnt signaling pathway. Each statement is based on a specified piece of evidence. [more](#)

Ontology structure

- ▶ Ontologies are represented as a directed acyclic graph (DAG).
- ▶ Parent-child relationship
 - ▶ is_a
 - ▶ part_of
- ▶ Ontology can be changed / updated



vesicle fusion

Term Information ?

Accession GO:0006906

Name vesicle fusion

Ontology biological_process

Synonyms None

Alternate IDs None

Definition Fusion of the membrane of a transport vesicle with its target membrane. *Source:* GOC:jjd

Comment None

History See term [history for GO:0006906](#) at QuickGO

Subset None

Related [Link](#) to all **genes and gene products** annotated to vesicle fusion.

[Link](#) to all direct and indirect **annotations** to vesicle fusion.

[Link](#) to all direct and indirect **annotations download** (limited to first 10,000) for vesicle fusion.

Data health ▼

[Annotations](#)

[Graph Views](#)

[Inferred Tree View](#)

[Neighborhood](#)

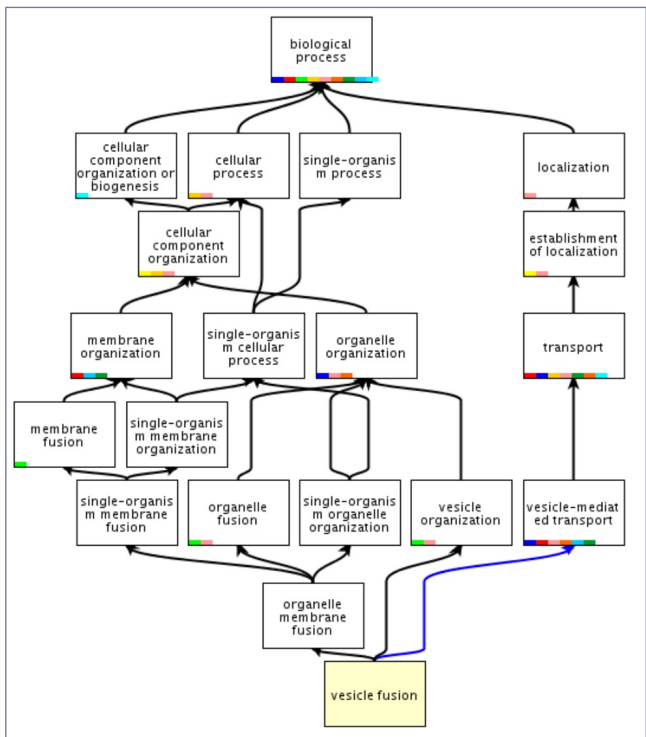
[Mappings](#)

- GO:0008150 biological_process
 - GO:0071840 cellular component organization or biogenesis
 - GO:0009987 cellular process
 - GO:0016043 cellular component organization
 - GO:0044699 single-organism process
 - GO:0051179 localization
 - GO:0061024 membrane organization
 - GO:0044763 single-organism cellular process
 - GO:0051234 establishment of localization
 - GO:0061025 membrane fusion
 - GO:0006996 organelle organization
 - GO:0044802 single-organism membrane organization
 - GO:0006906 vesicle fusion

<http://amigo.geneontology.org/amigo/term/GO:0006906>

- GO:0008150 biological_process
 - GO:0071840 cellular component organization or biogenesis
 - GO:0009987 cellular process
 - GO:0016043 cellular component organization
 - GO:0044699 single-organism process
 - GO:0051179 localization
 - GO:0061024 membrane organization
 - GO:0044763 single-organism cellular process
 - GO:0051234 establishment of localization
 - GO:0061025 membrane fusion
 - GO:0006996 organelle organization
 - GO:0044802 single-organism membrane organization
 - GO:0048284 organelle fusion
 - GO:0044801 single-organism membrane fusion
 - GO:1902589 single-organism organelle organization
 - GO:0006810 transport
 - GO:0090174 organelle membrane fusion
 - GO:0016050 vesicle organization
 - GO:0016192 vesicle-mediated transport
 - GO:0006906 vesicle fusion**
 - GO:0034058 endosomal vesicle fusion
 - GO:0048210 Golgi vesicle fusion to target membrane
 - GO:0031339 negative regulation of vesicle fusion
 - GO:0090385 phagosome-lysosome fusion
 - GO:0031340 positive regulation of vesicle fusion
 - GO:0031338 regulation of vesicle fusion
 - [capable_of part of relation] GO:0031201 SNARE complex
 - GO:0035493 SNARE complex assembly
 - GO:0099500 vesicle fusion to plasma membrane
 - GO:0048279 vesicle fusion with endoplasmic reticulum
 - GO:1990668 vesicle fusion with endoplasmic reticulum-Golgi int
 - GO:0048280 vesicle fusion with Golgi apparatus
 - GO:1990670 vesicle fusion with Golgi cis cisterna membrane
 - GO:0007086 vesicle fusion with nuclear membrane involved in r
 - GO:0019817 vesicle fusion with peroxisome
 - GO:0051469 vesicle fusion with vacuole
 - GO:0061782 vesicle fusion with vesicle

membrane




Gene association

- ▶ Gene <=> GO
- ▶ A gene may associate with multiple GO terms.
- ▶ Evidence codes.


| Evidence code | Evidence code description | Source of evidence | Manually checked |
|---------------|---|--|------------------|
| IDA | Inferred from direct assay | Experimental | Yes |
| IEP | Inferred from expression pattern | Experimental | Yes |
| IGI | Inferred from genetic interaction | Experimental | Yes |
| IMP | Inferred from mutant phenotype | Experimental | Yes |
| IPI | Inferred from physical interaction | Experimental | Yes |
| ISS | Inferred from sequence or structural similarity | Computational | Yes |
| RCA | Inferred from reviewed computational analysis | Computational | Yes |
| IGC | Inferred from genomic context | Computational | Yes |
| IEA | Inferred from electronic annotation | Computational | No |
| IC | Inferred by curator | Indirectly derived from experimental or computational evidence made by a curator | Yes |
| TAS | Traceable author statement | Indirectly derived from experimental or computational evidence made by the author of the published article | Yes |
| NAS | Non-traceable author statement | No 'source of evidence' statement given | Yes |
| ND | No biological data available | No information available | Yes |
| NR | Not recorded | Unknown | Yes |

nanos

Gene Product Information 

http://amigo.geneontology.org/amigo/gene_product/FB:FBgn0002962

Symbol nos
Name(s) nanos

Total annotations: 29; showing: 1-10
Results count: 10 

[«First](#) [<Prev](#) [Next>](#) [Last>](#) [Download \(up to 100000\)](#)

| <input type="checkbox"/> Gene/product | Gene/product name | Annotation qualifier | GO class (direct) | Annotation extension | Contributor | Organism | Evidence | Evidence with | PANTHER family | Isoform | Reference |
|---------------------------------------|-------------------|----------------------|---|----------------------|-------------|-------------------------|----------|----------------|-------------------------|---------|--------------------------------|
| <input type="checkbox"/> nos | nanos | | germ cell migration | | FlyBase | Drosophila melanogaster | TAS | | nanos protein pthr12887 | | FB:FBn0107500
PMID:9988212 |
| <input type="checkbox"/> nos | nanos | | oogenesis | | FlyBase | Drosophila melanogaster | IMP | | nanos protein pthr12887 | | FB:FBn0107609
PMID:10101171 |
| <input type="checkbox"/> nos | nanos | | spermatogenesis | | FlyBase | Drosophila melanogaster | IMP | | nanos protein pthr12887 | | FB:FBn0107609
PMID:10101171 |
| <input type="checkbox"/> nos | nanos | | pole plasm | | FlyBase | Drosophila melanogaster | TAS | | nanos protein pthr12887 | | FB:FBn0110978
PMID:10449356 |
| <input type="checkbox"/> nos | nanos | | anterior/posterior axis specification, embryo | | FlyBase | Drosophila melanogaster | TAS | | nanos protein pthr12887 | | FB:FBn0111327
PMID:10494038 |
| <input type="checkbox"/> nos | nanos | | oocyte anterior/posterior axis specification | | FlyBase | Drosophila melanogaster | NAS | | nanos protein pthr12887 | | FB:FBn0128774
PMID:10878576 |
| <input type="checkbox"/> nos | nanos | | protein binding | | FlyBase | Drosophila melanogaster | IPI | FB:FBgn0000392 | nanos protein pthr12887 | | FB:FBn0131417
PMID:11060247 |
| <input type="checkbox"/> nos | nanos | | germ-line stem cell division | | FlyBase | Drosophila melanogaster | NAS | | nanos protein pthr12887 | | FB:FBn0132358
PMID:11131516 |
| <input type="checkbox"/> nos | nanos | | protein binding | | UniProt | Drosophila melanogaster | IPI | FB:FBgn0010300 | nanos protein pthr12887 | | FB:FBn0135777
PMID:11274060 |
| <input type="checkbox"/> nos | nanos | | female meiosis chromosome segregation | | FlyBase | Drosophila melanogaster | IMP | | nanos protein pthr12887 | | FB:FBn0135802
PMID:11290718 |

How to annotate GO for non-model organisms?

- ▶ Ortholog grouping with a model organism and then transfer the GO terms from the reference organism to your target organism.
- ▶ BLAST2GO
- ▶ InterProScan

Gene Ontology enrichment analysis

- ▶ What is GO enrichment analysis?
- ▶ Why GO enrichment analysis is required in DEG studies?
- ▶ Type of GO enrichment analysis.
 - ▶ gene set
 - ▶ gene score
- ▶ Software
 - ▶ gene set type: DAVID (web), metascape (web), goseq (R), GOstat (R)
 - ▶ gene score: GSEA, roast, camera
 - ▶ both: ErmineJ

Basic over-representation test: 2 x 2 table and Fisher's exact test

- ▶ Suppose we perform a test of DE and find a list of 200 significant genes out of 10,000
- ▶ Consider a specific GO term, apoptosis. Among the 200 DE genes, 20 genes are annotated as apoptosis related, while 300 / 10,000 are associated with apoptosis in the whole gene set.
- ▶ Question: Is the gene set “apoptosis” over-represented among “significant” genes?

| | apoptosis | non-apoptosis | total |
|--------|-----------|---------------|--------|
| DE | 20 | | 200 |
| non-DE | | | |
| total | 300 | | 10,000 |

| | apoptosis | non-apoptosis | total |
|--------|-----------|---------------|--------|
| DE | 20 | 180 | 200 |
| non-DE | 280 | 9,520 | 9,800 |
| total | 300 | 9,700 | 10,000 |

```
> mat <- matrix(c(20,200-20,300-20, 10000-300-(200-20)),
nrow=2, byrow=T)
> fisher.test(mat, alternative="greater")
```

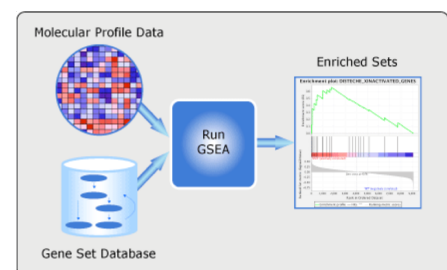
Fisher's Exact Test for Count Data

```
data:  mat
p-value = 2.269e-06
alternative hypothesis: true odds ratio is greater than 1
95 percent confidence interval:
 2.418508      Inf
sample estimates:
odds ratio
 3.777069
```

Gene score type enrichment analysis

- ▶ Drawback of basic 2x2 table method
 - ▶ Threshold value is arbitral
 - ▶ Magnitude of significance is ignored

- ▶ GSEA
 - ▶ <http://software.broadinstitute.org/gsea/index.jsp>
- ▶ ROAST, CAMERA
 - ▶ implemented within edgeR



Tutorial: ErmineJ

演習問題 ex11

▶ <http://erminej.chibi.ubc.ca/>



- ▶ Easy to use Java software with both GUI and CUI
- ▶ Three enrich methods supported
 - ▶ ORA: overrepresentation analysis
 - ▶ GSR: gene score resampling
 - ▶ ROC: rank-based gene score in receiver-operator curves