

Performing biological interpretation

- [Enrichment analysis](#)
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To learn more about the biology underlying gene expression changes, we can use gene ontology (GO) or pathway enrichment analysis. Enrichment analysis identifies over-represented GO terms or pathways in a filtered list of genes.

Enrichment analysis

- Click the filtered **Filtered feature list** data node
- Click **Biological interpretation** in the task menu
- Click **Gene set enrichment** then select **Gene set database** to perform GO enrichment analysis (Figure 1)

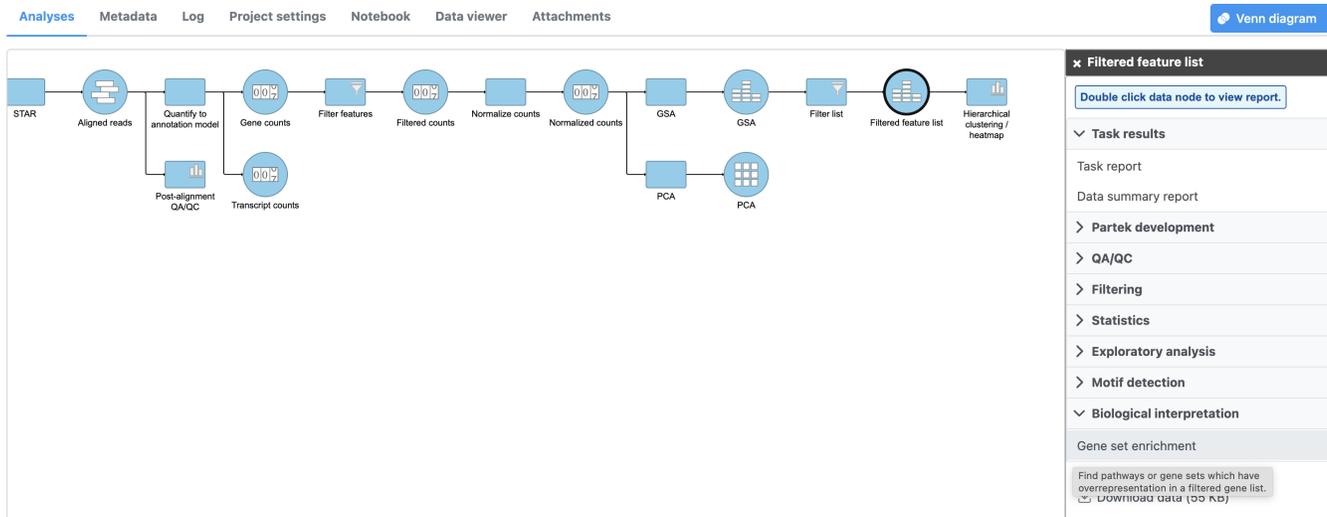
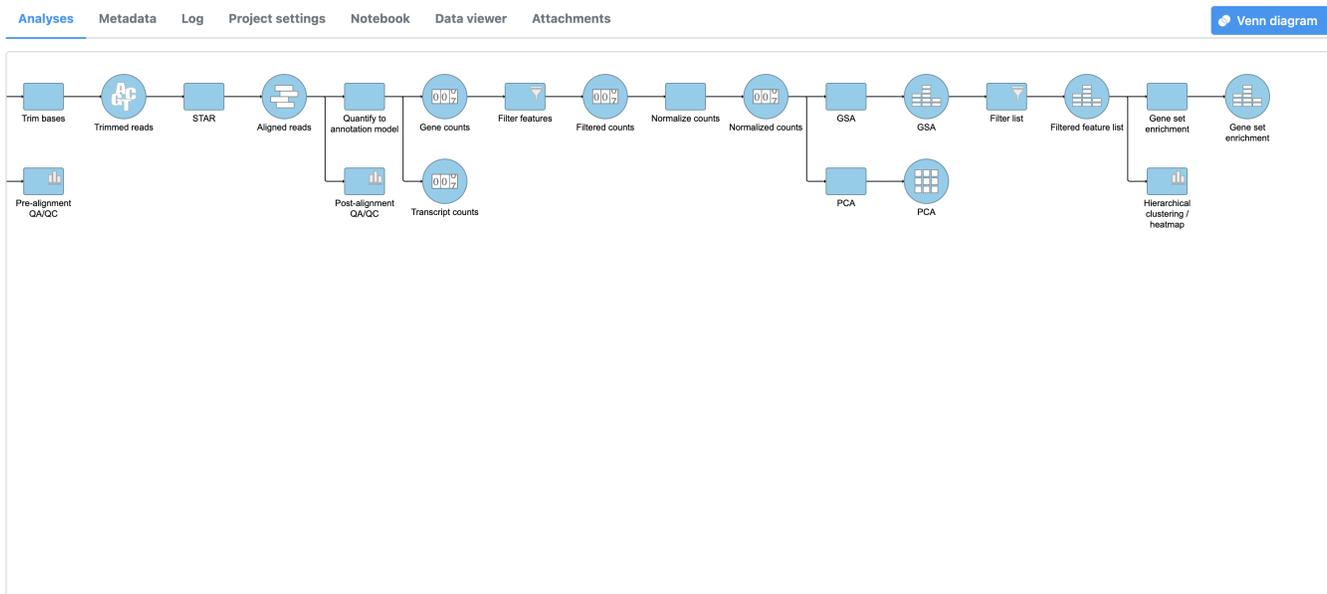


Figure 6. Invoking Enrichment analysis

- Select the latest gene set from geneontology.org from the *Gene set database* drop-down menu
- Click **Finish**

A *GO enrichment* task node will be added to the pipeline (Figure 2).



[Create new pipeline](#) [Import pipeline](#)

Figure 7. Enrichment task node

- Double-click the **Gene set enrichment** task node to open the task report (Figure 3)

Gene set ↑↓	Description ↑↓	Type ↑↓	Enrichment score ↑↓	P-value ↑↓	FDR step up ↑↓	Rich factor ↑↓	Genes in set ↑↓	Genes in list ↑↓	Genes not in list ↑↓	Genes in list, not in set ↑↓	Genes not in list, not in set ↑↓	
GO:0051703	biological process involved in intraspecies interaction between organisms	biological process	6.74	1.18E-3	1.00	0.75	4	3	1	26	385	☰ ☰
GO:0031644	regulation of nervous system process	biological process	6.74	1.18E-3	1.00	0.75	4	3	1	26	385	☰ ☰
GO:0035176	social behavior	biological process	6.74	1.18E-3	1.00	0.75	4	3	1	26	385	☰ ☰
GO:0043648	dicarboxylic acid metabolic process	biological process	5.35	4.73E-3	1.00	1.00	2	2	0	27	386	☰ ☰
GO:0071162	CMG complex	cellular component	5.35	4.73E-3	1.00	1.00	2	2	0	27	386	☰ ☰
GO:1901606	alpha-amino acid catabolic process	biological process	5.35	4.73E-3	1.00	1.00	2	2	0	27	386	☰ ☰
GO:0000724	double-strand break repair via homologous recombination	biological process	5.35	4.73E-3	1.00	1.00	2	2	0	27	386	☰ ☰
GO:0000725	recombinational repair	biological process	5.35	4.73E-3	1.00	1.00	2	2	0	27	386	☰ ☰
GO:0000727	double-strand break repair via break-induced replication	biological process	5.35	4.73E-3	1.00	1.00	2	2	0	27	386	☰ ☰
GO:0003688	DNA replication origin binding	molecular function	5.35	4.73E-3	1.00	1.00	2	2	0	27	386	☰ ☰
GO:0031261	DNA replication preinitiation complex	cellular component	5.35	4.73E-3	1.00	1.00	2	2	0	27	386	☰ ☰
GO:0006268	DNA unwinding involved in DNA replication	biological process	5.35	4.73E-3	1.00	1.00	2	2	0	27	386	☰ ☰

Figure 8. Viewing the GO enrichment task report

The *GO enrichment* task report spreadsheet lists GO terms by ascending p-value with the most significant GO term at the top of the list. Also included are the enrichment score, the number of genes from that GO term in the list, and the number of genes from that GO term that are not in the list.

To view the genes associated with each GO term, select  to open the extra details page. To view additional information about a GO term, click the blue gene set ID to open the linked geneontology.org entry in a new tab.

For more information about GO enrichment analysis, please see the [Gene Set Enrichment](#) user guide.

KEGG enrichment analysis

KEGG enrichment analysis identifies pathways that are over-represented in a gene list data node.

- Click the filtered **Filtered feature list** data node
- Click **Biological interpretation** in the task menu
- Click **Gene set enrichment** then select **KEGG database**
- Click **Finish** in the configuration dialog to run KEGG analysis with the *Homo sapiens* KEGG database

A *Pathway enrichment* task node will be added to the pipeline (Figure 4).

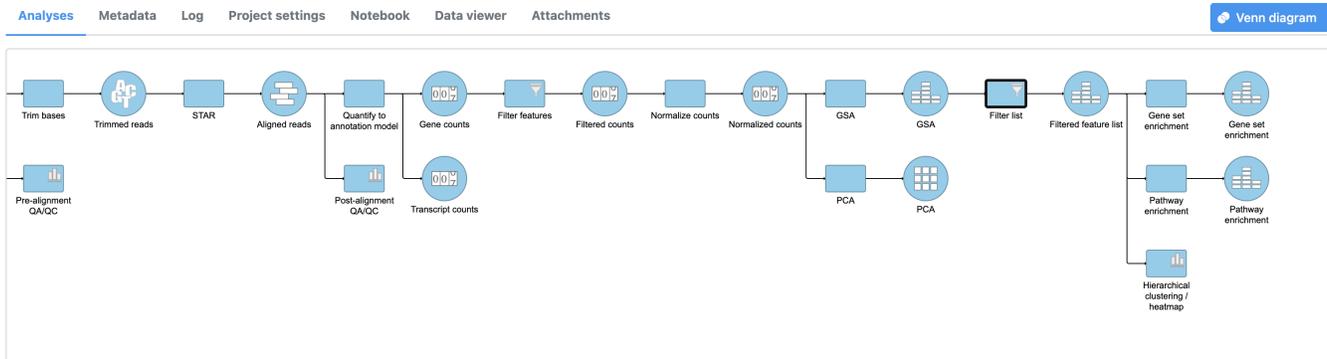


Figure 9. *Pathway enrichment* task node

- Double-click the **Pathway enrichment** task node to open the task report

The *Pathway enrichment* task report is similar to the *Enrichment analysis* task report (Figure 5).

Gene set ↑↓	Description ↑↓	Enrichment score ↑↓	P-value ↑↓	FDR step up ↑↓	Rich factor ↑↓	Genes in set ↑↓	Genes in list ↑↓	Genes not in list ↑↓	Genes in list, not in set ↑↓	Genes not in list, not in set ↑↓	
path:hsa04724	Glutamatergic synapse	3.20	0.04	1.00	0.50	4	2	2	14	161	🔍 📄
path:hsa04672	Intestinal immune network for IgA production	2.41	0.09	1.00	1.00	1	1	0	15	163	🔍 📄
path:hsa00430	Taurine and hypotaurine metabolism	2.41	0.09	1.00	1.00	1	1	0	15	163	🔍 📄
path:hsa04740	Olfactory transduction	2.41	0.09	1.00	1.00	1	1	0	15	163	🔍 📄
path:hsa03030	DNA replication	2.41	0.09	1.00	1.00	1	1	0	15	163	🔍 📄
path:hsa05340	Primary immunodeficiency	2.41	0.09	1.00	1.00	1	1	0	15	163	🔍 📄
path:hsa00240	Pyrimidine metabolism	2.41	0.09	1.00	1.00	1	1	0	15	163	🔍 📄
path:hsa05143	African trypanosomiasis	2.41	0.09	1.00	1.00	1	1	0	15	163	🔍 📄
path:hsa00260	Glycine, serine and threonine metabolism	2.41	0.09	1.00	1.00	1	1	0	15	163	🔍 📄
path:hsa00330	Arginine and proline metabolism	2.41	0.09	1.00	1.00	1	1	0	15	163	🔍 📄
path:hsa05150	Staphylococcus aureus infection	2.41	0.09	1.00	1.00	1	1	0	15	163	🔍 📄

Figure 10. *Pathway enrichment* task report

To view an interactive KEGG pathway map, click the pathway ID (*Gene set* column).

« [Generating a hierarchical clustering heatmap](#) [Saving and running a pipeline](#) »

Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



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