E.PathDash User Guide

Welcome

E.PathDash, ESKAPE Pathogen Pathway Dashboard, enables researchers to analyze cellular pathways using high-throughput gene expression data for ESKAPE pathogens from the Gene Expression Omnibus. The data has been processed for cellular pathway analysis of KEGG pathways and GO terms, common annotation databases.

This tool facilitates comparison of pathway activation across experimental conditions and studies, as well as targeted data exploring using a pathway of interest. For more information on each dashboard page, please refer to the "Study Explorer Info", "Pathway Explorer Info", "Term Explorer Info" and "Study Comparison Info" buttons.

Start your search by selecting a bacterial species and strain(s) of interest from **"Study Filters"**.

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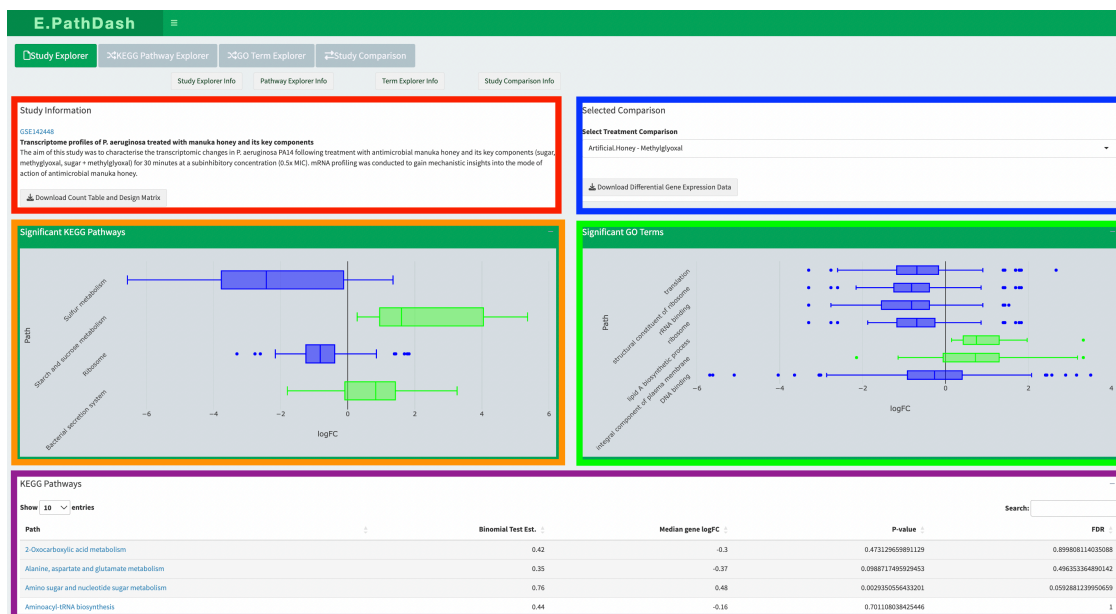4. Study Comparison
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Study Explorer

How to Use

Select a bacterial species, strain and GEO study in the filter sidebar. The page will populate with metadata and KEGG pathway/GO Term activation/repression information corresponding to the GEO study.

Page Components

1. **Study Information** Link to GEO study page, title and short study description
2. **Selected Comparison** Dropdown to select the study comparisons for which to view pathway/term analysis information. The pathways and terms are activated or repressed in the first sample group compared to the second sample group.
3. **Significant KEGG Pathways** A boxplot showing the distribution of the logFC values for genes in that significantly activated or repressed KEGG pathway. Significance is determined by a FDR value of <0.05 after conducting pathway analysis.
4. **Significant GO Terms** A boxplot showing the distribution of the logFC values for genes in that significantly activated or repressed GO term. Significance is determined by a FDR value of <0.05 after conducting pathway analysis.
5. **KEGG Pathway** A table of all KEGG pathways analyzed with corresponding binomial test statistic, median logFC value for genes in the pathway, P-value and FDR value for significance level of activation/repression. Pathway names link to functional pathway maps, with differentially expressed genes colored according to over (green) or under (blue) expression.
6. **GO Terms** A table of all GO terms analyzed with corresponding binomial test statistic, median logFC value for genes in the pathway, P-value and FDR value for significance level of activation/repression.
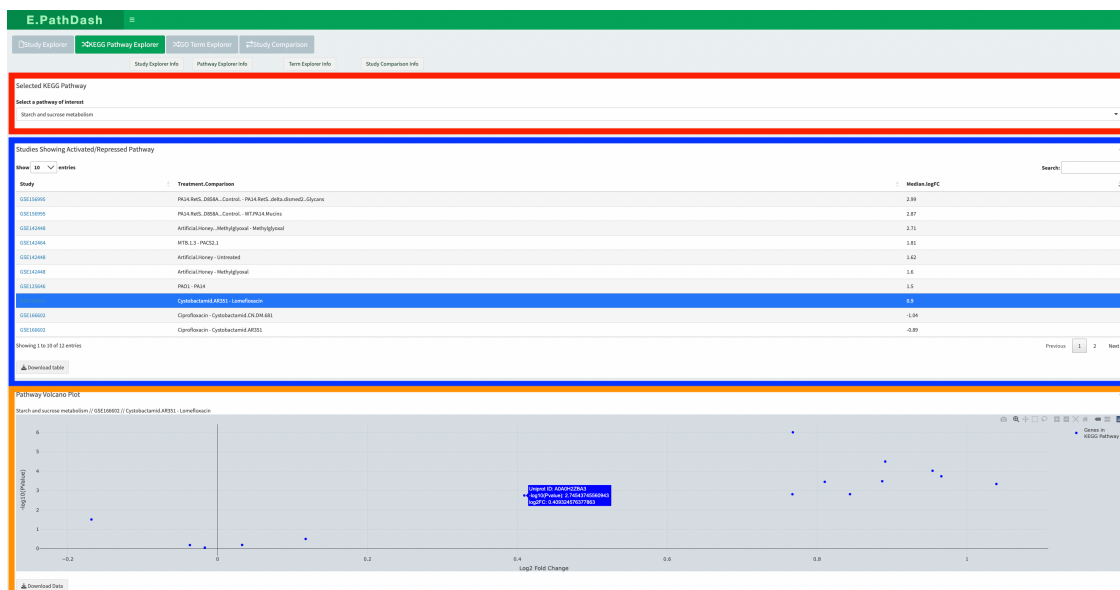
KEGG Pathway Explorer

How to Use

Explore the compendium of study data by a KEGG pathway of interest. Select a bacterial species for which to view KEGG pathways. After selecting a particular pathway, view studies and treatment comparisons in which that pathway was significantly activated or repressed.

Page Components

1. **Pathway Selection** Dropdown of KEGG pathways for bacterial species specified in filter.
2. **Study Table** List of studies for which the selected KEGG pathway was significantly activated or repressed. Information includes corresponding treatment comparison within the study for which the pathway was activated/repressed and median logFC of genes within the pathway. Study ID links to GEO page describing study.
3. **Pathway Volcano Plot** Selecting a row from the study table shows a volcano plot for the genes within that pathway. Hovering over a point shows the Uniprot ID of the gene along with its logFC between comparison groups and transformed P-value.

GO Term Explorer

How to Use

Explore the compendium of study data by a GO term of interest. Select a bacterial species for which to view GO terms. After selecting a particular term, view studies and treatment comparisons in which that term was significantly activated or repressed.

Page Components

1. **Term Selection** Dropdown of GO terms for bacterial species specified in filter.
2. **Study Table** List of studies for which the selected GO term was significantly activated or repressed. Information includes corresponding treatment comparison within the study for which the term was activated/repressed and median logFC of genes within the term. Study ID links to GEO page describing study.
3. **Term Volcano Plot** Selecting a row from the study table shows a volcano plot for the genes within that term. Hovering over a point shows the Uniprot ID of the gene along with its logFC between comparison groups and transformed P-value.

Study Comparison

How to Use

Explore common activated or repressed KEGG pathways and GO terms between studies. After filtering GEO studies by bacterial species and strain, you can select two studies for which to compare pathway analyses.

Page Components

1. **Select Studies** Dropdowns of GEO studies to compare.
2. **Pathway/Term Table** List of KEGG pathways and GO terms that are significantly activated or repressed in both selected studies.
3. **Process Activation/Repression Bar Plots** Selecting a pathway/term from the table populates bar plots representing the pathway or term's activation/repression level across the comparisons in each study. Activation/repression level is symbolized by the median logFC value for genes in the pathway/term under the comparison. Hovering over the bars shows the corresponding sample comparison.
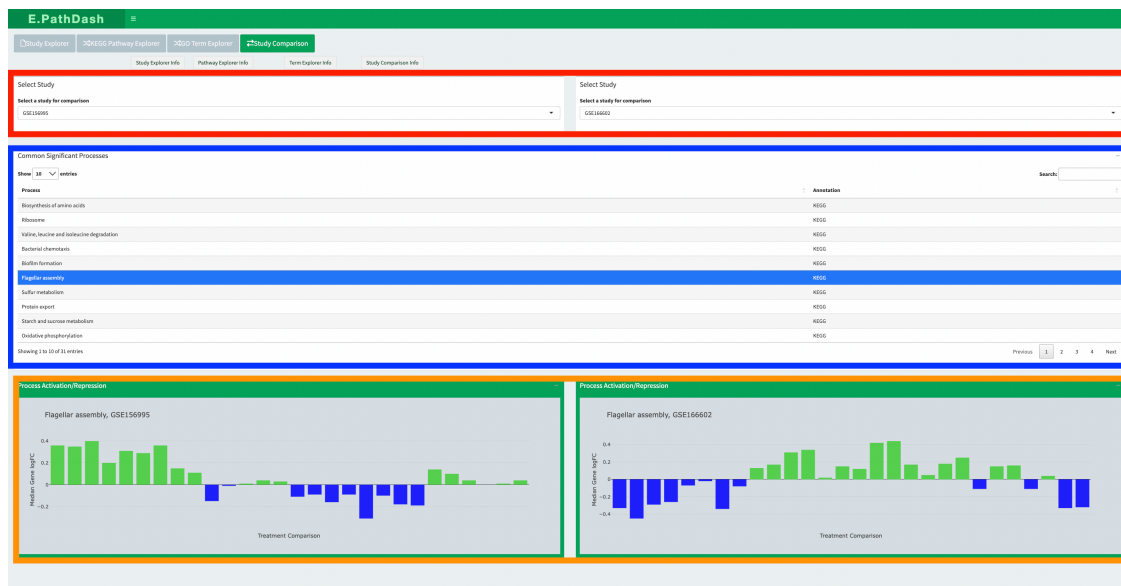
Supported Species

Table of bacterial species and strains supported by E.PathDash

Species	Strain	Link
Staphylococcus aureus	Newman	https://www.ncbi.nlm.nih.gov/datasets/taxonomy/426430/
Staphylococcus aureus	USA300	https://www.ncbi.nlm.nih.gov/datasets/taxonomy/367830/
Pseudomonas aeruginosa	PAO1	https://www.ncbi.nlm.nih.gov/datasets/taxonomy/208964/
Pseudomonas aeruginosa	PA14	https://www.ncbi.nlm.nih.gov/datasets/taxonomy/652611/
Bacteroides thetaiotaomicron	VPI-5482	https://www.ncbi.nlm.nih.gov/datasets/taxonomy/226186/
Streptococcus sanguinis	SK36	https://www.ncbi.nlm.nih.gov/datasets/taxonomy/388919/

Studies

Table of NCBI studies whose gene expression data composes the backend of E.PathDash.

Date	GEO.Accession	Strain	Link
11/2/20	GSE124385	PA14	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE124385
9/23/19	GSE125646	PA14, PAO1	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE125646
4/6/20	GSE142448	PA14	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE142448
1/2/20	GSE142464	PA14, MTB-1, B136-33, CF5, C3719, PACS2	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE142464
4/14/20	GSE148597	PA14	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE148597
8/28/20	GSE156995	PA14	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE156995
5/3/21	GSE166602	PA14	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE166602
6/8/17	GSE87213	PA14	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE87213
6/30/18	GSE110445	PAO1	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE110445
12/5/18	GSE123356	PAO1	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE123356
6/4/20	GSE130190	PAO1	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE130190
11/15/19	GSE136111	PAO1	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE136111
10/11/19	GSE138731	PAO1	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE138731
12/16/20	GSE163248	PAO1	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE163248
7/1/21	GSE179150	PAO1	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE179150
12/1/16	GSE71880	PAO1	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE71880
4/26/19	GSE129572	VPI-5482	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE129572
11/1/18	GSE122048	Newman	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE122048
1/29/19	GSE125741	USA300, AH1292, AH1263	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE125741
5/7/19	GSE130777	USA300, AH1263, AH3455	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE130777
6/12/19	GSE132179	USA300, JE2	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE132179
2/12/21	GSE148024	USA300, Cowan, Clinical isolates	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE148024
3/8/17	GSE89964	SK36	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89964
6/1/19	GSE90021	SK36	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE90021
3/30/18	GSE97218	SK36	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE97218
4/3/18	GSE97357	SK36	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE97357