

DEATS

VERSION 1.00

TITLE Differential Expression Anatomy Term Sheets

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Overview

How the DEATS Generator Works

By reviewing scientific research, the ZFIN database has been gathering data that connects zebrafish genes (starting with ENSDARGs) to zebrafish anatomy (ZFA & BSPO). The DEATS Generator leverages this information to help label unidentified cell-types from single-cell RNA seq. Our program goes into the ZFIN database, finds the zebrafish anatomy associated with the zebrafish genes the user has input, and generates a *differentially expressed anatomy term sheet*, or DEATS, table, displaying which anatomy terms are associated with the input and how many times these anatomy terms were found.

Why make a DEATS table?

DEATS tables were envisioned by the ZFIN organization as a method for labeling unidentified cell-types using single-cell RNA sequencing data. Single-cell RNA sequencing data, which can show genes differentially expressed between cell-types, provide tremendous insight into the differences between an organism, or a tissue's, cell-types. Unfortunately, one of the things currently unautomated is the use of data to label the cell-types present organism or tissue. The DEATS generator looks to solve this problem by using the expertly curated ZFIN database to create a simple table which shows the anatomy most often associated with the cell-types differentially expressed genes. In most cases the top values in the DEATS table can be used to determine a suitable label for the unidentified cell-type of interest.

This program uses the published anatomical locations of a gene's expression and a list of Differentially Expressed Genes for a Cell-Type to create a Differentially Expressed Anatomy Terms Sheet (DEATS). DEATS can be used to annotate one or multiple zebrafish cell-types.

TERMS:

Pete Score: $\text{Ratio of (Pct-1/ Pct-2) * Avg Log FC}$

Where,

Pct1 – Percentage of genes differentially expressed in a cluster

Pct2 – Percentage of genes differentially expressed in all cluster

Avg Log FC – Average Log Fold Change

2. How to use this tool:

1. Inputs

- a. Choose Developmental stage you are interested in, from the drop-down menu.

e.g.



1. Choose Developmental Stage

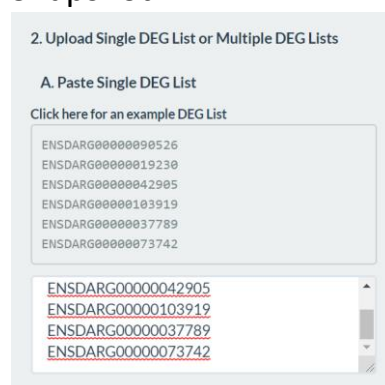
All Stages

In this example, we choose **All Stages**.

- b. Upload a list of Differentially Expressed Genes OR Multiple DEG Lists

In this example, we choose '[Click here for an example DEG List](#)' option.

Snapshot



2. Upload Single DEG List or Multiple DEG Lists

A. Paste Single DEG List

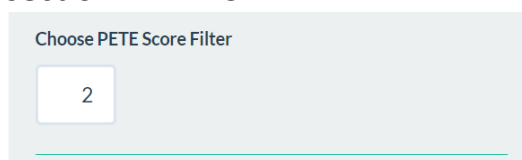
[Click here for an example DEG List](#)

ENSDARG00000090526
ENSDARG00000019230
ENSDARG00000042905
ENSDARG000000103919
ENSDARG00000037789
ENSDARG00000073742

[ENSDARG00000042905](#)
[ENSDARG000000103919](#)
[ENSDARG00000037789](#)
[ENSDARG00000073742](#)

- c. You can also use sample list which is already loaded in the box.

2. Choose PETE score. More explanation of PETE score can be found in section '**TERMS**'



Choose PETE Score Filter

2

3. Run!

Click on the '**Go**' button to start your data annotation.

4. Results

Based on Pete score, the program ranks the genes in each cluster in ascending order.

There are total 3 outputs:

1. Anatomy Term 2.Count 3. P value

Example snapshot:

Anatomy Term	Count	p val
brain	1	0.27
eye	1	0.69
immature eye	1	0.59
lens	1	0.44
musculature system	1	0.24
myotome	1	0.59
neural plate	1	0.47
presumptive neural plate	1	0.04

This program outputs list of anatomy terms associated with a particular cell cluster. All the results are in the tab called '**DEATS**'. Move over to the DEATS tab to view the results. The user can view as well as download the results as per the number of clusters through '**Download DEATS**' button.

A rectangular button with a dark grey background and white text that reads "Download DEATS". To the left of the text is a small white icon of a download arrow pointing into a document.

If the user is interested in a particular annotation term, the user has an option to search for the terms in cell-type annotation search-box

Cell-Type Annotation

Submit

[Read more about cell-type annotations here](#)

On the top-right corner, user also has an option to view Gene symbols by clicking '**See Gene Symbols**' button.