

timelineCreator.py is located at: in the "gene-timelines" folder on the carleton-spacehogs github page.

This Python script can create the figure above using the output from Jimmy's pipeline. Using either Deming or Baross you can run this script to create the timeline figure above using the steps below.

Create a relation file:

The script requires a CSV with the format in the table below so that the script knows which eccetterra output files to use.

Gene ID	Gene Name	Function
K03520	coxL	Carbon
Whatever ID was used to run gene in pipeline	Used for y-axis title	Categorical Identifier for experiment

^{**}Header names are required to be verbatim for script to work**

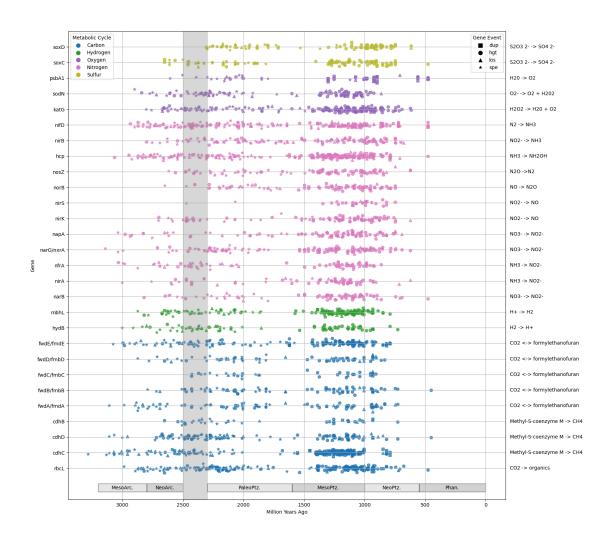
The sample relation file can be found at: ... to create the graph above.

As long as the spelling for each categorical variable is the same the script will automatically determine the function names from the relation file.

An example relation file can be found in carleton-spacehogs/timeline-creator github page as: relation_no_annotation.csv

Annotated timeline (optional)

If each timeline needs to be annotated in the timeline like in the graph below you can add an additional column to the relation file as seen below.



Gene ID	Gene Name	Function	Annotation
K03520	coxL	Carbon	CO -> CO2
Whatever ID was used to run file	Used for y-axis title	Categorical Identifier for experiment	Text to be annotated

^{**}Header names are required to be verbatim for script to work**

With a properly formatted 3-column or 4-column csv you can then run the script.

An example relation file can be found in carleton-spacehogs/timeline-creator github page as: relation_annotation.csv

USAGE

Python3 timelineCreator.py [relation file] [ecceterra output path] [output figure name]

Example usage:

python3 timelineCreator.py master1.csv

/workspace/data/Space_Hogs_shared_workspace/tree-reconciliation/cir1_ecceTERA_analysis/outputTest4.png

To change the title of the legend for function change the string on line 36 of timelineCreator.py