degenome

Release 0.0.1

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CONTENTS

DEGenome transforms differential gene expression (DGE) data to Ideogram JSON.

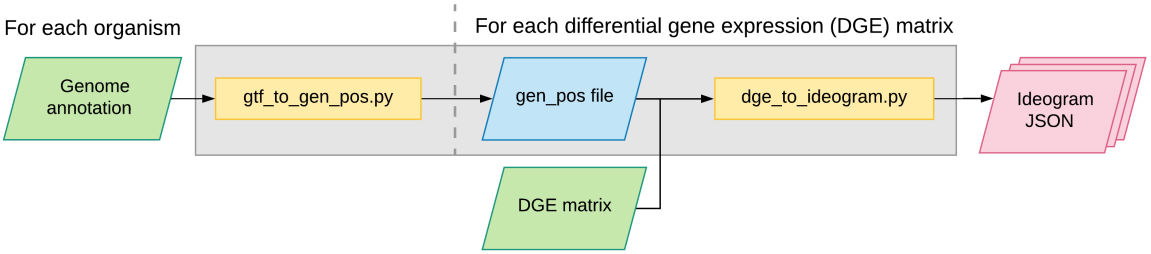
Written in Python, the DEGenome pipeline takes in genome annotations and DGE matrices, and outputs Ideogram.js JSON annotation files.

You can then upload Ideogram JSON to the cloud, and explore it in an interactive genome visualization at https://eweitz.github.io/ideogram/differential-expression.

For a walk-through example, see the DEGenome tutorial on Terra.

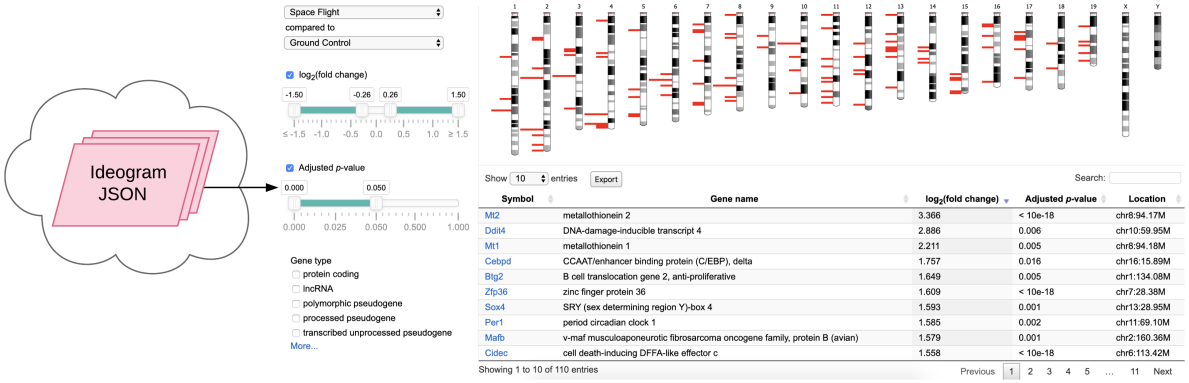
Explore differential expression across the genome

1. Run DEGenome pipeline



2. Upload your Ideogram JSON to the cloud

3. Go to https://eweitz.github.io/ideogram/differential-expression?annots-url=<your-annots-url>



CHAPTER

ONE

INSTALLATION

Run:

```
pip install degenome
```

Next, try the tutorial.

CHAPTER

TWO

REDUCE GTF

Each organism processed by DEGenome will need a reduced GTF, i.e. a "gen_pos.tsv" file.

The *gtf_to_gen_pos.py* CLI module converts a GTF genome annotation file from GENCODE, Ensembl, or NCBI into a smaller, simpler, and more metadata-rich TSV gene position ("gen_pos") file. The purpose is to speed up, simplify, and enrich downstream pipelines that require only data on genes, and not e.g. transcripts or exons.

2.1 Example GTF files

- Human (Homo sapiens), from GENCODE
- Mouse (Mus musculus), from GENCODE
- Thale cress (Arabidopsis thaliana), from Ensembl
- Worm (Caenorhabditis elegans), from Ensembl
- Rat (Rattus norvegicus), from Ensembl

CHAPTER

THREE

TRANSFORM DGE MATRIX

Each differential gene expression (DGE) matrix needs to be transformed to Ideogram JSON.

The dge_to_ideogram.py CLI module converts a DGE matrix file containing gene expression summary statistics into an Ideogram.js annotations JSON file. The resulting JSON file is used for exploratory data analysis as demonstrated at:

https://eweitz.github.io/ideogram/differential-expression

3.1 DGE matrix format

The DGE matrix has several groups of columns, with headers ordered like so:

- metadata: "REFSEQ","SYMBOL","GENENAME","ENSEMBL","ENTREZID","STRING_id","GOSLIM_IDS"
- replicates: <sample_prefix>-<group>-<replicate_number>, e.g. "Mmus-C57-6T-TMS-FLT-Rep1"
- stats: "All.mean","All.stdev","F.p.value"
- stats_by_group: Group.<stat>_(<group>), e.g. "Group.Mean_(Space Flight)"
- stats_by_comparison: <stat>_(<group1>)v(<group2>), e.g. "Log2fc_(Ground Control)v(Space Flight)"

3.2 Example DGE matrix

An example DGE matrix is GLDS-21_array_differential_expression.csv from GLDS-21, produced by NASA GeneLab. Below is an excerpt.

```
# Download example DGE matrix
curl -L https://genelab-data.ndc.nasa.gov/genelab/static/media/dataset/GLDS-21_array_
↪differential_expression.csv?version=1 > GLDS-21_array_differential_expression.csv

# Print first 10 lines of example DGE matrix
head GLDS-21_array_differential_expression.csv
"REFSEQ","SYMBOL","GENENAME","ENSEMBL","ENTREZID","STRING_id","GOSLIM_IDS","Mmus-C57-
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```

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CHAPTER

FOUR

TUTORIAL

For a walk-through example of using DEGenome to convert a differential gene expression matrix to Ideogram JSON, see the "DEGenome tutorial" Jupyter Notebook on Terra.