miRNA-Disease Database & Network Tool

Description

This command-line interface (CLI) tool is designed for bioinformatics research, specifically focusing on microRNAs (miRNAs) and their associations with diseases. With CLI, users can effortlessly query a local database to find diseases associated with a given miRNA or vice versa, and to browse available miRNAs and diseases. Its primary goal is to streamline the research process in understanding gene regulation and disease mechanisms through miRNA studies.

Installation

• Ensure Python and pandas are installed on your system.
• Download the **tools_v1.py** script and the **clean_data.tsv** database file.
• Place these files in the same directory or adjust the script to point to your data file's location.

Features

• Query diseases associated with specific miRNAs and vice versa.
• Customizable confidence score filters.
• Browsing functionality for available miRNAs and diseases.
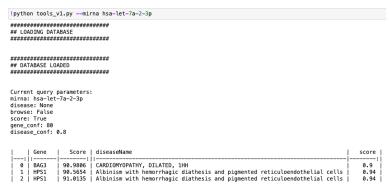• User-friendly output and error handling.

Usage

The tool can be run from the command line with various arguments to perform different tasks:

Basic Commands

• Display help information: 'python tools_v1.py --help'

```
!python tools_v1.py --help

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## LOADING DATABASE
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usage: tools_v1.py [-h] [--mirna MIRNA] [--disease DISEASE] [--browse]
                   [--score {True,False}] [--gene_conf GENE_CONF]
                   [--disease_conf DISEASE_CONF]

a simple local lookup database to look up diseases a given miRNA is associated
to, or look up miRNAs a disease is associated to

options:
  -h, --help          show this help message and exit
  --mirna MIRNA       Input mirna.
  --disease DISEASE   Input gene
```

Querying the Database

• To find diseases associated with a specific miRNA, whilst reporting the associated gene(s):
'python tools_v1.py --mirna [miRNA name]'

```
!python tools_v1.py --mirna hsa-let-7a-2-3p

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Current query parameters:
mirna: hsa-let-7a-2-3p
disease: None
browse: False
score: True
gene_conf: 80
disease_conf: 0.8

|   | Gene | Score   | diseaseName                                                    | score |
|--:|:-----|--------:|:---------------------------------------------------------------|------:|
| 0 | BAG3 | 90.9806 | CARDIOMYOPATHY, DILATED, 1HH                                   | 0.9   |
| 1 | HPS1 | 90.5654 | Albinism with hemorrhagic diathesis and pigmented reticuloendothelial cells | 0.94 |
| 2 | HPS1 | 91.0135 | Albinism with hemorrhagic diathesis and pigmented reticuloendothelial cells | 0.94 |
```

• To find miRNAs associated with a specific disease, whilst reporting the associated gene(s):
'python tools_v1.py --disease [disease name]'
Note: If the disease name contains commas, it must be enclosed in "" when entered in the command line. E.g. python tools_v1.py --disease "CARDIOMYOPATHY, DILATED, 1HH".
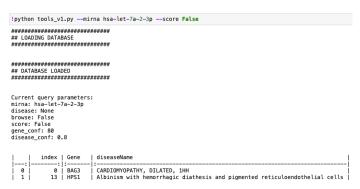
Advanced Options

Default report: Without a confidence score, list miRNA to Gene associations over 80 and all Gene to Disease associations over 0.8.
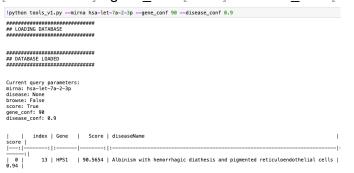
• Exclude score information from the output:

'python tools_v1.py --mirna [miRNA name] --score False'

```
!python tools_v1.py --mirna hsa-let-7a-2-3p --score False

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Current query parameters:
mirna: hsa-let-7a-2-3p
disease: None
browse: False
score: False
gene_conf: 80
disease_conf: 0.8


|   |   | index | Gene  | diseaseName                                                                  |
|---:|---------:|:-------|:----------------------------------------------------------------------------|
| 0 |        0 | BAG3  | CARDIOMYOPATHY, DILATED, 1HH                                                  |
| 1 |       13 | HPS1  | Albinism with hemorrhagic diathesis and pigmented reticuloendothelial cells |
```

• Set custom confidence thresholds for gene and disease associations:

'python tools_v1.py --mirna [miRNA name] --gene_conf [score] --disease_conf [score]'

```
!python tools_v1.py --mirna hsa-let-7a-2-3p --gene_conf 90 --disease_conf 0.9

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Current query parameters:
mirna: hsa-let-7a-2-3p
disease: None
browse: False
score: True
gene_conf: 90
disease_conf: 0.9


|   |   | index | Gene  |   Score | diseaseName                                                                  |
score |
|---:|---------:|:-------|---------:|:----------------------------------------------------------------------------|:
------:|
| 0 |       13 | HPS1  | 90.5654 | Albinism with hemorrhagic diathesis and pigmented reticuloendothelial cells |
0.94 |
```

Or 'python tools_v1.py --disease [disease name] --gene_conf [score] --disease_conf [score]'

Browsing the Database

Search partial miRNA or Disease names to list matching entries, like 'cfa' returning all 'cfa-miR' variants.

```
!python tools_v1.py --mirna 152 --browse

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Current query parameters:
mirna: 152
disease: None
browse: True
score: True
gene_conf: 80
disease_conf: 0.8


['hsa-miR-152-3p', 'hsa-miR-3152-3p', 'hsa-miR-7152-5p', 'hsa-miR-152-5p', 'hsa-miR-3152-5p', 'hsa-miR-7152-3p']
```

• To browse miRNAs matching a specific term: 'python tools_v1.py --mirna [search term] --browse'
• To browse diseases matching a specific term: 'python tools_v1.py --disease [search term] –browse'
• To browse all miRNAs or diseases:
   'python tools_V1.py --mirna ALL --browse' or 'python tools_V1.py --disease ALL --browse'

Error Handling

• If an incorrect input is provided, the system will respond with 'No relevant information was found.'
• If an incorrect argument is provided, the output will display the message 'error: unrecognized arguments.'

Contribution

Feedback and contributions to the tool are welcome. Please contact tuotuofei@gmail.com for more information.