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metaRNA finds potential target sites for the microRNAs in genomic sequences.

- Written in Python
- Built on miRanda.

It is built on miRanda, an algorithm for detection and ranking of the targets of microRNA.
Quickstart

```python
from metarna.target_scan import scan, free_energy

gene_sequence = {
    "ACAAGATGCATTGTCACCACCCGCTCTCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCC"
    "CCTGGAGGGTGCCCAACCAGCAGACACAGACACACTAGGACAGAGAAGGAGGCAGGAGGAGGAGGAGGACCTGCC""
    "CTCCTGACTTTCTCCCTGCTGGTTTGATTGGACCTCCAGCCCGAATTGAGGGCCCTCCTAGGAGGG"
}

mirna_sequence = "UGGCGAUUUUGGAACUAUGGGA"

# Get free Energy value:
delta_g = free_energy(gene_sequence, mirna_sequence)

# Get full targets information:
targets = scan(gene_sequence, mirna_sequence)

# Specifying Calculation Parameters
targets = scan(gene_sequence, mirna_sequence, scale=5.0)
```

Contents

Installing

Using PyPi

metaRNA can be installed very easily using pip.

```
pip install metarna
```
Using git

If you want to run the very latest, feel free to pull down the repo from github and install by hand.

```bash
git clone https://github.com/prashnts/metaRNA.git
cd metaRNA
python setup.py install
```

You can run the tests using the test-runner:

```bash
python setup.py test
```

Browse the source code online at https://github.com/prashnts/metaRNA

Pre-requisite

ViennaRNA is required to compile metaRNA C extensions. It is recommended to install ViennaRNA from source. On Unix-like systems, it usually involves:

```bash
wget 'http://www.tbi.univie.ac.at/RNA/download/sourcecode/2_2_x/ViennaRNA-2.2.10.tar.gz' -O viennarna.tar.gz
mkdir viennarna
tar -zxvf viennarna.tar.gz -C viennarna --strip-components=1
cd viennarna
./configure
make
sudo make install
```

Usual build essentials (automake, autoconf, gcc) are required.

You can download the above package from this link if the above link isn’t accessible. To download and verify the SHA checksum:

```bash
wget "https://noop.pw/etc/vienna224.tar.gz" -O vienna224.tar.gz
echo "71a4c4704228fd01eb6e39415400a904d5240cef vienna224.tar.gz" | shasum -c
```

Windows System

metaRNA hasn’t been tested or built on Windows systems yet. Contributions are welcome.

Calculation Parameters

miRanda algorithm used by metaRNA accepts the following optional parameters.
## Parameter Table

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Type</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>scale</td>
<td>float</td>
<td>4.0</td>
<td>The 5' miRNA scaling parameter.</td>
</tr>
<tr>
<td>strict</td>
<td>int</td>
<td>0</td>
<td>Perform a Strict Seed search when set to 1.</td>
</tr>
<tr>
<td>gap_open</td>
<td>float</td>
<td>-9.0</td>
<td>Gap-open Penalty</td>
</tr>
<tr>
<td>gap_extend</td>
<td>float</td>
<td>-4.0</td>
<td>Gap-extend Penalty</td>
</tr>
<tr>
<td>score_threshold</td>
<td>float</td>
<td>50.0</td>
<td>Score Threshold for reporting hits</td>
</tr>
<tr>
<td>energy_threshold</td>
<td>float</td>
<td>1.0</td>
<td>Energy Threshold for reporting hits</td>
</tr>
<tr>
<td>length_5p_for_weighting</td>
<td>int</td>
<td>8</td>
<td>The 5' sequence length to be weighed except for the last residue.</td>
</tr>
<tr>
<td>temperature</td>
<td>int</td>
<td>30</td>
<td>Used while calculating Free Energy</td>
</tr>
<tr>
<td>alignment_len_threshold</td>
<td>int</td>
<td>8</td>
<td>Minimum alignment.</td>
</tr>
</tbody>
</table>

### Passing Parameters

The parameters are passed as keyword arguments.

```python
targets = scan(gene_sequence, mirna_sequence, scale=5.0, strict=1)
```
CHAPTER 2

Indices and tables

- genindex
- modindex
- search