
PyKmers Documentation

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Alessio Zanga, Emanuele Cavenaghi

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CHAPTER 1

Getting Started with PyKmers

1.1 Dependencies

PyKmers relies on **pygfa library** to load GFA files. You can build this library downloading the source code from [this repository](#). In order to build and install pygfa, you need **python3**, **pip3** and **setuptools**.

```
python setup.py bdist_wheel  
pip install dist/pygfa*.whl
```

1.2 Build and Install PyKmers

Once pygfa is installed, you can build and install PyKmers from [here](#).

```
python setup.py bdist_wheel  
pip install dist/pykmers*.whl
```


CHAPTER 2

pykmers package

2.1 Module contents

PyKmers Module

Collection of functions to extract k-mers from GFA file.

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`pykmers.pykmers.com(base)`

Return complement base of given base

Parameters `base` – Input base

Returns Complement base

`pykmers.pykmers.get_kmers_from_file(file, kmer_length, sorted=False, debug=False)`

Find all the kmers that corresponds at the given sequence

Parameters

- `file` – Input GFA file
- `kmer_length` – Kmer length
- `sorted` – True to sort the kmers in lexicographical order
- `debug` – True to show debug info

Returns List of kmers

`pykmers.pykmers.get_kmers_from_string(sequence, k)`

Find all the kmers that corresponds at the given sequence

Parameters

- `sequence` – Sequence
- `k` – Kmer length

Returns List of kmers

`pykmers.pykmers.get_paths_from_graph(graph)`

Find paths in graph from root to leaf

Parameters `graph` – Graph

Returns List of path in the graph

`pykmers.pykmers.get_sequence_from_path(graph, path)`

Find the sequence that corresponds to the path without consider the overlap

Parameters

- `graph` – Graph

- `path` – Path

Returns Sequence that corresponds to the path

`pykmers.pykmers.get_subgraphs_from_graph(graph)`

Divide graph in connected components

Parameters `graph` – Graph

Returns List of subgraphs

`pykmers.pykmers.load_graph_from_file(file)`

Load a MultiGraph instance of Networkx from GFA file using pygfa library

Parameters `file` – Input GFA file

Returns MultiGraph instance

`pykmers.pykmers.rev_and_com(sequence)`

Return reverse and complement sequence of given sequence

Parameters `base` – Input sequence

Returns Reverse and complement sequence

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Indices and tables

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