# cortexpy Documentation

Release 0.46.2

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Apr 23, 2019

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### Overview of Cortexpy

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Cortexpy is a Python package for sequence analysis using linked and colored De Bruijn graphs such as the ones created by Cortex and Mccortex. This project aims to mirror many of the features contained in CortexJDK.

Cortexpy also comes with a command-line tool for basic inspection and manipulation of Cortex graphs with and without links.

#### 1.1 Audience

The audience of cortexpy is researchers working with colored De Bruijn graphs and link information in Cortex and Mccortex format.

### 1.2 Free software

Cortexpy is free software; you can redistribute it and/or modify it under the terms of the Apache License version 2.0. Contributions are welcome. Please join us on GitHub.

## 1.3 Installation

pip install cortexpy

#### **1.4 Documentation**

For more information, please see cortexpy documentation.

#### 1.5 Bugs

Please raise a github issue for any bugs.

#### **1.6 Development**

- 1. Install conda.
- 2. Download development and testing tools:

conda env create -f environment.yml -n my-dev-environment

3. Activate development environment:

conda activate my-dev-environment

All remaining commands in the development section need to be run in an activated conda dev environment.

#### 1.6.1 Tests

make test

#### 1.6.2 Deploy new cortexpy version to pypi

Requires access credentials for pypi.

make deploy

#### 1.6.3 Building the docs

The documentation is automatically built by read-the-docs on push to master. To build the documentation manually:

```
# install sphinx dependencies
pip install docs/requirements.txt
make docs
```

#### 1.6.4 Update the dev environment

This section is experimental because it does not work on travis-CI yet.

```
# Create a new env from the high-level requirements file
conda env create -f environment.yml -n another-dev-env
# activate the new environment
conda activate another-dev-env
# save new env to environment.lock.yml
make lock
```

### Usage examples

## 2.1 Python API

#### 2.1.1 Check if a cortex graph contains a kmer

We can use the After you have installed cortexpy, you can start using it to access cortex files from python:

```
from cortexpy.graph.parser.random_access import RandomAccess
# make sure to open the cortex graph in binary mode
with open('my_graph.ctx', 'rb') as fh:
    ra = RandomAccess(fh)
    # let's see if our favorite kmer is in the graph
    if 'AAA' in ra:
        print('AAA exists in my_graph.ctx!')
```

#### The cortexpy API reference

#### 3.1 Random access of cortexpy graphs

This module contains classes for inspecting cortex graphs with random access to their kmers.

```
___getitem__(lexlo_string)
```

Return kmer associated with kmer string

No check is performed to make sure that the input string is a lexicographically-lowest kmer string. Use  $get\_kmer\_for\_string()$  in order to convert a kmer string to its lexlo form before retrieving it from the cortex object.

\_\_\_iter\_\_()

Iterate over kmer strings in graph in order stored in graph

```
get_kmer_for_string(string)
```

Will compute the revcomp of kmer string before getting a kmer

items()

Iterate over kmer strings and kmers in graph in order stored in graph

```
values ()
Iterate over kmers in cortex graph
```

#### 3.2 Utility functions

This module contains utility functions that are used inside cortexpy. These functions may also be useful outside of cortexpy.

```
cortexpy.utils.kmerize_contig (contig, kmer_size)
Return generator of kmers in contig
```

The returned kmers are not lexicographically lowest.

```
>>> list(kmerize_contig('ATTT', 3))
['ATT', 'TTT']
```

```
cortexpy.utils.kmerize_fasta(fasta, kmer_size)
```

Return generator to all kmers in fasta

```
cortexpy.utils.lexlo
```

Return lexicographically lowest version of a kmer string and its reverse complement

The reverse complement of a kmer string is generated and the lexicographically-lowest kmer string is returned.

```
>>> lexlo('AAA')
'AAA'
```

```
>>> lexlo('TTT')
'AAA'
```

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