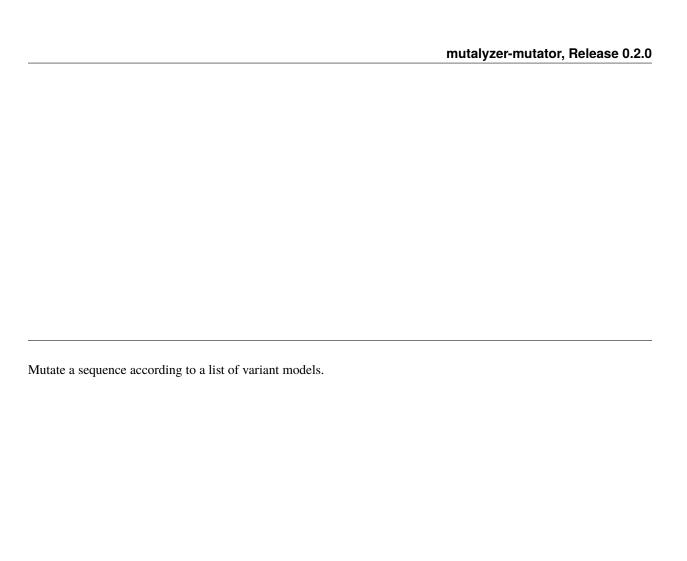
# mutalyzer-mutator

Release 0.2.0

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**CHAPTER** 

**ONE** 

# **INSTALLATION**

The software is distributed via PyPI, it can be installed with pip:

pip install mutalyzer-mutator

# 1.1 From source

The source is hosted on GitHub, to install the latest development version, use the following commands.

git clone https://github.com/mutalyzer/mutator.git
cd mutator
pip install .

### USAGE

The mutate() function provides an interface to mutate a sequence according to a list of variants. A dictionary with the reference ids as keys and their sequences as values should be provided as input. The reference with the reference key is the one to be mutate according to the variants model list, the second input of the mutate() function.

```
from mutalyzer_mutator import mutate
sequences = {"reference": "AAGG", "OTHER_REF": "AATTAA"}
variants = [
    # 2_2delinsOTHER_REF:2_4
        "type": "deletion_insertion",
        "source": "reference",
        "location": {
            "type": "range",
            "start": {"type": "point", "position": 2},
            "end": {"type": "point", "position": 2},
        },
        "inserted": [
            {"sequence": "CC", "source": "description"},
            {
                "source": {"id": "OTHER_REF"},
                "location": {
                    "type": "range",
                    "start": {"type": "point", "position": 2},
                    "end": {"type": "point", "position": 4},
                },
            },
       ],
   }
observed = mutate(sequences, variants) # observed = 'AACCTTGG'
```

6 Chapter 2. Usage

# THREE

# **API DOCUMENTATION**

## 3.1 Mutator

Module to mutate sequences based on a variants list.

### Assumptions for which no check is performed:

- Only deletion insertion operations.
- Only exact locations, i.e., no uncertainties such as 10+?.
- Locations are zero-based right-open with start > end.
- There is no overlapping between variants locations.

#### **Notes:**

- If any of the above is not met, the result will be bogus.
- There can be empty inserted lists.

mutalyzer\_mutator.mutator.mutate(sequences, variants)

Mutate the reference sequence under sequences ["reference"] according to the provided variants operations.

#### **Parameters**

- sequences (dict) Sequences dictionary.
- variants (list) Operations list.

Returns Mutated sequence.

Return type str

# 3.2 Util

Various util functions.

# The following code is adapted from biopython 1.77:

- https://github.com/biopython/biopython-177/Bio/Seq.py
- https://github.com/biopython/biopython/blob/biopython-177/Bio/Data/IUPACData.py

#### **Notes:**

- The alphabet check was removed.
- No previous custom errors are raised any longer.

mutalyzer\_mutator.util.complement(sequence)

Complement the sequence.

```
>>> sequence = 'CCCCCGATAG'
>>> complement(sequence)
'GGGGGCTATC'
```

You can use mix DNA with RNA sequences.

```
>>> sequence = 'CCCCCaTuAGD'
>>> complement(sequence)
'GGGGGuAaTCH'
```

Also, you can use mixed case sequences.

```
>>> sequence = 'CCCCCgatA-GD'
>>> complement(sequence)
'GGGGGcuaT-CH'
```

Note that in the above example, the ambiguous character D denotes G, A or T so its complement is H (for C, T or A).

**Parameters sequence** (*str*) – Input sequence.

Returns Complemented sequence.

Return type str

mutalyzer\_mutator.util.reverse\_complement(sequence)

Reverse complement the sequence.

```
>>> sequence = 'CCCCCGATAGNR'
>>> reverse_complement(sequence)
'YNCTATCGGGGG'
```

Note that in the above example, since R = G or A, its complement is Y (which denotes C or T).

You can use mix DNA with RNA sequences.

```
>>> sequence = 'CCCCCaTuAGD'
>>> reverse_complement(sequence)
'HCTaAuGGGGG'
```

You can of course used mixed case sequences,

```
>>> sequence = 'CCCCCgatA-G'
>>> reverse_complement(sequence)
'C-TaucGGGGGG'
```

**Parameters sequence** (str) – Input sequence.

**Returns** Reverse complemented sequence.

Return type str

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