# gff3-py Documentation

Release 0.1.0

Han Lin

#### Contents

1	gff3-py	3
	1.1 Features	3
2	Installation	5
3	Usage	7
4	Contributing 4.1 Types of Contributions	<b>9</b> 9
5	Credits5.1 Development Lead5.2 Contributors	11 11 11
6	History	13
7	0.1.0 (2014-12-11)	15
8	Indices and tables	17

Contents:

Contents 1

2 Contents

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# gff3-py

Manipulate genomic features and validate the syntax and reference sequence of your GFF3 files.

- Free software: BSD license
- Documentation: https://gff3-py.readthedocs.org.

# 1.1 Features

• TODO

4 Chapter 1. gff3-py

#### CHAPTER 2

# Installation

#### At the command line:

\$ easy\_install gff3

#### Or, if you have virtualenvwrapper installed:

\$ mkvirtualenv gff3
\$ pip install gff3

# CHAPTER 3

Usage

To use gff3-py in a project:

import gff3

8 Chapter 3. Usage

# Contributing

Contributions are welcome, and they are greatly appreciated! Every little bit helps, and credit will always be given. You can contribute in many ways:

### 4.1 Types of Contributions

#### 4.1.1 Report Bugs

Report bugs at https://github.com/hotdogee/gff3-py/issues.

If you are reporting a bug, please include:

- Your operating system name and version.
- Any details about your local setup that might be helpful in troubleshooting.
- Detailed steps to reproduce the bug.

#### 4.1.2 Fix Bugs

Look through the GitHub issues for bugs. Anything tagged with "bug" is open to whoever wants to implement it.

#### 4.1.3 Implement Features

Look through the GitHub issues for features. Anything tagged with "feature" is open to whoever wants to implement it.

#### 4.1.4 Write Documentation

gff3 could always use more documentation, whether as part of the official gff3 docs, in docstrings, or even on the web in blog posts, articles, and such.

#### 4.1.5 Submit Feedback

The best way to send feedback is to file an issue at https://github.com/hotdogee/gff3-py/issues.

If you are proposing a feature:

#### gff3-py Documentation, Release 0.1.0

- Explain in detail how it would work.
- Keep the scope as narrow as possible, to make it easier to implement.
- Remember that this is a volunteer-driven project, and that contributions are welcome :)

# **Credits**

# 5.1 Development Lead

• Han Lin <hotdogee@gmail.com>

# **5.2 Contributors**

None yet. Why not be the first?

12 Chapter 5. Credits

CHAPTER	6
Histor	ſy

14 Chapter 6. History

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0.1.0 (2014-12-11)

• First release on PyPI.

# CHAPTER 8

# Indices and tables

- genindex
- modindex
- search