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# **vcfpy Documentation**

***Release 0.2.1***

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Python 3 VCF parser that allows both reading and writing

- Free software: MIT license
- Documentation: <https://vcfpy.readthedocs.io>.

## 1.1 Why another VCF parser for Python!

I've been using PyVCF with quite some success in the past. However, the main bottleneck of PyVCF is when you want to modify the per-sample genotype information. There are some issues in the tracker of PyVCF but none of them can really be considered solved. I tried several hours to solve these problems within PyVCF but this never got far or towards a complete rewrite...

For this reason, VCFPy was born and here it is!

## 1.2 What's the State?

VCFPy is the result of two full days of development plus some maintenance work later now (right now). I'm using it in several projects but it is not as battle-tested as PyVCF.

## 1.3 Why Python 3 Only?

As I'm only using Python 3 code, I see no advantage in carrying around support for legacy Python 2 and maintaining it. At a later point when VCFPy is known to be stable, Python 2 support might be added if someone contributes a pull request.





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## Installation

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### 2.1 Stable release

To install vcfpy, run this command in your terminal:

```
$ pip install vcfpy
```

This is the preferred method to install vcfpy, as it will always install the most recent stable release.

If you don't have [pip](#) installed, this [Python installation guide](#) can guide you through the process.

### 2.2 From sources

The sources for vcfpy can be downloaded from the [Github repo](#).

You can either clone the public repository:

```
$ git clone git://github.com/holtgrewe/vcfpy
```

Or download the [tarball](#):

```
$ curl -OL https://github.com/holtgrewe/vcfpy/tarball/master
```

Once you have a copy of the source, you can install it with:

```
$ python setup.py install
```



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### Usage

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To use vcfpy in a project:

```
import vcfpy
```



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## Contributing

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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/bihealth/vcfpy/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” and “help wanted” is open to whoever wants to implement it.

#### 4.1.3 Implement Features

Look through the GitHub issues for features. Anything tagged with “enhancement” and “help wanted” is open to whoever wants to implement it.

#### 4.1.4 Write Documentation

vcfpy could always use more documentation, whether as part of the official vcfpy 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/bihealth/vcfpy/issues>.

If you are proposing a feature:

- 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 :)

## 4.2 Get Started!

Ready to contribute? Here's how to set up *vcfpy* for local development.

1. Fork the *vcfpy* repo on GitHub.
2. Clone your fork locally:

```
$ git clone git@github.com:your_name_here/vcfpy.git
```

3. Install your local copy into a virtualenv. Assuming you have virtualenvwrapper installed, this is how you set up your fork for local development:

```
$ mkvirtualenv vcfpy
$ cd vcfpy/
$ python setup.py develop
```

4. Create a branch for local development:

```
$ git checkout -b name-of-your-bugfix-or-feature
```

Now you can make your changes locally.

5. When you're done making changes, check that your changes pass flake8 and the tests, including testing other Python versions with tox:

```
$ flake8 vcfpy tests
$ python setup.py test or py.test
$ tox
```

To get flake8 and tox, just pip install them into your virtualenv.

6. Commit your changes and push your branch to GitHub:

```
$ git add .
$ git commit -m "Your detailed description of your changes."
$ git push origin name-of-your-bugfix-or-feature
```

7. Submit a pull request through the GitHub website.

## 4.3 Pull Request Guidelines

Before you submit a pull request, check that it meets these guidelines:

1. The pull request should include tests.

2. If the pull request adds functionality, the docs should be updated. Put your new functionality into a function with a docstring, and add the feature to the list in README.rst.
3. The pull request should work for Python 3.3, 3.4 and 3.5. Check [https://travis-ci.org/bihealth/vcfpy/pull\\_requests](https://travis-ci.org/bihealth/vcfpy/pull_requests) and make sure that the tests pass for all supported Python versions.

## 4.4 Tips

To run a subset of tests:

```
$ py.test tests.test_vcfpy
```





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## Indices and tables

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- `genindex`
- `modindex`
- `search`