

---

# **vcfpy Documentation**

***Release 0.11.0+0.g91ab788.dirty***

**Manuel Holtgrewe**

**Nov 22, 2017**



---

## Installation Getting Started

---

|          |                                   |          |
|----------|-----------------------------------|----------|
| <b>1</b> | <b>Quick Example</b>              | <b>3</b> |
| <b>2</b> | <b>Features</b>                   | <b>5</b> |
| <b>3</b> | <b>Frequently Asked Questions</b> | <b>7</b> |



VCFPy is a Python 3 library with good support for both reading and writing VCF files. The documentation is split into three parts (accessible through the navigation on the left):

**Installation & Getting Started** Instructions for the installation of the module and some examples to get you started.

**API Documentation** This section contains the API documentation for the module

**Project Info** More information on the project, including the changelog, list of contributing authors, and contribution instructions.



# CHAPTER 1

---

## Quick Example

---

```
#!/usr/bin/env python
# -*- coding: utf-8 -*-
import vcfpy

# Open input, add FILTER header, and open output file
reader = vcfpy.Reader.from_path('input.vcf')
reader.header.add_filter_line(vcfpy.OrderedDict([
    ('ID', 'DP10'), ('Description', 'total DP < 10')]))
writer = vcfpy.Writer.from_path('/dev/stdout', reader.header)

# Add "DP10" filter to records having less than 10 reads
for record in reader:
    ad = sum(c.data.get('DP', 0) for c in record.calls)
    if ad < 10:
        record.add_filter('DP10')
    writer.write_record(record)
```



## CHAPTER 2

---

### Features

---

- Support for reading and writing VCF v4.3
- Interface to `INFO` and `FORMAT` fields is based on `OrderedDict` allows for easier modification than `PyVCF` (also I find this more pythonic)
- Read (and jump in) and write BGZF files just using `vcfpy`



---

## Frequently Asked Questions

---

**Why another Python library for VCF?** 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!

**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.

**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.

**What's the difference to PyVCF?** The main difference is technical. Instead of using `collections.namedtuple` for storing the call annotation, VCFPy uses `collections.OrderedDict`. This has the advantage that (1) access to optional settings is much more pythonic using `.get(KEY, DEFAULT)` instead of `getattr()`. Further, (2) adding call annotations (FORMAT) fields is able without any performance penalty where for PyVCF, `copy.deepcopy` has to be used at some point which is very slow. There has not been any movement in supporting modifying FORMAT fields in PyVCF and here is a library that does this well.

**What's the aim?** The aim of the project is to provide simple yet efficient read and write access to VCF files. Eventually, PySAM will probably be a better choice once it has a Python wrapper for the VCF part of `htslib`. However, as this is still missing, VCFPy is a good solution for the time being.

## 3.1 Installation

### 3.1.1 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.

### 3.1.2 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/bihealth/vcfpy
```

Or download the [tarball](#):

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

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

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

## 3.2 Getting Started

After installation, you can use VCFPy in your project simply by importing the module.

```
import vcfpy
```

That's all, continue and look at the list of examples.

## 3.3 Examples

This chapter contains several examples for the most important use cases of VCFPy.

### 3.3.1 Reading VCF Files

The following is an example for reading VCF files and writing out a TSV file with the genotype calls of all SNVs. You can find the example Python and VCF file in the sources below the directory `examples/vcf_to_tsv`.

```
#!/usr/bin/env python
# -*- coding: utf-8 -*-
import vcfpy

# Open file, this will read in the header
reader = vcfpy.Reader.from_path('input.vcf')

# Build and print header
header = ['#CHROM', 'POS', 'REF', 'ALT'] + reader.header.samples.names
print('\t'.join(header))

for record in reader:
    if not record.is_snv():
        continue
    line = [record.CHROM, record.POS, record.REF]
```

```

line += [alt.value for alt in record.ALT]
line += [call.data.get('GT') or './.' for call in record.calls]
print('\t'.join(map(str, line)))

```

The program call looks as follows.

```

$ ./vcf_to_tsv.py
↪#CHROM      POS      REF      ALT      BLANK      NA12878      NA12891      NA12892
chr22      42522392      G      A      0/0      0/1      0/1      0/
↪0      0/0      0/0      0/0
chr22      42522597      C      T      0/1      0/0      0/0      0/
↪0      0/0      0/0      0/0
chr22      42522613      G      C      0/1      0/1      0/0      0/
↪1      0/1      0/1      0/1
chr22      42523003      A      G      0/1      1/1      0/1      0/
↪1      0/1      0/1      0/1
chr22      42523209      T      C      0/1      1/1      0/1      0/
↪1      0/1      0/1      0/1
chr22      42523211      T      C      0/0      0/1      0/1      0/
↪0      0/0      0/0      0/0
chr22      42523409      G      T      0/1      0/1      0/0      0/
↪1      0/1      0/1      0/1
chr22      42523491      C      T      0/1      0/0      0/0      0/
↪0      0/0      0/0      0/0
chr22      42523507      A      G      0/1      0/0      0/0      0/
↪0      0/0      0/0      0/0
chr22      42523805      C      T      0/0      0/0      0/1      0/
↪0      0/0      0/0      0/0
chr22      42523943      A      G      0/1      1/1      0/1      0/
↪1      0/1      0/1      0/1
chr22      42524435      T      A      0/1      0/0      0/0      0/
↪0      0/0      0/1      0/1
[...]

```

### 3.3.2 Writing VCF Files

The following shows how to add values to the FILTER column to records of an existing VCF file. Adding to existing records is simpler than constructing them from scratch, of course.

```

#!/usr/bin/env python
# -*- coding: utf-8 -*-
import vcfpy

# Open input, add FILTER header, and open output file
reader = vcfpy.Reader.from_path('input.vcf')
reader.header.add_filter_line(vcfpy.OrderedDict([
    ('ID', 'DP10'), ('Description', 'total DP < 10')]))
writer = vcfpy.Writer.from_path('/dev/stdout', reader.header)

# Add "DP10" filter to records having less than 10 reads
for record in reader:
    ad = sum(c.data.get('DP', 0) for c in record.calls)
    if ad < 10:
        record.add_filter('DP10')
    writer.write_record(record)

```

The program call looks as follows.

```
##fileformat=VCFv4.3
##contig=<ID=20,length=62435964>
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">
##INFO=<ID=AF,Number=A,Type=Float,Description="Allele Frequency">
##INFO=<ID=AA,Number=1,Type=String,Description="Ancestral Allele">
##INFO=<ID=DB,Number=0,Type=Flag,Description="dbSNP membership, build 129">
##INFO=<ID=H2,Number=0,Type=Flag,Description="HapMap2 membership">
##FILTER=<ID=q10,Description="Quality below 10">
##FILTER=<ID=s50,Description="Less than 50% of samples have data">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=HQ,Number=2,Type=Integer,Description="Haplotype Quality">
##FILTER=<ID=DP10,Description="total DP < 10">
```

| CHROM | POS     | ID        | REF | ALT            | QUAL | FILTER       | INFO             | FORMAT      |
|-------|---------|-----------|-----|----------------|------|--------------|------------------|-------------|
| 20    | 14370   | rs6054257 | G   | A              | 29   | PASS         | NS=3;            | GT:GQ:DP:HQ |
|       |         |           |     | 0 0:48:1:51,51 |      | 1 0:48:8:51, |                  |             |
|       |         |           |     |                |      |              |                  |             |
| 20    | 17330   | .         | T   | A              | 3    | q10          | NS=3;DP=11;AF=0. | GT:GQ:DP:HQ |
|       |         |           |     | 0 0:49:3:58,50 |      | 0 1:3:5:65,3 |                  |             |
|       |         |           |     |                |      |              |                  |             |
| 20    | 1110696 | rs6040355 | A   | G              |      |              |                  | GT:GQ:DP:HQ |
|       |         |           |     |                |      |              |                  |             |
|       |         |           |     |                |      |              |                  |             |
| 20    | 1230237 | .         | T   | .              | 47   | PASS         | NS=3;DP=13;      | GT:GQ:DP:HQ |
|       |         |           |     |                |      |              |                  |             |
|       |         |           |     |                |      |              |                  |             |
| 20    | 1234567 | microsat1 | GTC | G,GTCT         | 50   | PASS;        |                  | GT:GQ:DP    |
|       |         |           |     |                |      |              |                  |             |
|       |         |           |     |                |      |              |                  |             |

### 3.3.3 Jumping in Tabix-indexed Files

The following shows a small program that extracts a genomic region from the input VCF file and writes it to stdout.

```
#!/usr/bin/env python
# -*- coding: utf-8 -*-
import vcfpy

# Open input, add FILTER header, and open output file
reader = vcfpy.Reader.from_path('input.vcf.gz')
writer = vcfpy.Writer.from_path('/dev/stdout', reader.header)

# Fetch region 20:1,110,694-1,230,237. Note that the coordinates
# in the API call are zero-based and describe half-open intervals.
for record in reader.fetch('20', 1110695, 1230237):
    writer.write_record(record)
```

The program call looks as follows.

```
##fileformat=VCFv4.3
##fileDate=20090805
##source=myImputationProgramV3.1
```

```
##reference=file:///seq/references/1000GenomesPilot-NCBI36.fasta
##contig=<ID=1,length=249250621>
##contig=<ID=2,length=243199373>
##contig=<ID=20,length=62435964>
##phasing=partial
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">
##INFO=<ID=AF,Number=A,Type=Float,Description="Allele Frequency">
##INFO=<ID=AA,Number=1,Type=String,Description="Ancestral Allele">
##INFO=<ID=DB,Number=0,Type=Flag,Description="dbSNP membership, build 129">
##INFO=<ID=H2,Number=0,Type=Flag,Description="HapMap2 membership">
##FILTER=<ID=q10,Description="Quality below 10">
##FILTER=<ID=s50,Description="Less than 50% of samples have data">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=HQ,Number=2,Type=Integer,Description="Haplotype Quality">

#CHROM      POS      ID      REF      ALT      QUAL      FILTER      INFO      FOR
20          1110696  rs6040355  A      G,
#T          67      PASS      NS=2;DP=10;AF=0.333,0.667;AA=T;
#DB          GT:GQ:DP:HQ:1|2:21:6:23,27      2|1:2:0:18,2      2/2:35:4:40,30
20          1230237  .      T      .      47      PASS      NS=3;DP=13;
#AA=T      GT:GQ:DP:HQ      0|0:54:7:56,60      0|0:48:4:51,51      0/
#0:61:2:40,30
```

## 3.4 Best Practice

While not strictly part of the documentation of VCFPy, we include some notes on hints that we consider best practice when building VCF processing applications.

### 3.4.1 Keep Input Verbatim Where Possible

Try to keep the input verbatim if there is no strong reason for adjusting it. Strong reasons include fixing `Type` or `Number` in header lines describing arrays of strings, for example.

Whenever possible, keep the header order intact. VCFPy does this automatically for you (in contrast to PyVCF).

### 3.4.2 Prefer Soft-Filters over Hard-Filters

**Soft**-filters mean annotating your VCF records in the `FILTER` column whereas **Hard**-filters mean removing records from VCF file. In many situations, it is useful to keep around all VCF records and just annotate why they are to be dropped. Then, in the last step, only the interesting ones are kept.

This makes tracing back easier when and why a record was removed.

## 3.5 Header

## Contents

- *Header*
  - *vcfpy.OrderedDict*
  - *vcfpy.Header*
  - *vcfpy.HeaderLine*
  - *vcfpy.header\_without\_lines*
  - *vcfpy.SimpleHeaderLine*
  - *vcfpy.AltAlleleHeaderLine*
  - *vcfpy.MetaHeaderLine*
  - *vcfpy.PedigreeHeaderLine*
  - *vcfpy.SampleHeaderLine*
  - *vcfpy.ContigHeaderLine*
  - *vcfpy.FilterHeaderLine*
  - *vcfpy.CompoundHeaderLine*
  - *vcfpy.InfoHeaderLine*
  - *vcfpy.FormatHeaderLine*
  - *vcfpy.FieldInfo*
  - *vcfpy.SamplesInfos*

### 3.5.1 vcfpy.OrderedDict

Convenience export of `OrderedDict`. When available, the `cyorderreddict`, a Cython-reimplementation of `OrderedDict` is used for Python before 3.5 (from 3.5, Python ships with a fast, C implementation of `OrderedDict`).

**class** `vcfpy.OrderedDict`

Dictionary that remembers insertion order

**clear** () → None. Remove all items from od.

**copy** () → a shallow copy of od

**fromkeys** (*S* [, *v*]) → New ordered dictionary with keys from *S*.  
If not specified, the value defaults to None.

**items** () → a set-like object providing a view on D's items

**keys** () → a set-like object providing a view on D's keys

**move\_to\_end** ()

Move an existing element to the end (or beginning if `last=False`). Raises `KeyError` if the element does not exist. When `last=True`, acts like a fast version of `self[key]=self.pop(key)`.

**pop** (*k* [, *d*]) → *v*, remove specified key and return the corresponding value. If key is not found, *d* is returned if given, otherwise `KeyError` is raised.

**popitem()** → (k, v), return and remove a (key, value) pair.

Pairs are returned in LIFO order if last is true or FIFO order if false.

**setdefault(k[, d])** → od.get(k,d), also set od[k]=d if k not in od

**update([E], \*\*F)** → None. Update D from mapping/iterable E and F.

If E present and has a .keys() method, does: for k in E: D[k] = E[k] If E present and lacks .keys() method, does: for (k, v) in E: D[k] = v In either case, this is followed by: for k, v in F.items(): D[k] = v

**values()** → an object providing a view on D's values

### 3.5.2 vcfpy.Header

**class vcfpy.Header** (*lines=None, samples=None*)

Represent header of VCF file

While this class allows mutating records, it should not be changed once it has been assigned to a writer. Use **:py:method:~Header.copy** to create a copy that can be modified without problems.

This class provides function for adding lines to a header and updating the supporting index data structures. There is no explicit API for removing header lines, the best way is to reconstruct a new Header instance with a filtered list of header lines.

**add\_contig\_line(mapping)**

Add "contig" header line constructed from the given mapping

**Parameters mapping** – OrderedDict with mapping to add. It is recommended to use OrderedDict over dict as this makes the result reproducible

**Returns** False on conflicting line and True otherwise

**add\_filter\_line(mapping)**

Add FILTER header line constructed from the given mapping

**Parameters mapping** – OrderedDict with mapping to add. It is recommended to use OrderedDict over dict as this makes the result reproducible

**Returns** False on conflicting line and True otherwise

**add\_format\_line(mapping)**

Add FORMAT header line constructed from the given mapping

**Parameters mapping** – OrderedDict with mapping to add. It is recommended to use OrderedDict over dict as this makes the result reproducible

**Returns** False on conflicting line and True otherwise

**add\_info\_line(mapping)**

Add INFO header line constructed from the given mapping

**Parameters mapping** – OrderedDict with mapping to add. It is recommended to use OrderedDict over dict as this makes the result reproducible

**Returns** False on conflicting line and True otherwise

**add\_line(header\_line)**

Add header line, updating any necessary support indices

**Returns** False on conflicting line and True otherwise

**copy()**

Return a copy of this header

**filter\_ids()**

Return list of all filter IDs

**format\_ids()**

Return list of all format IDs

**get\_format\_field\_info(key)**

Return `FieldInfo` for the given INFO field

**get\_info\_field\_info(key)**

Return `FieldInfo` for the given INFO field

**get\_lines(key)**

Return header lines having the given `key` as their type

**has\_header\_line(key, id\_)**

Return whether there is a header line with the given ID of the type given by `key`

**Parameters**

- **key** – The VCF header key/line type.
- **id** – The ID value to compare fore

**Returns** `True` if there is a header line starting with `##${key}=` in the VCF file having the mapping entry ID set to `id_`.

**info\_ids()**

Return list of all info IDs

**lines = None**

list of `:py:HeaderLine` objects

**samples = None**

`SamplesInfo` object

### 3.5.3 vcfpy.HeaderLine

**class vcfpy.HeaderLine(key, value)**

Base class for VCF header lines

**copy()**

Return a copy

**key = None**

str with key of header line

**serialize()**

Return VCF-serialized version of this header line

### 3.5.4 vcfpy.header\_without\_lines

**vcfpy.header\_without\_lines(header, remove)**

Return Header without lines given in `remove`

`remove` is an iterable of pairs `key/ID` with the VCF header key and ID of entry to remove. In the case that a line does not have a mapping entry, you can give the full value to remove.

```
# header is a vcfpy.Header, e.g., as read earlier from file
new_header = vcfpy.without_header_lines(
    header, [('assembly', None), ('FILTER', 'PASS')])
# now, the header lines starting with "##assembly=" and the "PASS"
# filter line will be missing from new_header
```

### 3.5.5 vcfpy.SimpleHeaderLine

**class** vcfpy.**SimpleHeaderLine** (*key, value, mapping*)

Base class for simple header lines, currently contig and filter header lines

Don't use this class directly but rather the sub classes.

**Raises** vcfpy.exceptions.InvalidHeaderException in the case of missing key "ID"

**copy** ()

Return a copy

**mapping** = None

collections.OrderedDict with key/value mapping of the attributes

### 3.5.6 vcfpy.AltAlleleHeaderLine

**class** vcfpy.**AltAlleleHeaderLine** (*key, value, mapping*)

Alternative allele header line

Mostly used for defining symbolic alleles for structural variants and IUPAC ambiguity codes

**classmethod** **from\_mapping** (*klass, mapping*)

Construct from mapping, not requiring the string value

**id** = None

name of the alternative allele

### 3.5.7 vcfpy.MetaHeaderLine

**class** vcfpy.**MetaHeaderLine** (*key, value, mapping*)

Alternative allele header line

Used for defining set of valid values for samples keys

**classmethod** **from\_mapping** (*klass, mapping*)

Construct from mapping, not requiring the string value

**id** = None

name of the alternative allele

### 3.5.8 vcfpy.PedigreeHeaderLine

**class** vcfpy.**PedigreeHeaderLine** (*key, value, mapping*)

Header line for defining a pedigree entry

**classmethod** **from\_mapping** (*klass, mapping*)

Construct from mapping, not requiring the string value

**id = None**  
name of the alternative allele

### 3.5.9 vcfpy.SampleHeaderLine

**class** vcfpy.**SampleHeaderLine** (*key, value, mapping*)  
Header line for defining a SAMPLE entry

**classmethod** **from\_mapping** (*klass, mapping*)  
Construct from mapping, not requiring the string value

**id = None**  
name of the alternative allele

### 3.5.10 vcfpy.ContigHeaderLine

**class** vcfpy.**ContigHeaderLine** (*key, value, mapping*)  
Contig header line

Most importantly, parses the 'length' key into an integer

**classmethod** **from\_mapping** (*klass, mapping*)  
Construct from mapping, not requiring the string value

**id = None**  
name of the contig

**length = None**  
length of the contig, None if missing

### 3.5.11 vcfpy.FilterHeaderLine

**class** vcfpy.**FilterHeaderLine** (*key, value, mapping*)  
FILTER header line

**description = None**  
description for the filter, None if missing

**classmethod** **from\_mapping** (*klass, mapping*)  
Construct from mapping, not requiring the string value

**id = None**  
token for the filter

### 3.5.12 vcfpy.CompoundHeaderLine

**class** vcfpy.**CompoundHeaderLine** (*key, value, mapping*)  
Base class for compound header lines, currently format and header lines

Compound header lines describe fields that can have more than one entry.

Don't use this class directly but rather the sub classes.

**copy** ()  
Return a copy

**mapping = None**  
OrderedDict with key/value mapping

### 3.5.13 vcfpy.InfoHeaderLine

**class vcfpy.InfoHeaderLine** (*key, value, mapping*)  
Header line for INFO fields

Note that the `Number` field will be parsed into an `int` if possible. Otherwise, the constants `HEADER_NUMBER_*` will be used.

**description = None**  
description, should be given, `None` if not given

**classmethod from\_mapping** (*klass, mapping*)  
Construct from mapping, not requiring the string value

**id = None**  
key in the INFO field

**source = None**  
source of INFO field, `None` if not given

**type = None**  
value type

**version = None**  
version of INFO field, `None` if not given

### 3.5.14 vcfpy.FormatHeaderLine

**class vcfpy.FormatHeaderLine** (*key, value, mapping*)  
Header line for FORMAT fields

**description = None**  
description, should be given, `None` if not given

**classmethod from\_mapping** (*klass, mapping*)  
Construct from mapping, not requiring the string value

**id = None**  
key in the INFO field

**source = None**  
source of INFO field, `None` if not given

**type = None**  
value type

**version = None**  
version of INFO field, `None` if not given

### 3.5.15 vcfpy.FieldInfo

**class vcfpy.FieldInfo** (*type\_, number, description=None, id\_=None*)  
Core information for describing field type and number

**description = None**  
Description for the header field, optional

**id = None**  
The id of the field, optional.

**number = None**  
Number description, either an int or constant

**type = None**  
The type, one of INFO\_TYPES or FORMAT\_TYPES

### 3.5.16 vcfpy.SamplesInfos

**class vcfpy.SamplesInfos** (*sample\_names, parsed\_samples=None*)  
Helper class for handling the samples in VCF files

The purpose of this class is to decouple the sample name list somewhat from `Header`. This encapsulates subsetting samples for which the genotype should be parsed and reordering samples into output files.

Note that when subsetting is used and the records are to be written out again then the `FORMAT` field must not be touched.

**copy ()**  
Return a copy of the object

**is\_parsed (name)**  
Return whether the sample name is parsed

**name\_to\_idx = None**  
mapping from sample name to index

**names = None**  
list of sample that are read from/written to the VCF file at hand in the given order

**parsed\_samples = None**  
set with the samples for which the genotype call fields should be read; can be used for partial parsing (speedup) and defaults to the full list of samples, None if all are parsed

## 3.6 Input/Output

### Contents

- *Input/Output*
  - *vcfpy.Reader*
  - *vcfpy.Writer*

### 3.6.1 vcfpy.Reader

**class vcfpy.Reader** (*stream, path=None, tabix\_path=None, record\_checks=None, parsed\_samples=None*)  
Class for parsing of files from `file`-like objects

Instead of using the constructor, use the class methods `from_stream()` and `from_path()`.

On construction, the header will be read from the file which can cause problems. After construction, `Reader` can be used as an iterable of `Record`.

**Raises** `InvalidHeaderException` in the case of problems reading the header

---

**Note:** It is important to note that the `header` member is used during the parsing of the file. **If you need a modified version then create a copy, e.g., using `:py:method:~vcfpy.header.Header.copy`.**

---

---

**Note:** If you use the `parsed_samples` feature and you write out records then you must not change the `FORMAT` of the record.

---

**close()**

Close underlying stream

**fetch** (*chrom\_or\_region*, *begin=None*, *end=None*)

Jump to the start position of the given chromosomal position and limit iteration to the end position

**Parameters**

- **chrom\_or\_region** (*str*) – name of the chromosome to jump to if *begin* and *end* are given and a samtools region string otherwise (e.g. “chr1:123,456-123,900”).
- **begin** (*int*) – 0-based begin position (inclusive)
- **end** (*int*) – 0-based end position (exclusive)

**classmethod from\_path** (*klass*, *path*, *tabix\_path=None*, *record\_checks=None*,  
*parsed\_samples=None*)

Create new `Reader` from path

---

**Note:** If you use the `parsed_samples` feature and you write out records then you must not change the `FORMAT` of the record.

---

**Parameters**

- **path** – the path to load from (converted to `str` for compatibility with `path.py`)
- **tabix\_path** – optional string with path to TBI index, automatic inferral from `path` will be tried on the fly if not given
- **record\_checks** (*list*) – record checks to perform, can contain ‘INFO’ and ‘FORMAT’

**classmethod from\_stream** (*klass*, *stream*, *path=None*, *tabix\_path=None*, *record\_checks=None*,  
*parsed\_samples=None*)

Create new `Reader` from file

---

**Note:** If you use the `parsed_samples` feature and you write out records then you must not change the `FORMAT` of the record.

---

**Parameters**

- **stream** – file-like object to read from

- **path** – optional string with path to store (for display only)
- **record\_checks** (*list*) – record checks to perform, can contain ‘INFO’ and ‘FORMAT’
- **parsed\_samples** (*list*) – list of `str` values with names of samples to parse call information for (for speedup); leave to `None` for ignoring

**header = None**

the Header

**parsed\_samples = None**

if set, list of samples to parse for

**parser = None**

the parser to use

**path = None**

optional `str` with the path to the stream

**record\_checks = None**

checks to perform on records, can contain ‘FORMAT’ and ‘INFO’

**stream = None**

stream (`file`-like object) to read from

**tabix\_file = None**

the `pysam.TabixFile` used for reading from index bgzip-ed VCF; constructed on the fly

**tabix\_path = None**

optional `str` with path to tabix file

### 3.6.2 vcfpy.Writer

**class vcfpy.Writer** (*stream, header, path=None*)

Class for writing VCF files to `file`-like objects

Instead of using the constructor, use the class methods `from_stream()` and `from_path()`.

The writer has to be constructed with a `Header` object and the full VCF header will be written immediately on construction. This, of course, implies that modifying the header after construction is illegal.

**close()**

Close underlying stream

**classmethod from\_path** (*klass, path, header*)

Create new `Writer` from path

#### Parameters

- **path** – the path to load from (converted to `str` for compatibility with `path.py`)
- **header** – VCF header to use, lines and samples are deep-copied

**classmethod from\_stream** (*klass, stream, header, path=None, use\_bgzf=None*)

Create new `Writer` from file

Note that for getting bgzf support, you have to pass in a stream opened in binary mode. Further, you either have to provide a `path` ending in “.gz” or set `use_bgzf=True`. Otherwise, you will get the notorious “TypeError: ‘str’ does not support the buffer interface”.

#### Parameters

- **stream** – file-like object to write to
- **header** – VCF header to use, lines and samples are deep-copied
- **path** – optional string with path to store (for display only)
- **use\_bgzf** – indicator whether to write bgzf to `stream` if `True`, prevent if `False`, interpret `path` if `None`

**header = None**

the `:py:class:`~vcfpy.header.Header`` to write out, will be deep-copied into the `Writer` on initialization

**path = None**

optional `str` with the path to the stream

**stream = None**

stream (file-like object) to read from

**write\_record(record)**

Write out the given `vcfpy.record.Record` to this `Writer`

## 3.7 Exceptions

### Contents

- *Exceptions*
  - *vcfpy.VCFPyException*
  - *vcfpy.InvalidHeaderException*
  - *vcfpy.InvalidRecordException*
  - *vcfpy.IncorrectVCFFormat*
  - *vcfpy.HeaderNotFound*

### 3.7.1 vcfpy.VCFPyException

**exception vcfpy.VCFPyException**

Base class for module's exception

### 3.7.2 vcfpy.InvalidHeaderException

**exception vcfpy.InvalidHeaderException**

Raised in the case of invalid header formatting

### 3.7.3 vcfpy.InvalidRecordException

**exception vcfpy.InvalidRecordException**

Raised in the case of invalid record formatting

### 3.7.4 vcfpy.IncorrectVCFFormat

**exception** `vcfpy.IncorrectVCFFormat`  
Raised on problems parsing VCF

### 3.7.5 vcfpy.HeaderNotFound

**exception** `vcfpy.HeaderNotFound`  
Raised when a VCF header could not be found

## 3.8 Records

### Contents

- *Records*
  - *Record-Related Constants*
  - *vcfpy.Record*
  - *vcfpy.Call*
  - *vcfpy.AltRecord*
  - *vcfpy.Substitution*
  - *vcfpy.SV*
  - *vcfpy.BreakEnd*
  - *vcfpy.SingleBreakEnd*
  - *vcfpy.SymbolicAllele*

### 3.8.1 Record-Related Constants

The following constants are also available as `vcfpy.CONSTANT`.

`vcfpy.record.HOM_REF = 0`

Code for homozygous reference

`vcfpy.record.HOM_ALT = 2`

Code for homozygous alternative

`vcfpy.record.FIVE_PRIME = '5'`

code for five prime orientation BreakEnd

`vcfpy.record.THREE_PRIME = '3'`

code for three prime orientation BreakEnd

`vcfpy.record.FORWARD = '+'`

code for forward orientation

`vcfpy.record.REVERSE = '-'`

code for reverse orientation

### 3.8.2 vcfpy.Record

**class** `vcfpy.Record` (*CHROM, POS, ID, REF, ALT, QUAL, FILTER, INFO, FORMAT, calls*)

Represent one record from the VCF file

Record objects are iterators of their calls

**ALT = None**

A list of alternative allele records of type `AltRecord`

**CHROM = None**

A `str` with the chromosome name

**FILTER = None**

A list of strings for the FILTER column

**FORMAT = None**

A list of strings for the FORMAT column

**ID = None**

A list of the semicolon-separated values of the ID column

**INFO = None**

An `OrderedDict` giving the values of the INFO column, flags are mapped to `True`

**POS = None**

An `int` with a 1-based begin position

**QUAL = None**

The quality value, can be `None`

**REF = None**

A `str` with the REF value

**add\_filter** (*label*)

Add label to FILTER if not set yet, removing PASS entry if present

**add\_format** (*key, value=None*)

Add an entry to format

The record's `calls` `data[key]` will be set to `value` if not yet set and `value` is not `None`. If `key` is already in `FORMAT` then nothing is done.

**affected\_end**

Return affected start position in 0-based coordinates

For SNVs, MNVs, and deletions, the behaviour is based on the start position and the length of the REF. In the case of insertions, the position behind the insert position is returned, yielding a 0-length interval together with `affected_start()`

**affected\_start**

Return affected start position in 0-based coordinates

For SNVs, MNVs, and deletions, the behaviour is the start position. In the case of insertions, the position behind the insert position is returned, yielding a 0-length interval together with `affected_end()`

**begin = None**

An `int` with a 0-based begin position

**call\_for\_sample = None**

A mapping from sample name to entry in `self.calls`

**calls = None**

A list of genotype `Call` objects

**end = None**  
An `int` with a 0-based end position

**is\_snv()**  
Return `True` if it is a SNV

### 3.8.3 vcfpy.Call

**class vcfpy.Call** (*sample, data, site=None*)  
The information for a genotype callable

By VCF, this should always include the genotype information and can contain an arbitrary number of further annotation, e.g., the coverage at the variant position.

**called = None**  
whether or not the variant is fully called

**data = None**  
an `OrderedDict` with the key/value pair information from the call's data

**gt\_alleles = None**  
the allele numbers (0, 1, ...) in this calls or `None` for no-call

**gt\_bases**  
Return the actual genotype bases, e.g. if VCF genotype is 0/1, could return ('A', 'T')

**gt\_phase\_char**  
Return character to use for phasing

**gt\_type**  
The type of genotype, returns one of `HOM_REF`, `HOM_ALT`, and `HET`.

**is\_filtered** (*require=None, ignore=None*)  
Return `True` for filtered calls

**Parameters**

- **ignore** (*iterable*) – if set, the filters to ignore, make sure to include 'PASS', when setting, default is [ 'PASS' ]
- **require** (*iterable*) – if set, the filters to require for returning `True`

**is\_het**  
Return `True` for heterozygous calls

**is\_phased**  
Return boolean indicating whether this call is phased

**is\_variant**  
Return `True` for non-hom-ref calls

**plodity = None**  
the number of alleles in this sample's call

**sample = None**  
the name of the sample for which the call was made

**site = None**  
the `Record` of this `Call`

### 3.8.4 vcfpy.AltRecord

```
class vcfpy.AltRecord (type_=None)
    An alternative allele Record

    Currently, can be a substitution, an SV placeholder, or breakend

    serialize()
        Return str with representation for VCF file

    type = None
        String describing the type of the variant, could be one of SNV, MNV, could be any of teh types described
        in the ALT header lines, such as DUP, DEL, INS, ...
```

### 3.8.5 vcfpy.Substitution

```
class vcfpy.Substitution (type_, value)
    A basic alternative allele record describing a REF->AltRecord substitution

    Note that this subsumes MNVs, insertions, and deletions.

    value = None
        The alternative base sequence to use in the substitution
```

### 3.8.6 vcfpy.SV

`vcfpy.SV`

### 3.8.7 vcfpy.BreakEnd

```
class vcfpy.BreakEnd (mate_chrom, mate_pos, orientation, mate_orientation, sequence,
                      within_main_assembly)
    A placeholder for a breakend

    mate_chrom = None
        chromosome of the mate breakend

    mate_orientation = None
        orientation breakend's mate

    mate_pos = None
        position of the mate breakend

    orientation = None
        orientation of this breakend

    sequence = None
        breakpoint's connecting sequence

    serialize()
        Return string representation for VCF

    within_main_assembly = None
        bool specifying if the breakend mate is within the assembly (True) or in an ancillary assembly (False)
```

### 3.8.8 vcfpy.SingleBreakEnd

**class** vcfpy.**SingleBreakEnd** (*orientation, sequence*)  
A placeholder for a single breakend

### 3.8.9 vcfpy.SymbolicAllele

**class** vcfpy.**SymbolicAllele** (*value*)  
A placeholder for a symbolic allele

The allele symbol must be defined in the header using an `ALT` header before being parsed. Usually, this is used for succinct descriptions of structural variants or IUPAC parameters.

**value = None**  
The symbolic value, e.g. ‘DUP’

## 3.9 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:

### 3.9.1 Types of Contributions

#### 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.

#### Fix Bugs

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

#### Implement Features

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

#### 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.

## 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 :)

## 3.9.2 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.

## 3.9.3 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.

### 3.9.4 Tips

To run a subset of tests:

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

## 3.10 Credits

### 3.10.1 Development Lead

- Manuel Holtgrewe <[manuel.holtgrewe@bihealth.de](mailto:manuel.holtgrewe@bihealth.de)>

### 3.10.2 Contributors

None yet. Why not be the first?

## 3.11 History

### 3.11.1 v0.11.0 (2017-11-22)

- The field `FORMAT/FT` is now expected to be a semicolon-separated string. Internally, we will handle it as a list.
- Switching from warning helper utility code to Python `warnings` module.
- Return `str` in case of problems with parsing value.

### 3.11.2 v0.10.0 (2017-02-27)

- Extending API to allow for reading subsets of records. (Writing for sample subsets or reordered samples is possible through using the appropriate `names` list in the `SamplesInfos` for the `Writer`).
- Deep-copying header lines and samples infos on `Writer` construction
- Using `samples` attribute from `Header` in `Reader` and `Writer` instead of passing explicitly

### 3.11.3 0.9.0 (2017-02-26)

- Restructuring of `requirements.txt` files
- Fixing parsing of no-call `GT` fields

### 3.11.4 0.8.1 (2017-02-08)

- PEP8 style adjustments
- Using versioneer for versioning
- Using `requirements*.txt` files now from `setup.py`
- Fixing dependency on `cyordereddict` to be for Python <3.6 instead of <3.5
- Jumping by samtools coordinate string now also allowed

### 3.11.5 0.8.0 (2016-10-31)

- Adding `Header.has_header_line` for querying existence of header line
- `Header.add*_line` return a `bool` no indicating any conflicts
- Construction of `Writer` uses samples within header and no extra parameter (breaks API)

### 3.11.6 0.7.0 (2016-09-25)

- Smaller improvements and fixes to documentation
- Adding Codacy coverage and static code analysis results to README
- Various smaller code cleanup triggered by Codacy results
- Adding `__eq__`, `__neq__` and `__hash__` to data types (where applicable)

### 3.11.7 0.6.0 (2016-09-25)

- Refining implementation for breakend and symbolic allele class
- Removing `record.SV_CODES`
- Refactoring parser module a bit to make the code cleaner
- Fixing small typos and problems in documentation

### 3.11.8 0.5.0 (2016-09-24)

- Deactivating warnings on record parsing by default because of performance
- Adding validation for `INFO` and `FORMAT` fields on reading (#8)
- Adding predefined `INFO` and `FORMAT` fields to `pyvcf.header` (#32)

### 3.11.9 0.4.1 (2016-09-22)

- Initially enabling codeclimate

### 3.11.10 0.4.0 (2016-09-22)

- Exporting constants for encoding variant types
- Exporting genotype constants HOM\_REF, HOM\_ALT, HET
- Implementing `Call.is_phased`, `Call.is_het`, `Call.is_variant`, `Call.is_phased`, `Call.is_hom_ref`, `Call.is_hom_alt`
- Removing `Call.phased` (breaks API, next release is 0.4.0)
- Adding tests, fixing bugs for methods of `Call`

### 3.11.11 0.3.1 (2016-09-21)

- Work around `FORMAT/FT` being a string; this is done so in the Delly output

### 3.11.12 0.3.0 (2016-09-21)

- `Reader` and `Writer` can now be used as context manager (with `with`)
- Including license in documentation, including Biopython license
- Adding support for writing bgzf files (taken from Biopython)
- Adding support for parsing arrays in header lines
- Removing `example-4.1-bnd.vcf` example file because v4.1 tumor derival lacks ID field
- Adding `AltAlleleHeaderLine`, `MetaHeaderLine`, `PedigreeHeaderLine`, and `SampleHeaderLine`
- Renaming `SimpleHeaderFile` to `SimpleHeaderLine`
- Warn on missing `FILTER` entries on parsing
- Reordered parameters in `from_stream` and `from_file` (#18)
- Renamed `from_file` to `from_stream` (#18)
- Renamed `Reader.jump_to` to `Reader.fetch`
- Adding `header_without_lines` function
- Generally extending API to make it esier to use
- Upgrading dependencies, enabling pyup-bot
- Greatly extending documentation

### 3.11.13 0.2.1 (2016-09-19)

- First release on PyPI

## 3.12 License

### 3.12.1 VCFPy License

You can find the License of VCFPy below.

MIT License

Copyright (c) 2016, Berlin Institute of Health

Permission is hereby granted, free of charge, to any person obtaining a copy of this software and associated documentation files (the "Software"), to deal in the Software without restriction, including without limitation the rights to use, copy, modify, merge, publish, distribute, sublicense, and/or sell copies of the Software, and to permit persons to whom the Software is furnished to do so, subject to the following conditions:

The above copyright notice and this permission notice shall be included in all copies or substantial portions of the Software.

THE SOFTWARE IS PROVIDED "AS IS", WITHOUT WARRANTY OF ANY KIND, EXPRESS OR IMPLIED, INCLUDING BUT NOT LIMITED TO THE WARRANTIES OF MERCHANTABILITY, FITNESS FOR A PARTICULAR PURPOSE AND NONINFRINGEMENT. IN NO EVENT SHALL THE AUTHORS OR COPYRIGHT HOLDERS BE LIABLE FOR ANY CLAIM, DAMAGES OR OTHER LIABILITY, WHETHER IN AN ACTION OF CONTRACT, TORT OR OTHERWISE, ARISING FROM, OUT OF OR IN CONNECTION WITH THE SOFTWARE OR THE USE OR OTHER DEALINGS IN THE SOFTWARE.

### 3.12.2 Biopython License Agreement

The bgzf writing code is taken from the Biopython project. You can find a copy of the license below.

Biopython License Agreement

Permission to use, copy, modify, and distribute this software and its documentation with or without modifications and for any purpose and without fee is hereby granted, provided that any copyright notices appear in all copies and that both those copyright notices and this permission notice appear in supporting documentation, and that the names of the contributors or copyright holders not be used in advertising or publicity pertaining to distribution of the software without specific prior permission.

THE CONTRIBUTORS AND COPYRIGHT HOLDERS OF THIS SOFTWARE DISCLAIM ALL WARRANTIES WITH REGARD TO THIS SOFTWARE, INCLUDING ALL IMPLIED WARRANTIES OF MERCHANTABILITY AND FITNESS, IN NO EVENT SHALL THE CONTRIBUTORS OR COPYRIGHT HOLDERS BE LIABLE FOR ANY SPECIAL, INDIRECT OR CONSEQUENTIAL DAMAGES OR ANY DAMAGES WHATSOEVER RESULTING FROM LOSS OF USE, DATA OR PROFITS, WHETHER IN AN ACTION OF CONTRACT, NEGLIGENCE OR OTHER TORTIOUS ACTION, ARISING OUT OF OR IN CONNECTION WITH THE USE OR PERFORMANCE OF THIS SOFTWARE.



**A**

add\_contig\_line() (vcfpy.Header method), 13  
add\_filter() (vcfpy.Record method), 23  
add\_filter\_line() (vcfpy.Header method), 13  
add\_format() (vcfpy.Record method), 23  
add\_format\_line() (vcfpy.Header method), 13  
add\_info\_line() (vcfpy.Header method), 13  
add\_line() (vcfpy.Header method), 13  
affected\_end (vcfpy.Record attribute), 23  
affected\_start (vcfpy.Record attribute), 23  
ALT (vcfpy.Record attribute), 23  
AltAlleleHeaderLine (class in vcfpy), 15  
AltRecord (class in vcfpy), 25

**B**

begin (vcfpy.Record attribute), 23  
BreakEnd (class in vcfpy), 25

**C**

Call (class in vcfpy), 24  
call\_for\_sample (vcfpy.Record attribute), 23  
called (vcfpy.Call attribute), 24  
calls (vcfpy.Record attribute), 23  
CHROM (vcfpy.Record attribute), 23  
clear() (vcfpy.OrderedDict method), 12  
close() (vcfpy.Reader method), 19  
close() (vcfpy.Writer method), 20  
CompoundHeaderLine (class in vcfpy), 16  
ContigHeaderLine (class in vcfpy), 16  
copy() (vcfpy.CompoundHeaderLine method), 16  
copy() (vcfpy.Header method), 13  
copy() (vcfpy.HeaderLine method), 14  
copy() (vcfpy.OrderedDict method), 12  
copy() (vcfpy.SamplesInfos method), 18  
copy() (vcfpy.SimpleHeaderLine method), 15

**D**

data (vcfpy.Call attribute), 24  
description (vcfpy.FieldInfo attribute), 17

description (vcfpy.FilterHeaderLine attribute), 16  
description (vcfpy.FormatHeaderLine attribute), 17  
description (vcfpy.InfoHeaderLine attribute), 17

**E**

end (vcfpy.Record attribute), 23

**F**

fetch() (vcfpy.Reader method), 19  
FieldInfo (class in vcfpy), 17  
FILTER (vcfpy.Record attribute), 23  
filter\_ids() (vcfpy.Header method), 13  
FilterHeaderLine (class in vcfpy), 16  
FORMAT (vcfpy.Record attribute), 23  
format\_ids() (vcfpy.Header method), 14  
FormatHeaderLine (class in vcfpy), 17  
from\_mapping() (vcfpy.AltAlleleHeaderLine class method), 15  
from\_mapping() (vcfpy.ContigHeaderLine class method), 16  
from\_mapping() (vcfpy.FilterHeaderLine class method), 16  
from\_mapping() (vcfpy.FormatHeaderLine class method), 17  
from\_mapping() (vcfpy.InfoHeaderLine class method), 17  
from\_mapping() (vcfpy.MetaHeaderLine class method), 15  
from\_mapping() (vcfpy.PedigreeHeaderLine class method), 15  
from\_mapping() (vcfpy.SampleHeaderLine class method), 16  
from\_path() (vcfpy.Reader class method), 19  
from\_path() (vcfpy.Writer class method), 20  
from\_stream() (vcfpy.Reader class method), 19  
from\_stream() (vcfpy.Writer class method), 20  
fromkeys() (vcfpy.OrderedDict method), 12

**G**

get\_format\_field\_info() (vcfpy.Header method), 14

get\_info\_field\_info() (vcfpy.Header method), 14  
get\_lines() (vcfpy.Header method), 14  
gt\_alleles (vcfpy.Call attribute), 24  
gt\_bases (vcfpy.Call attribute), 24  
gt\_phase\_char (vcfpy.Call attribute), 24  
gt\_type (vcfpy.Call attribute), 24

## H

has\_header\_line() (vcfpy.Header method), 14  
Header (class in vcfpy), 13  
header (vcfpy.Reader attribute), 20  
header (vcfpy.Writer attribute), 21  
header\_without\_lines() (in module vcfpy), 14  
HeaderLine (class in vcfpy), 14  
HeaderNotFound, 22

## I

id (vcfpy.AltAlleleHeaderLine attribute), 15  
id (vcfpy.ContigHeaderLine attribute), 16  
id (vcfpy.FieldInfo attribute), 18  
id (vcfpy.FilterHeaderLine attribute), 16  
id (vcfpy.FormatHeaderLine attribute), 17  
id (vcfpy.InfoHeaderLine attribute), 17  
id (vcfpy.MetaHeaderLine attribute), 15  
id (vcfpy.PedigreeHeaderLine attribute), 15  
ID (vcfpy.Record attribute), 23  
id (vcfpy.SampleHeaderLine attribute), 16  
IncorrectVCFFormat, 22  
INFO (vcfpy.Record attribute), 23  
info\_ids() (vcfpy.Header method), 14  
InfoHeaderLine (class in vcfpy), 17  
InvalidHeaderException, 21  
InvalidRecordException, 21  
is\_filtered() (vcfpy.Call method), 24  
is\_het (vcfpy.Call attribute), 24  
is\_parsed() (vcfpy.SamplesInfos method), 18  
is\_phased (vcfpy.Call attribute), 24  
is\_snv() (vcfpy.Record method), 24  
is\_variant (vcfpy.Call attribute), 24  
items() (vcfpy.OrderedDict method), 12

## K

key (vcfpy.HeaderLine attribute), 14  
keys() (vcfpy.OrderedDict method), 12

## L

length (vcfpy.ContigHeaderLine attribute), 16  
lines (vcfpy.Header attribute), 14

## M

mapping (vcfpy.CompoundHeaderLine attribute), 16  
mapping (vcfpy.SimpleHeaderLine attribute), 15  
mate\_chrom (vcfpy.BreakEnd attribute), 25

mate\_orientation (vcfpy.BreakEnd attribute), 25  
mate\_pos (vcfpy.BreakEnd attribute), 25  
MetaHeaderLine (class in vcfpy), 15  
move\_to\_end() (vcfpy.OrderedDict method), 12

## N

name\_to\_idx (vcfpy.SamplesInfos attribute), 18  
names (vcfpy.SamplesInfos attribute), 18  
number (vcfpy.FieldInfo attribute), 18

## O

OrderedDict (class in vcfpy), 12  
orientation (vcfpy.BreakEnd attribute), 25

## P

parsed\_samples (vcfpy.Reader attribute), 20  
parsed\_samples (vcfpy.SamplesInfos attribute), 18  
parser (vcfpy.Reader attribute), 20  
path (vcfpy.Reader attribute), 20  
path (vcfpy.Writer attribute), 21  
PedigreeHeaderLine (class in vcfpy), 15  
plodity (vcfpy.Call attribute), 24  
pop() (vcfpy.OrderedDict method), 12  
popitem() (vcfpy.OrderedDict method), 12  
POS (vcfpy.Record attribute), 23

## Q

QUAL (vcfpy.Record attribute), 23

## R

Reader (class in vcfpy), 18  
Record (class in vcfpy), 23  
record\_checks (vcfpy.Reader attribute), 20  
REF (vcfpy.Record attribute), 23

## S

sample (vcfpy.Call attribute), 24  
SampleHeaderLine (class in vcfpy), 16  
samples (vcfpy.Header attribute), 14  
SamplesInfos (class in vcfpy), 18  
sequence (vcfpy.BreakEnd attribute), 25  
serialize() (vcfpy.AltRecord method), 25  
serialize() (vcfpy.BreakEnd method), 25  
serialize() (vcfpy.HeaderLine method), 14  
setdefault() (vcfpy.OrderedDict method), 13  
SimpleHeaderLine (class in vcfpy), 15  
SingleBreakEnd (class in vcfpy), 26  
site (vcfpy.Call attribute), 24  
source (vcfpy.FormatHeaderLine attribute), 17  
source (vcfpy.InfoHeaderLine attribute), 17  
stream (vcfpy.Reader attribute), 20  
stream (vcfpy.Writer attribute), 21  
Substitution (class in vcfpy), 25

SV (in module vcfpy), [25](#)

SymbolicAllele (class in vcfpy), [26](#)

## T

tabix\_file (vcfpy.Reader attribute), [20](#)

tabix\_path (vcfpy.Reader attribute), [20](#)

type (vcfpy.AltRecord attribute), [25](#)

type (vcfpy.FieldInfo attribute), [18](#)

type (vcfpy.FormatHeaderLine attribute), [17](#)

type (vcfpy.InfoHeaderLine attribute), [17](#)

## U

update() (vcfpy.OrderedDict method), [13](#)

## V

value (vcfpy.Substitution attribute), [25](#)

value (vcfpy.SymbolicAllele attribute), [26](#)

values() (vcfpy.OrderedDict method), [13](#)

VCFPyException, [21](#)

version (vcfpy.FormatHeaderLine attribute), [17](#)

version (vcfpy.InfoHeaderLine attribute), [17](#)

## W

within\_main\_assembly (vcfpy.BreakEnd attribute), [25](#)

write\_record() (vcfpy.Writer method), [21](#)

Writer (class in vcfpy), [20](#)