

Name

vcfparse

Description

Parses a vcf file and extracts the specified regions.

Dependencies

Python Modules

- [PyVCF](#)

Synopsis

```
vcfparse vcf_file [field1 field2 ... fieldN] [-h]
```

Arguments

- **vcf_file**: the vcf file to parse
- **fields**: a list of fields to extract from the vcf file.

Options

- **--help, -h**: print a helpful message and exit.

Examples

A command such as

```
vcfparse test.vcf gq dp sdp ad
```

will create four separate text files, one for each field. Each text file has a header of the form

```
Chromosome  Position      Sample1 [...]  SampleN
```

which is tab separated and each subsequent line will look something like this

```
chr10    181479  27      41
```

Thanks

Thanks to the people who have contributed to PyVCF for allowing me to write *way* less than one hundred lines of code:)