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# **epivizFileParser Documentation**

**jkanche**

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The package provides utilities to parse and query commonly used genomic file formats. Genomic files are usually indexed (BigWig, BigBed, Tabix etc) and the library will only read the necessary bytes of the file to query data. In addition, The library also works with remotely hosted files. This requires the remotely hosted file to support HTTP Byte-Range requests

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**Note:**

- package is open source and is available on [GitHub](#)
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# CHAPTER 1

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## Using PyPI

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will be on PyPI soon.. but for now install from GitHub below



# CHAPTER 2

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## From GitHub (devel version)

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To install the devel version from [GitHub](#): Install using pip

```
pip install git@github.com:epiviz/epivizFileParser.git
```

or clone the repository and install from local directory using *pip*

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**Note:** Depending on how python was setup, installing packages may sometime require sudo permission, in this case, add the –user option

```
pip install --user git@github.com:epiviz/epivizFileParser.git
```

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# CHAPTER 3

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## Usage

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For example, to read a BigWig file,

```
from epivizFileParser import BigWig

# initialize a file
bw = BigWig("tests/test.bw")

# extract header and zoom levels from the file
print(bw.header, bw.zooms)

# query the file
res, err = bw.getRange(chr="chr1", start=10000000, end=10020000)
print(res)

# summarize data into equals windows/bins
sres = bw.bin_rows(res, chr="chr1", start=10000000, end=10020000, columns=['score'],
                   bins=10)
print(sres)
```



# CHAPTER 4

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## Contents

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## 4.1 Installation

### 4.1.1 Using PyPI

will be on PyPI soon.. but for now install from GitHub below

### 4.1.2 From GitHub (devel version)

To install the devel version from [GitHub](#): Install using pip

```
pip install git@github.com:epiviz/epivizFileParser.git
```

or clone the repository and install from local directory using *pip*

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**Note:** Depending on how python was setup, installing packages may sometime require sudo permission, in this case, add the `--user` option

```
pip install --user git@github.com:epiviz/epivizFileParser.git
```

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## 4.2 Usage

For example, to read a BigWig file,

```
from epivizFileParser import BigWig  
  
# initialize a file  
bw = BigWig("tests/test.bw")
```

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```
# extract header and zoom levels from the file
print(bw.header, bw.zooms)

# query the file
res, err = bw.getRange(chr="chr1", start=10000000, end=10020000)
print(res)

# summarize data into equals windows/bins
sres = bw.bin_rows(res, chr="chr1", start=10000000, end=10020000, columns=['score'],
                   bins=10)
print(sres)
```

## 4.3 License

The MIT License (MIT)

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## 4.4 Contributors

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- Hector Corrada Bravo <hcorrada@gmail.com>

## 4.5 Changelog

### 4.5.1 Version 0.0.1

- Refactor parser module from the *epivizfileserver* package

## 4.6 epivizFileParser

### 4.6.1 epivizFileParser package

#### Submodules

`epivizFileParser.BamFile` module

`epivizFileParser.BaseFile` module

`epivizFileParser.BigBed` module

`epivizFileParser.BigWig` module

`epivizFileParser.GWASBigBedPIP` module

`epivizFileParser.GWASBigBedPval` module

`epivizFileParser.GtfFile` module

`epivizFileParser.GtfParsedFile` module

`epivizFileParser.GtfTabixFile` module

`epivizFileParser.HDF5File` module

`epivizFileParser.Helper` module

`epivizFileParser.InteractionBigBed` module

`epivizFileParser.S3HDF5File` module

`epivizFileParser.SamFile` module

`epivizFileParser.SplicingBamFile` module

`epivizFileParser.TbxFile` module

`epivizFileParser.TileDB` module

`epivizFileParser.TileDBTbxFile` module

`epivizFileParser.TranscriptTbxFile` module

`epivizFileParser.utils` module

#### Module contents



# CHAPTER 5

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## Indices and tables

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- genindex
- modindex
- search