VarFish CLI Documentation

Release 0.6.3

Core Unit Bioinformatics

MANUAL

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varfish-cli is a Python-based command line interface to the VarFish Server.

You can use it for the following tasks

- Listing information about projects, cases, etc. in the VarFish Server.
- Importing cases into VarFish based on their variant call files (VCFs) and quality reports.

This documentation will be expanded over time.

MANUAL 1

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ONE

INSTALLATION

1.1 Using Pip

Install varfish-cli into a new virtualenv:

```
virtualenv venv
source venv/bin/activate
pip install varfish-cli
varfish-cli --help
```

1.2 Using Conda

You can install VarFish via bioconda

```
## OR use "conda" below instead of mamba
mamba create -y -n varfish-cli varfish-cli
conda activate varfish-cli
varfish-cli --help
```

1.3 Creating Configuration

You must create a configuration file at ~/.varfishrc.toml with the URL to the server and the API token that you previously created. The following Bash snippet creaets such a file:

```
... code-block:: bash
cat >~/.varfishrc.toml <<EOF [global]

# URL to VarFish server. varfish_server_url = "https://varfish.example.com/" # API token to use for VarFish API. varfish_api_token = "XXX" EOF
```

TWO

CREDITS

- Manuel Holtgrewe
- Oliver Stolpe

6 Chapter 2. Credits

THREE

CHANGELOG

3.1 0.6.3 (2024-01-24)

3.1.1 Bug Fixes

• write out .sample_data in dragen-to-bam-qc (#101) (#102) (638c294)

3.1.2 Documentation

• fix link to pypi in README (#97) (8f25193)

3.2 0.6.2 (2024-01-23)

3.2.1 Bug Fixes

- properly assign version in release-please (#91) (3037f7a)
- version for release-please in CI (#89) (2aedb64)

3.2.2 Documentation

• add pypi and bioconda badges (#96) (88c7f79)

3.3 0.6.1 (2024-01-23)

3.3.1 Continuous Integration

• install setuptools to fix "python sdist" in release-please (#87) (9b03c68)

3.4 0.6.0 (2024-01-23)

3.4.1 Features

- add "projects project-list" command (#50) (057abd5)
- conversion from DRAGEN QC to legacy varfish format (#85) (#86) (043dbc3)
- migrate argparse code to typer (#48) (#61) (d1c86d4)
- migration from attrs to pydantic (#49) (#65) (2c9e402)

3.4.2 Documentation

- installation instructions in manual (#69) (0afb87c)
- updating README, adding terraform docs (#68) (f6dd1bf)

3.5 0.5.3 (2023-07-17)

3.5.1 Features

• force release of 0.6 (#46) (f003be8)

3.5.2 Bug Fixes

- allow varfish upload without SV effects (#43) (4aead65)
- fixing issue with logging (ab62f24)

3.5.3 0.5.2 (2023-07-17)

3.5.4 Bug Fixes

- allow varfish upload without SV effects (#43) (4aead65)
- Fixing case list API (#37) (ccaccfc)

3.5.5 0.5.2 (2023-06-12)

3.5.6 Bug Fixes

• Fixing case list API (#37) (ccaccfc)

3.5.7 0.5.1 (2023-02-09)

3.5.8 Bug Fixes

• manifest for readme and changelog (#35) (f14d647)

3.6 0.5.0 (2023-02-09)

3.6.1 Features

• replace python-Levenshtein with polyleven (#26) (#32) (73703bd)

3.6.2 Documentation

• fixing CI status badge (#34) (9967bbd)

3.7 0.4.0

• Adding support for varannos REST API (#24).

3.8 0.3.5

- Allowing to upload per-case gene annotation file (#20).
- Adding client endpoint for retrieving case from API (#18).

3.9 0.3.4

• Adding support for latest varfish-annotator output for svs (#16).

3.10 0.3.3

• Case importer distinguished smallvar and SV DB info files (#13).

3.11 0.3.2

• Fixing structuring/unstructuring of genomic region

3.12 0.3.1

• Allow disabling of verify_ssl in CLI

3.13 0.3.0

• Adding implementation of REST API (#7).

3.14 0.2.8

• Adding support to specify genome build on import (defaulting to GRCh37).

3.15 0.2.7

• Fix reading of non-compressed genotypes TSV file.

3.16 0.2.6

• Fixes to linting.

3.17 0.2.5

- Switching build system to Github Actions
- Adding many tests
- Fixing verify_ssl for case list.

3.18 0.2.4

• Added --no-verify-ssl.

3.19 0.2.3

- Added state field to VariantSetImportInfo class.
- Added endpoint for updating variant set import info.

3.20 0.2.2

• More MANIFEST.in fixes.

3.21 0.2.1

• Fixing package (MANIFEST.in).

3.22 0.2.0

- Adjusted to upstream REST API changes.
- Cases with all files can now be uploaded.

3.23 0.1.0

• everything is new

3.20. 0.2.2

FOUR

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