TACA Documentation

Release 1.0

Guillermo Carrasco

July 16, 2015

TACA stands for Tool for the Automation of Cleanup and Analyses, and basically it is a set of tools used in the National Genomics Infrastructure for easing the day-to-day tasks of managing and organizing projects and data.

To install TACA latest stable version, just use: `pip install taca`, for the latest development version, use `pip install git+git://github.com/SciLifeLab/TACA.git`.

Once it is installed, to get help just use the `--help` option. You can use the `--help` option on every TACA subcommand to get specific command help. For example `taca --help` will give you

```
Usage: taca [OPTIONS] COMMAND [ARGS]...

  Tool for the Automation of Storage and Analyses

Options:
  --version                   Show the version and exit.
  -c, --config-file FILENAME  Path to TACA configuration file
  --help                      Show this message and exit.

Commands:
  analysis  Analysis methods entry point
  storage   Storage management methods and utilities
```

And `taca storage --help` will give you

```
Usage: taca storage [OPTIONS] COMMAND [ARGS]...

  Storage management methods and utilities

Options:
  -d, --days INTEGER  Days to consider as thershold
  -r, --run PATH
  --help              Show this message and exit.

Commands:
  archive  Archive old runs to SWESTORE
  cleanup  Do appropriate cleanup on the given site i.e.
```

Project and Sample delivery

API documentation