Hypernets Processor User Guide

Release 2.0

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There are two main use cases for the **hypernets_processor** module. The primary function of the software is the automated preparation of data retrieved from network sites for distribution to users. Additionally, the software may also be used for ad-hoc processing of particular field acquisitions, for example for testing instrument operation in the field. For information on each these use cases read the following sections.

AD-HOC SEQUENCE PROCESSING

This section provides a user guide for running the **hypernets_processor** module to process specified field acquisitions, or sequences, on an ad-hoc basis outside of any automated processing.

1.1 Prerequisites

hypernets_processor is distributed using Git, from the project's GitHub repository. Git can be installed from the from the Git website.

Python 3 is required to run the software, the Anaconda distribution provides a convenient way to install this.

1.2 Installation

First clone the project repository from GitHub:

```
$ git clone https://github.com/HYPERNETS/hypernets_processor.git
```

Then install the module with pip:

```
$ pip install -e hypernets_processor/
```

This will also automatically install any dependencies.

If you are installing the module to contribute to its development, it is recommended you follow the install instructions on the developers_getting_started page.

1.3 Sequence Processing

Once installed the *hypernets_sequence_processor* command-line tool provides the means to process raw sequence data, it is run as follows:

```
$ hypernets_sequence_processor -i <input_directory> -o <output_directory> -n <network>
```

where:

- *input_directory* - directory of raw sequence product, or directory containing a number of raw sequence products, to process.
- *output_directory* - directory to write output data to.

- *network* - network name, *land* or *water*. The default configuration for this network is applied for the processing.

To see more options, try:

```
$ hypernets_sequence_processor --help
```

Alternatively, the processing can be specified with a job configuration file as follows:

```
$ hypernets_sequence_processor -j <job_config_path>
```

where:

- *job_config_path* - path of a job configuration file. See user_processor-job_setup for information on initialising a job configuration file.

Specifying processing with a custom job configuration file allows non-network-default configuration values to be set, for example, chosen calibration function. See also config for more details about the processing parameters that can be given.

1.4 Examples

Ad-hoc processing of a single sequence for a site called M1BE can be done with the following command:

```
$ hypernets_sequence_processor -i /home/waterhypernet/HYPSTAR/Raw/M1BE/DATA/
↪SEQ20231031T182051 -o /home/waterhypernet/HYPSTAR/Processed/test/ -n water --max-level␣
↪L2A
```

While processing all sequences within a single directory can be done with:

```
$ hypernets_sequence_processor -i /home/waterhypernet/HYPSTAR/Raw/M1BE/DATA/ -o /home/
↪waterhypernet/HYPSTAR/Processed/test/ -n water  --max-level L2A
```

If the adhoc processing arguments do not refer to a user defined job configuration path, input parameters for the processing configuration are taken by default from:

- /hypernets_processor/hypernets_processor/etc/processor_land_defaults.config, or,

- /hypernets_processor/hypernets_processor/etc/processor_water_defaults.config,

for the land and water network respectively. More details about the input parameters for the processing configuration can be found in config.