

API Reference

Technical Documentation.

It is recommended to open this via browser: <https://ms2206.github.io/FastQCParser/api>

Class Definitions

ParsedArg

Bases: dict

A class to represent parsed command-line arguments for sequence quality analysis.

This class maps command-line arguments to their corresponding search string and manages the required output types based on the argument.

Attributes:

Name	Type	Description
cli_argument	str	The command-line argument provided by the user.
value	bool	The bool command-line argument from 'store_true'
required_outputs	list	A list of required output types, defaulting to ['R', 'P', 'F'].
search_string	str	Search string to extract from FASTQC - retrieved from the arg_key_map.

- ▼ Class Attributes
- arg_key_map (dict): A mapping of command-line argument keys to their descriptions.

Methods:

Name	Description
configure_outputs	Adjusts the required outputs based on the command-line argument. If the argument is 'seq_len_dist' or 'over_seq', 'P' is removed from the required outputs.

- ▼ Example
- ```
parsed_arg = ParsedArg('per_base_seq_qual', 'some_value')
parsed_arg.configure_outputs()
['R', 'P', 'F']
```

- Source code in `src/class_definitions.py`

```
configure_outputs()
```

Removes 'P' from ['seq\_len\_dist', 'over\_seq'] :return:

- Source code in `src/class_definitions.py`

## Parsing

extract\_raw(filepath, search\_string)

Extracts a section of a CSV file based on a search string and returns it as a DataFrame.

This function reads a CSV file into a DataFrame, searches for a specified string within the 'raw' column, and extracts rows from the first occurrence of the search string to the corresponding 'END\_MODULE' marker. The function uses a predefined mapping to determine the correct 'END\_MODULE' for each search string.

Parameters: filepath (str): The path to the CSV file to be read. search\_string (str): The string to search for within the 'raw' column of the DataFrame.

Returns: DataFrame: A DataFrame containing the rows from the first occurrence of the search string to the corresponding 'END\_MODULE'.

Raises: FileNotFoundError: If the specified file does not exist, the function prints an error message and exits the program.

Example:

```
extract_raw('path/to/your/file.csv', 'Basic Statistics')
```

► Source code in `src/parser.py`

```
handle_cli_args(args)
```

This function further parses args from the ArgParse command line input. It unpacks all args with `store_true`. Then initiates and configures an instance of `Class::ParsedArg` for each optional arg that was supplied by the user.

:param args: cli arguments passed from user :return: a list of `ParsedArg` objects that have been configured to have their "Required outputs" adjusted based on expected output property.

► Source code in `src/parser.py`

```
parse_raw(raw_data)
```

Parses raw data from `extract_raw()`.

This function further processes a `DataFrame` from `extract_raw()`. It gathers all lines that do not start with '#' and splits on tab characters. These are the values from the FASTQC file. It also extracts the headers as lines that start with '#' and uses these two lists to return a pandas `DataFrame`.

Parameters: `raw_data` (`DataFrame`): The output from `extract_raw()`

Returns: `DataFrame`: A formatted `DataFrame` with the extracted values and headers.

Example:

```
raw_data = extract_raw('data/raw/fastqc_data1.txt', 'Sequence Duplication Levels')
formatted_df = parse_raw(raw_data)
print(formatted_df)
```

► Source code in `src/parser.py`

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## Plotting

```
plot_adap_cont(cli_arg, output_dir)
```

Plot and save `plot_adap_cont` to filepath :return: None

► Source code in `src/plotter.py`

```
plot_kmer_cont(cli_arg, output_dir)
```

Plot and save `per_base_N_cont` to filepath :return: None

► Source code in `src/plotter.py`

```
plot_per_base_N_cont(cli_arg, output_dir)
```

Plot and save `per_base_N_cont` to filepath :return: None

► Source code in `src/plotter.py`

```
plot_per_base_seq_content(cli_arg, output_dir)
```

Plot and save `per_base_seq_content` to filepath :return: None

► **Source code in** `src/plotter.py`

```
plot_per_base_seq_qual(cli_arg, output_dir)
```

Plot and save per\_base\_seq\_qual to filepath :return: None

► **Source code in** `src/plotter.py`

```
plot_per_seq_GC_cont(cli_arg, output_dir)
```

Plot and save per\_base\_seq\_content to filepath :return: None

► **Source code in** `src/plotter.py`

```
plot_per_seq_qual_scores(cli_arg, output_dir)
```

Plot and save per\_seq\_qual\_scores to filepath :return: None

► **Source code in** `src/plotter.py`

```
plot_per_tile_seq_qual(cli_arg, output_dir)
```

Plot and save per\_tile\_seq\_qual to filepath :return: None

► **Source code in** `src/plotter.py`

```
plot_seq_dup(cli_arg, output_dir)
```

Plot and save per\_base\_N\_cont to filepath :return: None

► **Source code in** `src/plotter.py`

```
plot_seq_len_dist(cli_arg, output_dir)
```

Plot and save per\_base\_N\_cont to filepath :return: None

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### Class Definitions

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A class to represent parsed command-line arguments for sequence quality analysis.

This class maps command-line arguments to their corresponding search string and manages the required output types based on the argument.

#### Attributes:

| Name             | Type | Description                                                            |
|------------------|------|------------------------------------------------------------------------|
| cli_argument     | str  | The command-line argument provided by the user.                        |
| value            | bool | The bool command-line argument from 'store_true'                       |
| required_outputs | list | A list of required output types, defaulting to ['R', 'P', 'F'].        |
| search_string    | str  | Search string to extract from FASTQC - retrieved from the arg_key_map. |

#### ▼ Class Attributes

arg\_key\_map (dict): A mapping of command-line argument keys to their descriptions.

#### Methods:

| Name                              | Description                                                                                                                                                 |
|-----------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <a href="#">configure_outputs</a> | Adjusts the required outputs based on the command-line argument. If the argument is 'seq_len_dist' or 'over_seq', 'P' is removed from the required outputs. |

#### ▼ Example

```
parsed_arg = ParsedArg('per_base_seq_qual', 'some_value')
parsed_arg.configure_outputs()
['R', 'P', 'F']
```

#### ► Source code in `src/class_definitions.py`

```
configure_outputs()
Removes 'P' from ['seq_len_dist', 'over_seq'] :return:
```

#### ► Source code in `src/class_definitions.py`

### Parsing

extract\_raw(filepath, search\_string)

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Returns: DataFrame: A DataFrame containing the rows from the first occurrence of the search string to the corresponding 'END\_MODULE'.

Raises: FileNotFoundError: If the specified file does not exist, the function prints an error message and exits the program.

Example:

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This function further parses args from the ArgParse command line input. It unpacks all args with `store_true`. Then initiates and configures an instance of `Class::ParsedArg` for each optional arg that was supplied by the user.

:param args: cli arguments passed from user :return: a list of `ParsedArg` objects that have been configured to have their "Required outputs" adjusted based on expected output property.

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Parameters: `raw_data (DataFrame)`: The output from `extract_raw()`

Returns: `DataFrame`: A formatted `DataFrame` with the extracted values and headers.

Example:

```
raw_data = extract_raw('data/raw/fastqc_data1.txt', 'Sequence Duplication Levels') formatted_df = parse_raw(raw_data)
print(formatted_df)
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plot_per_base_N_cont(cli_arg, output_dir)
```

Plot and save `per_base_N_cont` to filepath :return: None

► Source code in `src/plotter.py`

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Plot and save per\_base\_seq\_qual to filepath :return: None

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```

Plot and save per\_base\_seq\_content to filepath :return: None

► **Source code in** `src/plotter.py`

```
plot_per_seq_qual_scores(cli_arg, output_dir)
```

Plot and save per\_seq\_qual\_scores to filepath :return: None

► **Source code in** `src/plotter.py`

```
plot_per_tile_seq_qual(cli_arg, output_dir)
```

Plot and save per\_tile\_seq\_qual to filepath :return: None

► **Source code in** `src/plotter.py`

```
plot_seq_dup(cli_arg, output_dir)
```

Plot and save per\_base\_N\_cont to filepath :return: None

► **Source code in** `src/plotter.py`

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plot_seq_len_dist(cli_arg, output_dir)
```

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