

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

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

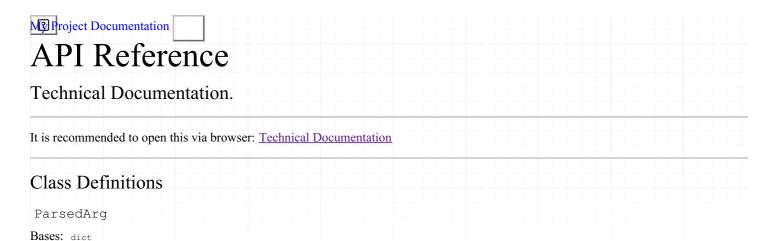
► Source code in src/plotter.py

plot seq len dist(cli arg, output dir)

Plot and save per_base_N_cont to filepath :return: None

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Documentation built with MkDocs.



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