DataPipeline

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Usage:

merger.py automatically attempts to read **'new_pubchem.csv'** and **'new_swiss.csv'** from **./data** and then outputs **./merger/merge.csv**

Altnernatively, use **merger.py -h** to show arguments that allow passing of specific files on input. populate_chem.py attempts to read data from **./merger/merge.csv** then output it to **./chem/new_attrib.csv**

2 Usage:

Namespace Index

2.1 Packages

re are the packages with brief descriptions (if available):	
cleaner	
crawler_orchestrator	13
dependencies	14
dependencies.pubchem	
dependencies.swissadme	
dependencies.swisstarget	14
merger	
pipe_handler	
populate_chem	15

4 Namespace Index

Hierarchical Index

3.	1	Class	Hiera	rchy
----	---	-------	-------	------

This inheritance list is sorted roughly, but not completely, alphabetically:	
object	
pipe handler.lanoreBrokenPipe	17

6 Hierarchical Index

Class Index

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Here are the classes, structs, unions and interfaces with brief descriptions:	
pipe_handler.lgnoreBrokenPipe	17

8 Class Index

File Index

5.1 File List

re is a list of all files with brief descriptions:	
cleaner.py	9
merger.py	20
pipe_handler.py	20
populate_chem.py	20
run_pipeline.py	21
crawlers/crawler_orchestrator.py	9
crawlers/dependencies/initpy	9
crawlers/dependencies/pubchem.py	20
crawlers/dependencies/swissadme.py	20
crawlers/dependencies/swisstarget ny	ייכ

10 File Index

Namespace Documentation

6.1 cleaner Namespace Reference

Functions

- def load_data (csv_file_name)
- def set_proper_data_type (df)
- def unique_count (column)
- def remove_useless_columns (df)
- list get_duplicit_correlated_descriptors (graphs, descriptors)
- def get_correlated_descriptors (df, threshold, fig_location)
- · def create correlation graphs (correlations, fig location, threshold)
- def save_mask (df, mask_name, [None, list] columns=None, [None, list] rows=None)
- pd.DataFrame check_correlated_column (df, threshold=0.9, remove=False, preserve_columns=[], graph_← location='./plot/correlations_grapgs_{}.jpeg', heatmap_location='./plot/correlations_heatmap_{}.jpeg')
- def remove_duplicits (pd.DataFrame df, subset, keep='first')
- def check_outliers (df, threshold=4.2, remove=False)
- def main (input_file, output_file, correlation_threshold=0.95, outliers_threshold=4.2, preserve_← columns=None, remove=False)
- dict process_config (config_file='conf/cleaner.ini')

Variables

dict args = process_config('conf/cleaner.ini')

6.1.1 Function Documentation

6.1.1.1 check_correlated_column()

6.1.1.2 check_outliers()

```
def cleaner.check_outliers ( df, \\ threshold = 4.2, \\ remove = False )
```

6.1.1.3 create_correlation_graphs()

6.1.1.4 get_correlated_descriptors()

6.1.1.5 get_duplicit_correlated_descriptors()

6.1.1.6 load_data()

6.1.1.7 main()

6.1.1.8 process_config()

6.1.1.9 remove_duplicits()

```
def cleaner.remove_duplicits (
    pd.DataFrame df,
    subset,
    keep = 'first' )
```

6.1.1.10 remove_useless_columns()

```
def cleaner.remove_useless_columns ( df )
```

6.1.1.11 save_mask()

6.1.1.12 set_proper_data_type()

6.1.1.13 unique_count()

6.1.2 Variable Documentation

6.1.2.1 args

```
dict cleaner.args = process_config('conf/cleaner.ini')
```

6.2 crawler_orchestrator Namespace Reference

Functions

• def main (file)

6.2.1 Function Documentation

6.2.1.1 main()

```
\begin{tabular}{ll} \tt def crawler\_orchestrator.main ( \\ \it file \end{tabular} )
```

6.3 dependencies Namespace Reference

Namespaces

- pubchem
- · swissadme
- swisstarget

6.4 dependencies.pubchem Namespace Reference

Functions

• def crawl (prefs)

6.4.1 Function Documentation

```
6.4.1.1 crawl() def dependencies.pubchem.crawl ( prefs )
```

6.5 dependencies.swissadme Namespace Reference

Functions

- def is_file_downloaded (filename, timeout=5)
- def crawl (prefs)

6.5.1 Function Documentation

```
6.5.1.1 crawl()
```

```
\begin{tabular}{ll} def dependencies.swissadme.crawl ( \\ prefs ) \end{tabular}
```

6.5.1.2 is_file_downloaded()

6.6 dependencies.swisstarget Namespace Reference

Functions

- def is_file_downloaded (filename, timeout=5)
- def crawl (prefs)

6.6.1 Function Documentation

6.6.1.1 crawl()

```
\begin{tabular}{ll} def dependencies.swisstarget.crawl ( \\ prefs ) \end{tabular}
```

6.6.1.2 is_file_downloaded()

6.7 merger Namespace Reference

Functions

• def merge ()

6.7.1 Function Documentation

```
6.7.1.1 merge()

def merger.merge ( )
```

6.8 pipe_handler Namespace Reference

Classes

• class IgnoreBrokenPipe

6.9 populate_chem Namespace Reference

Functions

• def populate ()

6.9.1 Function Documentation

6.9.1.1 populate()

```
def populate_chem.populate ( )
```

6.10 run_pipeline Namespace Reference

Variables

```
• parser = argparse.ArgumentParser()
```

- type
- str
- help
- args = parser.parse_args()

6.10.1 Variable Documentation

6.10.1.1 args

run_pipeline.args = parser.parse_args()

6.10.1.2 help

run_pipeline.help

6.10.1.3 parser

run_pipeline.parser = argparse.ArgumentParser()

6.10.1.4 str

run_pipeline.str

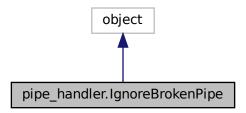
6.10.1.5 type

run_pipeline.type

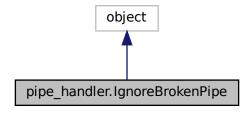
Class Documentation

7.1 pipe_handler.lgnoreBrokenPipe Class Reference

Inheritance diagram for pipe_handler.lgnoreBrokenPipe:



Collaboration diagram for pipe_handler.lgnoreBrokenPipe:



Public Member Functions

• def __init__ (self, stream)

Public Attributes

stream

18 Class Documentation

- write
- flush

7.1.1 Constructor & Destructor Documentation

7.1.2 Member Data Documentation

7.1.2.1 flush

pipe_handler.IgnoreBrokenPipe.flush

7.1.2.2 stream

pipe_handler.IgnoreBrokenPipe.stream

7.1.2.3 write

pipe_handler.IgnoreBrokenPipe.write

The documentation for this class was generated from the following file:

• pipe_handler.py

File Documentation

8.1 cleaner.py File Reference

Namespaces

cleaner

Functions

- def cleaner.load_data (csv_file_name)
- def cleaner.set_proper_data_type (df)
- def cleaner.unique_count (column)
- def cleaner.remove_useless_columns (df)
- list cleaner.get_duplicit_correlated_descriptors (graphs, descriptors)
- def cleaner.get correlated descriptors (df, threshold, fig location)
- def cleaner.create_correlation_graphs (correlations, fig_location, threshold)
- def cleaner.save mask (df, mask name, [None, list] columns=None, [None, list] rows=None)
- pd.DataFrame cleaner.check_correlated_column (df, threshold=0.9, remove=False, preserve_columns=[], graph_location='./plot/correlations_grapgs_{}.jpeg', heatmap_location='./plot/correlations_heatmap_{}.jpeg')
- · def cleaner.remove duplicits (pd.DataFrame df, subset, keep='first')
- def cleaner.check_outliers (df, threshold=4.2, remove=False)
- def cleaner.main (input_file, output_file, correlation_threshold=0.95, outliers_threshold=4.2, preserve_←
 columns=None, remove=False)
- · dict cleaner.process_config (config_file='conf/cleaner.ini')

Variables

dict cleaner.args = process config('conf/cleaner.ini')

8.2 crawlers/crawler_orchestrator.py File Reference

Namespaces

· crawler_orchestrator

Functions

· def crawler orchestrator.main (file)

8.3 crawlers/dependencies/__init__.py File Reference

Namespaces

dependencies

20 File Documentation

8.4 crawlers/dependencies/pubchem.py File Reference

Namespaces

• dependencies.pubchem

Functions

· def dependencies.pubchem.crawl (prefs)

8.5 crawlers/dependencies/swissadme.py File Reference

Namespaces

• dependencies.swissadme

Functions

- def dependencies.swissadme.is_file_downloaded (filename, timeout=5)
- def dependencies.swissadme.crawl (prefs)

8.6 crawlers/dependencies/swisstarget.py File Reference

Namespaces

· dependencies.swisstarget

Functions

- def dependencies.swisstarget.is_file_downloaded (filename, timeout=5)
- def dependencies.swisstarget.crawl (prefs)

8.7 merger.py File Reference

Namespaces

merger

Functions

• def merger.merge ()

8.8 pipe handler.py File Reference

Classes

• class pipe_handler.lgnoreBrokenPipe

Namespaces

· pipe handler

8.9 populate_chem.py File Reference

Namespaces

populate_chem

Functions

• def populate_chem.populate ()

8.10 README.md File Reference

8.11 run_pipeline.py File Reference

Namespaces

• run_pipeline

Variables

- run_pipeline.parser = argparse.ArgumentParser()
- run_pipeline.type
- run_pipeline.str
- run_pipeline.help
- run_pipeline.args = parser.parse_args()

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