D:\NHRI\AMR\amr-main\datasets\clean_SOURCE_2.py

```
import pandas as pd
 2
   import numpy as np
   import os
 3
 4
    from cod_prep.claude.configurator import Configurator
    from cod_prep.downloaders import (get_ages, get_cod_ages,
7
        get_current_location_hierarchy)
8
    from cod_prep.utils.formatting import ages
9
    from cod_prep.utils import report_if_merge_fail, print_log_message
10
11
   CONF = Configurator()
   SOURCE = "SOURCE_NAME"
12
13
   L_DIR = "FILEPATH"
14
15
   def read_in_data():
16
17
        df = pd.read_csv(L_DIR + 'FILENAME')
18
19
20
        df['cases'] = 1
21
        df['raw_specimen'] = df['source']
22
23
        df['raw_pathogen'] = df['species']
24
25
        df['sample_id'] = 'SOURCE-' + df['isolateid'].astype(str) + '-' + df['raw_specimen']
26
27
        df['year_id'] = df['year']
28
29
        return df
30
31
32
    def format_age_group_id(df):
33
34
        age_dict = {
35
        '0 to 2 Years': 244,
36
        '3 to 12 Years': 291,
        '13 to 18 Years': 15,
37
        '19 to 64 Years': 163,
38
39
        '65 to 84 Years': 281,
40
        '85 and Over': 160,
        'Unknown': 283}
41
42
43
        df['age_group_id'] = df['agegroup'].map(age_dict)
44
        assert df.age group id.notnull().values.all()
45
46
        return df
47
48
49
    def format_sex_id(df):
50
51
```

```
52
         df["sex_id"] = df["gender"].map({"Male": 1, "Female": 2, np.nan: 9})
         report if merge fail(df, "sex id", "gender")
53
54
55
         return df
56
57
    def format_location_id(df):
58
59
60
         location = get_current_location_hierarchy()
61
         df['location_name'] = df['country']
62
         df.loc[(df['location_name'] == 'United States') & (df['state'].notnull()),
63
     'location_name'] = df['state']
64
         df = df.merge(location[['location_name','location_id']], how = 'left', on =
65
     'location_name')
66
         df.loc[df['location_id'].isna(), 'location_name'].unique()
67
68
         df.loc[df['location_name'] == 'United States', 'location_id'] = 102
69
70
         df.loc[df['location_name'] == 'Hong Kong', 'location_id'] = 354
71
         df.loc[df['location_name'] == 'Czech Republic', 'location_id'] = 47
72
         df.loc[df['location_name'] == 'Russia', 'location_id'] = 62
         df.loc[df['location_name'] == 'Venezuela', 'location_id'] = 133
73
         df.loc[df['location_name'] == 'Korea, South', 'location_id'] = 68
74
75
         df.loc[df['location_name'] == 'Taiwan', 'location_id'] = 8
         df.loc[df['location_name'] == 'Vietnam', 'location_id'] = 20
76
         df.loc[df['location_name'] == 'Slovak Republic', 'location_id'] = 54
77
78
79
         assert df.location_id.notnull().values.all()
80
81
         return df
82
83
    def clean_drug(df):
84
85
         antibio = df.iloc[:, 13:101]
86
87
         antibio names = [x for x in list(antibio) if " i" in x]
         antibio_numbers = [x for x in list(antibio) if (x not in list(antibio_names))]
88
89
90
        df = df.drop(antibio_names, axis=1)
91
92
         df.loc[df[antibio numbers].isnull().apply(lambda x: all(x), axis=1), antibio numbers] =
     'unknown'
93
94
         keep = [x for x in list(df) if (x not in list(antibio numbers))]
95
96
         df = pd.melt(df, id_vars= keep, value_vars=antibio_numbers)
97
98
        df = df[df['value'].notnull()]
99
         df.rename(columns={'variable': 'raw_antibiotic', 'value': 'resistance'}, inplace=True)
100
101
102
         assert df.raw antibiotic.notnull().values.all()
```

```
103
         assert df.resistance.notnull().values.all()
104
105
         return df
106
107
    def clean_SOURCE():
108
         df = read_in_data()
109
110
         df = format_age_group_id(df)
111
         df = format_sex_id(df)
         df = format_location_id(df)
112
113
         df = clean_drug(df)
114
115
         df["nid"] = 410524
116
117
         return df
118
119
     if __name__ == '__main__':
120
121
         df = clean_SOURCE()
         demo_cols = ['nid', 'sample_id', 'location_id', 'year_id', 'age_group_id', 'sex_id']
122
         biology = ['raw_pathogen', 'raw_antibiotic', 'resistance', 'raw_specimen']
123
         other_values = ['cases']
124
125
         lowercase_cols = ['raw_pathogen', 'raw_antibiotic', 'raw_specimen']
         df = df[demo_cols + biology + other_values]
126
127
128
         # Lower case a few mapped columns
         for col in lowercase_cols:
129
130
             df[col] = df[col].str.lower().str.strip()
             assert df[col].notnull().values.all()
131
132
         df.to_csv("FILEPATH", index=False)
133
```