## D:\NHRI\AMR\amr-main\explore\top6\_pct\_by\_sr.py

```
import pandas as pd
2
   import numpy as np
   import seaborn as sns
   from pathlib import Path
    from db_tools import ezfuncs
6
7
8
    from cod_prep.downloaders import *
    from cod_prep.utils import *
    from cod_prep.claude.configurator import Configurator
9
    from amr prep.utils.amr io import get amr results
10
    from amr_prep.utils.amr_io import AmrResult
11
    from mcod_prep.compile_burden import summarize_draws
12
    from explore.number_plugging.rtr import *
13
    import warnings
    warnings.filterwarnings("ignore")
14
15
16
    CONF = Configurator()
   LSV_ID = CONF.get_id('location_set_version')
17
   CSV_ID = CONF.get_id('cause_set_version')
18
19
20
   lh = get_current_location_hierarchy(location_set_version_id=LSV_ID)
21
   ch = get_current_cause_hierarchy(cause_set_version_id=CSV_ID)
22
23
    print('Find top 6 pathogen percent against total by super region for both counterfactuals')
   supregs = lh.loc[lh['level'] == 1, ['location_id', 'location_name']].drop_duplicates()
24
25
    supregs_ids = supregs['location_id'].tolist()
26
    supregs_dict = dict(zip(supregs.location_id, supregs.location_name))
27
28
   df = get_results_wrapper('fatal', 1, 1, syndrome='all', abx_class='all_resistant',
        counterfactual='no_infection')
29
30
   top6 = df.loc[(df['pathogen'] != 'all'), ]
        .sort_values(by='amr_mean', ascending=False).head(6)['pathogen'].unique().tolist()
31
32
   df_f = get_results_wrapper('fatal', 1, 1, location_id=supregs_ids,
33
        pathogen=top6, syndrome='all', abx class='all resistant', draws=True)
34
   total_f = get_results_wrapper('fatal', 1, 1, location_id=supregs_ids,
35
        syndrome='all', pathogen='all', abx_class='all_resistant', draws=True)
36
37
   df_nf = get_results_wrapper('nonfatal', 2, 1, location_id=supregs_ids,
38
39
        pathogen=top6, syndrome='all', abx class='all resistant', draws=True)
    total_nf = get_results_wrapper('nonfatal', 2, 1, location_id=supregs_ids,
40
41
        syndrome='all', pathogen='all', abx_class='all_resistant', draws=True)
42
43
   dffs = []
44
   dfnfs = []
   for pathogen in top6:
45
        print("-----" + pathogen.capitalize() + "-----")
46
        for location_id, location_name in supregs_dict.items():
47
            print("----" + location name + '----')
48
            print('Deaths')
49
            df_f1 = df_f.loc[(df_f['pathogen'] == pathogen) & (df_f['location_id'] ==
50
    location_id), ]
            total_f1 = total_f.loc[(total_f['location_id'] == location_id), ]
51
```

```
df_f1, pct_f = aggregate_summarize_draws(df_f1, to_aggregate='pathogen',
52
    get_pct=True, denominator=total_f1)
53
            print(pathogen + ' attributable AMR death percentage out of total in :' +
   location_name)
            print_out_cf_lower_mean_upper(pct_f, 'deaths')
54
55
            print()
56
            pct_f['pathogen'] = pathogen
            dffs.append(pct_f)
57
58
59
            print('DALYS')
            df_nf1 = df_nf.loc[(df_nf['pathogen'] == pathogen) & (df_nf['location_id'] ==
60
    location_id)]
            total_nf1 = total_nf.loc[(total_nf['location_id'] == location_id), ]
61
            df_nf1, pct_nf = aggregate_summarize_draws(df_nf1, to_aggregate='pathogen',
62
    get_pct=True, denominator=total_nf1)
63
            print(pathogen + ' attributable AMR DALYs percentage out of total in :' +
    location_name)
64
            print_out_cf_lower_mean_upper(pct_nf, 'DALYs')
65
            pct_nf['pathogen'] = pathogen
66
            dfnfs.append(pct_nf)
67
68
        print()
69
   dff = pd.concat(dffs)
70
71
   dfnf = pd.concat(dfnfs)
72
73
   dff.to_csv('FILEPATH', index=False)
74 dfnf.to_csv('FILEPATH', index=False)
```