0_database-generation

February 14, 2020

1 Database generation

In this notebook we process the data into a database we can later query to make plots/do analysis etc. ### OBS: This notebook is only slightly edited from Zebedee Nicholls notebook, see here

1.1 Imports

/home/sarambl/PHD/IPCC/public/AR6_CH6_RCMIPFIGS/ar6_ch6_rcmipfigs/home/sarambl/PHD/IPCC/public/AR6_CH6_RCMIPFIGS/ar6_ch6_rcmipfigs/data_in

```
[2]: %load_ext nb_black
```

<IPython.core.display.Javascript object>

```
[]: import logging
import os.path
import re
from pathlib import Path
from distutils.util import strtobool

import pandas as pd
import tqdm
from scmdata import ScmDataFrame, df_append
```

```
TEST_RUN = strtobool(os.getenv("CI", "False")) or False
TEST_RUN
```

```
[]: logger = logging.getLogger()
```

1.2 Constants

```
[]: from ar6_ch6_rcmipfigs.utils.misc_func import make_folders

if not os.path.isdir(OUTPUT_DATABASE_PATH):
    make_folders(OUTPUT_DATABASE_PATH)

if not os.path.isdir(OBS_DATABASE_PATH):
    make_folders(OBS_DATABASE_PATH)
```

1.3 Protocol

```
[]: SCENARIO_PROTOCOL = os.path.join(INPUT_DATA_DIR, "data", "protocol", 

→"rcmip-emissions-annual-means.csv"
)
```

```
[ ]: protocol_db = ScmDataFrame(SCENARIO_PROTOCOL)
protocol_db.head()
```

```
[]: protocol_db["scenario"].unique()
```

```
1.4 Model output
[]: RESULTS_PATH = os.path.join(INPUT_DATA_DIR, "data", "results", "phase-1")
[]: _results_files = list(Path(RESULTS_PATH).rglob("*.csv")) + list(
         Path(RESULTS_PATH).rglob("*.xlsx")
     print(len(_results_files))
     sorted(_results_files)
[]: model_of_interest = [
          ".*acc2.*v2-0-1.*",
         ".*rcmip_phase-1_cicero-scm.*v5-0-0.*",
         ".*escimo.*v2-0-1.*",
        ".*fair-1.5-default.*v1-0-1.csv",
          ".*rcmip_phase-1_qir.*",
         ".*qreb.*v2-0-0.*",
         ".*hector.*v2-0-0.*",
          ".*MAGICC7.1.0aX-rcmip-phase-1.*",
         ".*rcmip_phase-1_magicc7.1.0.beta_v1-0-0.*",
         ".*MAGICC7.1.0aX.*",
         ".*mce.*v2-0-1.*",
         ".*oscar-v3-0*v1-0-1.*",
        ".*oscar-v3-0.*v1-0-1.*"
          ".*wasp.*v1-0-1.*",
     #
     ]
[]: if TEST_RUN:
         model_of_interest = [
             ".*escimo-phase-1-v2-0-1.*",
             ".*greb.*",
             ".*rcmip_phase-1_cicero-scm.*v5-0-0.*",
         ]
     results_files = [
         str(p)
         for p in _results_files
         if any([bool(re.match(m, str(p))) for m in model_of_interest]) and "$" not_
      \rightarrowin str(p)
```

```
print(len(results_files))
     sorted(results_files)
[ ]: [ ]
         str(p)
         for p in results_files
         if 'magicc' in str(p)] #for m in model_of_interest]) and "$" not in str(p)
     #]
[]: db = []
     for rf in tqdm.tqdm_notebook(results_files):
         if rf.endswith(".csv"):
             loaded = ScmDataFrame(rf)
         else:
             loaded = ScmDataFrame(rf, sheet_name="your_data")
         db.append(loaded)
     db = df_append(db).timeseries().reset_index()
     db["unit"] = db["unit"].apply(
         lambda x: x.replace("Dimensionless", "dimensionless") if isinstance(x, str)
     ⊶else x
     db = ScmDataFrame(db)
     db.head()
[]: db.filter(climatemodel="*cicero*").head()
```

```
[]: db["climatemodel"].unique()
```

1.4.1 Minor quick fixes

We relabel all the ssp370-lowNTCF data to remove ambiguity.

```
[]: db = db.timeseries().reset_index()
     db["scenario"] = db["scenario"].apply(
         lambda x: "ssp370-lowNTCF-gidden" if x == "ssp370-lowNTCF" else x
     db["scenario"] = db["scenario"].apply(
         {\tt lambda x: "esm-ssp370-lowNTCF-gidden" if x == "esm-ssp370-lowNTCF" else x}
     db["scenario"] = db["scenario"].apply(
         lambda x: "esm-ssp370-lowNTCF-gidden-allGHG"
         if x == "esm-ssp370-lowNTCF-allGHG"
         else x
```

```
db = ScmDataFrame(db)
```

```
[]: assert "ssp370-lowNTCF" not in db["scenario"].unique().tolist()
assert "esm-ssp370-lowNTCF" not in db["scenario"].unique().tolist()
assert "esm-ssp370-lowNTCF-allGHG" not in db["scenario"].unique().tolist()
```

The Hector and MCE data is mislabelled so we do a quick fix here. I also have changed my mind about how to format the quantiles so tweak the FaIR and WASP data too.

```
[]: hector_prob_data = db.filter(climatemodel="hector*HISTCALIB*")
   if not hector_prob_data.timeseries().empty:
     hector_prob_data = hector_prob_data.timeseries().reset_index()

   hector_prob_data["variable"] = (
        hector_prob_data["variable"]
        + "|"
        + hector_prob_data["climatemodel"].apply(hector_get_quantile)
    )

   hector_prob_data["climatemodel"] = hector_prob_data["climatemodel"].apply(
        lambda x: x.split("-")[0]
   )

   db = db.filter(climatemodel="hector*HISTCALIB*", keep=False).append(
        hector_prob_data
   )
```

```
db.filter(climatemodel="hector*HISTCALIB").head(10)
```

```
[]: wasp_prob_data = db.filter(climatemodel="*WASP*")
if not wasp_prob_data.timeseries().empty:
    wasp_prob_data = wasp_prob_data.timeseries().reset_index()

    wasp_prob_data["variable"] = wasp_prob_data["variable"].apply(
        lambda x: x.replace("|00th", "|0th").replace("|05th", "|5th")
)

    db = db.filter(climatemodel="*WASP*", keep=False).append(
        ScmDataFrame(wasp_prob_data)
    )

    db.filter(climatemodel="*WASP*").head(10)
```

1.5 Unify units and check names

Here we loop over the submissions and unify their units as well as checking their naming matches what we expect.

```
[]: base_df = db.timeseries()
    any_failures = False

    clean_db = []
    for climatemodel, cdf in tqdm.tqdm_notebook(
        base_df.groupby("climatemodel"), desc="Climate model"
):
        print(climatemodel)
        print("-" * len(climatemodel))

        any_failures_climatemodel = False
```

```
cdf = ScmDataFrame(cdf)
    cdf_converted_units = unify_units(cdf, protocol_variables)
        check_all_scenarios_as_in_protocol(cdf_converted_units,_
 →protocol_scenarios)
        check_all_variables_and_units_as_in_protocol(
            cdf converted units, protocol variables
    except AssertionError as e:
        print(e)
        any_failures_climatemodel = True
          # currently not possible as groups weren't told to obey variable
 \rightarrow hierarchy,
    #
          # add this in phase 2
          for v_top in cdf_converted_units.filter(level=0)["variable"].unique():
    #
              print(v top)
              cdf_pyam = cdf_converted_units.filter(variable="{}*".
 \rightarrow format(v_top)).timeseries()
    #
              cdf_pyam.columns = cdf_pyam.columns.map(lambda x: x.year)
              cdf_consistency_checker = pyam.IamDataFrame(cdf_pyam)
              if cdf_consistency_checker.check_internal_consistency() is not_
 \rightarrow None:
                  print("Failed for {}".format(v_top))
    #
    #
                  any_failures_climatemodel = True
                  failing_set = cdf_consistency_checker.copy()
    print()
    if not any_failures_climatemodel:
        clean_db.append(cdf_converted_units)
        print("All clear for {}".format(climatemodel))
    else:
        print("Failed {}".format(climatemodel))
        print("X" * len("Failed"))
        any_failures = True
    print()
    print()
if any_failures:
   raise AssertionError("database isn't ready yet")
else:
    clean_db = df_append(clean_db)
    clean_db.head()
```

```
[]: clean_db.head()
```

Notes whilst doing this:

• I wasn't clear that the variable hierarchy needs to be obeyed, hence doing internal consistency checks isn't going to work

For phase 2:

- checking internal consistency super slow, worth looping over top level variables when doing this to speed up filtering
- need to decide what a sensible tolerance is
- might have to go back to model notes to work out why there are inconsistencies
- will have to implement a custom hack to deal with the double counting in the direct aerosol forcing hierarchy

1.6 Creating a database

[]: save_into_database(clean_db, OUTPUT_DATABASE_PATH, "rcmip-phase-1")