Incremenetal Harmonization Install   
Dec. 2018

These directions assume you are not using INSTALL.sh which is recommended

Deliverables are two zip files: harm\_2018\_12\_11.zip and opt\_local\_harmonization.zip.   
Assumes you have PostgreSQL installed with a schema heart\_db\_v2 and at least basic OMOP.  
Also assumes Python3 is installed.

* In a directory of your choice, create and cd into a directory called harmonization.
* Unzip the zip files for harmonization harm\_2018\_12\_11.zip
* in /opt/local, unzip the zip files for /opt/local (probably already done for pardeep) opt\_local\_harmonization.zip
* copy real data into the following directories, maintain the filenames shown. /opt/local/harmonization/deployment/studies/STUDY/study\_file.csv
  + cp sample.csv /opt/local/harmonization/deployment/studies/CORONA/data/sample.csv
  + cp test.csv /opt/local/harmonization/deployment/studies/PARADIGM/test.csv
* cd to the harmonization/django\_harmonization directory
* set the PostgreSQL environment variables
  + check them: env | grep PG
    - should have PGHOST, PGPORT, PGUSER, PGPASSWORD, PGDATABASE
  + edit and  run ../bin/env.sh if necessary. Pardeep should have one kkkk
    - textedit ../bin/env.sh
    - . ../bin/env.sh. # runs it
* Add new Kao concepts: run ../sql/concept.sql by hand
  + cat ../sql/concept.sql | psql
  + verify in a psql prompt with “select \* from concept where concept\_id > 2000000000”
    - should see up to UCD-Kao-38
* run load\_mappings.sh by hand
  + . ../bin/load\_mappings.sh
  + vocabulary\_concept is big and takes a few minutes
  + The verify steps are noisy, but if you see and end with status 0, it’s good.
* start django
  + python3 manage.py runserver 0.0.0.0:8000
  + point browser to <http://localhost:8000/ui/pipeline.html>
* load\_studies: click on the load studies button
  + WARNINGS on other studies are OK
  + will error out if not all studies available (could edit study table)
  + test the presence of your data with SQL:
    - select count(\*) from corona.sample;
    - non trivial delete starts with removing rows in events\_mapping, table\_column then study
* reload the UI in the browser, see the studies appear in the menu
* choose a study, CORONA
* click the migrate button, note the text “running”. It will change to “COMPLETE”
* click the calculate button, note the text “running”. It will change to “COMPLETE”
* select and export configuration: paradigm-atmosphere
* click the extract button. Here too “running” changes to “COMPLETE”
  + /opt/local/harmonization/output/corona.csv