CalibratedVA Analysis pipeline on desktop

To run on the desktop:

1. Go to the portal
2. Run Analysis and download all\_WHO.csv from this analysis : <https://comsa.dashreport.io/analysis/ankfbjajdabfchdgabb>
3. Download eng\_ext\_child\_VASA.dta from this analysis : <https://comsa.dashreport.io/analysis/angebkaebbcdebchbbk>
4. Save 2 and 3 to Data subfolder
5. Any new data sent from CHAMPS also needs to be added to Data subfolder
6. Run scripts 1 through 8

Notes:

1. The formatted, final, data for CalibratedVA is in the folder Results/20200802\_comsa\_data
   1. Change line 12 of script #8 to the new formatted, final, subfolder date, if updating
   2. In the formatted final subfolder there is a checks.R to make sure that rows sum to 1 and rownames are consistent across methods
      1. Occasionally a row will sum to 2 because of a tied max getIndivProb(), in which case I’ve been using script #6a (lines 16-34) to getTopCOD(), and then manually assigning that single cause on a case-by-case basis in script #7 (eg. lines 173-179)
2. Script *X.Get new MITS broad categories.R* only needs to be run if we get more MITS from CHAMPS. I send the output of that script to Henry Kalter for broad categorization
   1. What he sends back becomes an additional input in script 5.
3. The table below shows how the input CalibratedVA matrices are named and organized

|  |  |  |  |
| --- | --- | --- | --- |
| **Results for Calibration 2x3x2x2 + 4 = 28 matrices)** | | | |
| Cause | Method | Age Group | Study |
| Single | InterVA | Neonate | COMSA |
| Multi | InSilicoVA | Child | CHAMPS |
|  | EAVA |  |  |
|  | MITS (CHAMPS only) |  |  |

|  |  |  |  |
| --- | --- | --- | --- |
| **Calibrated VA Analysis Pipeline** | | | |
| .R Script | Input | Output | Notes |
| 1. COMSA openVA results | all\_WHO.csv | openVA\_comsa.Rdata | 1h35m runtime |
| 2a. COMSA EAVA child results | all\_WHO.csv  eng\_ext\_child\_VASA.dta | eava\_child\_comsa.csv |  |
| 2b. COMSA EAVA neonate results | all\_WHO.csv | eava\_neonate\_comsa.csv |  |
| 3. CHAMPS openVA results | asr\_114\_va2016.csv  asr114\_va2016.csv | openVA\_champs.Rdata | 37m runtime |
| 4a. CHAMPS EAVA child results | asr\_114\_va2016.csv  asr114\_va2016.csv | eava\_child\_champs.csv |  |
| 4b. CHAMPS EAVA neonate results | asr\_114\_va2016.csv  asr114\_va2016.csv | eava\_neonate\_champs.csv |  |
| 5. CHAMPS combine mits | Initial and additional broad categorizations (from Henry) | mits\_child\_champs.csv  mits\_neonate\_champs.csv |  |
| X. Get new MITS broad categories | New MITS-VA from CHAMPS (compare to MITS-VA pairs from last run) | Send to Henry for reclassification | Only run when new MITS from CHAMPS |
| 6a. multi\_va\_comsa | openVA\_comsa.Rdata | multi\_interva\_child\_comsa.rds  multi\_interva\_neonate\_comsa.rds  multi\_insilicova\_child\_comsa.rds  multi\_insilicova\_neonate\_comsa.rds |  |
| 6b. multi\_eava\_comsa | eava\_neonate\_comsa.csv  eava\_child\_comsa.csv | multi\_eava\_child\_comsa.rds  multi\_eava\_neonate\_comsa.rds |  |
| 6c. multi\_va\_champs | openVA\_champs.Rdata | multi\_interva\_child\_champs.rds  multi\_interva\_neonate\_champs.rds  multi\_insilicova\_child\_champs.rds  multi\_insilicova\_neonate\_champs.rds |  |
| 6d. multi\_eava\_champs | eava\_child\_champs.csv  eava\_neonate\_champs.csv | multi\_eava\_child\_champs.rds  multi\_eava\_neonate\_champs.rds |  |
| 6e. multi\_mits\_champs | mits\_child\_champs.csv  mits\_neonate\_champs.csv | multi\_mits\_child\_champs.rds  multi\_mits\_neonate\_champs.rds |  |
| 6f. single\_mits\_champs | mits\_child\_champs.csv  mits\_neonate\_champs.csv | single\_mits\_child\_champs.rds  single\_mits\_neonate\_champs.rds |  |
| 7. multi\_to\_single\_VA | multi\_interva\_child\_comsa.rds  multi\_interva\_neonate\_comsa.rds  multi\_insilicova\_child\_comsa.rds  multi\_insilicova\_neonate\_comsa.rds  multi\_eava\_child\_comsa.rds  multi\_eava\_neonate\_comsa.rds | single\_interva\_child\_comsa.rds  single\_interva\_neonate\_comsa.rds  single\_insilicova\_child\_comsa.rds  single\_insilicova\_neonate\_comsa.rds  single\_eava\_child\_comsa.rds  single\_eava\_neonate\_comsa.rds |  |
| 8. match mits-va and format | All 28 matrices | All 28 matrices |  |