Running APK model sweeps on the ANL Bebop cluster

1. Pull changes from the bitbucket repository and run “APK main” launch in Eclipse to start a local GUI instance. Run the model to verify normal runs (no errors).
2. Reset the model via Repast GUI and run the batch mode from the Repast toolbar. Build a new complete\_model.jar which will be located in the project /output folder
3. The directory structure on Bebop is:
   1. \APK\_emews
      1. complete\_model
      2. data
      3. etc
      4. experiments
      5. scripts
      6. swift
   2. To update the model code, delete the contents of the complete\_model folder, and copy the new complete\_model.jar into the folder and unzip it there. Note that the scenario.rs folder may be named differently than the original model APK.rs folder.
   3. The bitbucket repo contains an “APK\_emews” folder which is a copy of the folder on bebop.
4. UPF files should be placed in the Bebop \APK\_emews\data folder
5. Generate UPF files as appropriate for the type of sweep being performed
   1. Vaccine sweep UPF files can be generated by the R scripts “generate\_vaccine\_upf…r”
6. The output analysis **may only** require the “populations” logging. Event and other logging will produce a large amount of output data that is not needed. Edit the **Bebop (double check)** **scenario.rs/batch\_parameters.xml** so that the “verbosity” parameter value is only “population”. The default is “events+populations+regularStatus+status”
7. Manually add a randomSeed parameter to the **batch\_parameters.xml** if it does not exist:

<parameter name="randomSeed" type="constant" constant\_type="int" value="1"></parameter>

1. The model run scripts are located in Bebop APK\_emews\swift\
2. Check for any updates to the bebop\_module\_load.sh in case the module deps have changed
3. Source the bebop\_module\_load.sh to set the environment modules
4. Edit the bebop\_run\_APK.sh as needed (number of procs, wall time, etc)
5. Run the bebop\_run\_APK.sh
6. (**Not recommended**) For local analysis, zip the experiment directory and download it for analysis on a local machine
   1. Copy the experiment zip on Bebop to /lcrc/project/EMEWS/bebop/data/hepcep
   2. Run **/analysis/run\_apk\_parallel\_analysis.py** or **??** on the local experiment folder
   3. Backup local experiment zip to external HDD
   4. **AFTER analysis is complete**, delete the experiment folder and zip in the run directory
7. For analysis on Bebop (best way!):
   1. Update or copy the needed /analysis/\*.py scripts in the /experiments folder and run directly, specifying the experiment subfolder to process
   2. SSH into a DIS condo node, run the module load script, and run the analysis script
      1. python run\_apk\_parallel\_analysis.py <experiment\_folder>
      2. This scripts calls functions in parse\_events\_function.py and trial\_analysis\_improved.py that in turn work with the runs output events and populations files.
   3. **Check** that the event history and summary table files are created:
      1. find ./vaccine\_experiment\_49\_Aug\_29\_2022/ -name \*\_history\_\* -print
      2. find ./vaccine\_experiment\_49\_Aug\_29\_2022/ -name summarytable\_\* -print
   4. **Copy** the stats results files in each /instance\_ folder into a common location
      1. find ./vaccine\_experiment\_49\_Aug\_29\_2022/ -name summarytable\_\* -exec cp {} ./vaccine\_experiment\_49\_Aug\_29\_2022\_results/ \;
      2. find ./vaccine\_experiment\_49\_Aug\_29\_2022/ -name \*\_history\_\* -exec cp {} ./vaccine\_experiment\_49\_Aug\_29\_2022\_results/ \;