This document outlines the code and processes to run the HIV-syphilis-HBV models using R. The models are split by disease and there are sub-models for each disease. Some model parts (i.e., the infant model, lifetable, etc.) may combine multiple diseases.

1. Model output:
2. HIV model:
   1. Main model: hiv\_model\_final.R
      1. **hiv\_maternal\_func:** main HIV maternal population estimation function
         1. inputs:
            1. population parameters
            2. testing frequency: **required** – early ANC, late ANC, optional – postpartum testing (not used for this project)
            3. syphilis testing (true/false): adjusts population of infants based on syphilis mortality if true. (default = FALSE)
            4. sensitivity parameters: incidence reduction, prevalence reduction, PrEP use. (default = 0)
         2. outputs: dataframe of number of women by HIV status and treatment, by week
            1. HIV-, acute HIV+ no ART, acute HIV+ on ART, chronic HIV+ unknown status, chronic HIV+ no ART, chronic HIV+ on ART
            2. Also includes # of deaths by week
         3. Requirements:
            1. Population parameters should be pulled in and filtered for population of interest.
            2. If running syphilis model that should be run first to get syphilis parameters for population and adjust infant mortality
      2. **pw\_func**: summarize person weeks from maternal HIV dataframe
         1. inputs:
            1. dataframe of number of women by HIV status and treatment, by week (from hiv\_maternal\_func)
         2. outputs: