# SHIELD components

The specification file provides the blueprint for the core model. definition of compartments and all the transitions in the model. The figure shows how it connects to other scripts required for running an engine test.

A diagram of a system

Description automatically generated with medium confidence

**Fig: High-level review of the SHIELD engine and scripts**

The specification file is organized as follow:

## Initial setup:

**SHIELD.SPECIFICATION:** defining the blueprint of compartments and various strata (age, race, sex, etc).

* The model represents the U.S. population through three distinct sex and sexual behavior categories: **heterosexual\_male**(males engaging in heterosexual sex), **msm** (men who have sex with men), and **female** (females, which may include both heterosexual and bisexual behaviors). These categories are further divided by race and ethnicity into three groups: **Black**, **Hispanic**, and **Other**, allowing for the analysis of differences in risk behaviors and infection transmission dynamics by demographic factors. The population is also subdivided into 11 age groups: 0-15 years, 16-20 years, 21-25 years, 26-30 years, 31-35 years, 36-40 years, 41-45 years, 46-50 years, 51-55 years, 56-65 years, and 65+ years. These age categories enable the model to track changes in risk and disease progression over the course of an individual's life.
* The population is further categorized into two main groups: **infected** and **uninfected**. The infected group is divided into two primary categories: the **continuum of infection**, which includes individuals who are either **undiagnosed** or **diagnosed but untreated**, and the **disease stages**, which represent the progression of infection through different phases: **ps** (primary or early stage), **el** (early latent stage), **ll** (late latent stage), and **ter** (terminal or advanced stage). This distinction allows for the modeling of the progression of infection from undiagnosed to untreated to advanced stages of disease.
* For the **uninfected** population, the model defines two key states: **susceptible**, representing individuals who are at risk of infection but have not yet been diagnosed, and **diagnosed.treated**, representing individuals who are diagnosed and receiving treatment for conditions related to HIV/STI. This helps differentiate between at-risk individuals and those who are under care, capturing both the uninfected and treated segments of the population.
* The model starts in 1940 and projects the population through to 2040, providing a dynamic view of infection dynamics, treatment, and transmission risks across time. This time span allows the model to simulate long-term trends and shifts in the population’s health status, helping to understand the impact of historical and future interventions on public health.

A diagram of a patient's process

Description automatically generated

## Simulation modules

The specification file includes several modules that define the composition of the initial population, as well as the various transitions that occur over time. These transitions are crucial for modeling the dynamics of the population and the spread of syphilis, with each module describing a different aspect of the population's health, behavior, and demographic changes.

* **Initial Population Composition:** The initial population composition is defined based on demographic characteristics such as age, sex, race/ethnicity, and sexual behavior. This underlying population is informed by U.S. census data, with full demographic composition only available from 2010 onward. As such, we assume a fixed population size and composition up to the year 2010. Capturing earlier periods prior to 2010 helps us reflect the syphilis epidemiology more closely, while after 2010, we allow for the natural evolution of population size and composition.
* **Births and Deaths:** The model captures demographic transitions related to births and deaths, which are key factors in shaping the population's size and structure over time. Births are modeled based on fertility rates, while deaths occur due to a combination of natural causes and disease progression. Deaths in the infected population, particularly those in the late latent and terminal stages of syphilis, are critical for modeling disease outcomes. These transitions ensure that the model reflects the reality of population turnover, with individuals entering and exiting the population through both natural processes and disease-related mortality.
* **Differential Aging Rates:** These rates are included in the model to reflect how the population ages at different rates across various demographic groups. Aging is modeled as a gradual process, where individuals transition between age categories over time. The rate of aging may vary by race or health status. This factor is crucial for capturing the evolution of the population's composition over time
* **Sexual Transmission:** One of the primary transitions modeled is sexual transmission, which describes how syphilis and other STIs are transmitted between individuals. This includes transitions between the uninfected and infected states (e.g. from susceptible to undiagnosed or diagnosed.untreated, and vice versa). Sexual transmission is influenced by behavior (e.g., whether individuals engage in heterosexual or MSM sexual activities) and demographic factors, including age and race/ethnicity. This dynamic allows the model to capture how infection spreads through the population over time, particularly within different sexual networks and risk groups.
* **Syphilis Continuum of Care:** The syphilis continuum of care defines the transitions that individuals with syphilis undergo as they progress through the stages of infection and treatment. This includes transitions from undiagnosed to diagnosed, from diagnosed to treated, and from untreated individuals progressing through various disease stages, including primary/early, early latent, late latent, and terminal. The model tracks these transitions to simulate the impact of treatment and diagnosis on the course of the disease, as well as the overall burden of syphilis in the population. This structure is critical for assessing how interventions at different points in the continuum—such as testing, treatment initiation, and follow-up—can affect disease outcomes and reduce transmission.

Together, these transitions provide a dynamic framework for modeling the spread of syphilis and other STIs in the population, as well as the health outcomes of different demographic groups. By capturing sexual transmission, births, deaths, aging, and the continuum of care, the model simulates the long-term effects of public health interventions and demographic changes. This helps in offering insights into how to reduce syphilis prevalence and improve population health outcomes over time

## Parameters

The specification file includes instructions for describing transitions between different compartments in the model, which are often represented by rates. In the simplest case, the rate of an event is fixed over time and informed by literature. However, in more advanced scenarios, the rate can be dynamic: changing over time and differentiated by factors such as age, sex, race, or other variables (i.e., it has a functional form). This allows the model to capture more complex behaviors and interactions within the population.

JHEEM uses a distinct construct for defining parameters in the model:

* **Elements:** These are *scalar* values or *functional forms*. They represent the basic building blocks of the model and can be constants or dynamic functions that describe various processes (e.g., infection rates, mortality rates). Elements can be used directly or combined to define more complex quantities.
* **Quantities:** These are more complex constructs that can represent combinations of elements and other quantities. A quantity can be equivalent to another quantity or an element, or it can be an expression or function of other quantities. Quantities are used to inform the model's compartments and the transitions between them, allowing the model to capture relationships between different variables in a more nuanced way.

Together, elements and quantities provide a flexible framework for modeling the dynamic relationships between different factors, enabling the specification of rates, transitions, and compartments that reflect real-world epidemiological processes.

## Outputs

There are two primary methods to capture outputs in the model: **Compartment Outputs** and **Transition Outputs**. These methods allow for tracking different aspects of the model's dynamics and assessing the impact of various processes on the population.

1. **Compartment Outputs:** Compartment outputs refer to the frequency values of specific compartments, such as the population size in each compartment. These outputs can be captured in different ways depending on the desired level of detail:
   1. **track.point.outcome():** This method captures a static outcome at a specific moment in time. For example, it could be used to track the number of individuals in a specific compartment at the start or end of a year (Jan 1st). This provides a snapshot of the population at a given point.
   2. **track.integrated.outcome():** This method integrates the point estimates over a specific time period, such as a year (Jan 1st to Dec 31st). It is more useful for calibration as it accounts for the average values across the entire timeframe rather than just a single moment. This method is preferred when looking for a more comprehensive measure of a compartment's population size or other attributes across time.

track.point.outcome(…, name='point.population', …)

track.integrated.outcome(…, name='population',

value.to.integrate = 'point.population',….)

1. **Transition Outputs:** Transition outputs capture the movement or event rates between compartments, representing the dynamics of individuals moving from one state to another (e.g., from susceptible to infected, or from diagnosed to treated). These outputs provide insight into how the population is changing over time due to various events and processes.
   1. **track.transition():** This method captures dynamic outcomes, indicating the movement of individuals between specific starting and ending compartments. It provides information on the flow between compartments, such as how many individuals transition from an undiagnosed to a diagnosed state over a specific period.
   2. **track.dynamic.outcome():** This method captures outcomes that account for individuals entering the model without specifying a starting or ending compartment. It is useful for tracking events that involve the population entering the model (e.g., through birth or migration) or when individuals do not fit neatly into defined starting or ending states.
   3. **track.cumulative.outcome():** This method sums multiple dynamic outcomes over time, providing an overall measure of the cumulative effect of transitions across different compartments. It is particularly useful for capturing the total impact of specific processes or events, such as the total number of individuals who have been diagnosed with syphilis over a set period.

track.**dynamic**.outcome(SHIELD.SPECIFICATION,

name='births.from',…)

track.**cumulative**.outcome(SHIELD.SPECIFICATION,

name='fertility.rate',

value=expression(births.from/population),….)

For dynamic transitions that change over time (e.g., testing), the anchor points are coded at the beginning of the year (e.g., if transmission changes from 2000 to 2020, these dates represent jan 1st of those years)

By using these output tracking methods, the model can provide valuable insights into both the state of the population at different times (compartment outputs) and the dynamics of transitions between compartments (transition outputs). These outputs are essential for understanding the long-term effects of interventions and changes in the model's parameters.