Supplementary S3 Text: Instructions for S3 Code

S3 Code: Compartmental Model

Section 1: Model Development

- **Explore Seasonality** Find a proper seasonality function to fit the pattern of the rainy seasons [1] that affects dengue transmission.
- **Generate States** The compartments are defined by currently exposed or infected serotype and the serostatus to previous infections, characterized as High (H), Low (L), or None (N). The formats and interpretations of the compartments are summarised in Table 4.
- **Define One-step Transitions** The transition rules are defined in Table 5. The *generate_next_states_SEIR* function returns all the possible next states given the current state.
- **Adjusted beta** Extract coefficients from the multinomial regression model in *S2 Code*, remember to change the model name accordingly (multi_modeli_low_high, where i refers to the analysis i in *S2 Code*). The estimates for having subsequent DENV3 infection are manually set to 0 (= 1 after log transformation which means base beta is used for DENV3) due to the unreliable coefficients estimated from the small sample size. The large impact of having an anti-DENV4 level on subsequent DENV2 infection is reset to 5 to make sure the effect is reasonably high but not too extreme.
- **SEIRS Model** The core model is defined by the *DENV_SEIRS_bd* function, with transitions specified by the differential equations. We added a counter to track the daily incidence, so the returned object has $378 + 1 = 379$ states. The total population calculated within the function should therefore be the sum of the number of individuals in the first 378 compartments.
- **Initial Condition**
  - **Total Population** According to the World Bank, there are 98 million people in Vietnam [2], and we assume half of the population is at risk of dengue [3].

- **Recovered States** In theory, the recovered state with fully susceptible individuals (R_NNNN) does not exist, so we assigned 0 individuals to this state. 10000 people were assigned for the rest of each recovered state.
- **Exposed and Infectious States** We allocated the individuals into exposed and infectious states according to the prevalence of each serotype estimated from the original data.
- **Susceptible States** The remaining population was assigned to susceptible states, with 80% of people going into the fully naive state (S_NNNN) and the remaining 20% is distributed based on the number of serotypes they lack immunity to (indexed by "N"). States with more "N"s are allocated a higher proportion of people. Similar to the recovered state, the susceptible states with measurable antibody levels against all serotypes (e.g. S_LLHH) do not exist, so 0 people are assigned to these states.

- **Model Period and Parameters** The simulation period in our analysis is 50 years and the model parameters are explained in *S3 Table*. The model takes hours to run.

Section 2: Visualization

After solving the differential equations, we store the results in a data frame for the following visualisation. The way to create the plots is the same for each simulation, just change the name of the result. The name is in the format: $datai + threshold\_low + threshold\_high + type$, where i is the data set i and type represents the base beta which is either homogeneous (homo) or heterogeneous (heter).

- Plot 1: Total population
- Plot 2: Yearly Incidence
- Plot 3: Number of people in the specified compartments
- Plot 4: Aggregated infection trends by serotype
- Plot 5: Aggregated SEIR plot over years
- Plot 6: Infection by Previous Infection History

References

1. Bett B, Grace D, Lee HS, Lindahl J, Nguyen-Viet H, Pham-Duc P, Quyen NH, Anh-Tu T, Phu T, Tan D, and Nam V. Spatiotemporal analysis of historical records (2001–2012) on dengue fever in Vietnam and development of a statistical model for forecasting risk. PLOS ONE 2019 Nov; 14:e0224353. DOI: 10.1371/journal.pone.0224353

2. World Bank. Vietnam. 2022. Available from: https://datacommons.org/place/country/VNM?utm_medium=explore&mprop=lifeExpectancy&popt=Person&hl=en [Accessed on: 2024 Jul 15]

3. Jones RT, Ant TH, Cameron MM, and Logan JG. Novel control strategies for mosquito-borne diseases. Philosophical Transactions of the Royal Society B: Biological Sciences 2020 Dec; 376:20190802. DOI: 10.1098/rstb.2019.0802. Available from: https://royalsocietypublishing.org/doi/full/10.1098/rstb.2019.0802 [Accessed on: 2023 Dec 19]