Algorithm 1: Generating the matrix M for the 4-disease model

Input: M_h, M_s, M_c, M_g
Output: M
D $\leftarrow \{h, s, c, g\}$;
m $\leftarrow 560$;
Y $\leftarrow$ createTableCompartments(D) ; `/* comment 1 */`
M $\leftarrow O_{m\times m}$;
`/* Inserting the matrices` M_i `into M */` ;
for *i in D* **do**
  D$'$ $\leftarrow$ D\{i} ;
  combD$'$ $\leftarrow$ getAllCombinations(D$'$) ; `/* comment 2 */`
  for *comb in combD$'$* **do**
    index $\leftarrow$ which(Y$_{\cdot,\text{D}'} == comb$);
    $M_{\text{index,index}} \leftarrow M_{\text{index,index}} + M_i(0)$; `/* comment 3 */`
  end
end
`/* Adding routine testing rates under PrEP */` ;
for ℓ *from 1 to m* **do**
  if $Y_{\ell,h}$ *in* $\{P, I_P, C_P\}$ **then**
    for *i in* $\{s, c, g\}$ **do**
      indexTo $\leftarrow$ getIndexTo(Y, ℓ, {i}) ; `/* comment 4 */`
      $M_{\ell,\ell} \leftarrow M_{\ell,\ell}$ - η_i^{PrEP} ; `/*` $\dot{X}_\ell = ... - \eta_i^{\text{PrEP}} X_\ell ...$ `*/`
      $M_{\text{indexTo},\ell} \leftarrow M_{\text{indexTo},\ell} + \eta_i^{\text{PrEP}}$; `/*` $\dot{X}_q = ... + \eta_i^{\text{PrEP}} X_\ell ...$ `*/`
    end
  end
end
`/* Adding voluntary testing rates */` ;
for `k` *in* `K` **do**
  for ℓ *from 1 to m* **do**
    indexTo $\leftarrow$ getIndexTo(Y, ℓ, `k`) ; `/* comment 4 */`
    allowVT = 1 ;
    for *i in* `k` **do**
      if $Y_{\ell,i}$ *in* $\{I_S, P, I_P, C_P\}$ **then**
        allowVT = 0 ;
      end
    end
    if allowVT **then**
      $M_{\ell,\ell} \leftarrow M_{\ell,\ell}$ - $\rho_{\texttt{k}}$; `/*` $\dot{X}_\ell = ... - \rho_{\texttt{k}} X_\ell ...$ `*/`
      $M_{\text{indexTo},\ell} \leftarrow M_{\text{indexTo},\ell} + \rho_{\texttt{k}}$; `/*` $\dot{X}_q = ... + \rho_{\texttt{k}} X_\ell ...$ `*/`
    end
  end
end

Comments supporting Algorithm 1, as indicated to the right of the pseudocode:
`comment 1`: creates the table Y with 4 columns and m rows that lists all possible 4-diseases stages created from using one and only one stage from each single-disease model. Hence, each row in Y corresponds to a unique compartment `C` in the 4-disease model, characterized by 4 letters corresponding to the stages of the 4 diseases (e.g., S, I, C, T, I_1,...). To each row also corresponds a time-dependent variable X_ℓ, ℓ from 1 to m, which corresponds to the number of individuals in the related compartment; see Table S70.
`comment 2`: creates a table of dimensions $3 \times m/m_i$ listing all possible infections, except j; e.g., if $j = 9$ then combD$'$ corresponds to the subtable Y(1:140, {'HIV', 'syphilis', 'Ct'}).
`comment 3`: the single-disease matrix $\mathrm{M}_i(0)$ of size $m_i \times m_i$ defined in section is inserted in the global matrix M at the columns and lines `index`; e.g., $\mathrm{M}_{1:7,1:7} \leftarrow \mathrm{M}_{1:7,1:7}+\mathrm{M}_h(0)$, $\mathrm{M}_{1:7:554,1:7:554} \leftarrow \mathrm{M}_{1:7:554,1:7:554}+\mathrm{M}_s(0)$.
`comment 4`: `getIndexTo(Y, ℓ, k)` returns the row index q of Y representing the compartment where individuals in compartment ℓ go once they have been tested with the kit `k`.