## S1 Appendix - Details of state transition model equations

We use the following example to illustrate how the state transition probabilities of the model are derived.

*Example:* With  $d_r(t)$  being the annual background probability of death, we let  $\sigma(t) = 1 - d_r(t)$ , which is the annual probability that an individual will not die of CHC-related causes. The number of individuals who, at the beginning of the year 2000, were in the undiagnosed F0 stage of CHC (stage X<sub>0</sub>) can be estimated to be equal to a proportion  $q_{chr}(1 - d_a)\sigma(t)$  of u(1999) (the number of new infections in 1999) plus a proportion  $\alpha_0^X(t) = (1 - q_{0,1})(1 - d_0)\sigma(t)$  of  $X_0(1999)$  (the number of individuals in state X<sub>0</sub> in 1999). Here,  $q_{chr}$  is the probability that a new hepatitis C infection will become chronic,  $d_a$  is the probability that an individual with an acute infection will be diagnosed before the infection turns chronic,  $q_{01}$  is the annual probability that an undiagnosed individual in fibrosis stage F0 will progress to fibrosis stage F1, and  $d_0$  is the annual probability that an undiagnosed individual in fibrosis stage F0 will be diagnosed with CHC. Therefore:

$$X_0(2000) = q_{chr}(1 - d_a)\sigma(t) u(1999) + \alpha_0^X(t)X_0(1999)$$

The first term represents the number of individuals who became infected with HCV in 1999 who survived until year 2000, and who remained undiagnosed throughout 1999, and whose infection became chronic between the 1999 and 2000. The second term represents the number of individuals who had CHC at stage F0 in 1999, and who survived until 2000, and who remained undiagnosed throughout 1999, and whose infection did not progress from F0 to F1 in 1999.

From the state transition model illustrated in Fig 1, we similarly arrive at the following expressions, which are functions of parameters in S1 Table:

Parameter formula	Description
$\alpha_{i}^{X}(t) = (1 - q_{i,i+1})(1 - d_{i})\sigma(t)$	Probability that an individual in state $X_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will
	remain in state $X_i$ in year $t + 1$ .
$\beta_i^X(t) = q_{i,i+1}(1 - d_i) \sigma(t)$	Probability that an individual in state $X_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will
	progress in liver fibrosis, transitioning to state $X_{i+1}$ in year $t + 1$ .

$\gamma^{X}(t) = (1 - d_{DC} - d_{HCC} - d_4)\sigma(t)$	Probability that an individual in state $X_4$ in year t will remain in state
	$X_4$ in year $t + 1$ .
$\delta_i^{\nu}(t) = (1 - q_{i,i+1})d_i\sigma(t)$	Probability that an individual in state $X_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will be diagnosed, transitioning to state $D_i$ in year $t + 1$ .
$\tau_i^D(t) = q_{ii+1} d_i \sigma(t)$	Probability that an individual in state $X_i$ ( <i>i</i> =0,1,2,3) in year t will
	progress in liver fibrosis and be diagnosed, transitioning to state $D_{i+1}$
	in year $t + 1$ .
$\varepsilon^{D}(t) = d_{A}\sigma(t)$	Probability that an individual in state $X_{A}$ in year t will be diagnosed.
	transitioning to state $D_4$ in year $t + 1$ .
$\alpha_i^D(t) = (1 - q_{ii+1})(1 - t_i(v))\sigma(t)$	Probability that an individual in state $D_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will
	remain in state $D_i$ in year $t + 1$ (for viral genotype $v$ ).
$\beta_{i}^{D}(t) = q_{ii+1}(1 - t_{i}(v)) \sigma(t)$	Probability that an individual in state $D_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will
	progress in liver fibrosis, transitioning to state $D_{i+1}$ in year $t + 1$ (for
	viral genotype $v$ ).
$\gamma^{D}(t) = (1 - d_{DC} - d_{HCC} - t_{4}(v))\sigma(t)$	Probability that an individual in state $D_4$ in year t will remain in state
	$D_4$ in year $t + 1$ (for viral genotype $v$ ).
$\delta_i^T(t) = (1 - q_{i,i+1})t_i(v) \sigma(t)$	Probability that an individual in state $D_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will be
	treated, transitioning to state $T_i$ in year $t + 1$ (for viral genotype $v$ ).
$\tau_i^T(t) = q_{ii+1} t_i(v) \sigma(t)$	Probability that an individual in state $D_i$ ( <i>i</i> =0.1.2.3) in year <i>t</i> will
	progress in liver fibrosis and be treated, transitioning to state $T_{i+1}$ in
	vear $t + 1$ (for viral genotype $v$ ).
$\varepsilon^{T}(t) = t_{A}(v) \sigma(t)$	Probability that an individual in state $D_{A}$ in year t will be diagnosed.
	transitioning to state $T_A$ in year $t + 1$ (for viral genotype $v$ ).
$\alpha_{i}^{T}(t) = 0$	Probability that an individual in state $T_i$ (i=0,1,2,3) in year t will
	remain in state $T_i$ in year $t + 1$ .
$\beta_i^T(t) = 0$	Probability that an individual in state $T_i$ ( <i>i</i> =0,1,2,3) in year t will
	progress in liver fibrosis, transitioning to state $T_{t+1}$ in year $t + 1$ .
$\gamma^T(t) = 0$	Probability that an individual in state $T_A$ in year t will remain in state
	$T_4$ in year $t + 1$ .
$\delta_i^S(t) = S_i(v)\sigma(t)$	Probability that an individual in state $T_i$ ( <i>i</i> =0,1,2,3) in year t will
	show SVR, transitioning to state $S_i$ in year $t + 1$ (for viral genotype
	v).
$\tau_i^S(t) = 0$	Probability that an individual in state $T_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will
	progress in liver fibrosis and show SVR, transitioning to state $S_{i+1}$
	in year $t + 1$ .
$\varepsilon^{S}(t) = s_{4}(v)\sigma(t)$	Probability that an individual in state $T_4$ in year t will show SVR,
	transitioning to state $S_4$ in year $t + 1$ (for viral genotype $v$ ).
$\alpha_i^S(t) = \sigma(t)$	Probability that an individual in state $S_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will
	remain in state $S_i$ in year $t + 1$ .
$\beta_i^S(t) = 0$	Probability that an individual in state $S_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will
	progress in liver fibrosis, transitioning to state $S_{i+1}$ in year $t + 1$ .
$\gamma^{S}(t) = (1 - d_{DC-SVR} - d_{HCC-SVR})\sigma(t)$	Probability that an individual in state $S_4$ in year t will remain in state
	$S_4$ in year $t + 1$ .
$\delta_i^N(t) = (1 - s_i(v))\sigma(t)$	Probability that an individual in state $T_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will not
	show SVR, transitioning to state $N_i$ in year $t + 1$ (for viral genotype
N	<i>v</i> ).
$\tau_i^N(t) = 0$	Probability that an individual in state $T_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will
	progress in liver fibrosis and not show SVR, transitioning to state
N / S / A / S / A / S / A / A / A / A / A	$N_{i+1}$ in year $t+1$ .
$\varepsilon^{\prime\prime}(t) = (1 - d_{DC} - d_{HCC} - s_4(v))\sigma(t)$	Probability that an individual in state $T_4$ in year t will not show SVR,
Ness	transitioning to state $N_4$ in year $t + 1$ (for viral genotype $v$ )
$\alpha_i^{\text{iv}}(t) = (1 - q_{i,i+1})\sigma(t)$	Probability that an individual in state $N_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will
	remain in state $N_i$ in year $t + 1$ .

$\beta_i^N(t) = q_{i,i+1}\sigma(t)$	Probability that an individual in state $N_i$ ( <i>i</i> =0,1,2,3) in year <i>t</i> will
	progress in liver fibrosis, transitioning to state $N_{i+1}$ in year $t + 1$ .
$\gamma^{N}(t) = (1 - d_{DC} - d_{HCC})\sigma(t)$	Probability that an individual in state $N_4$ in year t will remain in state
	$N_4$ in year $t + 1$ .
$b_{DC}(t) = d_{DC}\sigma(t)$	Probability that an individual in state $X_4$ , $D_4$ or $N_4$ in year t will
	develop decompensated cirrhosis, transitioning to state <i>DC</i> in year
	t+1.
$b_{DC-SVR}(t) = d_{DC-SVR}\sigma(t)$	Probability that an individual in state $S_4$ in year t will develop
	decompensated cirrhosis, transitioning to state $DC$ in year $t + 1$ .
$b_{HCC}(t) = d_{HCC}\sigma(t)$	Probability that an individual in state $X_4$ , $D_4$ or $N_4$ in year t will
	develop hepatocellular carcinoma, transitioning to state <i>HCC</i> in year
	t+1.
$b_{HCC-SVR}(t) = d_{HCC-SVR}\sigma(t).$	Probability that an individual in state $S_4$ in year t will develop
	hepatocellular carcinoma, transitioning to state <i>HCC</i> in year $t + 1$ .
$A_{DC}(t) = (\sigma(t) - a_4)(1 - a_3)$	Probability that an individual in state <i>DC</i> in year <i>t</i> will remain in state
	DC in year $t + 1$ .
$A_{HCC}(t) = (\sigma(t) - a_2)(1 - a_1)$	Probability that an individual in state <i>HCC</i> in year <i>t</i> will remain in
	state <i>HCC</i> in year $t + 1$ .
$A_{PT}(t) = \sigma(t) - a_6$	Probability that an individual in state <i>PT</i> in year <i>t</i> will remain in state
	PT in year $t + 1$ .
$B_{LT-DC}(t) = (\sigma(t) - a_4)a_3$	Probability that an individual in state <i>DC</i> in year <i>t</i> will receive a liver
	transplant, transitioning to state $LT$ in year $t + 1$ .
$B_{LT-HCC}(t) = (\sigma(t) - a_2)a_1$	Probability that an individual in state $HCC$ in year $t$ will receive a
	liver transplant, transitioning to state $LT$ in year $t + 1$ .
$B_{PT}(t) = \sigma(t) - a_5$	Probability that an individual that receives a liver transplant (state
	LT) in year t will survive, transitioning to state PT in year $t + 1$ .

The above state transition probabilities feed directly into the state transition matrices  $A_X(t)$ ,  $A_D(t)$ ,  $A_T(t)$ ,  $A_S(t)$ ,  $A_N(t)$  and  $B_D(t)$ ,  $B_T(t)$ ,  $B_S(t)$ ,  $B_N(t)$ , which take the form

$$A_{[\cdot]}(t) = \begin{bmatrix} \alpha_0^{[\cdot]} & 0 & 0 & 0 & 0 \\ \beta_0^{[\cdot]} & \alpha_1^{[\cdot]} & 0 & 0 & 0 \\ 0 & \beta_1^{[\cdot]} & \alpha_2^{[\cdot]} & 0 & 0 \\ 0 & 0 & \beta_2^{[\cdot]} & \alpha_3^{[\cdot]} & 0 \\ 0 & 0 & 0 & \beta_3^{[\cdot]} & \gamma^{[\cdot]} \end{bmatrix}$$

and

$$B_{[\cdot]}(t) = \begin{bmatrix} \delta_0^{[\cdot]} & 0 & 0 & 0 & 0 \\ \tau_0^{[\cdot]} & \delta_1^{[\cdot]} & 0 & 0 & 0 \\ 0 & \tau_1^{[\cdot]} & \delta_2^{[\cdot]} & 0 & 0 \\ 0 & 0 & \tau_2^{[\cdot]} & \delta_3^{[\cdot]} & 0 \\ 0 & 0 & 0 & \tau_3^{[\cdot]} & \varepsilon^{[\cdot]} \end{bmatrix}$$

where the placeholder [·] can be X, D, T, S, N. The structures of the matrices  $A_{[\cdot]}(t)$  and  $B_{[\cdot]}(t)$  arise directly from the state transition model illustrated in Fig 1.

In addition, we let

$$\begin{split} B_{HCC}(t) &= b_{HCC}(t) \begin{bmatrix} 0 & 0 & 0 & 0 & 1 \end{bmatrix} \\ B_{HCC-SVR}(t) &= b_{HCC-SVR}(t) \begin{bmatrix} 0 & 0 & 0 & 0 & 1 \end{bmatrix} \\ B_u &= \begin{bmatrix} q_{chr} & 0 & 0 & 0 & 0 \end{bmatrix}' \\ B_{DC}(t) &= b_{DC}(t) \begin{bmatrix} 0 & 0 & 0 & 0 & 1 \end{bmatrix} \\ B_{DC-SVR}(t) &= b_{DC-SVR}(t) \begin{bmatrix} 0 & 0 & 0 & 0 & 1 \end{bmatrix} \end{split}$$

The above-defined quantities are then combined into the following matrices, which are used in the statespace model equations (10), (11):

$$A(t) = \begin{bmatrix} A_X & & & & & \\ B_D & A_D & & & & \\ & B_T & A_T & & & & \\ & & B_S & A_S & & & \\ & & B_N & & A_N & & \\ B_{DC} & B_{DC} & B_{DC} & B_{DC-SVR} & B_{DC} & A_{DC} & & \\ & & & B_{HCC} & B_{HCC} & B_{HCC} & A_{HCC} & & \\ & & & & B_{LT-DC} & B_{LT-HCC} & & \\ & & & & & B_{PT} & A_{PT} \end{bmatrix}$$

$$B(t) = [(1 - d_a)B_u' \quad d_a B_u' \quad \mathbf{0}_5 \quad \mathbf{0}_5 \quad \mathbf{0}_5 \quad \mathbf{0} \quad \mathbf{0} \quad \mathbf{0} \quad \mathbf{0}]'$$

$$C(t) = \begin{bmatrix} \frac{B_{HCC}}{c_{HCC}} & \frac{B_{HCC}}{c_{HCC}} & \mathbf{0_5} & \frac{B_{HCC-SVR}}{c_{HCC}} & \frac{B_{HCC}}{c_{HCC}} & 0 & 0 & 0 \\ C_{CHC} & \mathbf{0_5} & \mathbf{0_5} & \mathbf{0_5} & \mathbf{0_5} & \mathbf{0_5} & 0 & 0 & 0 \end{bmatrix}$$

 $D(t) = \begin{bmatrix} 0 & d_a \end{bmatrix}'$ 

Where  $c_{HCC}$  is given in S3 Table,  $C_{CHC} = [d_0 \ d_1 \ d_2 \ d_3 \ d_4 + d_{HCC} + d_{DC}]$  and  $\mathbf{0}_5$  denotes a row vector of five zeros.