

Supplementary Tables and Figures

Supplementary Tables

Supp. Table 1: **Results of Profile Likelihood and Hessian-Based Calculations of Confidence Intervals (Using PottersWheel fitting toolbox)**. All results conclude to non-identifiability of model parameters, due to infinite confidence intervals.

Results for Flu data:

Parameter	Identifiability	Lower CI (PL)	Upper CI (PL)	Lower CI (Hessian)	Upper CI (Hessian)
1 mN	practically non-ident.	0	Inf	0	Inf
2 dNE	practically non-ident.	0	Inf	0	Inf
3 rE	practically non-ident.	0	Inf	0	1.3972e+243
4 mE	practically non-ident.	0	Inf	0	Inf
5 dEM	practically non-ident.	0	Inf	0	2.7777e+111
6 mM	practically non-ident.	0	Inf	0	1.7880e+294
7 rP	practically non-ident.	0	Inf	0	Inf
8 mP	practically non-ident.	0	Inf	0	Inf
9 mPO	practically non-ident.	0	Inf	0	Inf

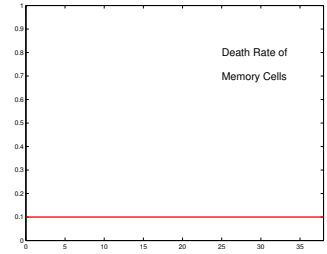
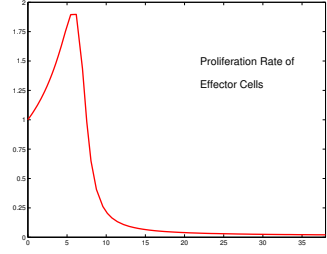
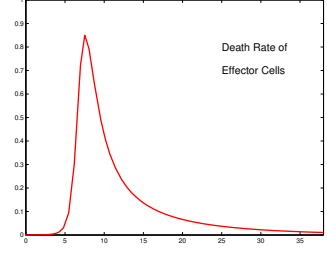
Results for VV data:

Parameter	Identifiability	Lower CI (PL)	Upper CI (PL)	Lower CI (Hessian)	Upper CI (Hessian)
1 mN	practically non-ident.	0	Inf	0	Inf
2 dNE	practically non-ident.	0	Inf	0	Inf
3 rE	practically non-ident.	0	Inf	0	Inf
4 mE	practically non-ident.	0	Inf	0	Inf
5 dEM	practically non-ident.	0	Inf	0	Inf
6 mM	practically non-ident.	0	Inf	0	2.7456e+28
7 rP	practically non-ident.	0	Inf	0	Inf
8 mP	practically non-ident.	0	Inf	0	Inf
9 mPO	practically non-ident.	0	Inf	0	Inf

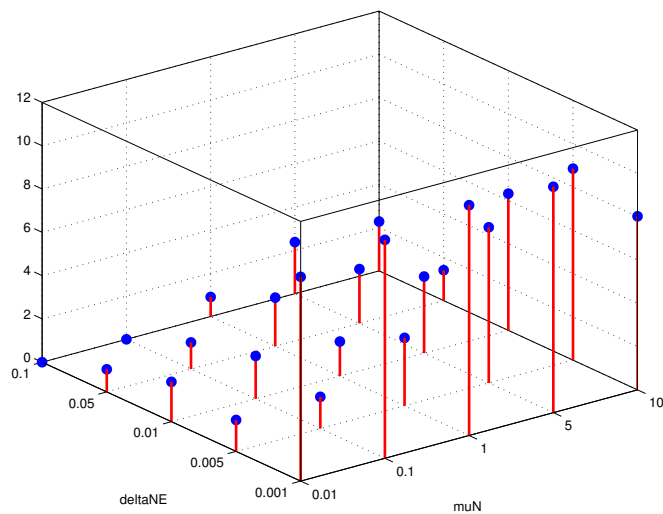
Results for *Lm* data:

Parameter	Identifiability	Lower CI (PL)	Upper CI (PL)	Lower CI (Hessian)	Upper CI (Hessian)
1 mN	practically non-ident.	0	Inf	0	Inf
2 dNE	practically non-ident.	0	Inf	0	Inf
3 rE	practically non-ident.	0	Inf	-1.9032	-1.9032
4 mE	practically non-ident.	0	Inf	-9.9575e-06	-9.9575e-06
5 dEM	practically non-ident.	0	Inf	-0.0300	-0.0300
6 mM	practically non-ident.	0	Inf	-0.1000	-0.1000
7 rP	practically non-ident.	0	Inf	-0.0158	-0.0158
8 mP	practically non-ident.	0	Inf	-2.1900e-07	-2.1900e-07
9 mPO	practically non-ident.	0	Inf	-0.0022	-0.0022

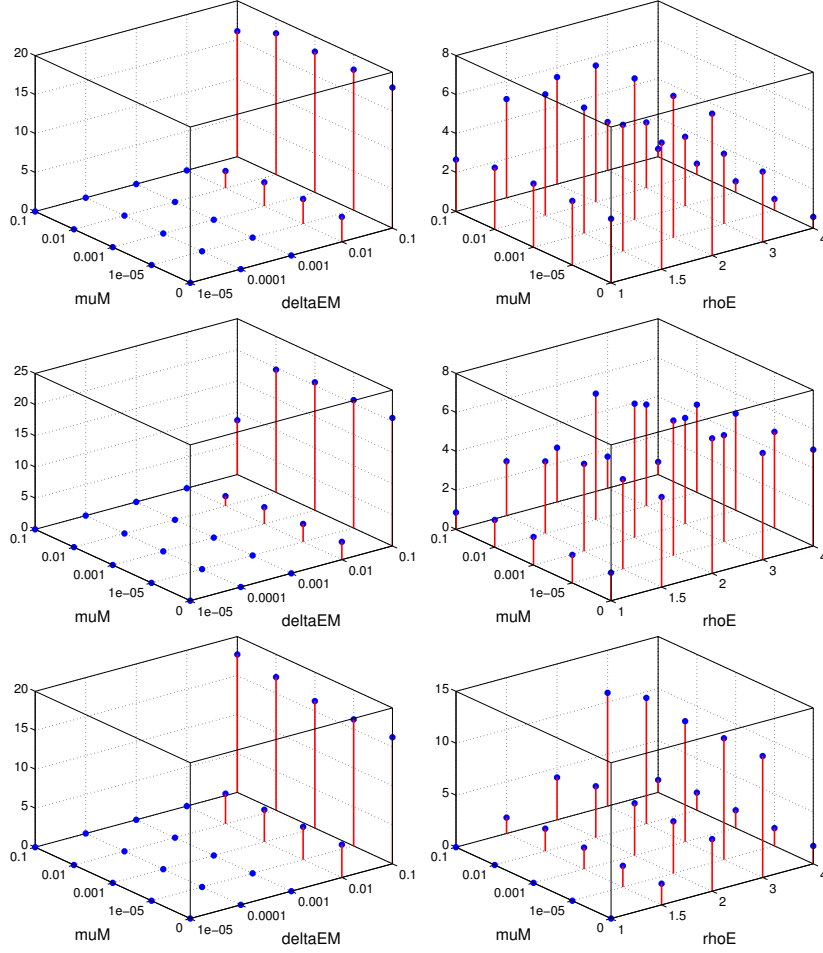
Supp. Table 2: **Relationship between the parameters and the biological rates of the model.** Graphic illustrations of biological rates are shown for the parameter values corresponding to the best result of the model using the influenza data. They correspond to the biological rate underlined in the third column.

	Notation (symbol)	Corresponding biological rates (d ⁻¹)	Evolution of the biological rate (d ⁻¹) during the response
Parameters which model <i>constant</i> biological rates (d ⁻¹)	$\mu_N, \delta_{EM},$ μ_M, μ_P^0	$\mu_N, \delta_{EM},$ <u>μ_M, μ_P^0</u>	
Parameters associated with <i>non constant</i> biological rates (d ⁻¹)	$\delta_{NE}, \rho_E,$ ρ_P	$\delta_{NEP}, \rho_{EP},$ <u>ρ_{PP}</u>	
Parameters associated with <i>non constant</i> biological rates (cell ⁻¹ .d ⁻¹)	μ_E, μ_P	<u>$\mu_E E,$</u> $\mu_P E$	

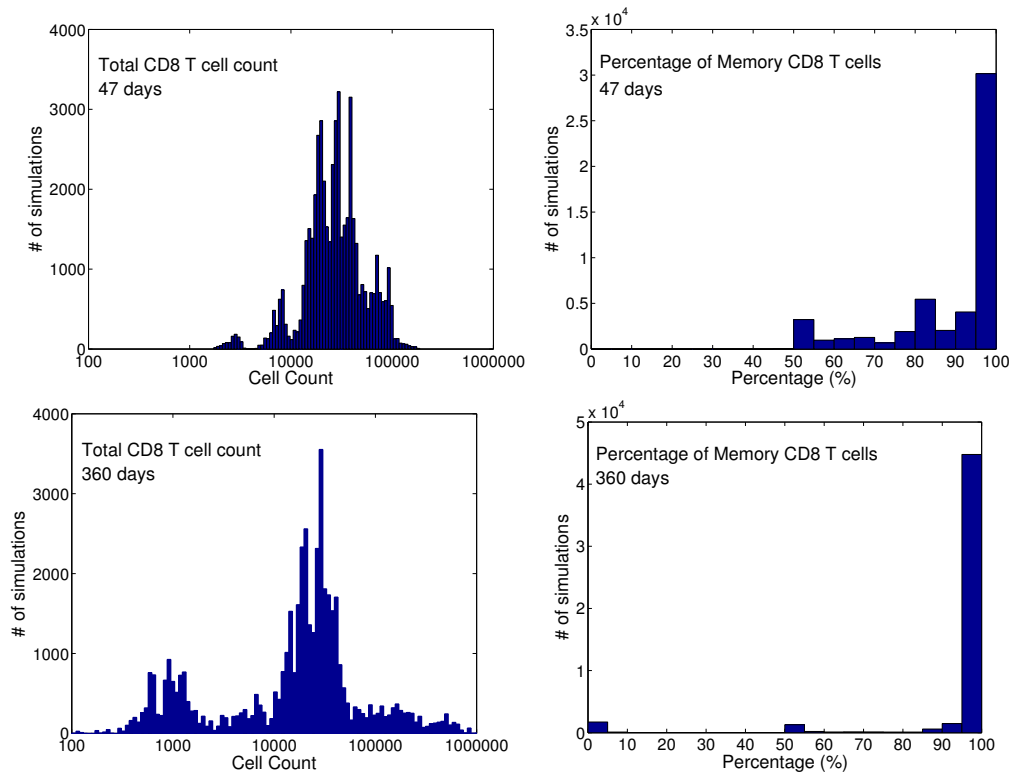
Supplementary Figures



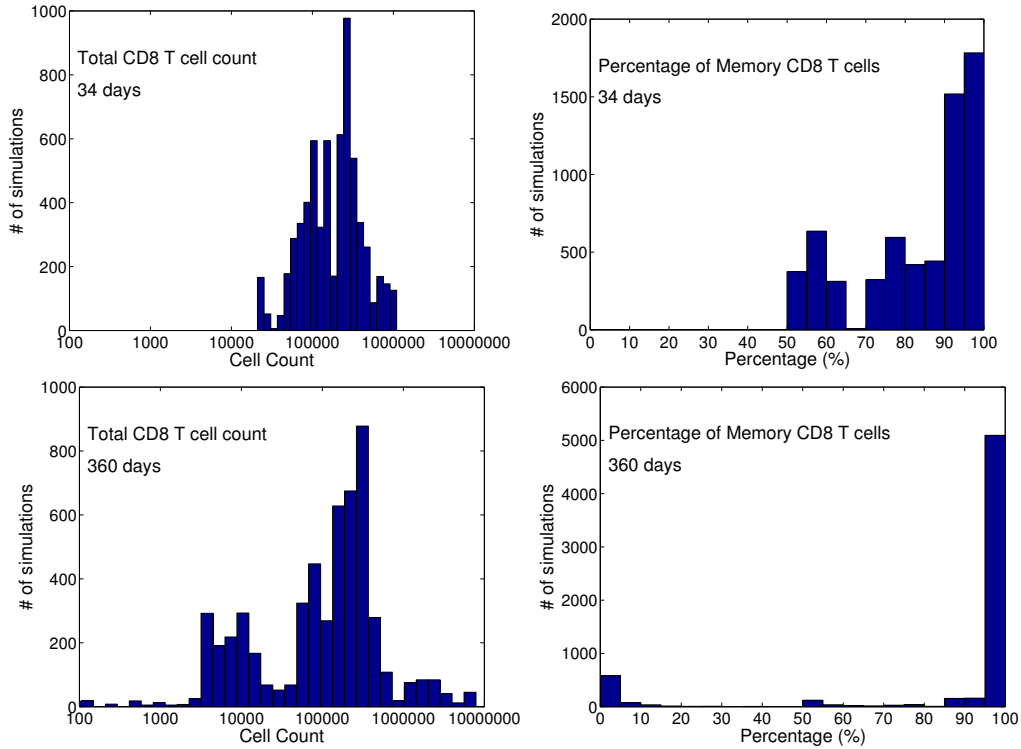
Supp. Fig. 1: **Frequencies of appearance of values of (μ_N, δ_{NE}) among the acceptable parameter value sets for Lm infection.** The height of red vertices indicates the percentage of parameter sets using the associated pair-value. For correlated parameters, values of one parameter are strongly associated with one or two values of the other parameter. Here, low values of δ_{NE} are preferentially associated with high values of μ_N .



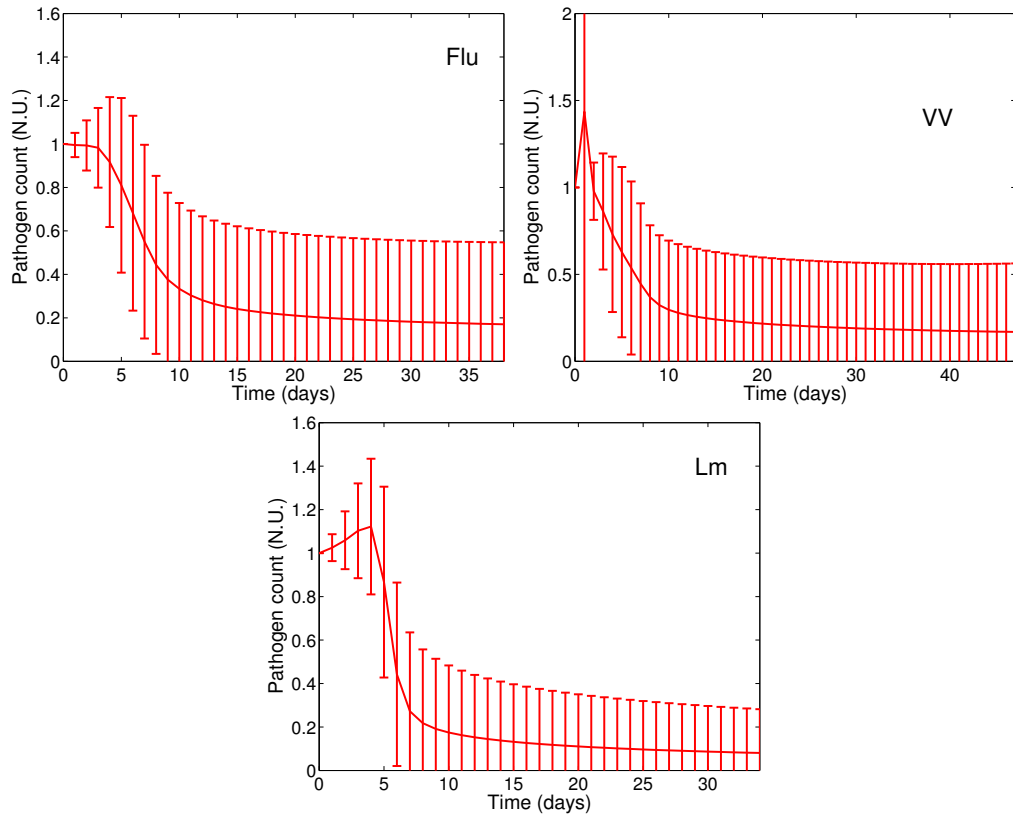
Supp. Fig. 2: **Uncorrelated parameter values.** Frequencies of appearance of every pair (δ_{EM}, μ_M) (left) and (ρ_E, μ_M) (right) among the acceptable parameter value sets are presented, for the three infections. The height of red vertices indicates the percentage of parameter sets using the associated pair-value. Uncorrelated parameters are characterized by a similar distribution of parameter values whatever the value of the other parameter. One observes no correlation between parameter values for experiments on Flu (top), VV (middle), and *Lm* (bottom).



Supp. Fig. 3: **Total number of CD8 T cell counts and percentages of memory cells among the total CD8 T cell population predicted by the model for VV infection.** For every parameter value set among the acceptable ones, the histograms of the number of simulations associated with a given count of total CD8 T cells (left panel) and with a given percentage of memory cells among the total CD8 T cell population (right panel) are presented, both at the end of the experiment (D47, top) and at D360 (bottom).



Supp. Fig. 4: **Total number of CD8 T cell counts and percentages of memory cells among the total CD8 T cell population predicted by the model for *Lm* infection.** For every parameter value set among the acceptable ones, the histograms of the number of simulations associated with a given count of total CD8 T cells (left panel) and with a given percentage of memory cells among the total CD8 T cell population (right panel) are presented, both at the end of the experiment (D34, top) and at D360 (bottom).



Supp. Fig. 5: **Pathogen count evolution.** For the 3 experiments (top left: Flu; Top right: VV; Bottom: *Lm*), the average evolution of the pathogen count, with standard deviation, is shown over the duration of each experiment. This evolution is computed from each individual evolution among the acceptable parameter value sets.