Supplementary figures and datasets

Tina Toni, Michael P. H. Stumpf

Table 1: Simulated dataset for the chemical reaction kinetics example.

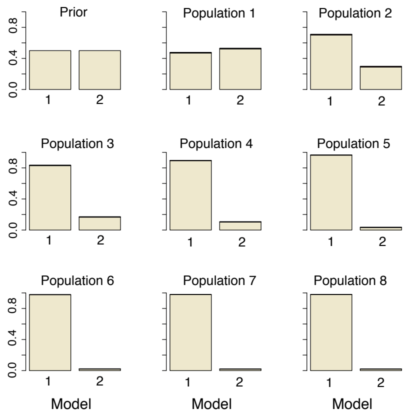
time	0.000	0.005	0.010	0.015	0.020	0.025	0.030	0.035	0.040	0.045
Y	3	8	15	18	23	27	32	35	37	37
time	0.050	0.055	0.060	0.065	0.070	0.075	0.080	0.085	0.090	0.095
Y	38	39	40	41	41	42	42	42	42	42

Table 2: Influenza A (H3N2) infection in 1977-78 (middle column) and 1980-81 (right column) epidemics, Tecumseh, Michigan [1].

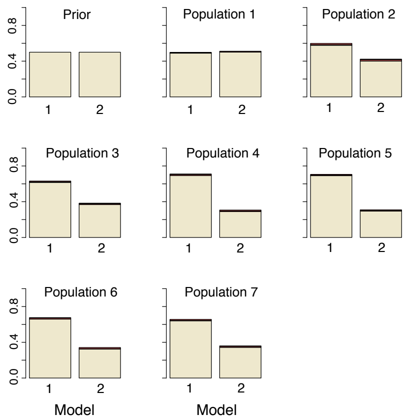
Nr. infected individuals	1	2	3	4	5	1	2	3	4	5
0	66	87	25	22	4	44	62	47	38	9
1	13	14	15	9	4	10	13	8	11	5
2		4	4	9	1		9	2	7	3
3			4	3	1			3	5	1
4				1	1				1	0
5					0					1

Table 3: Influenza B infection in 1975-76 epidemic (middle column) and influenza A (H1N1) infection in 1978-79 epidemic (right column), Seattle, Washington [2].

Nr. infected individuals	1	2	3	4	5	1	2	3
0	9	12	18	9	4	15	12	4
1	1	6	6	4	3	11	17	4
2		2	3	4	0		21	4
3			1	3	2			5
4				0	0			
5					0			

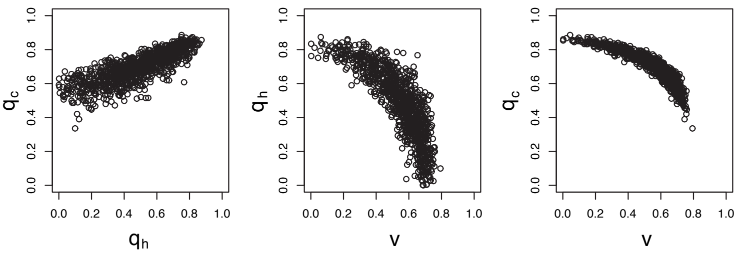


(a)

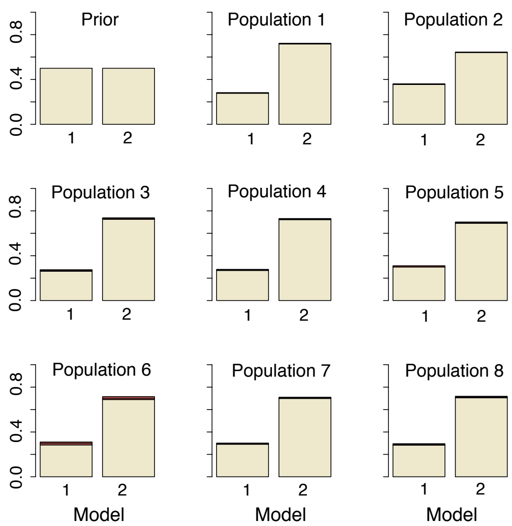


(b)

Figure 1: Estimation of marginal intermediate distributions of (a) Two- and four-parameter models (1) and data from Suppl. Table 2. Tolerance schedule: $\epsilon = \{100, 80, 50, 30, 20, 15, 13, 12\}$. Population 8 is the target distribution, which approximates $P(m|D_0)$.(b) Two- and three-parameter models (1) and data from Suppl. Table 3. Tolerance schedule: $\epsilon = \{40, 20, 15, 10, 8, 6, 5\}$. This tolerance schedule is lower the tolerance schedule in example (a) because the dataset used in this example is smaller. Population 7 is our target distribtuion. Perturbation kernels used in both examples are: $KM_t(m|m^*) = 0.7$ if $m = m^*$ and 0.3 otherwise; $KP_t(\theta|\theta^*) = U(-\sigma, \sigma)$, $\sigma = 0.5(\max\{\theta\}_{t-1} - \min\{\theta\}_{t-1})$. $N = 1000$. $B_t = 1$.



(a)



(b)

Figure 2: (a) Two dimensional projections of the posterior parameter distributions of model (2). Note the deviation from normality. (b) Estimation of marginal intermediate distributions. Population 8 the a target distribution, which approximates $P(m|D_0)$. Model 1 is a basic two-parameter model (1), model 2 is model (2). We use the combined data from Suppl. Table 2 and the tolerance schedule $\epsilon = \{100, 80, 50, 30, 20, 15, 13, 12\}$. Perturbation kernels are: $KM_t(m|m^*) = 0.7$ if $m = m^*$ and 0.3 otherwise; $KP_t(\theta|\theta^*) = U(-\sigma, \sigma)$, $\sigma = 0.5(\max\{\theta\}_{t-1} - \min\{\theta\}_{t-1})$. $N = 1000$. $B_t = 1$.

References

[1] Addy C, Jr IL and Haber M. A generalized stochastic model for the analysis of infectious disease final size data. *Biometrics*, 961–974, 1991.

[2] Jr IL and Koopman J. Household and community transmission parameters from final distributions of infections in households. *Biometrics*, 115–126, 1982.