

SUPPLEMENTARY INFORMATION

Analysis of heterogeneous dengue transmission in Guangdong in 2014 with multivariate time series model

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Table S1. Shows the mean scores based on one-step-ahead predictions. Model D3 is compared with the remaining models; the Monte Carlo p-values are based on permutation tests for paired observations (9999 permutations). Bold indicates the best model, i.e. the model with the lowest score

Model	S	$\overline{\log S}$	(p-value)	\overline{RPS}	(p-value)
With Fo weight model					
A1	1	1.638	(0.0796)	5.542	(0.0071)
A2	2	1.611	(0.0766)	6.158	(0.0081)
A3	3	1.595	(0.0573)	5.232	(0.0076)
With Fo+pop. weight model					
B1	1	1.650	(0.0801)	5.748	(0.0074)
B2	2	1.610	(0.0909)	6.168	(0.0085)
B3	3	1.589	(0.0599)	5.197	(0.0076)
With PL weight model					
C1	1	1.599	(0.1451)	5.644	(0.0091)
C2	2	1.569	(0.0215)	5.226	(0.0076)
C3	3	1.524	(0.1066)	1.509	(0.7993)
With PL+pop. weight model					
D1	1	1.599	(0.1424)	5.665	(0.007)
D2	2	1.574	(0.0154)	5.347	(0.0081)
D3	3	1.520		1.506	