

**Supplementary Table 1. Summary of model selection and parameter estimation for transmission data from uncontrolled outbreaks**

Dataset	Model	$\Delta AIC_c$	Akaike weight	Negative binomial parameters		
				$\hat{R}_0$ or $\hat{R}$ 90% CI	$\hat{k}$ 90% CI	$t_{20}$ 90% CI
SARS	P	250.4	0	1.63 <sup>†</sup>	0.16	0.88
Singapore 2003	G	41.2	0	0.54-2.65	0.11-0.64	0.60-0.94
$N=57$	NB	0	1			
SARS	P	49.2	0	0.94 <sup>†</sup>	0.17	0.87
Beijing 2003	G	10.6	0	0.27-1.51	0.10-0.64	0.60-0.95
$N=33$	NB	0	1			
Measles <sup>v95</sup>	P	-	-	0.63 <sup>#</sup>	0.23	0.81
US 1997-1999	G	-	-	0.47-0.80	0.16-0.39 <sup>pz</sup>	0.70-0.92
$N=165^{s,pz}$	NB	-	-			
Measles <sup>v95?</sup>	P	-	-	0.82 <sup>#</sup>	0.21	0.83
Canada 1998-2001	G	-	-	0.72-0.98	0.12-0.65 <sup>pz</sup>	0.64-0.96
$N=49^{s,pz}$	NB	-	-			
Smallpox (V. major) <sup>v80?</sup>	P	129.3	0	3.19	0.37	0.71
Europe 1958-1973	G	7.4	0.02	1.66-4.62	0.26-0.69	0.59-0.79
$N=32^s$	NB	0	0.98			
Smallpox (V. major) <sup>v20-70</sup>	P	13.0	0	0.80	0.32	0.74
Benin 1967	G	0.8	0.45	0.32-1.20	0.16-1.76	0.44-0.88
$N=25$	NB	0	0.55			
Smallpox (V. major) <sup>v</sup>	P	-	-	1.49 <sup>#</sup>	0.72	0.58
W. Pakistan	G	-	-		0.44-2.05 <sup>pz</sup>	0.41-0.74
$N=47^{s,pz}$	NB	-	-			
Smallpox (V. minor) <sup>v50-70?</sup>	P	16.4	0	1.60	0.65	0.60
England 1966	G	0	0.71	0.88-2.16	0.34-2.32	0.41-0.73
$N=25$	NB	1.7	0.29			
Monkeypox <sup>v70</sup>	P	10.6	0	0.32	0.58	0.62
Zaire 1980-84	G	0	0.62	0.22-0.40	0.32-3.57	0.36-0.74
$N=147^s$	NB	1.0	0.37			
Pneumonic plague	P	15.5	0	1.32	1.37	0.47
6 outbreaks	G	0	0.67	1.01-1.61	0.88-3.53	0.37-0.54
$N=74$	NB	1.5	0.33			
Hantavirus (Andes virus)*	P	1.0	0.31	0.70	1.66	0.45
Argentina 1996	G	0	0.52	0.20-1.05	0.24- $\infty$	0.20-0.80
$N=20$	NB	2.3	0.17			
Ebola HF*	P	0	0.56	1.50	5.10	0.34
Uganda 2000	G	1.4	0.28	0.85-2.08	1.46- $\infty$	0.20-0.46
$N=13$	NB	2.4	0.17			

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J.O. Lloyd-Smith, S.J. Schreiber, P.E. Kopp, W.M. Getz

## Table notes

P, Poisson; G, geometric; NB, negative binomial offspring distribution.

$\Delta\text{AIC}_c$ , Akaike information criterion, modified for sample size, relative to lowest score.

Akaike weight, approximate probability that each model is the best of the models considered.

$\hat{R}_0$  (or  $\hat{R}$ ) and  $\hat{k}$ , maximum likelihood estimates of mean and dispersion parameter of negative binomial distribution, from full observed distribution of  $Z$  except where noted.

$t_{20}$ , expected proportion of transmission due to most infectious 20% of cases, calculated from  $\hat{k}$ .

90% CI, bootstrap confidence intervals based on 10,000 resamples and bias-corrected non-parametric percentile method.

$N$ , number of infectious individuals in dataset.

$v^{XX}$  vaccinated population with XX% coverage ( ? coverage estimated or unknown).

\*results should be interpreted with caution due to small sample size, incomplete contact tracing, or atypical nature of outbreak.

<sup>s</sup>surveillance data.

<sup>pz</sup>only mean of  $Z$  and proportion of zeros known. Estimation of  $\hat{k}$  and confidence interval on  $\hat{k}$  described in Supplementary Notes; AIC model selection was not possible.

<sup>†</sup>see Supplementary Notes for relation to other  $R_0$  estimates for SARS.

<sup>#</sup> $R_0$  from source article (including 95% CI when given).

Data and analysis described in the Supplementary Notes and Supplementary Table 2.