

## Supplementary Table 2. Results of data analyses

### Uncontrolled outbreaks

<u>Parameter estimation</u>	SARS, Singapore	SARS, Beijing (gen 2 only)	SARS, Beijing (gens 1 and 2)	Measles, USA	Measles, Canada	Pneumonic plague, 6 outbreaks	Hantavirus, Argentina		
<i>N</i>	57	33	34	165	49	74	20		
mean ( <i>R</i> <sub>0</sub> or <i>R</i> )	1.63	0.94	1.88	0.63	0.82	1.32	0.7		
<i>k</i> <sub>mle</sub>	0.16	0.17	0.12			1.37	1.66		
<i>k</i> <sub>pz</sub>	0.17	0.17	0.13			1.25	1.94		
var( <i>Z</i> )/mean( <i>Z</i> )	15.31	5.45	18.7			1.84	1.52		
Number of zeros in dataset ( <i>Z</i> =0)	38	24	24			122	35	30	11
<i>p</i> <sub>0</sub>	0.6667	0.7273	0.7059	0.7394	0.7143	0.4054	0.5500		
Binomial 90CI on <i>p</i> <sub>0</sub>	0.5503,0.7695	0.5724,0.8497	0.5524,0.8309	0.6772, 0.7950	0.5899,0.8183	0.3090,0.5076	0.3469,0.7414		
<b><u>Model selection</u></b>									
ΔAIC(P)	250.4	49.2	183.4			15.5	1		
ΔAIC(G)	41.2	10.6	31.4			0	0		
ΔAIC(NB)	0	0	0			1.5	2.3		
Akaike weight(P)	0	0	0			0	0.31		
Akaike weight(G)	0	0	0			0.67	0.52		
Akaike weight(NB)	1	1	1			0.33	0.17		
P-W test <i>p</i> -value	<1e-6	<1e-6	<1e-6			1.6e-5	0.068		
<b><u>90% Confidence intervals for <i>k</i></u></b>									
Non-parametric bootstrap (uncorrected)	0.10, 0.36	0.08, 0.46	0.06, 0.31					0.82, 3.00	0.46, inf
1. Non-parametric bootstrap (bias-corrected)	0.11, 0.64	0.10, 0.64	0.08, 0.42					0.88, 3.53	0.65, inf
Number of all-zero bootstrap datasets	0	0	0					0	0
Parametric bootstrap (uncorrected)	0.09, 0.28	0.08, 0.49	0.06, 0.27					0.80, 3.61	0.44, inf
2. Parametric bootstrap (bias-corrected)	0.10, 0.30	0.11, 0.78	0.08, 0.33	0.88, 4.58	0.68, inf				
Number of all-zero bootstrap datasets	0	1	0	0	0				
3. Maximum-likelihood sampling variance	0.10, 0.32	0.10, 0.79	0.07, 0.37			0.84, 3.86	0.54, inf		
4. Large-sample variance on <i>k</i> <sub>pz</sub>	0.11, 0.36	0.09, 0.80	0.07, 0.38			0.16, 0.39	0.12, 0.65	0.75, 3.76	0.57, inf
5. Binomial sampling variance on <i>p</i> <sub>0</sub>	0.09, 0.34	0.06, 0.58	0.05, 0.30			0.13, 0.44	0.08, 0.64	0.56, 5.12	0.20, inf

#### Legend

Quantity cannot be calculated with available data

From:


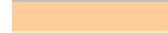

Superspreading and the impact of individual variation on disease emergence

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

## Uncontrolled outbreaks (cont'd)

<u>Parameter estimation</u>	Smallpox surveillance, Europe	Smallpox, Benin	Smallpox, W. Pakistan	Variola minor, England	Monkeypox surveillance, Zaire	Rubella, Hawaii*	Ebola HF, Uganda
<i>N</i>	32	25	47	25	147	19	13
mean ( <i>R</i> <sub>0</sub> or <i>R</i> )	3.19	0.8	1.49	1.6	0.32	1	1.5
<i>k</i> <sub>mle</sub>	0.37	0.32		0.65	0.58	0.032	5.1
<i>k</i> <sub>pz</sub>	0.42	0.29	0.72	0.53	0.58	0.032	2.31
var( <i>Z</i> )/mean( <i>Z</i> )	8.73	2.81		2.71	1.58	17	1.37
Number of zeros in dataset ( <i>Z</i> =0)	13	17	21	12	114	17	4
<i>p</i> <sub>0</sub>	0.4063	0.6800	0.4468	0.4800	0.7755	0.8947	0.3077
Binomial 90CI on <i>p</i> <sub>0</sub>	0.2597,0.5665	0.4964,0.8297	0.3223,0.5766	0.3051,0.6586	0.7116,0.8309	0.7042,0.9810	0.1127,0.5726
<b><u>Model selection</u></b>							
ΔAIC(P)	129.3	13		16.4	10.6	83.5	0
ΔAIC(G)	7.4	0.8		0	0	25.4	1.4
ΔAIC(NB)	0	0		1.7	1	0	2.4
Akaike weight(P)	0	0		0	0	0	0.56
Akaike weight(G)	0.02	0.45		0.71	0.62	0	0.28
Akaike weight(NB)	0.98	0.55		0.29	0.37	1	0.17
P-W test <i>p</i> -value	<1e-6	5e-6		1.2e-5	8.6e-6	<1e-6	0.17
<b><u>90% Confidence intervals for <i>k</i></u></b>							
Non-parametric bootstrap (uncorrected)	0.24, 0.63	0.13, 1.20		0.30, 1.91	0.29, 2.41		0.86, inf
1. Non-parametric bootstrap (bias-corrected)	0.26, 0.69	0.16, 1.76		0.34, 2.32	0.32, 3.57		1.48, inf
Number of all-zero bootstrap datasets	0	1		0	0	1192	0
Parametric bootstrap (uncorrected)	0.23, 0.71	0.13, 1.95		0.32, 2.28	0.30, 2.20		1.11, inf
2. Parametric bootstrap (bias-corrected)	0.26, 0.82	0.18, inf		0.40, 3.97	0.33, 3.57		1.91, inf
Number of all-zero bootstrap datasets	0	0		0	0	1397	0
3. Maximum-likelihood sampling variance	0.24, 0.83	0.16, 11.2		0.36, 3.32	0.32, 2.86	0.013,inf	1.28, inf
4. Large-sample variance on <i>k</i> <sub>pz</sub>	0.27, 0.98	0.15, 10.5	0.44, 2.05	0.29, 2.70	0.32, 2.97	0.013,inf	0.76, inf
5. Binomial sampling variance on <i>p</i> <sub>0</sub>	0.20, 0.88	0.08, 2.69	0.32, 2.15	0.18, 2.08	0.18, inf	0.003, 0.19	0.31, inf

### Legend

	Quantity cannot be calculated with available data
	>5% of bootstrap datasets contained all zeros
	Not shown in Supplementary Table 1 due to broad CIs and atypical nature of outbreak.

From:

Superspreading and the impact of individual variation on disease emergence

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

## Controlled outbreaks

	<u>SARS, Singapore</u>		<u>SARS, Beijing</u>		<u>Pneumonic plague, Mukden</u>		<u>Smallpox, Kuwait</u>	
<u>Parameter estimation</u>	Before control	During control	Before control	During control	Before control	During control	Before control	During control
<i>N</i>	57	114	33	43	12	27	4	23
mean ( <i>R</i> <sub>0</sub> or <i>R</i> )	1.63	0.68	0.94	0.28	2	0.41	2.75	0.91
<i>k</i> <sub>mle</sub>	0.16	0.071	0.17	0.0062	2.63	0.32	2.64	0.026
<i>k</i> <sub>pz</sub>	0.17	0.074	0.17	0.0061	2	0.28		0.025
var( <i>Z</i> )/mean( <i>Z</i> )	15.31	22.81	5.45	12	1.82	1.75	3	10.25
Number of zeros in dataset ( <i>Z</i> =0)	38	96	24	42	3	21	0	21
<i>p</i> <sub>0</sub>	0.6667	0.8421	0.7273	0.9767	0.2500	0.7778	0.0000	0.9130
Binomial 90CI on <i>p</i> <sub>0</sub>	0.5503,0.7695	0.7749,0.8954	0.5724,0.8497	0.8944,0.9988	0.0719,0.5273	0.6079,0.8985	0,0.4377	0.7508,0.9843
<b><u>Model selection</u></b>								
ΔAIC(P)	250.4	318.1	49.2	74.7	0.8	3.8	0.8	79.9
ΔAIC(G)	41.2	85.7	10.6	37.8	0	0	0	29.4
ΔAIC(NB)	0	0	0	0	1.8	1.1	11.3	0
Akaike weight(P)	0	0	0	0	0.33	0.09	0.4	0
Akaike weight(G)	0	0	0	0	0.48	0.58	0.6	0
Akaike weight(NB)	1	1	1	1	0.2	0.34	0	1
P-W test <i>p</i> -value	<1e-6	<1e-6	<1e-6	<1e-6	0.045	0.011	0.029	<1e-6
<b><u>90% Confidence intervals for <i>k</i></u></b>								
Non-parametric bootstrap (uncorrected)	0.10, 0.36	0.041, 0.28	0.08, 0.46		0.82, inf	0.11, 1.52	1.86, inf	
1. Non-parametric bootstrap (bias-corrected)	0.11, 0.64	0.049, 0.41	0.10, 0.64		1.26, inf	0.12, 2.15	2.63, inf	
Number of all-zero bootstrap datasets	0	0	0	3608	0	13	0	1219
Parametric bootstrap (uncorrected)	0.09, 0.28	0.042, 0.12	0.08, 0.49		0.86, inf	0.11, inf	0.60, inf	
2. Parametric bootstrap (bias-corrected)	0.10, 0.30	0.046, 0.13	0.11, 0.78		1.47, inf	0.15, inf	2.96, inf	
Number of all-zero bootstrap datasets	0	0	1	5612	0	6	3	1407
3. Maximum-likelihood sampling variance	0.10, 0.32	0.047, 0.15	0.10, 0.79	0.002, inf	0.97, inf	0.14, inf	0.76, inf	0.01, inf
4. Large-sample variance on <i>k</i> <sub>pz</sub>	0.11, 0.36	0.049, 0.15	0.09, 0.80	0.002, inf	0.73, inf	0.12, inf		0.01, inf
5. Binomial sampling variance on <i>p</i> <sub>0</sub>	0.09, 0.34	0.037, 0.15	0.06, 0.58	0.0002, 0.069	0.33, inf	0.05, inf	0.40, inf	0.003, 0.14

### Legend

	Quantity cannot be calculated with available data
	>5% of bootstrap datasets contained all zeros
	One-tailed 90% CI reported

From:

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