Beds, burials and tracers: the timing and the size of an Ebola response

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Summary. One imported case of Ebola is simulated in a Sierra Leone district of 500,000 people, with three responses that can each start late and run out: treatment beds, safe-burial teams and contact tracing. Every parameter is a published estimate and nothing is fitted. Beds are the only lever that brings the reproduction number below one alone (2.53 to 0.89), and timing matters more than size: 40 beds opened on the day the first case is found leave 10 deaths, the same beds 90 days later leave 191,764. Whether the response is worth its cost depends on what would have happened without it, which is this study's largest uncertainty and is reported both ways.

1 The model

Structure and equations

The model extends the Ebola structure of Legrand et al. [1], with transmission from the community, from treatment beds and from unburied bodies, by making the response finite. A susceptible person (S) who is infected becomes latent (E), then infectious in the community (I). A community case is detected and joins a queue for a bed (Q), is admitted when a bed is free (H), recovers, or dies and becomes a body awaiting burial (F). Latent and infectious people who are listed contacts of a known case are tracked separately (E^T, I^T) because they are detected sooner (Fig. 1). The simulations are stochastic; their deterministic skeleton is

$$\begin{aligned}
\frac{dS}{dt} &= -\lambda S, & \frac{dQ}{dt} &= \gamma_d I + \gamma_T I^T - (\delta + \rho)\, Q - A,\\
\frac{dE}{dt} &= (1-p)\,\lambda S - \alpha E, & \frac{dE^T}{dt} &= p\,\lambda S - \alpha E^T,\\
\frac{dI}{dt} &= \alpha E - (\gamma_d + \delta + \rho)\, I, & \frac{dI^T}{dt} &= \alpha E^T - (\gamma_T + \delta + \rho)\, I^T,\\
\frac{dH}{dt} &= A - (\delta_H + \rho_H)\, H, & \frac{dF}{dt} &= \delta\,(I + I^T + Q) - \gamma_F F - \mu \min(F, K),
\end{aligned} \tag{1}$$

with force of infection

$$\lambda = \frac{\beta_I (I + I^T + Q) + \beta_H H + \beta_F F}{N}. \tag{2}$$

Here A is the admission flow, K the number of burial teams, each completing $\mu = 5$ burials a day [2], and p the share of new infections that are listed contacts. A patient who dies in a bed is buried safely and never enters F.

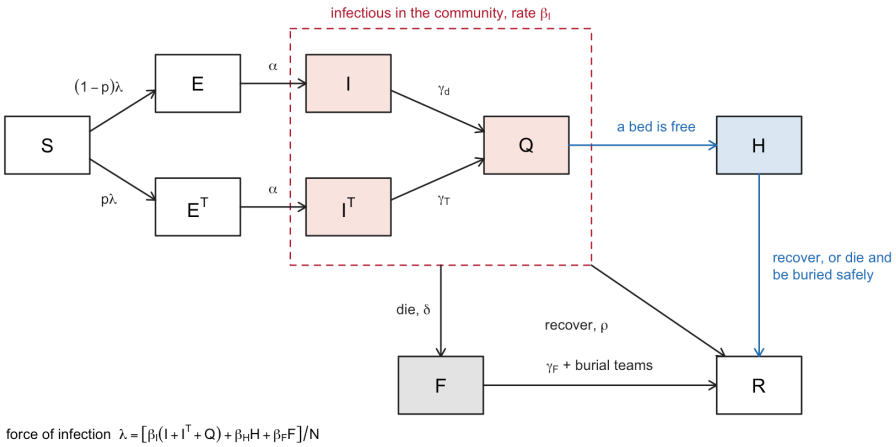


Figure 1: The model. Shaded states transmit: the community states at rate β_I, a treatment bed at β_H and an unburied body at β_F. A detected case waits in Q, still infectious, until a bed is free.

The three levers as capacities

Each lever is inactive until its own start delay has passed since the **first detected case**, so every scenario shares the same history up to that moment.

- **Beds** are a stock of B beds. Admission is immediate while $H < B$, so A empties the queue; once the beds are full a detected case stays in Q and transmits at the community rate.
- **Burial teams** are servers. Bodies leave F at rate $\gamma_F F + \mu \min(F, K)$, and a backlog builds when deaths outrun the teams.
- **Contact tracing** is a daily throughput of C contacts under follow-up. With $m = 8.5$ contacts listed per detected case [3], the traced share is $p = p_{\max}\, c \min\{1, C/[m(\gamma_d I + \gamma_T I^T)]\}$, where $p_{\max} = 0.8$ is its ceiling and $c = 0.878$ the share of contacts followed to completion [4].

Detection moves a case into the queue, not out of the community, so **tracing changes nothing unless a bed exists**. This follows Kucharski et al. [5] and is the model's strongest structural assumption.

Parameters and the derivation of the transmission rates

Table 1: Model parameters. Every duration is a mean; rates are their reciprocals. Unit costs and health weights are in `parameters.R` with their sources.

Symbol	Meaning	Value	Source
N	district population	500,000	design
$1/\alpha$	infection to onset	10.3 d	[6]
$1/\gamma_d$	onset to detection	5.0 d	[6]
$1/\gamma_T$	onset to detection, traced contact	1.0 d	design
	onset to death, community	8.2 d	[6]
	onset to recovery, community	15.1 d	[6]
	admission to death	4.3 d	[6]
	admission to discharge	11.2 d	[6]
$1/\gamma_F$	death to traditional burial	2.0 d	[1]
	case fatality, community	0.690	[7]
	case fatality, in a bed	0.614	[7]
R_0	reproduction number, no response	2.53	[8]
f	share of R_0 from funerals	0.43	[9]
ε	reduction in transmission in a bed	0.90	[9]

The death and recovery rates δ and ρ are set so that $\delta/(\delta+\rho)$ equals the case fatality ratio while each exit keeps its own mean duration, as in [1]; δ_H and ρ_H likewise for a bed (Table 1).

The split of transmission between the three routes cannot be taken from the literature. Legrand et al. fitted all three rates for two outbreaks and found two thirds of transmission at funerals in one and almost none in the other [1], and Camacho et al. show that several routes cannot be identified from one incidence curve [10]. The rates are therefore derived. With no response nobody is admitted, so

$$R_0 = \frac{\beta_I}{\delta+\rho} + \mathrm{CFR}\,\frac{\beta_F}{\gamma_F} \quad\Rightarrow\quad \beta_I = (1-f)\,R_0\,(\delta+\rho), \qquad \beta_F = \frac{f\,R_0\,\gamma_F}{\mathrm{CFR}}, \qquad \beta_H = (1-\varepsilon)\,\beta_I. \tag{3}$$

R_0 is not carried over from WHO's estimate of 2.02 [7]. That figure was derived from a doubling time of 12.84 days assuming a 15.3-day serial interval, and this model's generation interval is longer because 43% of its transmission happens after death. The base case uses 2.53, Althaus's independent fit to the Sierra Leone series [8], at which the model's doubling time is 12.8 days. The value 2.02 is kept as a sensitivity case.

Simulation and design

Runs use the Gillespie direct method [11] while at most 50 people are infected and binomial leaps of 0.1 days above that [12], so the early phase, where fade-out and timing are decided, is exact. Each scenario is run on the same 1,000 seeds for 365 days from one infection and compared with no response pair by pair. Results are means over the 348 **established** outbreaks, those with at least 2 infections before the first detection, a subset fixed before

any lever acts and therefore identical in every scenario. Brackets give 95% Monte Carlo intervals, and a paired difference whose interval excludes zero is called resolved.

2 Verification

Reproduction numbers, fade-out and final size against independent references

The code passes 25 tests with 619 expectations. The closed-form reproduction number agrees with the dominant eigenvalue of the next-generation matrix [13] to machine precision in all 8 response configurations. Feeding Legrand et al.'s own parameters through the same code reproduces 8 of their 8 published reproduction numbers and route shares [1]. The check also exposes a trap: their transmission rates are per week, and reading them as daily inflates R_0 sevenfold.

Early in an outbreak the model is a branching process, so the probability that one introduction takes off is known exactly [14]. Over 10,000 exact runs it was 0.6715 on the study's seed stream and 0.6665 on an independent one, against 0.6727 in theory, with every Wilson interval [15] covering the theoretical value (Fig. 2 b). Exact simulation matches the final-size relation $z = 1 - e^{-R_0 z}$ [16] to 0.004%; the leap step used in production runs +0.5% high. The step and switch threshold were accepted against pure exact simulation on an unanswered outbreak and on one answered 90 days late (Table 7).

One quantity was measured in the field and not used to build the model. The derivation in Eq. 3 implies $\beta_F/\gamma_F = 1.58$ secondary cases per unsafe burial, inside the 0.64 to 4.74 that Tiffany et al. estimated from 45 unsafe burials [17].

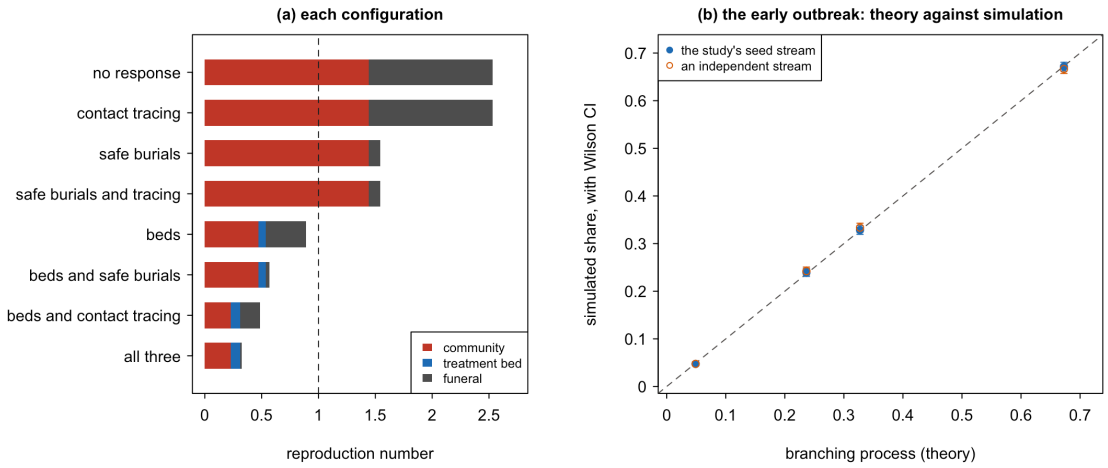


Figure 2: Verification. (a) The reproduction number of each response configuration with unlimited capacity, split by route; the dashed line is one. (b) Simulated probabilities of early outcomes (final size one, final size two, fade-out, take-off) against the branching process, with 95% Wilson intervals.

3 Results

Q1 - Where transmission comes from, and which lever can bring the reproduction number below one

With no response $R_0 = 2.53$, of which 1.44 arises in the community and 1.09 at funerals (Fig. 2 a). Beds reduce it to 0.89, because an admitted patient transmits little and is buried safely if they die. Safe burials alone reach only 1.54, since community transmission alone exceeds one. Contact tracing alone leaves it at 2.53: a traced case is found sooner but has nowhere to go. With beds, tracing has the largest further effect of any addition, 0.89 to 0.48, and all three give 0.33.

These are analytic values for capacity that never binds from the first day. The simulations below ask what remains of them when capacity is finite and late.

Q2 - Earlier or bigger: deaths against the start delay and the capacity of each lever

With no response an established outbreak kills 275,457 (265,693 to 285,221) people within a year. Fig. 3 and Table 2 show each lever alone.

Delay costs more than capacity buys. 40 beds opened on the day of the first detected case leave 10 (8 to 13) deaths, and after 30 days 68 (59 to 78). After 60 days the same beds leave 36,714 (26,322 to 47,107) and after 90 days 191,764 (176,248 to 207,280). Quadrupling to 160 beds at 90 days still leaves 54,331 (42,156 to 66,506). An epidemic doubling every 12.8 days is about 129 times larger after 90 days, so capacity that would have been ample is overwhelmed: with 40 beds at 90 days the queue peaks at 24,251 detected cases, and the beds are full with someone waiting on 161 days of the year. Capacity only starts to matter once the response is late: at 0 and 30 days, 40 and 160 beds give the same result.

Burial teams reduce deaths but do not contain; tracing alone does nothing. 8 teams from day 0 leave 48,595 (40,950 to 56,239) deaths, with 34% of outbreaks contained. Of the 16 tracing-only scenarios, none differs resolvably from no response, as Q1 predicts. The small differences in Fig. 3 c are Monte Carlo noise, most likely because moving people between traced and untraced states changes the random numbers later events draw.

Table 2: Mean deaths within one year over established outbreaks, by lever, capacity and start delay (days after the first detected case). Intervals are in `summary_levers_established.csv`.

Lever	Capacity	0 days	30 days	60 days	90 days
beds	20	10	1,847	119,340	222,782
beds	40	10	68	36,714	191,764
beds	80	10	68	6,527	130,588
beds	160	10	68	395	54,331
burial teams	1	117,975	191,017	235,101	257,867
burial teams	2	92,692	160,868	217,726	249,207
burial teams	4	67,684	135,471	197,431	238,556
burial teams	8	48,595	106,990	173,760	222,825

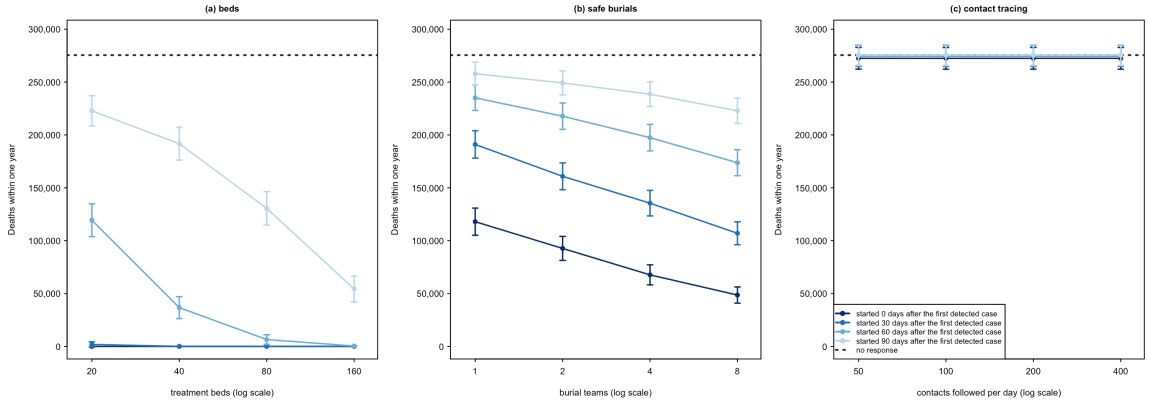


Figure 3: Deaths within one year against the capacity of each lever alone, one line per start delay. Means over 348 established outbreaks with 95% Monte Carlo intervals; the dotted line is no response.

Q3 - The best mix of beds, teams and tracers at a fixed budget

Every affordable split of $0.5, $1 and $2 million between the three levers was simulated, each starting 30 days after the first detected case (Fig. 4, Table 3). Bundles are sized so that their capacity fits the budget at the planning prices. The cost reported for a bundle is its expected cost over the economic draws, which can sit on either side of the budget: a programme stops being paid for once its outbreak has ended, and the draws let the price of a burial team and of a tracer range from one to three times the planning price, because that price is a lower bound. Bundles with no beds therefore show an expected cost up to 1.7 times their budget.

The best bundle at every budget is beds with burial teams, and none of the 3 best bundles buys tracing. At the smallest budget the best all-beds bundle averts 213,390 deaths against 260,992 for the best mix, and the mix stays ahead by less at the larger budgets. The worst bundles are those that put most of the money into tracing; tracing alone averts 705 to 723 deaths, which is noise.

The second purchase is therefore burial teams, not tracers, the opposite of the analytic ranking in Q1. The two answer different questions: the reproduction numbers assume unlimited capacity from the first day, and these bundles are finite and start 30 days late.

Table 3: The best affordable bundle at each budget, by deaths averted against no response.

Budget	Beds	Burial teams	Contacts per day	Deaths averted	Cost per death averted
$500,000	5	2	0	260,992	$0.95
$1,000,000	11	4	0	273,836	$1.58
$2,000,000	22	9	0	275,432	$3.22

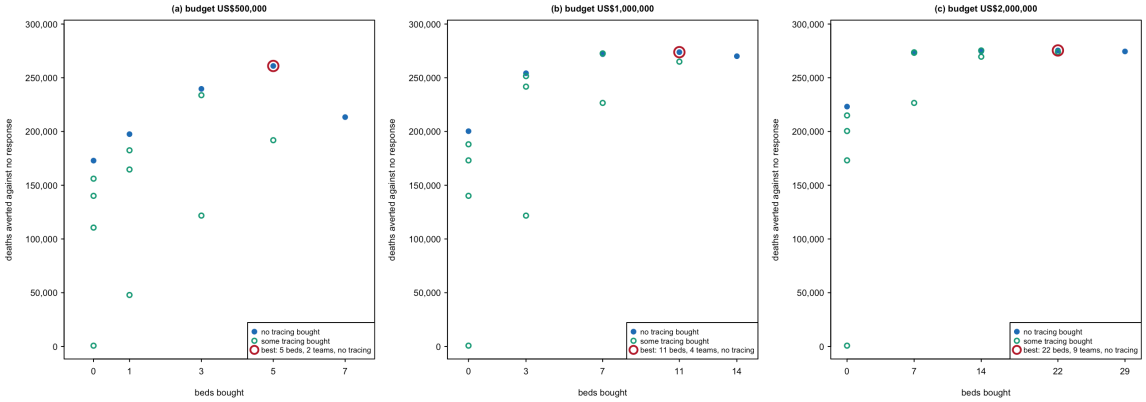


Figure 4: Deaths averted by every affordable bundle at three budgets, against the number of beds it buys. The circled bundle is the best at that budget.

Q4 - Cost per death and per DALY averted, under two counterfactuals

Costs are from the health system's perspective over one year, against no response. A bed costs $200.90 a day [18]. No published unit cost exists for a safe burial or a contact traced in West Africa, so teams and tracers are costed from the weekly incentives the Sierra Leone government paid [19], which is a lower bound, and break-even prices are reported (Table 8). Deaths are converted to DALYs at 19.5 discounted life-years each (3% a year); deaths account for 99.5% of the burden, as in [20]. The threshold is $105 to $137 per DALY averted [21], and the real response achieved $154 [22].

The answer depends on the counterfactual, which this study cannot pin down. If only the response can stop the epidemic, the unanswered outbreak kills 275,457 people. In 2014 transmission also fell as people changed how they cared for the sick and buried the dead; with the decline Althaus fitted [8], it kills 127. Sierra Leone's real epidemic, scaled to this district, killed about 279 over two years. The first counterfactual is an upper bound on what a response is worth and the second a lower bound, because the fitted decline partly reflects the real response.

Only the response stops the epidemic. All three levers cost $0.96 million, avert 275,436 deaths and cost $0.18 per DALY averted (Fig. 5 a). Every package is far below the threshold. This describes how severe an unchecked epidemic is in a closed, homogeneously mixing population, not the value of the 2014 response.

Behaviour change also reduces transmission. All three levers avert 112 deaths for $0.87 million, or $395 per DALY averted, above the threshold. The packages separate into two groups (Fig. 5 b, Table 4): safe burials alone cost $52 per DALY and burials with tracing $57, whereas every package with beds costs $395 to $446, because beds are paid for all year whether or not they are filled. The best package at the threshold is safe burials only, where under the first counterfactual it was all three.

Table 4: The reference packages (40 beds, 2 teams, 100 contacts a day, each from day 30) under both counterfactuals. Costs per DALY averted are against no response; the tracing-only rows divide by a difference that is not resolved.

Package	(i) Deaths	Averted	$/ DALY	(ii) Deaths	Averted	$/DALY
no response	275,457	0		127	0	
beds only	68	275,388	0.30	20	107	446
safe burials only	160,868	114,589	0.08	36	91	52
contact tracing only	274,684	773	1.23	123	4	187
beds and burials	25	275,432	0.20	16	111	407
beds and tracing	30	275,427	0.20	18	109	405
burials and tracing	164,379	111,078	0.09	36	91	57
all three	21	275,436	0.18	15	112	395

In Table 4, (i) is the counterfactual in which only the response stops the epidemic and (ii) the one with behaviour change.

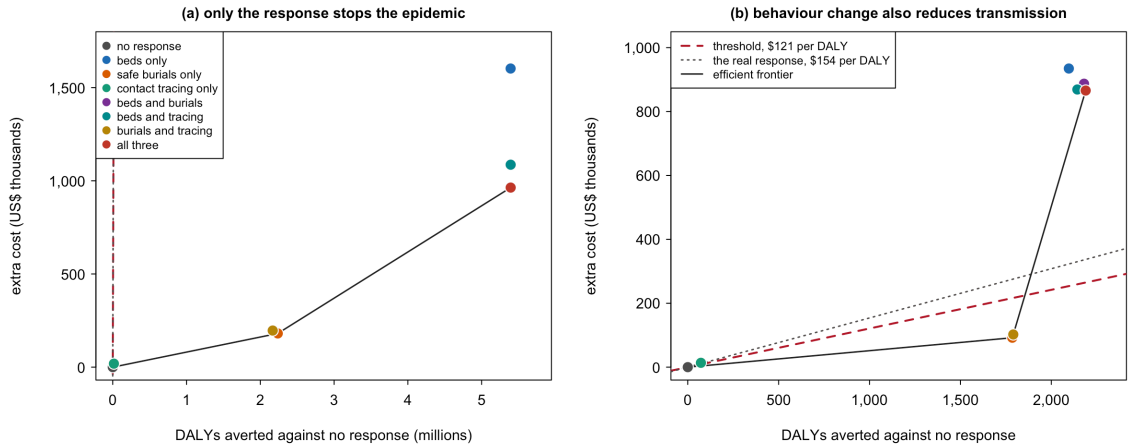


Figure 5: Cost-effectiveness planes for the reference packages under the two counterfactuals. In (a) the threshold line is almost vertical at this scale: every package lies far below it.

4 Sensitivity

One change at a time, and the economics re-valued

18 changes were applied one at a time to no response and to three reference packages (Fig. 6). All 57 paired differences in deaths are resolved and favour the response. In every case all three levers avert at least as many deaths as beds alone, and beds alone at least as many as burials alone. The gap between beds and burials is not constant: burials alone avert more than 85% of what beds avert under 4 changes (reproduction number 2.02 (WHO's own figure); reproduction number 1.79; two thirds at funerals (Congo 1995); behaviour change also reduces transmission). Apart from the second counterfactual, the totals move most with reproduction number 1.79 and reproduction number 2.02 (WHO's own figure).

14 economic re-valuations of the first counterfactual (discount rates, both ends of the bed-cost range, extensive care, tracer workload, disability weights and four thresholds from $105 to $1,118 per DALY) leave all three as the best package in 14 of them.

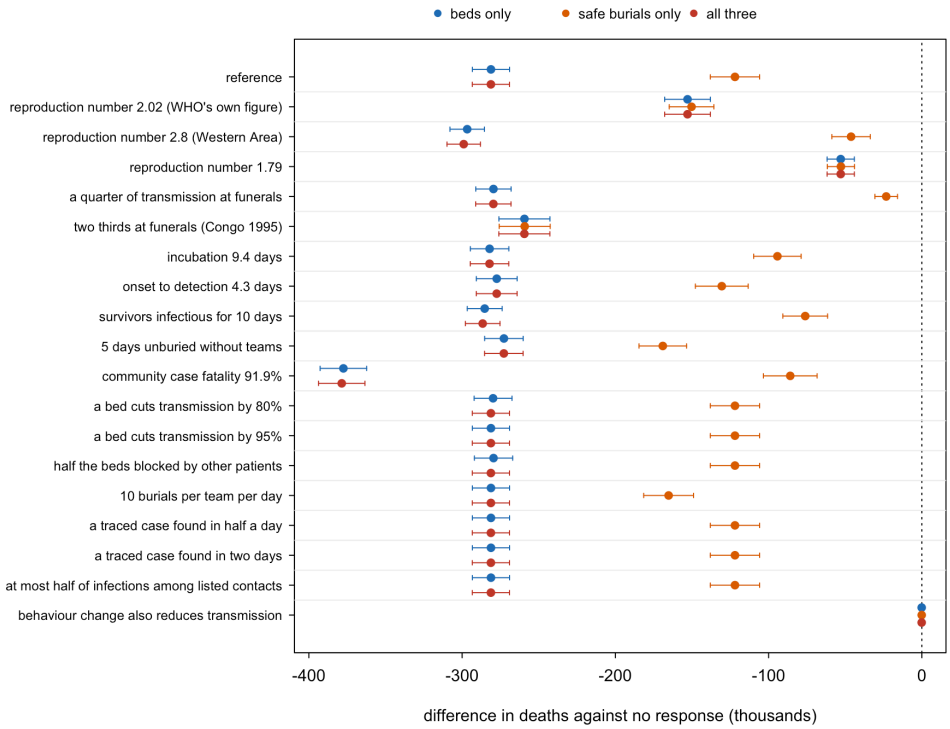


Figure 6: Paired differences in deaths against no response under each one-at-a-time change, for three reference packages, with 95% Monte Carlo intervals.

5 Limitations

What the model cannot say

The unanswered outbreak is far too large. With homogeneous mixing, one introduction and no behaviour change, an established outbreak infects 81% of the district within a year. Sierra Leone's whole epidemic, scaled to a district of this size, was about 996 cases over two years (Fig. 7). The model is wrong about scale by more than two orders of magnitude. The second counterfactual brackets the absence of behaviour change; nothing brackets homogeneous mixing. Absolute numbers are therefore properties of the model, and the paired comparisons between responses are more robust than the levels.

Other limits. The district is closed, with no movement in or out. The reproduction number is an anchor and the funeral share a single published value. There is no isolation outside a treatment bed, which is what makes tracing worthless without beds; a real response had holding centres and home isolation. Two of the three unit costs are lower bounds. The run counts were kept at their planned values although the pilot rule, which projected 38.2 minutes against a 30-minute budget, would have scaled them by 0.75; this costs run time and no precision. Stigma, orphanhood and the collapse of routine care are outside the model.

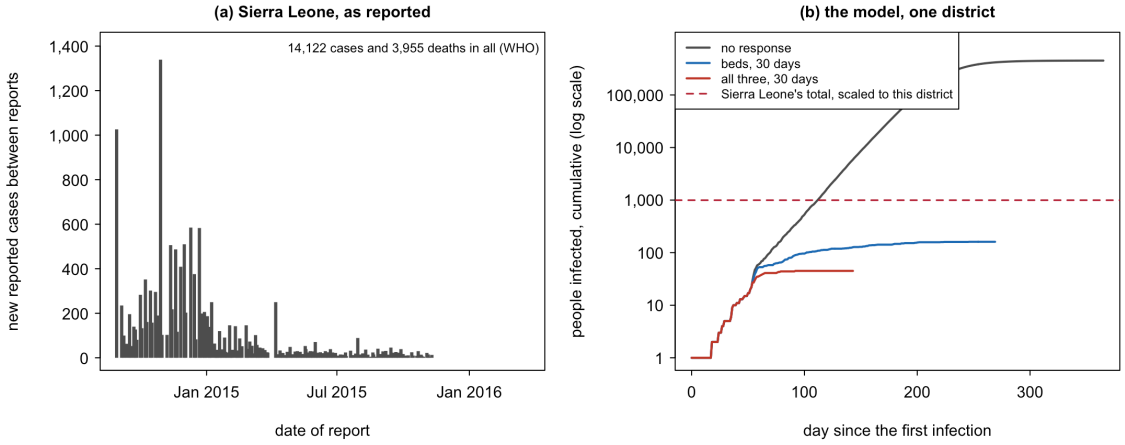


Figure 7: (a) Sierra Leone's epidemic as reported by WHO. (b) One simulated district outbreak under three responses, against Sierra Leone's total scaled to a district of this size.

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Appendix

A - Verification tables

Table 5: The reproduction number of each response configuration with unlimited capacity, by closed form and by next-generation eigenvalue, with its three routes.

Configuration	Closed form	Eigenvalue	Community	Bed	Funeral	Doubling time (d)
no response	2.5300	2.5300	1.442	0.000	1.088	12.8
beds	0.8902	0.8902	0.470	0.065	0.355	no growth
safe burials	1.5410	1.5410	1.442	0.000	0.099	29.7
contact tracing	2.5300	2.5300	1.442	0.000	1.088	12.8
beds and safe burials	0.5678	0.5678	0.470	0.065	0.032	no growth
beds and contact tracing	0.4838	0.4838	0.229	0.082	0.173	no growth
safe burials and tracing	1.5410	1.5410	1.442	0.000	0.099	29.7
all three	0.3266	0.3266	0.229	0.082	0.016	no growth

Table 6: Legrand et al.'s published reproduction numbers, recomputed from their parameters by this project's code.

Outbreak	Quantity	Published	Recomputed	Agrees
Congo1995	R0	2.70	2.697	yes
Congo1995	R0 community	0.50	0.500	yes
Congo1995	R0 hospital	0.40	0.423	yes
Congo1995	R0 funeral	1.80	1.775	yes
Uganda2000	R0	2.70	2.678	yes
Uganda2000	R0 community	2.60	2.603	yes
Uganda2000	R0 hospital	0.01	0.007	yes
Uganda2000	R0 funeral	0.10	0.069	yes

Table 7: Leap step and switch threshold against pure exact simulation, on two cases. A setting is accepted only if containment, cases, deaths and the peak bed queue are all within 1% of the exact value or inside its Monte Carlo interval, on both cases.

Case	Setting	Contained	Cases	Deaths	Peak queue	Passes both
no response	exact	0.314	304,638	207,374	25,916	yes
no response	switch20_tau0.1	0.314	306,471	208,867	26,462	yes
no response	switch20_tau0.25	0.314	309,092	210,948	27,278	no
no response	switch50_tau0.1	0.314	306,486	208,794	26,470	yes
no response	switch50_tau0.25	0.314	309,067	210,850	27,284	no
no response	switch200_tau0.1	0.314	306,386	208,679	26,447	yes
no response	switch200_tau0.25	0.314	309,036	210,780	27,279	no
all three, 90 days late	exact	0.418	106,200	70,591	9,069	yes
all three, 90 days late	switch20_tau0.1	0.420	113,886	76,463	9,794	yes
all three, 90 days late	switch20_tau0.25	0.416	142,419	95,278	12,565	no
all three, 90 days late	switch50_tau0.1	0.418	118,835	79,654	10,283	yes
all three, 90 days late	switch50_tau0.25	0.418	129,267	87,530	11,331	no
all three, 90 days late	switch200_tau0.1	0.418	114,464	76,618	9,873	yes
all three, 90 days late	switch200_tau0.25	0.418	125,463	84,067	11,076	no

The rule's pick is the cheapest setting that passes on both cases, switch20_tau0.1. Production runs use switch50_tau0.1, fixed in `parameters.R`, which also passes on both cases and keeps more of the early phase exact. Table 7 shows the settings with steps of 0.1 and 0.25 days; all twelve are in `checks_methods.csv`.

The deterministic model gives 447,503 infections by day 365 with no response, against 447,379 (445,797 to 448,962) over the simulated outbreaks that took off. Deaths trail infections, and there the simulated outbreaks are 1.0% behind, as expected of a stochastic epidemic that spends a random time small before it grows.

B - Break-even prices and one outbreak in detail

Table 8: Break-even unit costs under the first counterfactual: the price per day at which a package stops paying for itself at the threshold, beside the price used. The tracing-only value rests on an unresolved difference.

Package	Bed-day used	break-even	Team-day used	break-even	Contact-day used	break-even
beds only	200.90	95,757	163.30		0.327	
safe burials only	200.90		163.30	496,112	0.327	
contact tracing only	200.90		163.30		0.327	64
all three	200.90	170,194	163.30	3,400,034	0.327	67,998

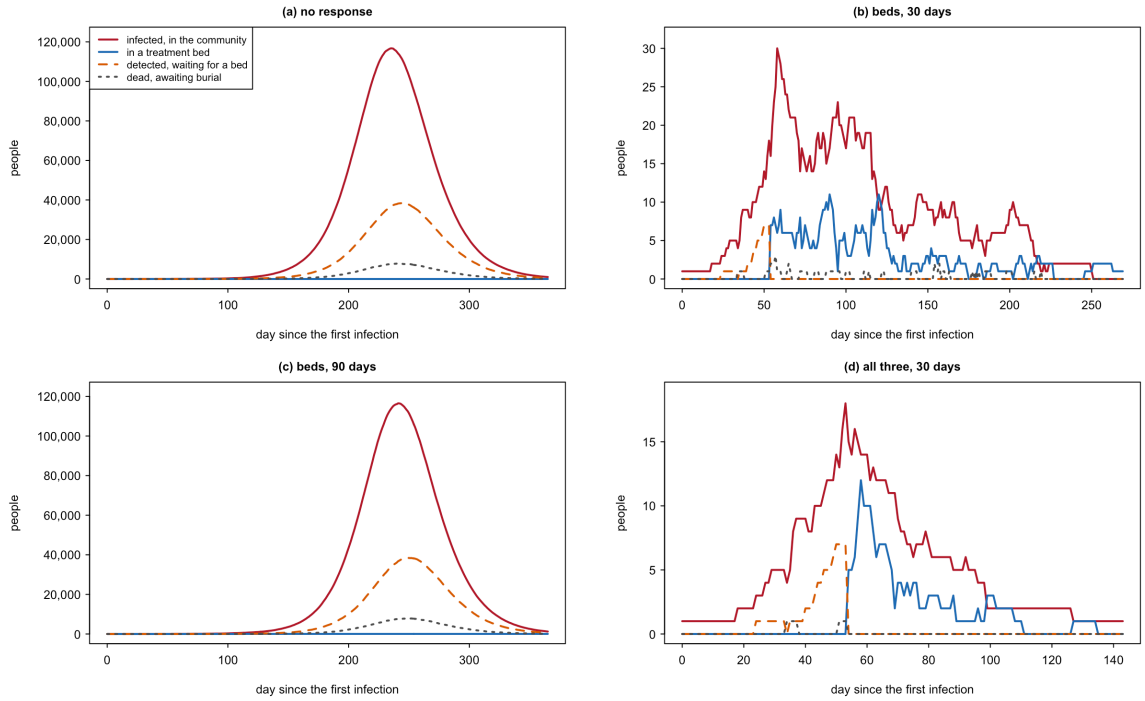


Figure 8: One simulated outbreak, at the 75th percentile of unanswered outbreaks, under four responses. Beds opened at 30 days hold the outbreak to tens of cases; the same beds at 90 days are too few to change its course.

C - Reproducing the results

`make test` runs the unit tests, `make all` every stage of `run_all.R`, and `make report` renders this document, and the longer guided web report beside it, from the saved tables. Every number in the text is read from a table in `output/tables/`; none is typed by hand. Parameters, with units and sources, are in `parameters.R`.