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Measuring the impact of Ebola control measures in Sierra Leone

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Between September 2014 and February 2015, the number of Ebola virus disease (EVD) cases reported in Sierra Leone declined in many districts. During this period, a major international response was put in place, with thousands of treatment beds introduced alongside other infection control measures. However, assessing the impact of the response is challenging, as several factors could have influenced the decline in infections, including behaviour changes and other community interventions. We developed a mathematical model of EVD transmission, and measured how transmission changed over time in the 12 districts of Sierra Leone with sustained transmission between June 2014 and February 2015. We used the model to estimate how many cases were averted as a result of the introduction of additional treatment beds in each area. Examining epidemic dynamics at the district level, we estimated that 56,600 (95% CI: 48,300–84,500) Ebola cases were averted in Sierra Leone up to 2nd February 2015 as a direct result of additional treatment beds being introduced. We also found that if these beds had been introduced one month earlier, it could have averted a further 12,500 cases. Our results suggest the unprecedented local and international response led to a substantial decline in EVD transmission during 2014/15. In particular, the introduction of additional beds had a direct impact on reducing EVD cases in Sierra Leone, although the effect varied considerably between districts.

Ebola virus disease | Sierra Leone | mathematical model | control measures | treatment beds

Significance Statement: Between June 2014 and February 2015, thousands of Ebola treatment beds were introduced in Sierra Leone, alongside other infection control measures. However, there has been criticism of the timing and focus of this response, and it remains unclear how much it contributed to curbing the 2014–15 Ebola epidemic. Using a mathematical model, we estimated how many Ebola virus disease cases the response averted in each district of Sierra Leone. We estimated that 56,600 (95% CI: 48,300–84,500) Ebola cases were averted in Sierra Leone as a direct result of additional treatment beds. Moreover, the number of cases averted would have been even greater had beds been available one month earlier.

The 2013–15 Ebola virus disease (EVD) epidemic in West Africa has seen more cases than all past outbreaks combined [1], and has triggered a major international response. In Sierra Leone, where there have been over 8,600 confirmed cases reported as of 1st August 2015, the Sierra Leone and UK governments and NGOs have supported the gradual introduction of over 1,500 beds in Ebola Holding Centres (EHCs) and Community Care Centres (CCCs), as well as over 1,200 beds in larger-scale Ebola Treatment Units (ETUs) [2, 3]. As well as the humanitarian value of providing treatment and care to sick patients, there is a secondary benefit to expanding bed capacity that is more difficult to quantify; by isolating the ill and removing them from the community, further infections might be prevented.

Since the peak of the epidemic in Sierra Leone in November 2014, when there were over 500 confirmed EVD cases reported per week, the level of infection has dropped, with fewer than 100 confirmed cases reported per week in February 2015. Although the nation-wide decline in cases coincided with an increase in the number of beds available [4], as well as improved case detection, tracing of contacts and safe burials of patients who had died [3, 5], there has been criticism of the timing and focus of the international response

in Sierra Leone [6, 7]. To properly evaluate the control efforts, and plan for future outbreaks of EVD, it is therefore crucial to understand how many cases were likely averted as a result of the response.

Mathematical models have been used prospectively to estimate the potential impact of additional beds [8, 9, 10, 11]. However, evaluating the effect of control measures retrospectively is more challenging, because a model must disentangle the reduction in transmission due to improved bed capacity from other factors. Behaviour changes [12], community engagement, improved case finding and an increase in safe burials [5] could all have contributed to a reduction in transmission. Indeed, many Ebola facilities were designed to be part of a package of interventions, combining treatment beds with community-based infection control [3].

To estimate how EVD transmission changed as interventions were introduced, we developed a stochastic mathematical model of Ebola transmission in Sierra Leone. The model was stratified by district, and incorporated available data on bed capacity in ETUs, EHCs and CCCs [13]. As beds were not the only control measure in place, we also included a time-varying transmission rate in the model [4, 14], to capture any variation in transmission which was not explained by the introduction of beds.

As not all new cases in Sierra Leone occur among known contacts of EVD patients [15], we accounted for potential under-reporting in our model. In our main analysis, we assumed that 60% of infectious individuals would be ascertained (i.e. would be reported and seek treatment), and that it took an average of 4.5 days for these individuals to be reported [16]. We also included the possibility of variability in the accuracy of reporting, with weekly reported cases following a negative binomial distribution. In the model, stochasticity could therefore be generated by both the transmission process and the reporting process. We assumed infectious individuals who were ascertained attended EHC/CCCs if beds were available [16]; the average time between onset and attendance declined over time, based on reported values for Sierra Leone (Fig. S1). Once test results were received, patients were transferred to an available ETU; we assumed this took two days on average. If no beds were available at any facility, cases remained in the community. The model structure is shown in Fig. 1, and the full set of parameter values in Table S1.

To allow for a time-varying community transmission rate, we used a flexible sigmoid function [14, 17]; depending on parameter values, transmission could be constant over time, or increase or decline. Our model structure therefore made it possible to separate the reduction in infection as a result of additional treatment beds and variation resulting from other effects, such as behaviour changes and implementation of safe burials.

Reserved for Publication Footnotes

We used a Bayesian approach to fit the model to weekly EVD confirmed and probable case data reported in each district of Sierra Leone [18, 19], and estimate how community transmission varied over time. We then used the fitted model to simulate multiple stochastic epidemic trajectories, and measured the number of cases that could have occurred in each area had additional beds not been introduced.

Results

We found that the temporal change in community transmission varied considerably between different regions (Fig. 2). In Bo and Moyamba, for example, the level of community transmission remained relatively flat, whereas in Bombali, Kailahun, Port Loko and Western Area, a significant decline in community transmission occurred alongside the reduction in transmission resulting from additional beds. In districts where there was greater variation in disease incidence, such as Kambia and Kenema, there was considerable uncertainty in our estimates of the community transmission rate. We found that the decline in community transmission in each of the 12 districts was strongly associated with the initial basic reproduction number, but less so with the total number of cases (Table S2). There was also a geographical structure to the decline, with a greater drop occurring in districts in the north and east of the country (Fig. S2).

To measure how many cases control measures may have averted, we removed all CCC, EHC and ETU beds introduced during the period of observation and simulated stochastic epidemic trajectories using our estimates for the time varying level of community transmission (Fig. S3). In this scenario, transmission reductions from factors other than beds, such as reduced infection as a result of behaviour changes, were still included. Any difference in epidemic dynamics between this scenario and the original model was therefore only the result of the removal of treatment beds.

Our results suggest that the increase in beds averted a limited number of cases in districts without ongoing transmission (e.g. Pujehun) but in districts with large outbreaks – such as Bombali and Western Area – there would have been thousands more infections without the introduction of beds. In Kenema, which had highly variable incidence data, there was substantial variation in the background transmission rate, and hence it was not possible to detect a significant effect of interventions; the 95% credible interval for cases averted included zero in Table 1. Across all 12 districts, we estimated that 56,600 (95% CI: 48,300–84,500) cases were averted in total between June 2014 and February 2015 as a result of additional beds.

As a sensitivity analysis, we also estimated how many cases would have been averted if 40% or 80% cases were ascertained, rather than 60% as in our main analysis (Tables S3–S4). If 80% of cases were ascertained, we estimated that 148,000 (95% CI: 115,000–219,000) cases were potentially averted across all districts as a result of the introduction of beds; when ascertainment was 40%, the additional beds averted 29,200 (95% CI: 24,500–47,700) cases. In our main analysis, we also assumed an infectious period of 10.9 days, based on reported time from onset-to-death, and onset-to-hospital discharge (details in SI Appendix). As some cases may have ceased to be infectious before discharge, as a sensitivity analysis we refit the model with a 9 day infectious period, equal to the average time of infectiousness for fatal cases. Our results did not change substantially under this assumption (Table S5).

In the model, we also assumed that transmission in each district was independent of the others. In reality, however, infectious individuals occasionally travelled between different areas [20]. To assess how this could affect our estimates of cases averted, we re-simulated outbreaks using the fitted model, but with additional infectious individuals introduced at a rate of either one per day or one per week in each district. When there was an average of one additional infection introduced per week, our estimates increased slightly (Table S6);

when one additional infection was introduced per day, the increase was larger, with an estimated 72,900 (95% CI: 61,700–87,900) cases averted across the country.

As well as measuring the effect of actual control measures, we were also able to estimate what impact the introduction of beds would have had earlier in the epidemic. Using the fitted model, we simulated epidemic trajectories under the assumption that the same numbers of beds were introduced 4 weeks earlier than in reality (Fig. S4). In this scenario, we estimated 69,100 (95% CI: 59,500–122,000) cases would have been averted, which is 12,500 higher than the number we estimated were actually averted (Table 1).

Discussion

Using a district-level mathematical model of EVD transmission, we have examined the effect of control measures on epidemic dynamics in Sierra Leone. In particular, we estimated the effect of the reduction in community transmission and additional treatment beds on the number of EVD cases. We found considerable geographic variation: in some districts, there was a noticeable shift in epidemic dynamics as a result of changes in community transmission and increased bed capacity; in other areas, the impact of control measures was less clear.

Although we could measure the number of beds available over time, there were some additional components of the treatment process that were less well known. We used reported data on time to hospital admission in Sierra Leone to parameterise our model [16, 1], but this may have varied between districts. We also assumed that individual infectiousness remained constant throughout the symptomatic period. If most transmission occurs in the later stages of infection, as viral load data might suggest [21], treatment beds could have had a greater impact on transmission reduction by isolating cases at their most infectious. This would make our estimate for cases averted as a result of additional beds conservative.

In the model, patients also sought treatment within their home district. However, in the early stages of the epidemic, several cases admitted to the ETU in Kailahun were from outside the district [20]. This may have increased the benefits of bed introduction, by reducing transmission in locations without treatment beds; it may also have impeded control efforts, by making contact tracing and safe burials more difficult [20]. In addition, faster turnaround time in lab testing may have reduced the time spent in EHC/CCCs before moving to ETUs [22], and led to more EHC beds becoming available per day. While there were occasional details of the number of patients in isolation in different districts in Ministry of Health situation reports [15], overall these data were incomplete. If more complete EHC/CCC/ETU data were available, it would be possible to validate our model estimates for the number of cases hospitalised over time.

Our results also emphasise the highly variable nature of Ebola transmission. Even in retrospect, it was difficult to measure the effect of changes in transmission and additional beds on the number of EVD cases in some areas. It is also likely that the introduction of Ebola facilities helped stimulate other infection control measures, including safe burials and improved contact tracing [3]. In our simulated scenarios, we removed only treatment beds; in practice, a lack of treatment centres would also likely have led to fewer safe burials, and hindered investigation of cases' contacts. With better data on the timing and role of different interventions – both clinical and non-clinical – it would be possible to obtain more accurate estimates about the precise contribution of different factors to the dynamics of EVD in Sierra Leone. In particular, it is important to understand how awareness of EVD influences behaviour during an outbreak [23], and how this change in behaviour might affect disease dynamics [24, 25].

In the absence of such data, we concentrated on the impact of additional treatment beds alone; we assumed the level of community transmission declined regardless of the number of beds. An alternative approach would be to assume that transmission would remain at the same level as was in the early phase of the epidemic [9, 10]. As

our estimate of the basic reproduction number, R_0 , was above one in most districts initially (Table 1), epidemic theory suggests the outbreak would have continued to grow exponentially in these regions under the assumption of no change in transmission, until there were insufficient susceptible individuals for the infection to persist. The corresponding number of cases averted would therefore have been extremely large. However, it not clear that R_0 would have remained unchanged for such a long period of time. Evidence from past EVD epidemics indicates that changes in behaviour can reduce transmission independently of external interventions [23, 26].

Even under our conservative assumption that the introduction of EHC/CCC/ETUs reduced transmission only by isolating more patients, we estimated that around 57,000 cases were averted in Sierra Leone as a result of additional treatment beds. Given that the case fatality rate of Ebola in Sierra Leone is near 70% [16], this suggests that the scale-up of local and international efforts to combat the epidemic is likely to have averted around 40,000 Ebola deaths in the country between June 2014 and February 2015. Moreover, the reduction in Ebola transmission will also have halted the damaging secondary effects of the epidemic, including the suspension of access to maternal health and vaccination programmes [27, 28].

Materials and Methods

Transmission model. To model the effect of treatment beds on Ebola transmission, we used an SEIR framework that incorporated ETUs and EHC/CCCs [8]. We used a relatively simple framework as we were fitting to only a single case time series for each district [14]. In the model, individuals started off susceptible to infection (S). Upon infection with Ebola they entered an incubation period (E), then at symptom onset they became infectious. As there is evidence that not all Ebola cases have been reported [1], we assumed that only a proportion r of newly infectious individuals would eventually be ascertained and seek treatment. This category was denoted I^A . The other proportion $1 - r$ would not be ascertained; this group were denoted I^N . We assumed that it took an average of $1/\tau_r$ days for ascertained cases to be reported to the Ministry of Health. After becoming symptomatic in the model, cases in I^A sought health care in EHC/CCCs (H). They took an average of $1/\tau_H$ days to attend these centres. If no EHC/CCC beds were available, the patient would attend an ETU. If no ETUs bed were available, the patient remained infectious in the community until the infection was resolved (R) i.e. they had recovered, or were dead and buried. Once in an EHC/CCC, patients were tested for Ebola (we assumed this took an average of 2 days) then progressed to an ETU if a bed was available. Patients stayed for an average of $1/\tau_D$ days in an ETU before the disease was resolved (either through recovery or death). The probability Ebola-positive individuals were admitted to an EHC/CCC, p_H , when they attended the centre depended on whether the centre was full or not. We assumed that some patients attending EHC/CCCs were Ebola-negative, which had the effect of reducing the available bed capacity by a factor α . The probability Ebola-positive individuals were admitted to an EHC/CCC upon attendance was therefore:

$$p_H = \begin{cases} 1 & \text{if } \alpha B_H > H \\ 0 & \text{if } \alpha B_H = H \end{cases} \quad [1]$$

where B_H denotes the total capacity of the EHC/CCCs. Likewise, the probability individuals were admitted/transferred to an ETU was:

$$p_U = \begin{cases} 1 & \text{if } B_U > U \\ 0 & \text{if } B_U = U \end{cases} \quad [2]$$

where B_U denotes the capacity of the ETUs. We assumed that the population was initially fully susceptible to infection. We assumed the average latent period, $1/\nu$ was 9.4 days, and the average duration of infectiousness in the community, $1/\gamma$, to be 10.9 days in our main analysis; as a sensitivity analysis we also considered an infectious period of 9 days. The average time from onset-to-outcome for individuals that seek treatment was assumed to be 11.3 days (details in SI Appendix).

We obtained EHC/CCC/ETU opening dates from the Humanitarian Data Exchange [13], and cleaned ambiguous or missing dates using reports from WHO, MSF, UNICEF and other partners. If the precise date of opening, or change in capacity was not known, we used the first date for which we could find confirmation of the centre being open with a given capacity. This could have made our analysis more conservative, as some centres may in reality have opened earlier than we presumed. One field study in Bo estimated that 54% EVD cases made it into the district-level situation

reports [29]; in turn the numbers of cases in these reports are typically slightly lower than the numbers in the final WHO patient database [1]. Therefore we made the assumption that 60% of symptomatic cases were ascertained in our main analysis [4], and considered 40% and 80% ascertainment as a sensitivity analysis. We assumed that it took an average of 4.5 days for these cases to be reported after symptom onset [16]. In the model, the time between onset and attendance of EHC/CCCs declined from 4.6 days to 1.3 days between July 2014 and April 2015 (Fig. S1); the average duration spent in EHC/CCC before moving to an ETU was 2 days; and the average time spent in an ETU was initially 11.3-4.6-2=4.7 days. We assumed that 50% of beds in EHC/CCCs were occupied by Ebola-negative patients [15] (i.e. $\alpha=0.5$). We also allowed community transmission to potentially vary over time by modelling the transmission rate at time t , β_t , as a sigmoid [14, 17]:

$$\beta_t = \hat{\beta} \left(1 - \frac{a_2}{1 + e^{-a_1(t-a_\tau)}} \right) \quad [3]$$

where $\hat{\beta}$, a_1 , a_2 and a_τ were parameters to be fitted. We modelled transmission dynamics using a stochastic model, with environmental noise acting on the transmission rate [30]:

$$dS_t = -\beta_t \xi_t \frac{S_t(I_t^A + I_t^N)}{N} dt \quad [4]$$

$$dE_t = \beta_t \xi_t \frac{S_t(I_t^A + I_t^N)}{N} dt - \nu E_t dt \quad [5]$$

$$dI_t^A = r\nu E_t dt - p_H \tau_H I_t^A dt - (1 - p_H)(1 - p_U) \gamma I_t^A dt + (1 - p_H) p_U \tau_H I_t^A dt \quad [6]$$

$$dI_t^N = (1 - r)\nu E_t dt - \gamma I_t^N dt \quad [8]$$

$$dH_t = p_H \tau_H I_t^A dt - p_U \tau_U H_t dt - (1 - p_U) \tau_F H_t dt \quad [9]$$

$$dU_t = (1 - p_H) p_U \tau_H I_t^A dt + p_U \tau_U H_t dt - \tau_D U_t dt \quad [10]$$

$$dR_t = \gamma I_t^N dt + \tau_D U_t dt + (1 - p_H)(1 - p_U) \gamma I_t^A dt + (1 - p_U) \tau_F H_t dt \quad [11]$$

$$dX_t = r\nu \tau_r E_t dt \quad [12]$$

$$dX_t = r\nu \tau_r E_t dt \quad [13]$$

Here N is the total population size, X_t is the cumulative total of ascertained Ebola cases, β_t is the rate of transmission at time t , and ξ_t is a lognormal (and hence positive) noise term with mean 1 and variance σ :

$$\log(\xi_t) dt = \sigma dW - \frac{\sigma^2}{2} dt \quad [14]$$

where W is Brownian motion [30]. Model structure and parameters are shown in Fig. S6. The model was simulated using the Euler-Maruyama method with intervals of $dt=1/10$ days. Population size N for each district was taken from Sierra Leone census data [31].

Model fitting. We fitted the model to weekly incidence data (i.e. number of new confirmed and probable cases per week) from Sierra Leone reported in the WHO patient database [1]. As described in a previous study, we also used data from the Sierra Leone Ministry of Health [15] when more recent case data were not available in the WHO database [4]. We excluded Bonthe district from the analysis as there were small numbers of confirmed or probable cases, which were spaced several weeks apart. It is therefore unlikely there was sustained transmission in this area. For each of the other districts, we used the first reported week of sustained transmission (i.e. there were cases in that week and the following week) as the first data point in the time series. The last data point for all districts was 2nd February 2015, as the number of cases had declined to minimal levels in most areas by this point. In the model, incidence in week t , denoted x_t , was given by the difference in cumulative reported cases over the previous 7 days i.e. $x_t = X(t) - X(t-7)$. As situation reports were only issued on w out of 7 days in some weeks, we scaled these weeks by a factor $\kappa_t = w/7$. We also included the possibility of variability in the accuracy of reporting in the situation reports. We assumed the number of reported cases in week t followed a negative binomial distribution with mean $x_t \kappa_t$ and variance $\kappa_t(1 - \kappa_t)x_t + \phi^2 \kappa_t^2 x_t^2$ [4].

Model fitting was performed using a particle MCMC algorithm [19] with an adaptive multivariate normal proposal distribution [32]. For each district, we fitted: the initial number of infective individuals (including both ascertained and missed) at the start of the outbreak, $I_0 = I(0)$; the volatility of the transmission rate, σ ;

over-dispersion of reporting, ϕ ; the initial transmission rate $\hat{\beta}$; and the two shape parameters for the transmission rate sigmoid, a_1 , a_2 and a_r . We used uniform positive priors for all parameters, with the exception of a_2 , which we constrained to the interval $(-\infty, 1)$ by imposing reflective boundary conditions during parameter resampling. Posterior estimates for $R_0 = \beta_0/\gamma$, I_0 , σ , ϕ and the 4 sigmoid parameters (taken from 50,000 MCMC iterations, following a burn-in period of 10,000 iterations) are given in Figs. S6–17; the posterior distribution of the sigmoid is shown in Fig. 2 (blue line and shaded region). The model was implemented in R version 3.1.3, and parallelised for multiple districts using the doMC library [33, 34].

Estimating cases averted. To estimate the number of infections averted as a result of control measures, we first estimated the total number of infections (i.e. the cumulative number of individuals who leave the S compartment) up to 2nd February 2015 using the posterior parameter estimates from our fitted model. We define this as the 'baseline scenario'. Next, we assumed that the community transmission rate varied as in the baseline scenario, but no additional EHC/CCC/ETU were introduced.

This was equivalent to assuming that changes aside from bed introductions – such as shifts in behaviour, increased number of safe burials, improved infection control – would have happened regardless of whether additional beds were made available. We ran 1000 bootstrap simulations under this scenario, and compared the total number of infections with the baseline scenario. In our main analysis, we assumed that 60% of cases were ascertained (i.e. $r=0.6$). To test how sensitive our results were to this assumption, we also refitted the model to each district with $r=0.4$ and 0.8, and used these fitted models to estimate the number of cases averted in the two different scenarios above. The results are given in Tables S3–S4.

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Table 1. Estimated number of cases averted up to 2nd February 2015 as a result of additional treatment beds. For each district, we estimated the median number of additional cases that would result in the original fitted model, with community transmission rate varying as Fig. 2. We then considered two scenarios: additional EHC/CCC/ETU beds introduced as in reality, and the same additional beds introduced 4 weeks earlier, and estimated the number of cases averted in each scenario (95% credible interval in parentheses). The median posterior estimates for initial R_0 (95% credible interval in parentheses), and total numbers of additional EHC/CCC/ETU beds introduced in each district are shown for comparison.

District	Initial R_0	Beds introduced	Additional beds	Beds 4 weeks earlier
Bo	1.6 (1.4–1.7)	124	6,310 (4,150–9,040)	6,820 (4,730–9,620)
Bombali	5.2 (2.9–7.9)	506	6,480 (1,800–22,900)	7,630 (2,320–34,500)
Kailahun	8.4 (5.3–16.2)	123	3,650 (2,250–6,750)	4,580 (3,290–7,460)
Kambia	1.5 (1.4–3.6)	55	545 (2–4,430)	748 (4–15,400)
Kenema	7.4 (2.1–19.4)	75	1 (0–10,500)	3 (0–23,800)
Koinadugu	0.7 (0.3–1.1)	92	35 (11–104)	97 (48–206)
Kono	1.6 (1.4–1.9)	83	1,570 (928–2,430)	2,060 (1,490–3,060)
Moyamba	1 (0.9–1.2)	34	130 (77–197)	237 (145–366)
Port Loko	1.8 (1.6–2.2)	546	3,850 (853–13,400)	5,660 (1,180–26,900)
Pujehun	0.5 (0.2–1.2)	24	11 (2–34)	22 (6–55)
Tonkolili	3.5 (1.3–8.4)	349	568 (140–2,900)	959 (272–5,940)
Western Area	2.5 (2.2–2.8)	960	32,600 (25,500–40,200)	39,200 (32,100–47,100)
Total		2971	56,600 (48,300–84,500)	69,100 (59,500–122,000)

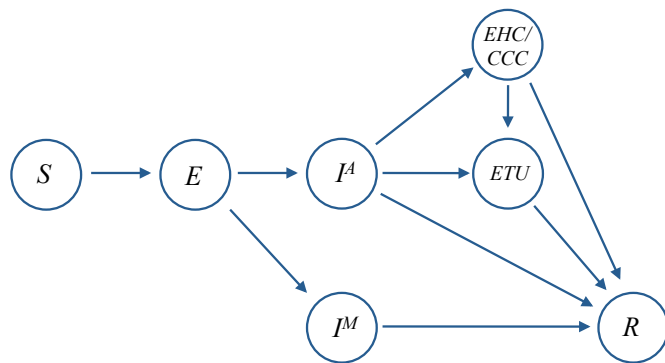


Fig. 1. Model structure. Individuals start off susceptible to infection (S). Upon infection with Ebola they enter an incubation period (E), then at symptom onset they become infectious; these individuals either eventually become ascertained (I^A) or do not (I^M). Individuals who are ascertained initially seek health care in EHC/CCCs (or ETUs if these are full); if no beds are available, they remain infectious in the community until the infection is resolved (R) i.e. they have recovered, or are dead and buried. Patients in EHC/CCCs are transferred to ETUs once they have been tested for Ebola, which takes an average of 2 days. Patients remain in ETUs until the infection is resolved. We assume the latent period is 9.4 days, the average time from onset to EHC/CCC attendance declines from an initial value of 4.6 days (Fig. S1), and individuals who do not seek treatment are infectious for 10.9 days on average (details in SI Appendix).

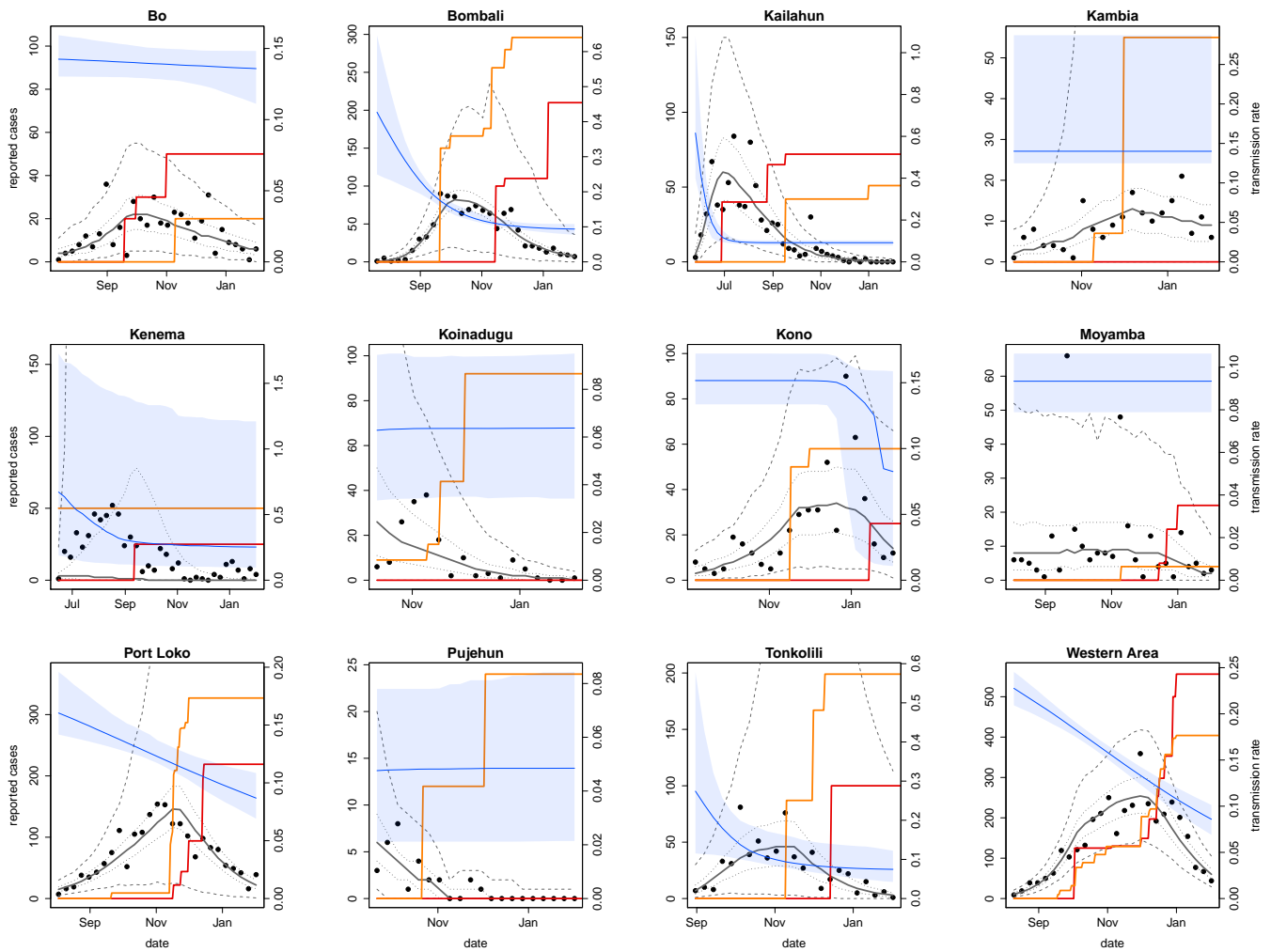


Fig. 2. Community transmission and bed capacity in Sierra Leone over time. Blue line shows estimated median community transmission rate, shaded area shows 95% credible interval (right hand axis). Black dots show weekly reported confirmed and probable cases in each district up to 2nd February 2015 (left hand axis). Gray line shows median number of cases generated from 1000 simulations of the fitted model, with 50% credible intervals given by dotted gray lines and 95% intervals given by dashed lines. Solid red line, ETU bed capacity; orange line, EHC/CCC bed capacity.