Response to reviewers

We thank the two reviewers for their pertinent, constructive and positive comments. These comments have helped us make several improvements to the paper, particularly in terms of clarifying details within the Materials and Methods and Annex 2. We include with this resubmission a file called diff.pdf, which uses colour to highlight changes within the paper. We have also made cosmetic changes to figure 1.

Reviewer 1 (Hetsron Nyandjo Bamen)

(1) Page 3, Line 82: Since that some parameters of your model are random process, we are not longer talking about a system of ordinary differential equations but a system of random ordinary differential equations.

- The reviewer has questioned our use of terminology in the very first line of the section describing our mechanistic model. We confirm that what we originally wrote in the paper is correct, that our system *is* a system of ordinary differential equations. We are unsure why the reviewer thought that the system invovled stochastic parameters, so we have modified the sentence to emphasise that the model is indeed deterministic. Moreover, in the section "Limitations and future research" we re-emphasise that the model neglects stochasticity.

(2) Mechanistic Model(Page 3;4): Describe the infection process.

- We have modified the second paragraph of the section entitled **Mechanistic Models** (page 3). We have also clarified the notation I_Σ following it's use in equations 1-19.

(3) Table 2: Describe the choice of the other prior distributions except the three described in Annex 2.

- Desciptions of all priors are now included in annex 2. We also changed the header of column 3 in table 2 to include constants.

(4) Page 6, Equation (3): What is Σ in I_Σ ?

- We thank the reviewer for spotting this omission of detail. We have added, just after equations 1-19, that I_Σ is the total density of all infectious bats.

(5) Page 6, Equation (20) and (21): Highlight the dependency of $\widetilde{\mu}$ with time. It should be $\widetilde{\mu}_A(t)$ and $\widetilde{\mu}_Y(t)$.

- We prefer to keep the mathematical notation as simple as possible, and have therefore chosen not to included (t) every time we represent density dependance in mortality. The $\sim$ notation is intended to indicate density dependance, which in a dynamic model is always time-varying. We have added a sentence following equation 21 to clarify this point.

(6) Page 6, Equation (22): Maybe it is a typo. Otherwise clarify the difference between S_A and $\mathcal{S}_A$. There is a confusion in the whole manuscript.

- We have changed the font for annual survival (now $\boldsymbol{\mathcal{S}}$) in order to generate contrast with the symbol for survival function ($\mathcal{S}$) and with the S used for susceptibles. We have also text in the materials and methods where we introduce and use $\boldsymbol{\mathcal{S}}$ and $\mathcal{S}$.

(7) Page 7, line 120: Explain the reason of choosing the start of the year 2017 as initial time despite the fact your data started in December 2018 (Table 1).

- We have restructured this paragraph, adding two sentences justifying our choice of starting simulations in 2017.

(8) Page 8, line 131: its carrying capacity. . . (not it's).

- Corrected

(9) Page 16: The gap between the current results and the previous one is not well supported.

- It is unclear which results gap the reviewer is refering to. If they are refering to the estimated short duration of maternal anti-bodies, compared to the Epstein et al 2013 study, well that study considered a different bat-virus system so we would not expect to replicate their results. If the reviewer is refering to the estimated short duration of antibodies, compared to Peel et al 2018, again, that study did not consider the same virus and so replication would not be expected. If the reviewer is refering to the mismatch between PCR and serology results, then we agree that there is a paradox and have dedicated an entire page to discussing this paradox (pages 17-18) - indeed, the other

reviewer noted that "The authors suggest many possible explanations to this apparent discrepancy."

(10) Page 18 and 19: Recommendations suggested in the limitations will required a lot of resources. Is it realistic to build such models

- It is clear that logitudinal sampling of bats is resource intense. However, it is also important for modellers to be honest about the sorts of data that they require in order for us to advance in characterising the dynamics in bat-virus systems. In other bat-virus systems (coronaviruses in Rhinophilus species, for example) non-invasive methods, such as guano sampling, can provide a less resource intensive alternative to sampling live bats. For example, in La Reunion a team has been collecting bat guano each month for six years providing a unique dataset for modelling, whilst also contributing to the surveilance of potentially zoonotic viruses. A realistic way forward is to exploit synergies between the needs of public health surveillance and research in disease ecology, in order to provide attractive solutions for funders interested in financing One Health initiatives.

Reviewer 2 (Anonymous)

My main comment is related to a choice of notation that would require some clarification in my opinion. Indeed, the notation S_A in the section "Mechanistic model" corresponds to the number of susceptible adults in the population. This notation is also used just before equation 22 to describe the survival over one year of adults. In equation 22, it is also used to describe $S_A(t)$, the survival probability which implicitly depends on time (i.e. the survival probability over time t). I think that using the same notation for so many different concepts can confuse the reader (actually, it did in my case). I would suggest to (i) use different notations for survival probabilities and number of susceptible adults, and (ii) use different notations when a survival probability describes the survival over one year and when it describes the survival over a time-lag (or maybe use a common notation $S_A(t)$ with $S_A(52)$ corresponding to annual probabilities).

- We agree with both reviewers that the notation for survival, annual survival and susceptibles was confusing. As described in our response

to reviewer 1, we have modified the notation to employ clearer fonts to distinguish between these three different entities. We have also added a footnote (following equation 22) to clarify these differences.

I would be curious to know approximately the duration of the MCMC simulations (40 million iterations).

- From memory, these MCMC simulations took between two to three days on a HP Z440 work station.

Section "Probability of not sampling an infectious bat. The model identify a high probability of infectious individual around week 31 (thus end of July). The authors may wish to note that this date is very consistent with table 1, where a simple visual examination suggests that the proportion of positive animals increase suddenly increases at this approximate date (July 17).

- We agree with the reviewer. Based on the raw data we knew that there was massive seroconversion occuring in July and August - this was discussed already in Djomsi et al 2022. A key aim of the model was to explore in details the dynamics of the seroconversion and the mismatch with the PCR results – these aims required fitting a mechanistic model in order to quantify the dynamics within the viral transmission system.

I noted that the survival probability of animals did not depend on whether they were infected by Ebola virus or not. I am not a specialist of Ebola: is it a reasonable assumption?

- It is. Firstly, no mortality events have ever been observed in the wild. Secondly, experimental infection in bats with Ebola viruses have shown several species of bats are tolerant to Ebola infection. For example, Paweska et al (2016) infected 24 Rousettus aegyptiacus with Ebolavirus and concluded that "No mortality, morbidity or gross pathology was observed in these bats."