Derivation of equation 7

The following is the derivation of equation 7 in the main text. Please note, full details can be found in [1] and that this simplified model and these assumptions are only used as a way to estimate the transmission coefficient parameter, β , and not to model the filovirus dynamics within bats *per se*. The basic model is a susceptible (*S*), infected (*I*), recovered (*R*) model.

The assumptions are that infection transmission is direct, horizontal and not vertical (*in utero*), and that individuals are born susceptible (*S*), then infected (*I*) and recover from infection, with life-long immunity (*R*). Here age homogeneity is assumed and thus parameters are constant with respect to age. Births occur at a rate *b*, deaths at rate μ , infections at rate λ and recovery from infection at rate *v*, with no disease-induced mortality. The population size is assumed to be constant and thus the population birth rate, *b*, is assumed to be equal to the mortality rate, μ .

This leads to the following differential equation for the SIR system:

$$\frac{dS(t)}{dt} = \mu N - \beta I(t)S(t) - \mu S(t)$$
(S1)
$$\frac{dI(t)}{dt} = \beta I(t)S(t) - \nu I(t) - \mu I(t)$$

$$\frac{dR(t)}{dt} = \nu I(t) - \mu R(t)$$

By dividing the variables by the population size, N, the number susceptible S, becomes the fraction s, number infected I the fraction infected, i, and likewise for the recovered (R becomes r). As noted in [1], the transmission then becomes frequency-dependent (and see [2]). However, though the units of the β change, because the population size is constant the two terms are the same in this instance [1]. Following [1], I use the $\tilde{\beta}$ to denote the change in units and that $\tilde{\beta}$ now reflects βN .

This division leads to the revised set of differential equations, with the population now in proportions (s, i, and r):

$$\frac{ds(t)}{dt} = \mu - \tilde{\beta}i(t)s(t) - \mu s(t)$$
(S2)
$$\frac{di(t)}{dt} = \tilde{\beta}i(t)s(t) - \nu i(t) - \mu i(t)$$

$$\frac{dr(t)}{dt} = \nu i(t) - \mu r(t)$$

This simple set of differential equations is what allows equation 7 in the main text to be derived. Assuming the system is at equilibrium (∞), ds(t)/dt = di(t)/dt = dr(t)/dt = 0. The term for the infected class becomes:

$$\frac{di(t)}{dt} = 0 \to \tilde{\beta}i(t)s(t) - \nu i(t) - \mu i(t) = 0 \to i(t)(\tilde{\beta}s(t) - \nu - \mu) = 0 \to i(\infty) = 0, (S3)$$

$$or\left(\tilde{\beta}s(t) - \nu - \mu\right) = 0 \to s(\infty) = \frac{(\nu + \mu)}{\tilde{\beta}}$$
(S4)

Thus, the term:

$$S(\infty) = \frac{(\nu + \mu)}{\tilde{\beta}} = \frac{1}{R_0}$$
(S5)

To derive the term for $i(\infty)$ the term for $s(\infty)$ is simply substituted into the $i(\infty)$ term di(t)/dt=0 and rearranged so that:

$$\frac{ds(t)}{dt} = 0 \to i(\infty) = \frac{\mu}{\tilde{\beta}}(R_0 - 1)$$
(S6)

This leads to the final equation 7 in the main text, where:

$$s(\infty) = \frac{1}{R_0}$$
, and $i(\infty) = \frac{\mu}{\tilde{\beta}}(R_0 - 1)$ (S7)

Sensitivity analysis

The partial-rank correlation coefficients (PRCC) between each parameter and model output determined the relative importance of each parameter. In a *K*+1 by *K*+1 symmetric matrix, *C*, where *K* is the number of parameters, and 1 to *N* is the rank of each column defined by the set (r_{1i} , r_{2i} , ..., r_{ki} , R_i), where i = run number, $\mu =$ the average rank ((1+N)/2), the matrix *C* is defined with elements C_{ij} , such that:

$$C_{ij} = \frac{\sum_{t=1}^{N} (r_{it} - \mu)(r_{jt} - \mu)}{\sqrt{\sum_{t=1}^{N} (r_{it} - \mu)^2 \sum_{s=1}^{N} (r_{js} - \mu)^2}} \quad i, j = 1, 2, \dots K.$$
(S8)

 R_i replaces r_{ij} and r_{is} for the C_j , $_{K+1}$ elements, and the inverse of C becomes b_{ij} for matrix B. The PRCC between the *i*th parameter and yth variable is then:

$$PRCC_{iy} = \frac{-b_{i,K+1}}{\sqrt{b_i b_{K+1,K+1}}}$$
(S9)

In the PRCC analysis a positive PRCC indicates that as the parameter increases, virus persistence in the population increases and a negative PRCC indicates virus persistence decreases with increasing parameter values [3, 4]. Significance (t_{iy}) of PRCC_{iy} is determined by a student's *T* distribution with *N*-2 degrees of freedom, thus:

$$t_{iy} = PRCC_{iy} \sqrt{\frac{N-2}{1-PRCC_{iy}}}$$
(S10)

Supplementary Figures

Figure S1: The periodic Gaussian function used to model seasonal births. A fixed birth rate of close to 1 birth per female per year (0.49 per capita per year) with synchrony (s), from 1.43 (low synchrony, dotted lines) to 143.5 (high synchrony, dashed lines) (the range used in the partial rank correlation coefficient sensitivity analysis), with the default for the analyses (14.35, solid lines) shown. One (grey) or 2 (black) birth pulses (ω) per year are shown.



Figure S2: The proportion of 500 simulations for which filovirus infection was present after 25 years for different population sizes. Models have either 1 (a and b) or 2 (c and d) birth pulses per year and with two different incubation periods $(1/\sigma)$ estimated from data. The remaining parameter values are given in Table 1.





Figure S3: The mean prevalence (a), antibody prevalence (seroprevalence, b) and probability of persistence (c) predicted by the model for a range of population sizes. These are calculated from 500 simulations after a 25 year model run for different population sizes with 2 birth pulses per year and a 21 day incubation period $(1/\sigma)$. Adult (close circles) and juvenile (open circles) seroprevalence is shown in b. Remaining parameters are in Table 1.



Figure S4: Sensitivity analysis results using partial rank correlation coefficients (PRCC) for the output variable infection persistence. Parameter values and results are in Table 1. Infection persistence was calculated as the proportion of the 500 simulations infection was present after a 25 year time period for each of the 500 parameter sets. Positive PRCC indicate increasing a parameter increases virus persistence. Parameters are: transmission rate β ; adult mortality rate μ ; juvenile mortality rate δ ; disease induced mortality α ; 1/incubation period σ ; carrying capacity *K*; rate of seroconversion τ ; annual birth synchrony s (where increasing s increases synchrony) and offset during the year φ . Significance at $\alpha = 0.05$ is demarcated by the (red) dashed line.



Figure S5: The effect of altering the incubation period $(1/\sigma)$ and infectious period $(1/\tau)$ on pathogen persistence (z axis and panel). Persistence was estimated as the proportion of 500 simulations for which filovirus infection was present after 25 years for 100 incubation $(1/\sigma)$ – infectious period $(1/\tau)$ combinations. All simulations had 2 annual birth pulses per year and the remaining perameters were the default parameters given in Table 1.



Figure S6: The proportion of bats seropositive with 95% confidence limits reported for 40 bat species. Those species with two or more seasonal birth pulses are in plotted in (a) and those with one annual birth pulse in (b). See Table S1 for details. Where a species is named twice, results for *Ebolavirus* and *Marburgvirus* are presented separately.



Supplementary Tables

Table S1: Serological findings for filovirus - bat systems.

virus	bat species	antibody positive	number tested	annual birth pulses	virus reference	birth pulse reference
Marburgvirus	Epomops franqueti	2	679	2	[5]	[6]
Marburgvirus	Hypsignathus monstrosus	1	103	2	[5]	[7]
Marburgvirus	Miniopterus pusillus	1	177	NA	[5]	
Marburgvirus	Rhinolophus eloquens	20	209	NA	[8]	
Marburgvirus	Rousettus aegyptiacus	21	229	2	[5]	[9]
Marburgvirus	Rousettus aegyptiacus	35	156	2	[8]	[9]
Marburgvirus	Rousettus aegyptiacus	13	546	2	[10]	[9]
Marburgvirus	Rousettus aegyptiacus	29	438	2	[11]	[9]
Marburgvirus	Rousettus aegyptiacus	250	1622	2	[9]	[9]
Marburgvirus	Hipposideros caffer	0	10	1	[5]	[12]
Marburgvirus	Hipposideros commersoni	0	16	1	[5]	[13]
Marburgvirus	Nycteris hispida	0	1	1	[5]	* [14]
Marburgvirus	Lissonycteris angolensis	0	3	2	[5]	[15]
Marburgvirus	Miniopterus inflatus	0	34	1	[5]	[16]
Reston	Cynopterus sphinx	2	2	2	[17]	[18, 19]

ebolavirus						
Reston ebolavirus	Hipposideros pomona	3	37	1	[17]	[20]
Reston ebolavirus	Miniopterus schreibersii	2	23	1	[17]	[21]
Reston ebolavirus	Myotis pilosus	4	83	NA	[17]	
Reston ebolavirus	Pipistrellus pipistrellus	4	35	1	[17]	[22]
Reston ebolavirus	Rousettus amplexicaudatus	5	16	2	[23]	[24]
Reston ebolavirus	Rousettus leschenaultii	11	126	2	[17]	[25]
Reston ebolavirus	Scotophilus kuhlii	1	25	1	[17]	[26]
Reston ebolavirus	Rousettus leschenaultii	15	141	2	[27]	[25]
Reston ebolavirus	Hipposideros cineraceus	0	111	NA	[17]	[28]
Reston ebolavirus	Hipposideros armiger	0	41	1	[17]	[29]
Reston ebolavirus	Hipposideros larvatus	0	21	1	[17]	[30]
Reston	Rhinolophus affinis	1	69	1	[17]	[26]*

ebolavirus						
Reston	Rhinolophus	0	15	1	[17]	[31]
ebolavirus	ferrumequinum					
Reston	Rhinolophus sinicus	0	6	1	[17]	* [26]
ebolavirus						
Reston	Rhinolophus pusillus	0	14	1	[17]	* [26]
ebolavirus						
Reston	Rhinolophus pearsonii	0	3	1	[17]	* [26]
ebolavirus	I I I I I I I I I I I I I I I I I I I			1	[1,]	[20]
Reston	Mvotis davidii	0	5	1	[17]	[26]
ebolavirus	niyons aavaar					[-~]
Reston	Mvotis chinensis	0	6	NA	[17]	
ebolavirus						
Reston	Mvotis daubentonii	0	24	1	[17]	[32]
ebolavirus						
Reston	Myotis fimbriatus	0	2	NA	[17]	
ebolavirus						
Reston	Eonycteris spelaea	0	5	2	[23]	[33]
ebolavirus						
Reston	Cynopterus brachyotis	0	35	2	[23]	[26]
ebolavirus						
Reston	Ptenochirus jagori	0	38	2	[23]	[34]
ebolavirus						
Reston	Haplonycteris fischeri	0	6	1	[23]	[35, 36]

ebolavirus						
Reston ebolavirus	Macroglossus minimus	0	2	2#	[23]	[26]
Reston ebolavirus	Rhinolophus rufus	0	2	1	[23]	[26]*
Reston ebolavirus	Rhinolophus arcuatus	0	1	1	[23]	[26]*
Reston ebolavirus	Emballonura alecto	0	9	NA	[23]	
Reston ebolavirus	Pipistrellus javanicus	0	2	3	[23]	[37]
Reston ebolavirus	Scotophilus kuhlii	0	5	1	[23]	[26]
Reston ebolavirus	Miniopterus australis	0	8	1	[23]	[38]
Reston ebolavirus	Miniopterus schreibersii	0	8	1	[23]	[21]
Reston ebolavirus	Miniopterus tristis	0	1	1	[23]	[26]*
Reston ebolavirus	Hipposideros diadema	0	1	1	[23]	[39, 40]
Reston ebolavirus	Miniopterus macrotarsus	0	1	NA	[23]	
Zaire ebolavirus	Eidolon helvum	1	262	1	[41]	[42]

Zaire ebolavirus	Epomops franqueti	36	805	2	[5]	[26]
Zaire ebolavirus	Epomops franqueti	20	355	2	[43]	[26]
Zaire ebolavirus	Epomops franqueti	5	370	2	[43]	[26]
Ebolavirus [¶]	Epomops franqueti	10	27	2	[44]	[26]
Zaire ebolavirus	Epomops franqueti	8	17	2	[45]	[26]
Ebolavirus [¶]	Epomophorus gambianus	14	37	2	[44]	[46]
Zaire ebolavirus	Hypsignathus monstrosus	9	125	2	[5]	[47]
Zaire ebolavirus	Hypsignathus monstrosus	9	44	2	[43]	[47]
Zaire ebolavirus	Hypsignathus monstrosus	4	67	2	[43]	[47]
Ebolavirus [¶]	Hypsignathus monstrosus	7	16	2	[44]	[47]
Zaire ebolavirus	Hypsignathus monstrosus	4	17	2	[45]	[47]
Zaire ebolavirus	Micropteropus pusillus	4	197	2	[5]	[26]
Zaire ebolavirus	Myonycteris torquata	19	573	2	[5]	[26]
Zaire ebolavirus	Myonycteris torquata	1	323	2	[43]	[26]
Zaire ebolavirus	Myonycteris torquata	9	231	2	[43]	[26]
Zaire ebolavirus	Myonycteris torquata	4	58	2	[45]	[26]
Zaire ebolavirus	Rousettus aegyptiacus	24	307	2	[5]	[48]

Zaire ebolavirus	Rousettus leschenaultii	15	141	2	[27]	[26]
Ebolavirus [¶]	Nanonycteris veldkampii	1	4	Not seasonal	[44]	[26]
Ebolavirus [¶]	Epomops buettikoferi	0	1	NA	[44]	

* based on records for related species in the region. [#]Not seasonal at lower latitudes. [¶] Initial

screening results using R-EBOV and Z-EBOV antigen ELISAs are used here. See [44] for

further details.

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