

Estimating the impact of sarcoptic mange epidemic on the population size of wild raccoon dogs (*Nyctereutes procyonoides*) from wildlife rescue data

Ryota Matsuyama^{a,*}, Nobuhide Kido^{b,2}, Ryosuke Omori^{c,**,1}

^a School of Veterinary Medicine, Rakuno Gakuen University, 582 Midorimachi, Bunkyo-dai, Ebetsu, 069-0836, Japan

^b Kanazawa Zoological Gardens, 5-15-1, Kamariyahigashi, Kanazawa-ku, Yokohama, 236-0042, Japan

^c International Institute for Zoonosis Control, Hokkaido University, Kita-20, Nishi-10, Kita-Ku, Sapporo, 001-0020, Japan

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ABSTRACT

The impact of infectious diseases on host populations is often not quantified because it is difficult to observe the host population and infectious disease dynamics. To address this problem, we developed a state-space model to simultaneously estimate host population and disease dynamics using wildlife rescue data. Using this model, we aimed to quantify the impact of sarcoptic mange on a Japanese raccoon dog population by estimating the change in their relative population size. We classified the status of rescued raccoon dogs into four categories: i) rescued due to infection with mange, ii) rescued due to traffic accidents without mange, iii) rescued due to traffic accidents with mange, and iv) rescued due to causes other than traffic accidents or mange. We modelled the observation process for each category and fitted the model to the reported number of raccoon dogs rescued between 1990 and 2010 at three wildlife rescue facilities in Kanagawa Prefecture, Japan. The mortality rate induced by mange was estimated to be 1.09 (95% credible interval (CI): 0.47–1.72) per year. The estimated prevalence of sarcoptic mange ranged between 4 and 80% in the study period. When a substantial prevalence of mange was observed (1995–2002), the host population size decreased by 91.2% (95% credible intervals: 86.3–94.7). We show that the impact of infectious disease outbreak on the wildlife population can be estimated from the time-series data of wildlife rescue events due to multiple causes. Our estimates suggest that sarcoptic mange triggered a substantial decrease in the Japanese wild raccoon dog populations.

1. Introduction

Estimating population size of wildlife is important in the context of their conservation and management. Furthermore, the population size of wildlife should be measured for disease control to estimate the probability of transmission in the case that the wildlife is involved as a host species (Artois et al., 2009; Sweetapple and Nugent, 2018). Several factors affect the change in the population size of wildlife; as one of them, outbreaks of infectious diseases affect host population size (McCallum and Dobson, 1995; De Castro and Bolker, 2005; Salkeld et al., 2023). As a classical example, a large population crash of wild or introduced free-ranging rabbits was observed owing to an outbreak of the myxoma virus in the US, European countries, and Australia (Fenner, 1953; Alves et al., 2019). In addition, numerous emerging infectious

diseases caused a decline in the population size of endangered species and important species as a disease reservoir, such as white nose syndrome in little brown myotis (*Myotis lucifugus*) (Frick et al., 2010), canine distemper in lions (*Panthera leo*) (Roelke-Parker et al., 1996), African swine fever in wild boar (*Sus scrofa*) (Morelle et al., 2020), and peste des petits ruminants in saiga antelopes (*Saiga tatarica*) (Pruvot et al., 2020). The impact on host population size by infectious disease outbreak should be elucidated qualitatively and quantitatively.

Sarcoptic mange (hereinafter, mange) is one of the diseases that can give influence on host population. Mange is caused by the pathogenic mite *Sarcoptes scabiei* (Pence and Ueckermann, 2002). *S. scabiei* is maintained in a multi-mammalian host system (Alasaad et al., 2013; Matsuyama et al., 2019) and detected from more than 140 mammalian species (Escobar et al., 2022). In particular, mange is associated with

* Corresponding author.

** Corresponding author.

E-mail addresses: r-matsuyama@rakuno.ac.jp (R. Matsuyama), omori@cvc.hokudai.ac.jp (R. Omori).

¹ Ryota Matsuyama and Ryosuke Omori contributed equally to this work.

² Present address: M.S.K Inc. Dai3-Tendai Building 2F 4-9-1, Higashienokicho, Shinjuku-ku, Tokyo 162-0807, Japan.

high morbidity and mortality in many canid species, such as: coyotes (*Canis latrans*) (Pence et al., 1983; Pence and Windberg, 1994; Chronert et al., 2007), red foxes (*Vulpes vulpes*) (Soulsbury et al., 2007; Uruguchi et al., 2014; Willebrand et al., 2022), and raccoon dogs (*Nyctereutes procyonoides*) (Kido et al., 2013; Kołodziej-Sobocińska et al., 2014; Matsuyama et al., 2015) and ruminants, such as: Iberian ibex (*Capra pyrenaica*) (León-Vizcaíno et al., 1999), vicuña (*Vicugna vicugna*) and guanaco (*Lama guanicoe*) (Ferreira et al., 2022). The impacts of mange on host population have been discussed based on the decline in the population abundance index estimated by a field survey (Martin et al., 2018; Ferreira et al., 2022), hunting bags (Mörner, 1992; Shibata and Kawamichi, 1999; Soulsbury et al., 2007) and number of reported cases including rescued animals (Kido et al., 2013; Cypher et al., 2017). Meanwhile, simulation (Willebrand et al., 2022) and modelling (Leung and Grenfell, 2003; Lunelli, 2010; Uruguchi et al., 2014; Beeton et al., 2019) using well-studied ecological data are also applied to understand the impact of mange on its host population.

To quantitatively assess the impact of infectious diseases on wildlife populations (Barroso et al., 2024), the dynamics of: i) the host population and ii) disease outbreaks should be obtained. Although the population size of endangered species, invasive alien species, or important species for game or wildlife damage management were analyzed, the population size of most species were not (Witmer, 2005). Furthermore, surveillance and monitoring of wildlife diseases are often not sufficiently implemented. It is challenging to estimate the impact of infectious diseases on wildlife populations. The development of more feasible framework is necessary in the absence of observation regarding the dynamics of host population and infectious diseases (Barroso et al., 2024).

Unobservable population dynamics have been estimated using statistical models such as the state-space model (SSM) (Buckland et al., 2004; Newman et al., 2006). The SSM is composed of two parts: i) the latent process describing the system of chronological change in the host population and ii) the observation process characterizing the generating process of observational data. As in the case of wildlife population size estimation, the latent process is the time-series change in wildlife population size (which is characterized and modulated by demographic parameters such as growth rate), and observational data are provided as population abundance indices, such as the number of hunted animals per hunting activity (Buckland et al., 2004). The SSM has also been used to estimate the dynamics of infectious diseases. The dynamics of infectious diseases can be measured by the time-series change of infected population. Since a lot of surveillance do not capture all infected individuals, it can be the latent process behind observed surveillance data (Cooper and Lipsitch, 2004).

Wildlife rescue activities involves the treatment and release of injured wildlife. When wildlife rescue facilities receive rescued animals, their health status is typically recorded. Wildlife rescue activities have an aspect of the surveillance of infectious diseases in local wildlife populations (Trocini et al., 2008; Camacho et al., 2016; Kelly et al., 2021; Miller et al., 2023). Furthermore, given that their rescue activities are stable, medical records of rescued animals should contain information related to trend in the population size of rescued animal over time. Thus, using data on the infection status and the number of rescued animals, disease and host population dynamics can be estimated, and subsequently, the impact of infectious diseases on wildlife populations can be quantified.

This study aimed to develop a method to quantify the impact of infectious diseases on wildlife populations using a SSM and wildlife rescue data. Using this method, we estimated the impact of sarcoptic mange epidemic on the population size of Japanese raccoon dogs (*Nyctereutes procyonoides viverrinus*) using medical records from wildlife rescue facilities in Japan.

2. Materials and methods

2.1. Model

The concept of our SSM for estimating impact of epidemic from wildlife rescue data is illustrated in Fig. 1. As for the latent process, in our previous studies (Matsuyama et al., 2021, 2022), we developed a mathematical model to derive the relation between the dynamics of Japanese wild boar and an infectious disease (classical swine fever). Using the population size of the host animal at time t , $N(t)$, and the number of infected animals at time t , $I(t)$, the host population dynamics during the epidemic can be written as

$$\frac{dN(t)}{dt} = r(t)N(t) - \mu_d I(t), \quad (1)$$

where $r(t)$ and μ_d are the population growth rate of the host animals and the mortality rate induced by the disease, respectively. The population growth rate is defined by the birth and natural mortality rates at time t . Taking the variation in population growth between different years into account, we assume that the growth rate follows a certain probability distribution (e.g., $r(t) \sim r + \varepsilon(t)$, $\varepsilon(t) \sim N(0, \sigma^2)$, where r is the average growth rate and $\varepsilon(t)$ is the variation of growth rates at time t which follows a normal distribution with mean = 0 and variance = σ^2). By integrating Equation (1), $N(t)$ can be written as

$$N(t) = N(0) \exp \left(\int_{\tau=0}^t r(\tau) d\tau - \mu_d \int_{\tau=0}^t \frac{I(\tau)}{N(\tau)} d\tau \right), \quad (2)$$

where $I(\tau)/N(\tau)$ in equation (2) denotes the proportion of infected individuals at time τ (i.e., prevalence of the disease). Hereafter, we add the notation $q(t)$ to express the proportion of infected individuals $I(t)/N(t)$. Equation (2) demonstrates the latent process (i.e., change in the host population size).

Regarding the observation process of infected/non-infected animals through wildlife rescue, host animals are rescued not only by infection but also by several other causes, such as car accidents, trauma, and poisoning (Miller et al., 2023). Let p_i and D be the relative frequency of rescue incidences by cause i and the sets of rescue causes with disease conditions, respectively. The probability of rescue by cause i can be modelled by the product of p_i and the probability of disease infection at time t (which can be described using the prevalence, $q(t)$):

$$(\text{Number of rescued animals by cause } i) \propto \begin{cases} N(t)p_i q(t) & (\text{if } i \in D) \\ N(t)p_i(1 - q(t)) & (\text{if } i \notin D) \end{cases} \quad (3)$$

The aim of this study was to estimate the impact of infectious diseases on host population size by estimating host population and disease dynamics. We focused only on the relative change of population size with respect to time or rescue cause. We set $N(0)p_1 = 1$ as baseline of rescue population size.

2.2. Data and model settings for sarcoptic mange in Japanese raccoon dogs

Data on rescued raccoon dogs were extracted from Kido et al. (2013) as shown in Fig. 2, demonstrating the number of rescued raccoon dogs and the causes of their rescue in 1989 and 2010 at wildlife rescue facilities in Yokohama, Japan. As shown in Fig. 2, the reasons for rescue were as follows: i) infection with mange, ii) car accident with mange infection, iii) car accident without mange infection, and iv) other reasons, such as the protection of pups isolated from their parents. The number of rescued raccoon dogs showed two peaks: a large peak in 1995 and a small peak in 2009. The first case of a mangy raccoon dog was reported in 1987, with no subsequent detection until 1991. The sudden increase in the number of mangy animals began in 1993. For our analysis, we used data from 1990 (Fig. 2).

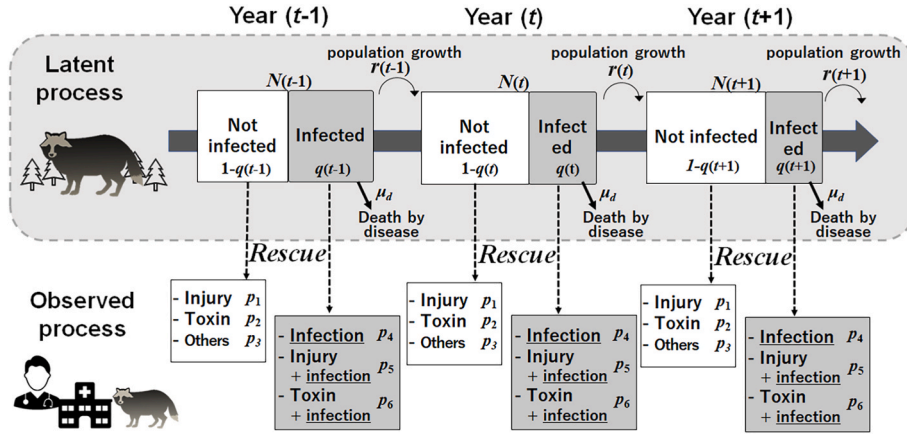


Fig. 1. State-space model for wildlife rescue data. The upper grey area illustrates the latent process, which consists of host population dynamics and disease dynamics. The host population dynamics are modulated by the population growth and mortality of the infected fraction of the population. The observed process demonstrates that wildlife rescue provides the observation of animals with a certain rescue cause. $N(t)$, $r(t)$, $q(t)$, μ_d , p_1 , p_2 , p_3 , p_4 , p_5 , and p_6 denote the population size, population growth rate, proportion of infected animals (i.e., prevalence of the disease), disease induced mortality rate, relative frequency of rescue due to cause 1 (injury), cause 2 (toxin), cause 3 (others), cause 4 (infection), cause 5 (injury with infection), and cause 6 (toxin by infection) at time t , respectively. The rescue cause categories shown in this figure are examples and any other rescue cause can be incorporated in the model.

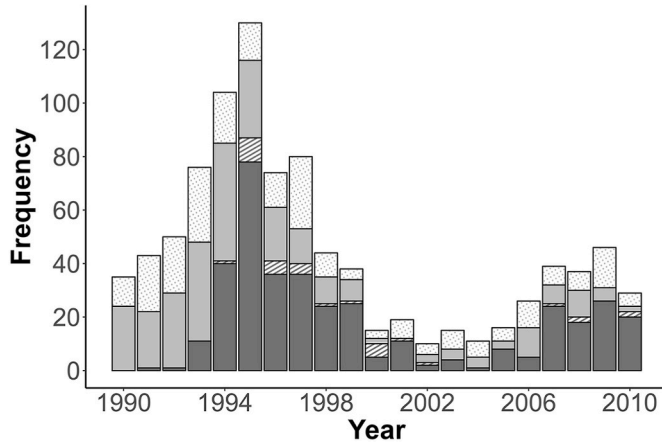


Fig. 2. Yearly number of rescued Japanese raccoon dogs and the cause of rescue at wildlife rescue facilities in Yokohama, Japan. The original figure is cited as Fig. 2 in Kido et al. (2013). Grey, stripe-pattern, light grey, and dot-pattern bars denote the number of rescued animals due to sarcoptic mange (mange), car accidents with mange, car accidents without mange, and causes other than car accidents and mange, respectively.

We constructed a model regarding the time series of four rescue events occurrences: the number of animals that were rescued due to infection with mange at time t , $\hat{M}(t)$; the number of those without mange infection and rescued due to injury from traffic accidents at time t , $\hat{C}(t)$; the number of those with mange infection and rescued due to traffic accidents at time t , $\hat{C}_m(t)$; and the number of those rescued due to other reasons, $\hat{O}(t)$. These events can be written as

$$\hat{M}(t) = p_1 N(t) q(t), \quad (4)$$

$$\hat{C}(t) = p_2 N(t) \{1 - q(t)\}, \quad (5)$$

$$\hat{C}_m(t) = p_3 N(t) q(t), \quad (6)$$

$$\hat{O}(t) = p_4 N(t) \{1 - q(t)\}, \quad (7)$$

where $N(t)$ denotes the population size of raccoon dogs at time t and $q(t)$ denotes the proportion of infected animals at time t . p_1 , p_2 , p_3 , and p_4

denote the relative frequency with which a mangy raccoon dog is rescued due to mange infection, a non-mangy raccoon dog is rescued due to an injury from a traffic accident, a mangy raccoon dog is rescued due to an injury from a traffic accident but not due to mange infection, and a non-mangy raccoon dog is rescued due to causes other than traffic accidents and mange infections, respectively. Note that $N(t)$ is modelled by Equation (2) and discretized as

$$N(t) = N(0) \exp \left(\sum_{s=0}^t r(s) - \mu_d \sum_{s=0}^t \frac{I(s)}{N(s)} \right), \quad (8)$$

to handle observed yearly data. Since the prior information on the population growth rate, $r(t)$, among Japanese raccoon dogs was not available, we employed three modelling approaches; i) estimating $r(t)$ by assuming that they have a constant value r_c (Model 1), ii) estimating $r(t)$ by assuming that they are normally-distributed (Model 2), and iii) assuming a constant value $r_u = 0.148$, which is an average growth rate among Ussuri raccoon dogs in Finland (*Nyctereutes procyonoides ussuriensis*) extracted from a literature (Kauhala and Helle, 1995) (Model 3). Regarding Model 2, we modelled the yearly variation in growth using a non-centered parameterization of a normal distribution (Papaspiliopoulos et al., 2007) as follows:

$$r(t) = \bar{r} + \sigma \epsilon, \quad (9)$$

where \bar{r} is the average growth rate, $\sigma \epsilon$ describes the variation of growth rate, and ϵ follows a normal distribution with mean = 0 and variance = 1.

Assuming that the time series of the rescue were observed through Poisson process, the likelihood to estimate parameter sets ($\theta = \{\mu_d, r(t), p_2, p_3, p_4, q(t)\}$) can be written as,

$$L(\theta) = \prod_t \{ \text{pmf}(\text{Poisson}(\hat{M}(t)), M_{\text{data}}(t)) \times \text{pmf}(\text{Poisson}(\hat{C}(t)), C_{\text{data}}(t)) \\ \times \text{pmf}(\text{Poisson}(\hat{C}_m(t)), C_{m,\text{data}}(t)) \times \text{pmf}(\text{Poisson}(\hat{O}(t)), O_{\text{data}}(t)) \}, \quad (10)$$

where $\text{pmf}(\text{Poisson}(\lambda), x)$, denotes the probability mass function of the Poisson distribution with the expected value = λ and the observational value = x . $M_{\text{data}}(t)$, $C_{\text{data}}(t)$, $C_{m,\text{data}}(t)$, and $O_{\text{data}}(t)$ correspond to the observed numbers of raccoon dogs rescued due to the progress of mange, non-mangy raccoon dogs rescued due to traffic accidents, mangy raccoon dogs rescued due to traffic accidents, and non-mangy raccoon dogs rescued due to other reasons, respectively.

We conducted a Bayesian estimation to estimate the parameters. We obtained 10,000 thinned samples from 40,000 Markov chain Monte Carlo iterations, with a burn-in of 2000 iterations on four chains. Table 1 shows the prior distributions used for the estimation. The convergence was checked using the Gelman-Rubin convergence diagnostic. The models were compared using a widely applicable information criterion (WAIC) (Watanabe and Oppen, 2010). The model with the lowest WAIC value was selected as the best-fit model. R.4.3.1 (R Core Team, 2023) and Stan 2.26.1 (Stan Development Team, 2023). were used.

3. Results

Among the three models constructed, Model 2 showed the lowest WAIC (WAIC in Models 1, 2, and 3 were 477.4, 453.6, and 476.4, respectively). The fit of Model 2 is shown in Fig. 3, which demonstrates that the observed number of rescued animals was appropriately explained by the model. The mange-induced mortality rate, μ_d , the average growth rate between 1990 and 2010, \bar{r} , and the coefficient of the variance of the growth rate, σ , were estimated to be 1.09 (95% credible interval (CI): 0.47–1.72) per year, 0.49 (0.18–0.86), and 0.29 (0.16–0.47), respectively (Table S1, available in Supporting Information). As a result, the estimated population growth rates ranged between 0.19 (95% CI: 0.29–0.67) in 1997 and 0.78 (95% CI: 0.35–1.35) in 2005. The estimates of the relative frequency that non-mangy raccoon dogs are rescued due to traffic accidents, p_2 , that mangy raccoon dogs are rescued due to traffic accidents, p_3 , and that non-mangy raccoon dogs are rescued due to causes other than traffic accidents or mange, p_4 , were 0.77 (95% CI: 0.43–1.38), 0.09 (95% CI: 0.06–0.13), and 0.66 (95% CI: 0.37–1.18), respectively. The estimate of the prevalence in year (t), $q(t)$, ranged between 0.04 (95% CI: 0.02–0.08) in 1990 and 0.80 (95% CI: 0.59–0.91) in 2010.

Using the estimated parameter values, the relative population size of raccoon dogs (Fig. 4) and annual prevalence of mange (Fig. 5) were reconstructed. The estimated annual prevalence of mange demonstrated a bimodal shape with peaks in 1999 and 2010. The time series of the relative population size also showed a bimodal shape, with the first and second peaks occurring in 1995 and 2009, respectively. The relative population size ranged from 0.40 (95% CI: 0.23–0.71) in 2002 to 4.56

Table 1

Prior distributions for the parameters used to model the population dynamics and disease dynamics of sarcoptic mange among Japanese raccoon dogs. Uniform (x, y) denotes a uniform distribution with a range of x to y , Cauchy (x, y) denotes a Cauchy distribution with location parameter = x and scale parameter = y , and Beta (x, y) denotes a Beta distribution with shape parameters x and y , respectively.

Variable	Model	Parameter	Prior distribution
Mortality rate induced by sarcoptic mange	All	μ_d	\sim Uniform (0, 5)
Mean population growth rate	only in Model 2	r	\sim Uniform (0, 5)
Constant population growth rate	only in Model 1	r_c	\sim Uniform (0, 5)
Coefficient of the variance of the population growth rate	only in Model 2	σ	\sim Cauchy (0, 5)
Relative frequency of non-mangy individuals rescued due to traffic accidents	All	p_2	\sim Uniform (0, 3)
Relative frequency of mangy individuals rescued due to traffic accidents	All	p_3	\sim Uniform (0, 3)
Relative frequency of non-mangy individuals rescued due to other causes other than sarcoptic mange infection/traffic accidents	All	p_4	\sim Uniform (0, 3)
Proportion of infected animals in year (t) (between 1990 and 2010, 21 parameters)	All	$q(t)$	\sim Beta(1,1)

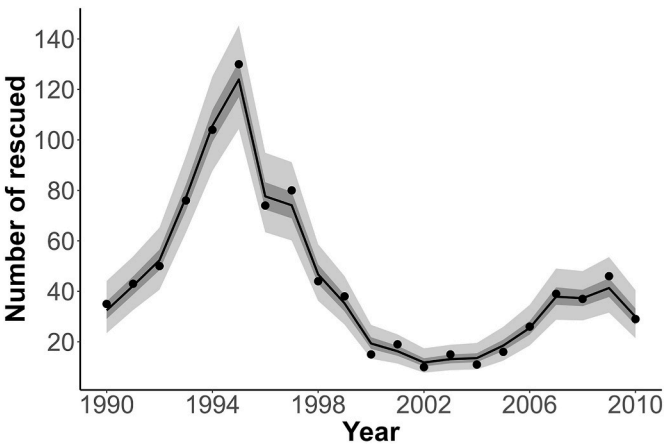


Fig. 3. Model fitting to the time-series data of the number of rescued Japanese raccoon dogs. Black dots denote the observed number of rescued Japanese raccoon dogs each year. The black line, dark grey band, and light grey band denote the median, 50%, and 95% credible intervals of the estimated number of rescued animals, respectively.

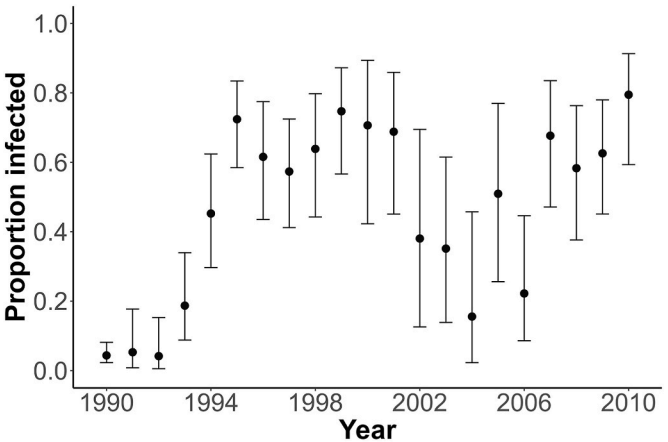


Fig. 4. Time series of estimated yearly prevalence of sarcoptic mange among Japanese raccoon dogs. The black dots denote the median values and the error bars denote the 95% credible intervals.

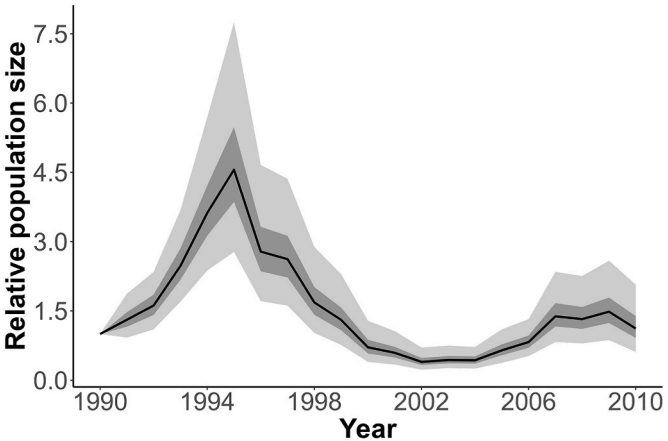


Fig. 5. Chronological change in the estimated relative population size of Japanese raccoon dogs. The black line, dark grey band, and light grey band denote the median, 50%, and 95% credible intervals, respectively.

(95% CI: 2.78–7.74) in 1995, resulting in the ratio of the smallest

population size to the largest one being 0.088 (95% CI: 0.053–0.137).

4. Discussion

In this study, a state-space model was developed to estimate the impact of infectious diseases on wild animal populations using wildlife rescue data. The host population and disease dynamics regarding sarcoptic mange on raccoon dogs were estimated using time-series data for each rescue cause. During the outbreak, the ratio of the population size at the end of substantial prevalence (when the smallest population size was estimated) to that at the beginning (when the largest population was estimated) was estimated to be 0.088 (95% CI: 0.053–0.137). This implies that the population size changed by 91.2% (95% CI: 86.3–94.7) from its peak to the bottom when the substantial prevalence of mange was observed.

An advantage to use wildlife rescue data is reducing the cost of estimating disease impact. Estimating the impact of disease on wildlife requires extensive ecological investigations. For instance, several studies have estimated the impact using population abundance indices obtained from long-term investigations, e.g., West Nile fever in wild birds (LaDeau et al., 2007) and white nose syndrome in bats (Frick et al., 2010). Other studies have used tracing data of host individuals obtained by radio tracking (e.g., disease mortality in koalas (*Phascolarctos cinereus*) (Rhodes et al., 2011) and African wild dogs (*Lycaon pictus*) (Woodroffe et al., 2007)). Furthermore, intensive camera trapping data are used for the estimation (the impacts of African swine fever (Morelle et al., 2020) and classical swine fever (Ikeda et al., 2020, 2021) on wild boars). In contrast, our estimation method requires only wildlife rescue data, which are accumulated in wildlife rescue facilities as routine products. Hence, our approach enables cost savings.

The estimated decline in the population size of raccoon dog population during the mange outbreak, approximately 90% reduction, is comparable with that of other carnivores. The reduced proportion of population size was reported to be approximately 90% in Swedish red foxes (Mörner, 1992; Willebrand et al., 2022) and 92% in the red fox population in Bristol (Soulsbury et al., 2007). In contrast, some lower estimates were reported in a red fox population in Japan (75.8% (Uraguchi et al., 2014)), a coyote population in Texas (70% (Pence and Windberg, 1994)), and an endangered kit fox (*Vulpes macrotis mutica*) population in California (approximately 50% (Foley et al., 2023)). The difference in the impacts of the disease can be explained by host susceptibility (Oleaga et al., 2011; Moroni et al., 2021), host sociality (Kołodziej-Sobocińska et al., 2014), density (Pence and Windberg, 1994), and virulence of the *S. scabiei* strain circulating in the host population.

The present study has a few limitations. First, the rescue probability per cause was assumed to be constant over time. The rescue probability can change owing to the time-dependent differences in the intensity of wildlife rescue activities. The intensity of wildlife rescue activity can vary with several artificial factors, such as the availability of economic and human resources and the criteria for animal rescue adopted by rescue facilities. Although the wildlife rescue activity in the present study could be assumed to be stable (Kido, personal communication), time-dependent changes in these variables should be measured and integrated in future studies to obtain more accurate estimates. Second, we assumed a constant disease-induced mortality, though weakening pathogen virulence and/or strengthening host resistance have been reported in many diseases, e.g., myxomatosis (Fenner, 1953) and the European brown hare syndrome (Scicluna et al., 1994) in wild rabbits and the classical swine fever in wild boar (Kramer-Schadt et al., 2007). Measuring the susceptibility of hosts and virulence of pathogens through infection experiments allows us to expand our model to consider time-varying susceptibility and virulence. Third, age-dependent behavioral changes in raccoon dogs were not assumed in our estimation due to the lack of detailed age data in the rescue data. Traffic accidents occur more frequently in young raccoon dogs during the subadult dispersal

period (Saeki and Macdonald, 2004). If epidemics and subsequent population crashes increase the birth rate of raccoon dogs, an increase in subadults will lead to a higher frequency of traffic accidents. Further studies are required to clarify the age structure and age-dependent disease ecology of raccoon dogs.

5. Conclusions

In conclusion, this study demonstrates the usefulness of wildlife rescue data in estimating the population dynamics of wildlife, disease dynamics, and impact of disease on wildlife populations. Our study suggests that wildlife rescue data provide important information for the management of wildlife diseases, i.e., the time-series changes in populations size and disease prevalence.

CRediT authorship contribution statement

Ryota Matsuyama: Writing – original draft, Visualization, Methodology, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Nobuhide Kido:** Writing – review & editing, Investigation, Data curation. **Ryosuke Omori:** Writing – review & editing, Validation, Methodology, Funding acquisition, Formal analysis, Conceptualization.

Ethics statement

Ethical approval was not required because the authors used only secondary data. The original data were collected by Kido et al. (2013) and have been published previously.

Availability of data

The data supporting the findings of this study are available from the corresponding author upon reasonable request.

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Declaration of competing interest

The authors declare that they have no competing interests or personal relationships that may have influenced this study.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.ijppaw.2024.101010>.

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