

The Importance of Epidemiology and R_0 in Wildlife Rehabilitation

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Abstract: Wildlife rehabilitators are at the intersection between individual and population-level wildlife health. Epidemiology is the study of diseases at population levels and mounting evidence suggests that disease outbreaks can impact wildlife populations significantly. The basic reproduction number (R_0) is used as a threshold value to predict whether a disease will result in an outbreak or die out. It is defined as the expected number of secondary cases caused by one infectious individual (the index or primary case) during this individual's entire infectious period in a fully susceptible population. Rehabilitators should be familiar with the concept of R_0 and the important effect on and contribution to wildlife disease epidemiology that they can have.

Keywords: basic reproduction number, disease, epidemiology, R_0 , wildlife rehabilitation

INTRODUCTION

Historically, wildlife biologists have speculated that parasites and disease have little impact on wildlife populations, believing that most infections are relatively benign (Hudson et al 2002). Disease outbreaks may cause high mortality within a population, but typically these outbreaks were considered unusual exceptions resulting from environmental factors interrupting the delicate natural balance. However, evidence is mounting that disease, particularly wildlife epidemics, is a serious concern for the long-term health of wildlife populations (Daszak et al 2000) and even is capable of causing species extinction (Smith et al 2006).

Disease can be unpredictable in wildlife populations. Why do some diseases suddenly emerge, sweep through a population, and then suddenly disappear without infecting all individuals? Why do other diseases remain endemic in many populations, causing high mortality each year? Investigating the answers to these questions is the labor of wildlife disease epidemiologists, with the goal of helping to manage and protect wildlife populations.

Epidemiology is the study of disease (in this case infectious), and how often and why diseases occur in different groups of animals. The key term is *groups of animals*. Epidemiologists work at the level of populations. Individual animals are not a concern until they are included into categories such as “susceptible,” “infected,” “dead,” or “recovered” (either temporarily or permanently immune) individuals. Wildlife rehabilitators, on the other hand, are primarily concerned with the health and well-being of individual animals and may find the population approach somewhat coldhearted. Nevertheless, individual wild animals unite epidemiologists and rehabilitators in many critical ways, the most fundamental being R_0 , the basic reproduction number.

BASIC REPRODUCTION NUMBER

How an infection behaves when it first appears in a population of susceptible individuals is critical to the health of the population. Being able to predict how an infection will act is important for management of the disease and the animal population. In most cases, the infection will follow one of three paths; either it will start an epidemic; burnout, meaning, after a few cases of infection it will disappear; or it will become endemic, meaning it will become stable within the population. Which path the infection follows can be predicted by the basic reproduction number (symbolized as R_0). The strict definition for the basic reproduction number is the expected number of secondary cases caused by *one infectious individual* during this individual's entire infectious period in a fully susceptible population (Heesterbeek 2002).

The concept of R_0 can be illustrated best by evaluating a practical example, such as the *fictitious* introduction of canine distemper virus into the raccoon population on Galveston Island, TX by a single infected raccoon. Assuming that the local raccoons have had no previous exposure to the distemper virus

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and therefore have no immunity to protect them from the virus, they all are susceptible to infection. Distemper virus is highly contagious, often fatal, and easily spread by direct contact (usually by inhalation) with infected bodily fluids. Raccoons that survive the infection should be immune to future infections. The single infected raccoon (the index or primary case) will be infectious for three weeks after arriving on the island. The question to consider is: How many local raccoons will the infected raccoon contact—in close enough proximity to transmit the virus—during the 21-day infectious period? Although many factors could influence this scenario, one of the most important is the number of contacts that occur between infected and susceptible raccoons. Imagine, for instance, if the infected raccoon was released following the breeding season when many curious young juveniles were in the population versus being released during the coldest part of the year (as cold as it can get in Texas) when activity and potential contacts would be relatively low.

In reality, calculating R_0 according to the strict definition is almost impossible in wildlife populations that are experiencing an infectious disease outbreak. Epidemics rarely are identified at the moment an infected individual enters a susceptible population, and the number of contacts between susceptible and infectious individuals is difficult, if not impossible, to estimate for most infections in the field. Yet, despite the challenges with calculating the actual value of R_0 , it is still an essential concept in epidemiology and infectious diseases and arguably “one of the foremost and most valuable ideas that mathematical thinking has brought to epidemic theory” (Heesterbeek and Dietz 1996).

The significance of R_0 is not in the actual number, but in what it represents—a theoretical threshold. In simplified disease scenarios, R_0 is a cutoff point that predicts whether an infection will spread, which is what we really are interested in knowing. Is the disease likely to result in an epidemic, a sudden outbreak of the disease? Or will the disease die out? Under more complicated scenarios, R_0 helps predict whether a disease will become endemic, indicating that it will persist in the population, often at some low level. In order for an infection to spread and result in an outbreak, R_0 must be greater than one. This means that every infected individual, on average, infects more than one new individual, resulting in a chain reaction of new cases (Figure 1). If R_0 is less than one, each infected individual produces, on average, less than one new infected individual, indicating that the infectious disease eventually will die out in the population.

When R_0 equals one, the disease is likely to remain in the population with roughly the same number of individuals infected all the time (Kermack and McKendrick 1927).

- $R_0 < 1$ – disease will eventually disappear
- $R_0 = 1$ – disease will become endemic
- $R_0 > 1$ – disease will result in an epidemic

Threshold levels are familiar concepts in wildlife ecology. You may be familiar with the analogous threshold property of λ , the Greek letter lambda (also written as just R), which represents the fundamental net reproductive rate of a population under simplified conditions. Lambda combines the birth of new individuals with the survival of existing individuals. The value of the concept lies in its threshold property similar to R_0 . If λ is greater than one the population will grow; if λ is less than one the population will decline (Dublin and Lotka 1925).

R_0 has other important uses for wildlife diseases in addition to its threshold property. The magnitude of R_0 can be used to gauge the risk and severity of an epidemic of an emerging infectious disease (Heesterbeek 2002) and the final size of the epidemic—specifically the number of susceptible individuals remaining at the end of the epidemic (Andreasen 2011). If a disease is endemic, R_0 helps evaluate control strategies. Different control efforts can be incorporated into mathematical disease models to test which strategy and how much effort (cost) it would require to reduce R_0 below one, and theoretically eliminate the infection from the population (Li et al 2011). For example, R_0 calculations were used to illustrate that mosquito control would probably be much more effective in controlling an outbreak of West Nile virus (WNV) than would be attempting to control bird populations (Wonham et al 2004). In fact, it was shown that reducing American crow (*Corvus brachyrhynchos*) densities—the bird species that has suffered some of the greatest mortality in the United States due to WNV—might actually increase the chance of disease transmission and result in an outbreak.

CALCULATING R_0

Because it is virtually impossible to calculate R_0 according to the strict definition discussed above, there are numerous methods to estimate R_0 -like thresholds for a specific disease and population. Some methods are very basic and incorporate the bare minimum information necessary. Other methods use complicated models to incorporate more sophisticated data about the population under study, such as different age and social groups, physical distribution in the

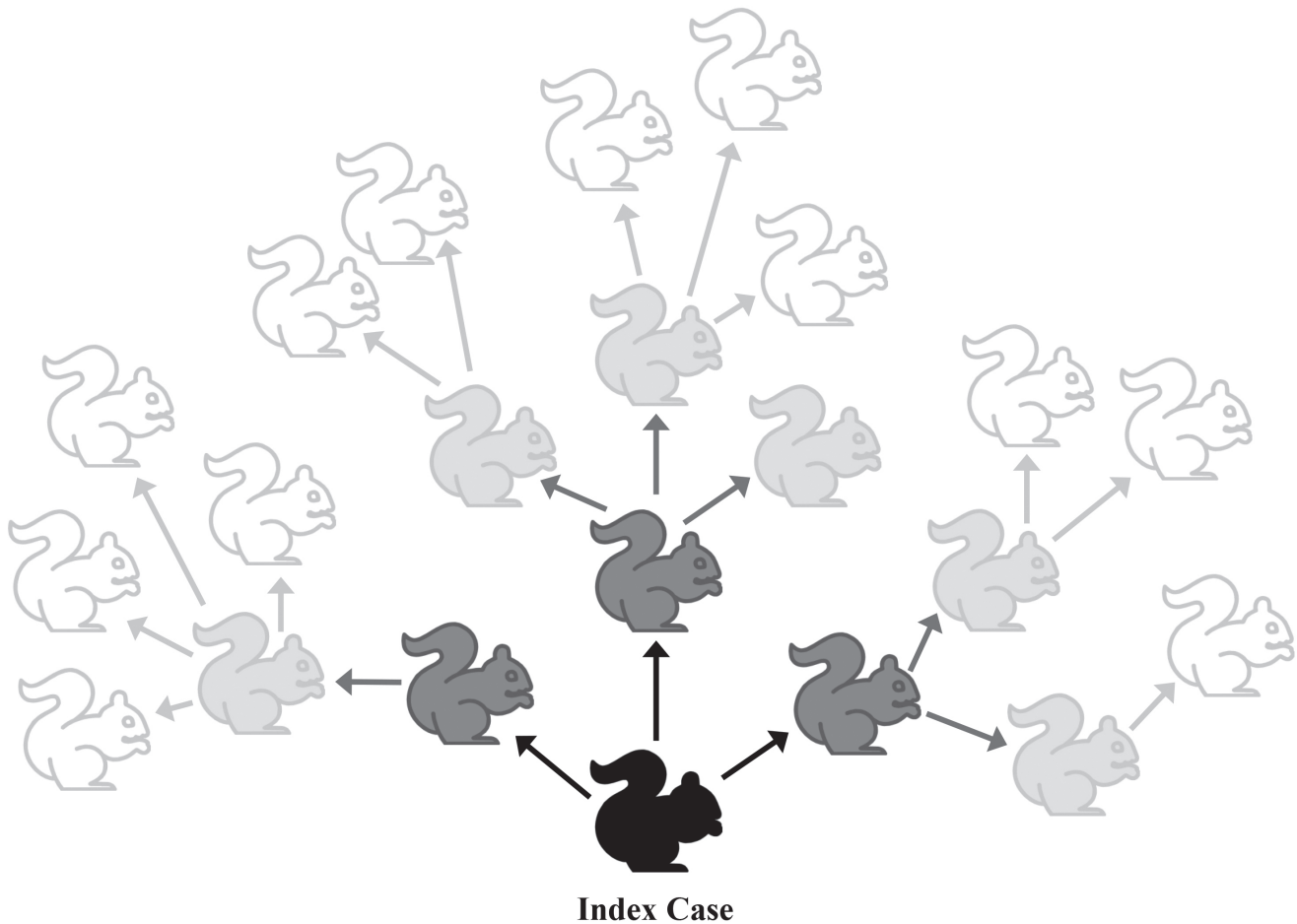


Figure 1. Graphical representation of new cases of infection during an outbreak. In this case, each infected squirrel spreads the infection to 0 to 4 other susceptible squirrels. The average number of new cases is 2.1.

environment, and status of immunity. An important point to consider is that there is no universal R_0 for a disease (Li et al 2011). For example, R_0 for squirrel pox virus (*Squirrel parapoxvirus*) will not always be 2.1 because it depends on the situation where and when this value was calculated. The R_0 for another outbreak of squirrel pox may be 2.12, but it should never reach a hugely different value such as 19.0, assuming the same method was used for calculation, because such a large value would be inconsistent with the disease's behavior. What this means is that R_0 must be interpreted within the context of the disease and population at the time it is investigated and, most importantly, the method used to calculate R_0 .

Most methods to calculate R_0 include aspects of the three main factors of infectious disease epidemiology: (1) the natural history or progression of the infection in an individual; (2) how the infection is spread from infected to susceptible individuals; and, (3) the environment and behavioral characteristics of the specific population (Ward et al 2009). Calculating

an R_0 -like threshold value for a hypothetical outbreak of distemper virus on Galveston Island can be done relatively easily by using basic disease information published in the scientific literature regarding distemper epidemiology (Deem et al 2000) and previously studied outbreaks in raccoons (Roscoe 1993). Important values to estimate are the transmission probability (how likely is it that the disease will be passed from an infectious to susceptible individual), the contact rate (how many individuals, on average, will the infected raccoon contact on a daily basis), and how long the infected raccoon will remain infectious. Estimates for these values, along with several simplifying assumptions, can be used to calculate R_0 for a susceptible raccoon population of 1,000 individuals on the island. By using one particular method (Roberts 2007), R_0 would be approximately 8.45. Since this threshold value is greater than one, it strongly suggests that there would be an epidemic of distemper in the raccoons on the island.

CONCLUSION

Wildlife rehabilitators are at the intersection between individual and population-level wildlife health. From an individual perspective, rehabilitators deliver a valuable service providing care and assisting wild animal welfare. From a population perspective, rehabilitators collectively observe and handle a large sample of wild animal populations from across the United States. These observations have been critical for surveillance programs such as West Nile virus (Nemeth et al 2006), but overall have been sorely under-utilized. Recent efforts are encouraging rehabilitators to use standardized on-line patient record systems to maximize the collection and distribution of wildlife health information generated by rehabilitators across the country; WILD-ONE, which stands for Wildlife Incident Log/Database and Online Network, recently launched by the Wildlife Center of Virginia is one example. Collating records across geographic regions and standardizing data entry will make the underlying data in these records more accessible and more broadly useful.

Lastly, rehabilitators interact with wildlife populations every time an individual animal is released back to the wild. By definition, the basic reproduction number, R_0 , is an individual-based metric that sheds valuable light on potential impacts of disease on wildlife populations. By definition, a single infected individual can cause an epidemic, which should be enough to cause all of us to pause the next time we release an animal.

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