Chapter 11
Filling the Gaps: Improving Sampling and Analysis of Disease Surveillance Data in Galápagos

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Abstract Emerging infectious diseases in wildlife are of conservation concern worldwide, including on the Galápagos Archipelago, where isolation, small population sizes, and naïve immune systems place the birds of Galápagos at potentially higher risk of devastating impacts of disease. Wildlife disease data from surveillance efforts, whether active or passive, are invaluable because they provide a baseline understanding of what diseases are present in a system, serve as an early warning sign of an ecosystem health issue, and provide managers with information about the efficacy of disease mitigation efforts. We have learned an enormous amount about diseases affecting Galápagos avifauna in the last 20 years or so, but gaps in our understanding exist because of the challenges posed by issues with imperfect detection of hosts, parasites and pathogens, and the diseases they cause as well as uncertainty about the size of the population of the target host. Nonetheless, sampling design and analytical approaches borrowed from population and community ecology offer a suite of tools to help fill the gaps in our knowledge about diseases in wildlife in Galápagos and beyond.

Keywords Detection probability • Occupancy models • Wildlife disease surveillance • Dependent double-observer method • False positive

11.1 The Values of Wildlife Disease Surveillance Data

Emerging infectious diseases (EIDs) are an important threat to wildlife as disease contributes to changes in system dynamics at multiple scales. Work on emerging diseases in the avifauna of the Galápagos Archipelago over the last two decades, as detailed in this volume, illustrates well the impact disease has at these different

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layers of organization. *Philornis downsi*'s devastating influence on nestling survival in Darwin's finches (Fessl et al. 2006a, Chap. 9, this volume) will likely reverberate from the individual host nest that is affected, up through island populations of these iconic passerines. Disease resonates to higher scales, as well. The discovery of antibodies to *Toxoplasma gondii* in endemic Galápagos Penguins (*Spheniscus mendiculus*) and Flightless Cormorants (*Phalacrocorax harrisi*) on both islands with and without felid definitive hosts (Deem et al. 2010, Chap. 8, this volume) highlights pathogen transmission as yet another negative impact feral cats can have on bird communities. Further, while largely ubiquitous across the globe (Dubey 2009), the presence of *T. gondii* in an isolated system like Galápagos might serve to signal a potential public health issue (Levy et al. 2008) reflecting an ecosystem that is not as "healthy" as we might wish.

Despite recognition of these impacts echoing throughout wildlife host-parasite-environment systems, important challenges remain in part because wildlife disease management at all stages—from the initial incursion of the pathogen to its possible elimination—often lacks relevant or sufficient data (McCallum 2016) or appropriate management actions (Langwig et al. 2015). After highlighting the values of health survey data in the context of the avifauna of the Galápagos, my goals for this chapter are twofold. One goal is to describe some of the challenges posed by wild systems that lead to gaps in data collection and analysis needed to fully characterize the complex interactions and dynamics of disease in wildlife systems (McClintock et al. 2010). The second is to describe approaches for data collection and analysis—borrowed from population and community ecology—to address the gaps in our knowledge about these critically important wildlife diseases.

Disease surveillance comprises the systematic and ongoing collection and analysis of health data (Toma et al. 1999) which, in our case, pertains to infectious diseases in wildlife with the eventual application to wildlife disease management. Ryser-deGiorgis (2013) nicely captured the goal of wildlife disease surveillance as gathering "information for action." The principal roles such disease surveillance data play are: (a) as a catalog of the diseases affecting hosts and the pathogens or parasites that cause them; and (b) as a long-term record of changes in host population disease status over time. Initial questions are often "What is present and whom does it affect?" and many of the early papers on disease in birds in Galápagos provide the baseline for future work tackling deeper questions that could not be addressed had the baseline not been established. Avian pox in the Waved Albatross (*Phoebastria irrorata*) presents a good example. Initial detection of external, wart-like gross lesions (Tompkins et al. 2017) like those characteristic of "dry" cutaneous pox infection (Tripathy 1993) is typically high. Detection of the lesions triggers tissue sampling to confirm by histopathology and electron microscopy (i.e., presence of inclusion bodies) or molecular methods (Tripathy 1993) that the lesions were caused by an avipoxvirus and not another agent. In addition, previous reports of active or targeted disease surveillance (Ryser-Degiorgis 2013) in the same or related host taxa, like Galápagos seabirds (Padilla et al. 2003, Padilla et al. 2006) in the albatross case, must be checked to confirm whether pox had been seen in these

hosts in the past; in this case, we know that the virus has been present in Galápagos for at least a century (Parker et al. 2011), but never previously reported in the Waved Albatross. This work then forms the foundation for continued surveillance for disease as a factor contributing to changes in the status of this critically endangered seabird.

Passive or scanning surveillance takes place as incidents of disease occur (Ryser-Degiorgis 2013). Such opportunistic surveys present some issues with respect to detection because the sample is not designed to represent a target population, but such surveillance data provide another important stream of information to document "What is present?" The advantages of passive surveillance arise from the broad scope covered by the survey in terms of host distribution and causes of morbidity or mortality. For example, passive surveillance efforts using submission of dead birds for necropsy in Galápagos (Gottdenker et al. 2008) included findings from 28 different species in 9 different avian orders and representing 10 different causes of mortality. Incidental findings included reports of cutaneous lesions consistent with avian pox, including in an Audubon's Seawater (*Puffinus lherminieri*); these are all discoveries that would never have been made had the authors not taken advantage of the opportunity presented by the carcass submissions.

Both active and passive surveillance data serve the critically important role as an early warning sign of a potential conservation threat; this is particularly germane to the Galápagos where populations are isolated, small, and likely immunologically naïve to introduced pathogens (Wikelski et al. 2004). Reports of antibodies to *Toxoplasma gondii* in Galápagos Penguins (Deem et al. 2010; Chap. 8, this volume) illustrate the utility of a sentinel species. Penguins interface with both the terrestrial and marine environments for nesting and foraging, respectively, such that they can experience stressors from both environments and track changing conditions in both environments in a way similar to sea turtles (Aguirre and Lutz 2004). Coupled with their response to the changing environmental conditions, changes in the incidence of disease in the sentinel species may reflect human-induced environmental change indicating an emerging threat to ecosystem health (Newman et al. 2007).

Lastly, surveillance data are valuable for tracking the efficacy of disease management activities when collected before, during, and following a disease management intervention. These monitoring data track changes to the host population disease status and can be used to evaluate the prediction that the intervention contributes to declines in disease incidence or prevalence. Infestation of nests with the parasitic larvae of the fly *Philornis downsi* has been connected to the declines of at least two finch species in Galápagos (Fessl et al. 2006b; Chap. 9, this volume), including the critically endangered Mangrove Finch (*Camarhynchus heliobates*). Population viability analyses suggested that reducing parasite prevalence would lead to important reductions in the risk of finch extinction (Koop et al. 2016), a hypothesis that could be tested with an active intervention to reduce infestation and the effectiveness tracked by disease surveillance to see if the intervention contributed to declines in fly infestation in finches.

11.2 Challenges Studying Disease in Wild Systems

So much of what we know about disease in Galápagos avifauna has come from the proverbial "blood, sweat, and tears" and much has been learned from this very hard work, perseverance, and a dash of serendipity. Indeed, as the contributors to this volume will attest, collecting surveillance data on disease in the field can be expensive and the logistical challenges are sometimes intractable. Nonetheless, several additional challenges to effective disease data collection are posed by the very nature of the system. A first challenge in studying disease in wild systems is that detection is imperfect (McClintock et al. 2010). Given their long isolation, island host populations tend to be relatively smaller and have lower genetic variation than their mainland counterparts (Chap. 4 this volume, Frankham 1996). Sources of uncertainty in detecting disease in wild birds might then arise, first, because host populations are small and the density of occurrences of disease may be concomitantly small and difficult to detect.

Host status further complicates detection of the incidence of disease and estimates of prevalence. Sick animals may behave differently than healthy conspecifics, making their detection more or less difficult and this leads to biased estimates of prevalence. Hunter harvest of mule deer with chronic wasting disease (CWD) increased over the course of a hunting season perhaps because they were more susceptible to harvest due to behavioral changes associated with disease. This differential susceptibility to harvest, the authors speculate, may have led to estimates of CWD prevalence that were biased high (Conner et al. 2000). House Finches (*Carpodacus mexicanus*) experimentally inoculated with the bacterium *Mycoplasma gallisepticum* exhibited more "sickness behaviors" (e.g., lethargy) than uninoculated individuals (Love et al. 2016); in a field setting, changes in behavior due to disease could translate to lower capture probabilities—infected birds are not captured in mist nets—and attendant lower detection of diseased birds.

Another issue relates to the actual size of the host population affected. Prevalence is typically calculated as the proportion of the sample examined that is classified as infected or "diseased" and this proportion is assumed to represent the true population prevalence. Often, estimates of prevalence are limited to the small subset of the population that is actually sampled, which is likely limited by the resources available for field sampling and subsequent analysis, without knowledge of the size of the total population the sample represents. This is likely unimportant when host population size is stable, as in many populations of domestic animals, but not accounting for fluctuations in wildlife population size and disease prevalence over time can lead to surveillance efforts that do not provide an effective assessment of disease risk (Walton et al. 2016) in what may be a very vulnerable wildlife population.

Imperfect detection of disease in wild systems may also arise because of issues related to the test or assay used to detect the parasite, pathogen, or disease itself. Prominent among the issues with tests used to detect parasites and the disease they cause is that many assays have been developed using well-understood domestic animal models, like domestic chickens, and then applied to a phylogenetically

closely related wild organism (Pedersen and Babayan 2011). In particular, the issue is that the wild host's immune response likely does not parallel that of the domestic analog; the wild organism's immune response occurs under natural conditions and in the face of natural genetic variation (Pedersen and Babayan 2011). In many but not all cases, application of domestic animal assays to the immune response of a wild organism can result in low test sensitivity, because the test is not very good at detecting disease in a non-target host, and concomitant false negatives. False negatives are problematic in the context of Galápagos and other sensitive avifauna if management decisions are made based on the results of the assay used to detect disease: scarce financial resources may be committed to other projects when they are urgently needed to mitigate a disease outbreak that goes undetected. This urgency is compounded when a novel and virulent pathogen arrives in the archipelago, rapidly becomes established, and spreads among immunologically naïve hosts. The challenge is in detecting the incursion before rapid transmission and deleterious effects on hosts occur.

We can look to the tests used to detect infection with avian blood parasites as a case study illustrating the issues that arise when tests are not sufficiently sensitive to detect parasites or the diseases they cause. Infections with protozoan blood parasites in the genera *Haemoproteus*, *Plasmodium*, and *Leucocytozoon* are typically identified using microscopy to examine thin blood smears or by polymerase chain reaction (PCR) and sequencing, to confirm the presence of parasite DNA in a peripheral blood sample from a bird. Work by Fallon et al. (2003) showed that detection of avian blood parasites from the genera *Plasmodium* and *Haemoproteus* was different for microscopy compared to three different PCR-based assays (i.e., three different primer sets) and none of the assays alone detected all infections. *Plasmodium* blood parasites have been detected in at least 4 Galápagos bird species so far out of 22 tested (Levin et al. 2013) and we know from Hawaii that the impacts of *Plasmodium* infection on host populations can be devastating, contributing to the declines and extinction of many Hawaiian forest bird species (van Riper et al. 1986). Given this, imperfect detection of the parasite or the disease can have profound consequences for disease management because a missed detection of this sort of parasite could lead to rapid spread without our knowing.

A related but distinct issue may be more prominent in Galápagos than in other settings. Detection of *Plasmodium* in the Archipelago is thought to be poor in endemic species like the Galápagos Penguin because they do not appear to be competent hosts for the *Plasmodium* Lineage A. Gametocytes detected in host erythrocytes indicate the final stage in the completion of the portion of the life cycle that takes place in the vertebrate host, meaning that that host species is a competent host (Valkiunas 2005), but gametocytes have never been documented in any species of infected endemic bird in Galápagos (Levin et al. 2013). Two types of early intraerythrocytic development (meronts and trophozoites) have been observed in blood smears and the working hypothesis is that the host and parasite are poorly adapted to each other, as may happen when hosts and parasites have co-occurred for only a short time. Thus, by applying typical blood parasite PCR assays to blood samples, many infections likely remain undetected, and the "gold standard" microscopic inspection of thin blood smears is even worse at detecting existing infections.

11.3 Tools for Enhancing the Study of Wildlife Disease

To tackle the variety of challenges I have detailed related to evaluating the dynamics of wild host-pathogen-environment systems, we can borrow sampling designs and analytical approaches from population and community ecology that recognize—and allow us to account for—variation in detection probabilities of hosts, parasites, and the diseases they can cause. Several excellent works provide extensive detail on the development of these approaches (e.g., Jennelle et al. 2007, Conn and Cooch 2009, McClintock et al. 2010); my intent is to provide an overview that will allow workers to identify useful new approaches to apply to surveillance in their wildlife disease systems.

11.3.1 Accounting for Imperfect Detection

When the probability of detecting a target species, whether a host or parasite, is <1.0, it is "imperfect"; estimates of parameters like abundance or prevalence that use counts of the target species will be biased low when detection is assumed to be perfect (Cooch et al. 2012). Helpfully, many approaches exist that acknowledge that detection of a target species can be imperfect; that is, false negatives can occur. Occupancy modeling presents one approach where uncertainty in detection can be evaluated by making repeated visits to a site during which the presence or absence of the species of interest is recorded as a "1" or "0," respectively. The repeated visits to the site are collated into an encounter history, recorded as a series of 1s or 0s indicating the state of the species at each sequential visit to the site, and maximum likelihood methods are used to estimate the probability of detection (p) and the probability that the site is occupied, or sometimes "used," by the species of interest (ψ) (MacKenzie et al. 2006).

In a disease setting, the target species could be the host, the pathogen/parasite, or both, and occupancy approaches are finding increasingly widespread use with applications to hosts, parasites, and the tests used to evaluate disease status (arguably the interface of a host and a parasite). For example, multi-state occupancy approaches have been applied to arctic-nesting geese and *Toxoplasma gondii* (Elmore et al. 2014), a pathogen that has also been detected in cats in Galápagos (Levy et al. 2008) as well as some vulnerable Galápagos seabird species (Deem et al. 2010). In the arctic goose example, the risk of transmission to other potential hosts in the ecosystem, as well as to humans through harvest for consumption, motivated the need for reliable estimates of seroprevalence in geese. Estimates of seroprevalence under an occupancy framework were compared to naïve estimates that assumed that the diagnostic tests were error-free, a strong assumption, particularly in wild systems where the arsenal of tools available is absent or limited to phylogenetically similar laboratory analogs (Pedersen and Babayan 2011). Estimates of seroprevalence under an occupancy framework were ~10% higher than those using

a traditional estimator of prevalence (Elmore et al. 2014). Further, the occupancy approach revealed important differences between two available serological tests where one (Indirect Fluorescent Antibody Test, IFAT) had a higher probability of detecting antibodies and a higher probability of classifying a positive sample as positive than the other (Direct Agglutination Test, DAT), given that the antibodies were present (Elmore et al. 2014). Taken together, these results emphasize that an occupancy approach could be particularly useful in surveillance of wildlife disease systems where a positive test result at some point in time could indicate a serious threat to the conservation of an iconic species.

Applications of occupancy models have recently been extended far beyond the serosurvey to include the analysis of the amphibian chytrid fungus *Batrachochytrium dendrobatidis* in eDNA (water) samples (Schmidt et al. 2013), fleas on prairie dogs (Eads et al. 2013), and *Borrelia* in ticks infesting seabirds (Gomez-Diaz et al. 2010), among others. In all of these instances, inferences about the disease system were improved by making multiple "visits" to a target host, site, or sample to account for imperfect detection inherent in these wild systems. Further, later visits to focal or study sites in subsequent seasons or years can be appended to the encounter histories and incorporated into updated analyses as necessary for long-term surveillance. Thus, I echo McClintock et al. (2010) that occupancy approaches are so valuable because they allow researchers to account for the imperfect detection inherent in wildlife host-parasite-environment systems and advance our understanding of the dynamics and consequences of disease in wild populations, getting us one step closer to closing gaps in our knowledge.

11.3.2 Estimating Population Size

It is a rare case when every animal is detected and perhaps it is rarer still when the detection probability for both infected and uninfected animals is the same and equals 1.0. In challenging field settings, we tend to be limited by opportunity or resources to only those few animals that we can sample easily; inferences suffer when we assume that we are perfect at detecting all types of animals and when we extrapolate information about a small sample to a much larger and unknown population. When host population size is unknown, the extent of disease risk is also, arguably, unknown.

We can do better by estimating population size directly. A number of techniques exist for estimating population size (Williams et al. 2002); I highlight a few here that I think could be useful in improving our understanding of disease in Galápagos avifauna though their utility is certainly not limited to just this setting. An option that is especially attractive for use in field settings like Galápagos is the double-observer method detailed by Nichols et al. (2000). The method was initially described for use in (avian) point counts to estimate the probability of detection and sources of variation in detection, such as those that arise because of differences among bird species or observers doing the counts. In practice, the method requires

two observers, a primary and a secondary. The primary observer indicates to the secondary target individuals that should be tallied. The secondary observer records the number of those indicated by the primary observer while also recording any additional individuals that the primary does not detect. Key to the application considered here is that the information on the numbers of birds not detected by the primary is used to estimate abundance (Nichols et al. 2000).

Data collected using this dependent double-observer protocol can then be summarized as individual encounter histories where observation by the two observers functions as two separate encounters. For instance, those animals seen by the primary observer would have an encounter history of "10" and those seen by just the secondary have an encounter history of "01." Using a Huggins closed captures model (Huggins 1989, 1991), like those implemented in Program MARK (White and Burnham 1999), we can get estimates of detection probability (p), we can evaluate competing hypotheses, or models, incorporating covariates to explain heterogeneity in detection (like that between observers or sites or timing of the survey, etc.), and we can obtain estimates of abundance ($\hat{N}$). Double-observer methods have been applied to estimate population size of blue-footed boobies in Galápagos (Anchundia et al. 2014) but disease-related applications have not yet been explored. It is especially appealing that this approach can be extended to counts—and therefore estimates of abundance—of individuals in different states as might be germane for estimating the abundance of classes of birds with and without ectoparasites, for example, or other syndrome with readily observed external signs. Though I have not seen applications of this sort, a dependent double-observer protocol also could be applied to microscopic evaluation of thin blood smears to estimate abundance of particular cell types like different stages of intraerythrocytic parasites such as *Plasmodium*.

Capture-mark-recapture approaches are useful when estimates of vital rate parameters like survival and population rate of change (λ) are also of interest. These time, effort, and cost-intensive methods require marking or banding a portion of the population initially, then revisiting the marked individuals by observing or by capturing them again to read their unique band numbers. Encounter histories are built from the series of encounters with the marked individuals over time in the same way that encounter histories were developed for occupancy and double-observer approaches. The relevant time steps—days, weeks, months, or seasons—for reencountering the marked animals will depend on the question of interest. Importantly, variables such as disease status, age, sex, or other individual covariates can be collected at the same time and incorporated into models of detection probability (p) and the vital rates of interest (e.g., survival). Mark-recapture models incorporating disease status have been used to document improving survival of little brown bats in the face of white-nose syndrome (Maslo et al. 2015) and to track the impacts of avipoxvirus infection on great tits (Lachish et al. 2012), among others. Occasionally, information about an individual is ambiguous—such as disease state—and one way of handling ambiguous states is to censor those data at the expense of precision of the estimates of parameters of interest such as the rate of transition from, say, a diseased state to a not-diseased state. Multi-state capture-recapture models using a hidden Markov process (Conn and Cooch 2009) offer an approach to estimate state transition probabilities and survival in the face of uncertain classification of disease states.

11.4 Parting Thoughts

Emerging infectious diseases are increasing globally for humans, domestic animals, and wildlife alike (Tompkins et al. 2015); they pose a critical conservation concern for many wildlife species. In Galápagos, we have learned a great deal about the diseases affecting wild bird populations, yet gaps in our knowledge about disease persist because of challenges posed by elements of this wild system. I have described some approaches borrowed from, but not exclusive to, population and community ecology. At the same time, here I add a few parting thoughts to make the most of these approaches should they be amenable to another wildlife disease surveillance application.

While a number of excellent works exist that describe these methods in detail, freely available software with online guides exist for all of the approaches described. Prominent among them is Program Mark (White and Burnham 1999, http://www.phidot.org/software/mark/) which has a robust user's forum (http://www.phidot.org/forum/index.php), a "gentle" online book introducing the growing list of model types and how to implement them in MARK (http://www.phidot.org/software/mark/docs/book/), and workshops are offered frequently. Occupancy models can also be implemented in Program PRESENCE (MacKenzie et al. 2006) and PRESENCE can be called from R (http://cran.r-project.org/). The R package RMark is also available for mark-recapture analyses for those who are accustomed to the R environment.

The focus of the discussion presented here has been on the empirical components—study design, data collection, and analysis—of a discovery process in which mathematical models have important roles at all steps (Restif et al. 2012). I suggest that transdisciplinary collaborations with modelers, empiricists, and those whose expertise are in the field and the laboratory will bear important fruit for wildlife disease management (Chap. 12 this volume). Moreover, just as we can borrow approaches initially described by population and community ecology, we can learn a good deal by sharing ideas across the discipline of wildlife disease management with disease ecology theory to maximize learning about both enterprises (Joseph et al. 2013).

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