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Analysis of Population Monitoring Data

In numerous areas that we call science, we have come to like our habitual ways, and our studies that can be continued indefinitely. We measure, we define, we compute, we analyze, but we do not exclude. And this is not the way to use our minds most effectively or to make the fastest progress in solving scientific questions.

—Platt (1964:352)

What Is Monitoring?

Monitoring is a system for detecting trends over a period of time in areas such as habitat, water, and more. Herein we focus on animal populations and evaluate common quantitative methods for monitoring wildlife species. Animal distribution, abundance, survival, and productivity are examples of important biological parameters that can show trends based on ecosystem condition. Although there are different monitoring types (Morrison and Marcot 1995), monitoring is at its best with *targeted* (or *focused*) monitoring (Nichols and Williams 2006), when specific goals and objectives are identified and evaluated under rigorous sampling designs. Herein we focus on targeted monitoring. The process of defining goals and objectives, sampling, evaluating population response, and directing further monitoring and/or management actions should be classified as scientific research (Morrison et al. 2008).

We first distinguish between the biological versus sampled population, as these are seldom the same entity. Since it is rare to census all individuals in a population, the sampled population usually represents a subset of the biological population, but processes in the former may not fully reflect those in the latter (Morrison 2012). The related biological and

sampled populations are a result of a hierarchical framework of processes (see Chapter 10): the true underlying ecological process (state process) and the observation process (sampling process) (Fig. 8.1). A biological population consists of all individuals of the same species that occur in the same area at a specific time and is characterized by births, deaths, emigration, and immigration. A community (or assemblage) of species consists of multiple populations of different species that occur in the same area at a specific time. The current state of a community is characterized by number of species (species richness), species composition, number of species and relative abundance of each species (diversity), and local species extinction and colonization.

A robust monitoring data set requires careful planning and adequate support to ensure durability. Researchers and managers should

- formulate clear questions and objectives;
- select appropriate state variables (variables that describe system state, such as abundance) and vital rates to assess study questions;
- determine if there is sufficient power to answer questions within limitations (optimization);
- develop sampling design that fulfills four main questions of what, where, when, and how;

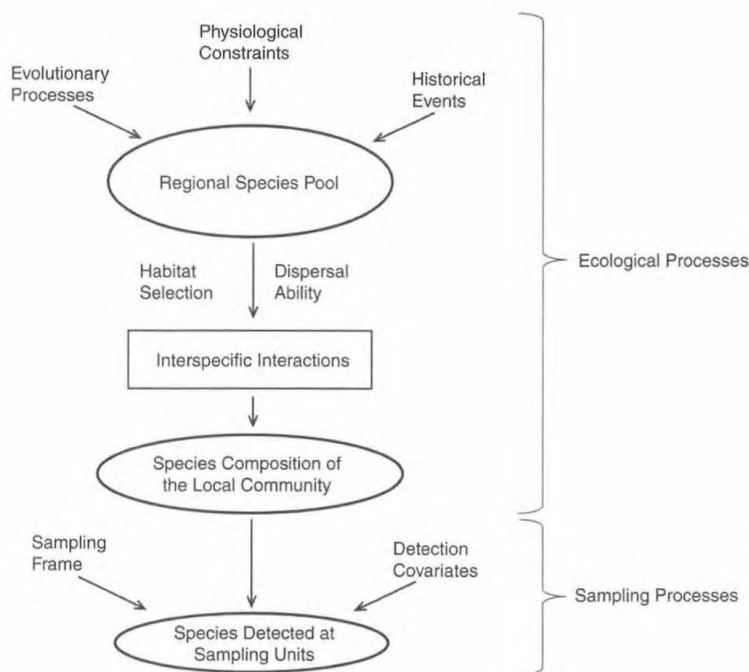


Fig. 8.1. Example of ecological and sampling processes with a study of species in a community. The sampling frame includes the study design and target population. Source: Adapted from Morin (1999).

- ensure data quality controls are in place before collecting data;
- conduct study, and simultaneously conduct quality assurance and quality control (QA/QC), as well as complete QA/QC after study is completed;
- use appropriate models for questions to analyze data;
- modify sampling design or models based on current status.

Qualities of a Robust Monitoring Approach

Collecting robust monitoring data is challenging, but not impossible. A critical first step is to clearly articulate monitoring questions and objectives (Yoccoz et al. 2001). In conjunction with clear objectives, selection of appropriate parameters to assess change over time is paramount. For example, abundance may not change over the course of a monitoring study, but vital rates such as survival or reproduction could change and thus represent more informative variables. If abundance changes, monitoring of addi-

tional vital rates provides understanding of the causes underlying those changes. The reason for change, however, may not be the monitoring objective. Therefore, the appropriate parameters ultimately depend on what will provide the strongest inference for the monitoring objective(s).

Given appropriate state variables and vital rates, the next crucial step is determining if the study design provides sufficient power (probability of correctly rejecting the null hypothesis) to answer questions with a given effect size (magnitude of change with a given precision during a certain time frame). Effort level (sampling frequency and intensity) required to meet study objectives is an important part of determining if there is sufficient power. Expected sampling time frame for state variables and vital rates depends on the rate that population processes function; they could be short (i.e., monitoring small mammal abundance change after a disturbance event) or long (i.e., monitoring adaptation). Ideally, pilot studies can help identify if sufficient power is available with a given effect size for study parameters. We recognize, however, that pilot studies are not al-

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ways feasible. Information from previous studies (i.e., variance of important parameter[s]) on similar systems could be useful in sampling design development. The pilot study can also pinpoint potential sampling efficiencies for a monitoring study (see "How" section below). Inventories, which quantify metrics of species at one point in time, may be used as pilot studies. Many monitoring schemes consist of repeat inventories, which allow us to estimate state variables at discrete points in time and then extract trends; an alternate approach involves estimating change metrics through demographic modeling, which does not require repeat sampling, *per se*. Multiple inventories require more effort, but usually provide more accurate trend depictions. Monitoring is pragmatic; thus, whatever approach provides more accurate trend estimates at reduced effort should be adopted.

With an appropriate study design, we assume the sampled population is an unbiased random sample representative of the biological population. This is a critical assumption for all estimation methods we discuss below. Given limited resources, it is also important to optimize study designs for maximum parameter accuracy at reduced effort. Additional robust monitoring data-set qualities are well-designed data input options (see "Data Quality Controls for Monitoring Data" section below) and use of appropriate models (see "Analytical Methods" below, and Table 8.1). Finally, a robust monitoring data set results from a process of feedback loops used to modify sample design and/or models based on current monitoring objective status in an adaptive management framework. All of these steps increase likelihood of success with a monitoring scheme, but monitoring may still not work, even with well-designed efforts, due to reasons beyond the researcher's or manager's control (i.e., reduced budgets and/or commitment to collect data half-way through a study).

Study Design

Given state variables and vital rates that correspond to monitoring objectives, study design then dictates

choice of analysis method. Study designs for monitoring data sets can include (from strong to weak inference): experimental, quasi-experimental, and observational approaches (Table 8.2). Experimental approaches test biological relationships, and can be classified as true or quasi-experimental approaches. True experimental approaches have randomly assigned and replicated experimental units to treatments and controls, whereas quasi-experimental approaches, which often occur with ecological studies, rarely have randomly assigned treatments and controls with experimental units or treatment replication. Experimental approaches directly measure cause and effect, while observational approaches are correlational and evaluate patterns. Most monitoring can be classified as observational (although see Russell et al. 2009).

The basic principles (what, where, when, how) of establishing a monitoring study are the same, regardless of temporal or spatial scales. Monitoring objectives dictate whether data sets are massive (i.e., monitoring animal population responses to global climate change or forest succession) or specific to a targeted area (i.e., animal population response to a localized disturbance event). There are challenges, however, with long-term data sets. Often, researchers or managers are limited by number of sampling locations due to budgetary and time constraints. Limits on sampling locations may also restrict abilities to address study objectives. Thus, innovative approaches (i.e., citizen science [Dickinson et al. 2010]) may be needed. Regardless of monitoring study scale or duration, a valid study design fulfills four main questions of what, where, when, and how.

1. *What?* What parameter(s) are most sensitive to index change? The most essential study design aspect is determining the most informative parameter(s) and precision needed for monitoring objectives. *A priori* knowledge and literature review of species' biology should assist with this aspect. Since these preconditions are not always possible with rare species,

Table 8.1. Animal population state variables and vital rates for monitoring, analysis methods, analysis programs, and sampling considerations. Sampling considerations were condensed from Williams et al. (2002), unless otherwise noted. Although there are several more, we list the most common analysis methods and programs used for monitoring state variables and vital rates. Analysis approaches could be frequentist or Bayesian (Gelman et al. 2004; see Chapter 14 in this volume). With Bayesian approaches, state-space models (see Chapter 10 in this volume) and programs OpenBUGS (Speigelhalter et al. 2007; Lunn et al. 2000) and JAGS (Plummer 2003) are typically used with these state variables and vital rates, with the exceptions of genetic measures.

Monitoring state variable(s) and vital rates	Analysis method	Analysis program(s)	Sampling considerations
Abundance, density, λ (finite rate of increase)	Closed (Otis et al. 1978) and open (Jolly-Seber model [Jolly 1965; Seber 1965]) CMR models (or both closed and open models, <i>sensu</i> robust design models [Pollock 1982]), distance-based methods (Buckland et al. 2001; see Chapter 6, this volume), spatially-explicit capture recapture (SECR; Royle and Young 2008), matrix models ² (Caswell 2001)	MARK, ¹ CAPTURE (Otis et al. 1978; Rexstad and Burnham 1991), DISTANCE (Laake et al. 1996), SPACECAP (Gopalaswamy et al. 2012)	- Requires extensive effort to capture, mark, and recapture animals (CMR), although physical marks not necessary (i.e., noninvasive genetic CMR, camera traps). - Population closure, tag loss (or with genetic CMR, genotyping error [Taberlet et al. 1999]), and sampling nonindependence (from mates, siblings, or animal clusters) should be minimized or incorporated into population models (i.e., Wright et al. 2009). Assumptions include tags are read correctly and marking does not influence animal behavior. Population closure is minimized by limiting number of repeat sample days and avoiding sampling during migration or high rates of mortality/recruitment. For animals that naturally cluster and show high site fidelity, multiple independent groupings need to be sampled. - Multiple sampling methods (Abadi et al. 2010) may improve abundance or density estimates. Evaluation of costs and precision gain is needed with joint data models (Sanderlin et al. 2019). - For distance-based methods: accurate estimation of distance/angles from observer to animal; animals located on the line/post have a detection probability of one; animals are not influenced by observation (see Buckland et al. 2001 for specific considerations). - For density methods, the effective trapping area may not be known, and Spatially Explicit Capture-Recapture (SECR) methods are preferable (Royle and Young 2008).
Survival, nest success	Known-fate analyses (i.e., Kaplan-Meier method [Kaplan and Meier 1958; Pollock et al. 1989a,b]), band-recovery analyses (Brownie et al. 1978; Brownie and Pollock 1985, Barker 1997), Cormack-Jolly-Seber model (CJS; Cormack 1964; Jolly 1965; Seber 1965), nest survival (Dinsmore et al. 2002)	MARK ¹	- Effort for nest survival can be allocated toward increased time searching for nests or more visits. - For known-fate analyses, survival probability should be restricted to days when the fate could be observed and disturbance minimized to nests and surrounding habitat during visits. - Accurate estimation of death times and well-specified origin times are needed with telemetry studies. - Censoring is random and independent of survival. - Sampling periods are instantaneous, and recaptured animals are released immediately. - Emigration from the sampled area is permanent.
Reproduction, recruitment	Jolly-Seber model (Jolly 1965; Seber 1965), reverse-time models (Pollock et al. 1974; Nichols et al. 2000; Nichols 2016)	MARK ¹	- Sampling periods are instantaneous, and recaptured animals are released immediately. - Emigration from the sampled area is permanent.

Table 8.1. (continued)

Monitoring state variable(s) and vital rates	Analysis method	Analysis program(s)	Sampling considerations
Movement/dispersal	Multi-strata (multistate) CMR (Arnason 1972, 1973; Brownie et al. 1993; Schwarz et al. 1993), least cost models (Adriaensen et al. 2003), geneflow via population substructure (Hedrick 2005), genetic assignment tests (Waser and Strobeck 1998)	MARK, ¹ GIS, STRUCTURE (Pritchard et al. 2000), GENELAND (Guillot et al. 2005)	• Simultaneous sampling of multiple sites is preferable. • CMR sampling is often costly, while telemetry may provide more information. • Indirect methods (e.g., genetic monitoring) may increase sample sizes and power to detect changes.
Occupancy, local extinction and colonization probability	occupancy models (MacKenzie et al. 2006; see Chapter 7, this volume)	PRESENCE (Hines 2006), MARK, ¹ R package <i>unmarked</i> (Fiske and Chandler 2011)	• Require repeat surveys (visits and/or sampling points) during a period of closure. • Sampling unit and definition of season appropriate for species. • See MacKenzie and Royle (2005) for more details on occupancy study design.
Range distribution	Maximum entropy modeling with presence-only data (Phillips et al. 2006), occupancy models with presence-absence data (MacKenzie et al. 2006; see Chapter 7, this volume), abundance/density models (see above), abundance indices	MaxEnt (Phillips et al. 2005), PRESENCE (Hines 2006), R package <i>unmarked</i> (Fiske and Chandler 2011)	• Yackulic et al. (2013) provide recommendations based on detection probability (equal to one, less than one, and constant, varies) and sampling probability (varies, constant). • Many assumptions (e.g., constant sampling and detection probability with respect to environmental covariates that determine occupancy) of presence-only data are difficult to meet in practice (Yackulic et al. 2013).
Genetic measures	Hybridization, geographic range, genetic variation, effective population size, movement, population substructure	STRUCTURE (Pritchard et al. 2000), GENEPOP (Raymond and Rousset 1995), ARLEQUIN (Schneider et al. 2000), GENELAND (Guillot et al. 2005)	• Methods rely on reduced genotyping errors (Bonin et al. 2004). Quality and quantity of DNA is important. • Genetic changes with population changes are easier to detect after severe disturbances (Schwartz et al. 2007).
Diversity, species richness, species turnover, species evenness	Multi-species occupancy models (Dorazio et al. 2006; MacKenzie et al. 2006), hierarchical Bayesian analyses and MCMC (see Chapter 14, this volume)	JAGS (Plummer 2003), OpenBUGS (Speigelhalter et al. 2007; Lunn et al. 2000), R (R Development Core Team 2016)	• Require repeat surveys (visits and/or sampling points) during a period of closure. • Sampling unit and definition of season appropriate for all species in the community. • Optimal methods for species richness include focusing on number of sampling occasions, while sampled area percentage is more important for rare species occupancy probability in a community (Sanderlin et al. 2014). • Sampling design recommendations are needed with multi-season, multi-species occupancy models.

¹ Program MARK (White and Burnham 1999).² This analysis method results in a change metric, not a metric derived from repeated inventories.

Table 8.2. Differences in the design aspects of true experiments and quasi-experiments

Design aspect	Type of experimental design	
	True experiment	Quasi-experiment
Treatments	Randomly allocated to experimental units	Self-assigned to experimental units
Controls	Randomly allocated to experimental units	Randomly allocated to experimental units, self-assigned, or lacking
Confounding factors	Controlled by design	Not controlled by design
Cause and effect	Directly inferable	Not directly inferable
Inference	Strong	Weak
Potential design	Randomized complete block; completely randomized; factorial treatments; split plot	Nonequivalent controls; interrupted time series; before-after-control-impact

Table from Block et al. (2001).

studies with similar species may contribute to identifying important parameters with rare species.

2. *Where?* What is the geographic scale for sampling? Researchers and managers should first identify, as closely as possible, the extent of the biological population of interest. For example, there may be interest in monitoring population trend of black bears (*Ursus americanus*) on a wildlife management area (WMA) to make harvest management decisions specific to the WMA, even though black bears have a larger distribution across the landscape. In this case, the target population, and thus geographic scale, would be the WMA only, even though this is a subset of the biological population. This is a cautionary example, however, since black bears that do not reside on the WMA may be subject to different pressures than those that influence the WMA population subset. Any valid study design should extend beyond the WMA because population processes are unlikely to be captured fully on the WMA.

3. *When?* Length of time for monitoring depends on the study system and monitoring questions. For example, results of a study of fire effects on birds would be different for one year, five years, and 20 years after the fire, respectively. The time frame for detecting change will also affect power to detect change and monitoring feasibility.

4. *How?* The sampling method will depend on objectives and biology of the species. For example, mist-netting and banding with capture-mark-resight

might be more advantageous for estimating passerine bird survival than point counts, which are more suitable for estimating occupancy (MacKenzie et al. 2006) or density (Buckland et al. 2001). Potential sampling designs include: simple random sampling, stratified random sampling, systematic sampling, adaptive sampling, cluster sampling, and two-stage cluster sampling (Thompson 2004; Morrison et al. 2008). Several sampling designs can be implemented based on species rarity and elusiveness (Thompson 2004) and animal distribution across space (clumped versus randomly distributed). Rare or elusive species may be easier to detect via non-invasive methods with DNA (Waits 2004) or camera traps (Karanth et al. 2004), as opposed to traditional capture-mark-recapture (CMR) animal trapping methods.

Timing (i.e., season, day or night) and sampling length depend on the species and monitoring goals. Is the species available for detection (i.e., birds during the breeding season will sing more often)? Is it better to sample before or after breeding? Should sampling occur over different seasons (i.e., birds could be sampled during the spring migratory season versus winter for residents)? It is important to sample during the same season so comparisons can be made between and among years.

Lifespan of the species should also be considered: short life spans may not require as many monitoring years as long-lived individuals. For example,

for a small mammal, such as the white-footed mouse (*Peromyscus leucopus*), the full life cycle could be monitored over the course of a year, but the full life cycle of a northern goshawk (*Accipiter gentilis*) could require a decade to monitor. Species with shorter life spans could add more variance to abundance estimate trends than long-lived species of a population.

Without an adequate budget and commitment to collect data by investigators, well-planned studies can fail. Monitoring should not be done if there is inadequate support, since objectives will not be met with available resources (Legg and Nagy 2006). Resources are better allocated to projects that could meet study objectives. Optimal (increased parameter accuracy with reduced effort) study designs (i.e., Field et al. 2005; Sanderlin et al. 2014; Williams et al. 2018) for monitoring are critical for allocating limited resources to key monitoring parameters.

Depending on analysis method, there are important study design sampling considerations (Table 8.1). Methods of increasing capture probabilities reduce bias in monitoring parameter estimates for all analyses (Williams et al. 2002). CMR methods tend to be more labor intensive than occupancy methods, although advances in technologies such as noninvasive genetic sampling and camera traps have improved sampling capacity and observer safety, especially with rare or elusive species. Noninvasive methods are usually more cost efficient for efforts to detect rare or elusive species (compared to physically capturing animals), although genotyping error (Bonin et al. 2004) and other potential biases (Foster and Harmsen 2012) should be considered when designing a monitoring program. For example, De Barba et al. (2010) demonstrated that it was more cost-effective to sample and monitor a small brown bear (*Ursus arctos*) population using noninvasively collected hair and fecal genetic samples than radio-telemetry or physical trapping. They further showed that noninvasive genetic sampling designs (hair traps and opportunistic sampling) have different costs and efficiencies.

Value Added

Most sampling methods have ancillary data that are collected in addition to the main objectives. These additional data could be valuable to project objectives, and may sway decisions about which sampling methods to use. For example, known-fate methods could be selected to estimate survival changes, but the use of Global Positioning System (GPS) or Very High Frequency (VHF) collars could also provide information to develop habitat maps. It is important, however, that ancillary data collection does not increase sampling effort substantially because that would detract from the main study objective(s).

Adaptive Management

Adaptive management, or adaptive decision-making, is an iterative process for simultaneously managing and gaining knowledge about natural resources. Adaptive management is important to ensuring a robust monitoring data set, as it allows sample design and/or model modification based on current status or monitoring objective. The monitoring phase in adaptive management contributes to knowledge of progress toward objectives, resource status and dynamics, and decisions on modifications to resource dynamics models (Williams 2011). Monitoring under adaptive management, if done correctly via valid study design, will have thresholds that trigger specific actions (Nie and Schultz 2012; Schultz et al. 2013). Biological or management relevance will determine thresholds and triggers, which are important for ensuring efficient monitoring efforts (Schwartz et al. 2015). Adaptive management is distinctly different from a "trial and error" approach, wherein one watches what is happening and then decides on a management option. Moir and Block (2001) identify three monitoring feedback loops that address the following questions and prompt specific actions: (1) Are the right things being monitored? (2) Is the monitoring design being implemented correctly? (3) Has the project met stated goals and objectives, or are modifications in order?

Data Quality Controls for Monitoring Data

Without foresight and planning, consistent monitoring data collection is unmanageable. Monitoring data usually include population data from multiple sampling years, locations, and observers, as well as several environmental and biological covariates. Careful attention to detail when training observers to collect data, develop a data management plan, and archive data is essential for ensuring data integrity with data analyses. Data quality steps also ensure that appropriate data are collected to answer study questions and meet project goals and that covariates are collected at correct scale(s).

Relational Databases

Relational database programs (i.e., MySQL, Microsoft Access) offer project flexibility in electronically

storing and retrieving data for quality control and analysis steps. A relational database is a collection of linked tables that contain records (e.g., rows), with each record having fields (e.g., columns). Relationships between entities can be classified as one-to-one, one-to-many, or many-to-many (Figs. 8.2 and 8.3), linked by pairs of values from a primary key (e.g., unique identifier) and foreign key (e.g., a field in a second table that is a primary key in a first table).

Designing a database and import forms before data collection ensures consistency and allows data to be imported and checked for quality as data are collected. Computer and field data logger-data import forms allow users to restrict import fields to valid data input values (i.e., only integer values that are valid with study year field).

Relational databases can also be used to sort and clean data fields for errors by using queries. For example, a common error in multiple-species avian

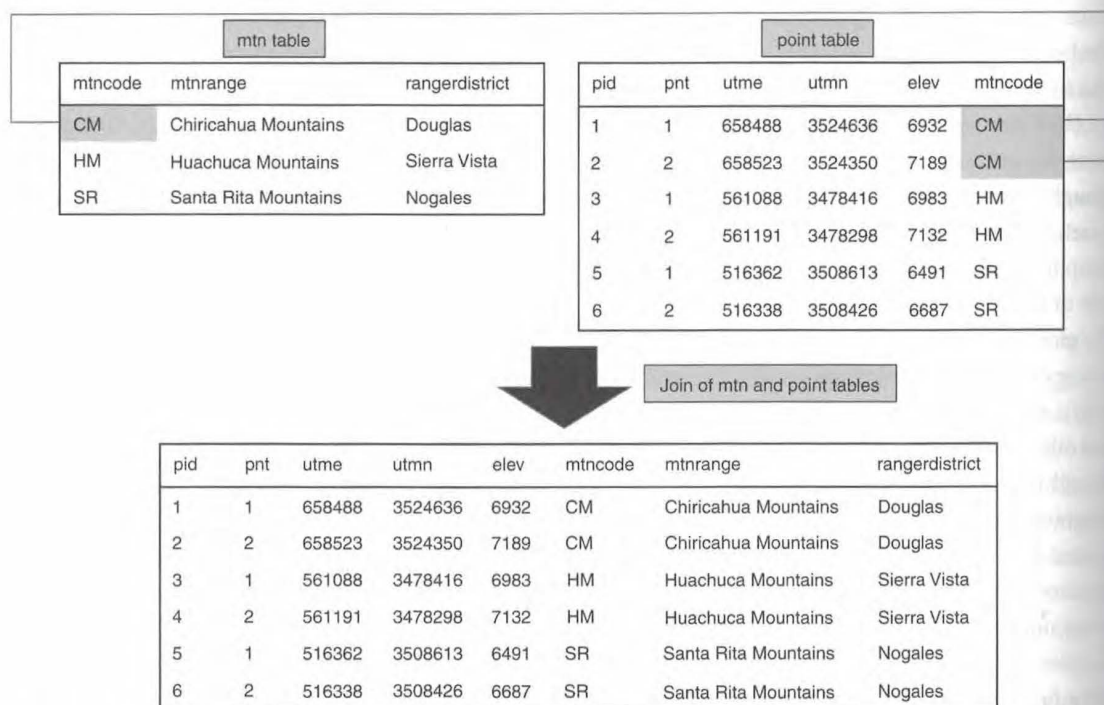


Fig. 8.2. Bird monitoring examples of one-to-one (*mtn* table) and one-to-many (*mtn* table and *point* table) relationships. Each "mtncode" in the *mtn* table is unique to each *mtnrange*. The one-to-many relationship is illustrated with multiple points having the same *mtncode*. Data are stored more efficiently in two tables than in the bottom "join" table.

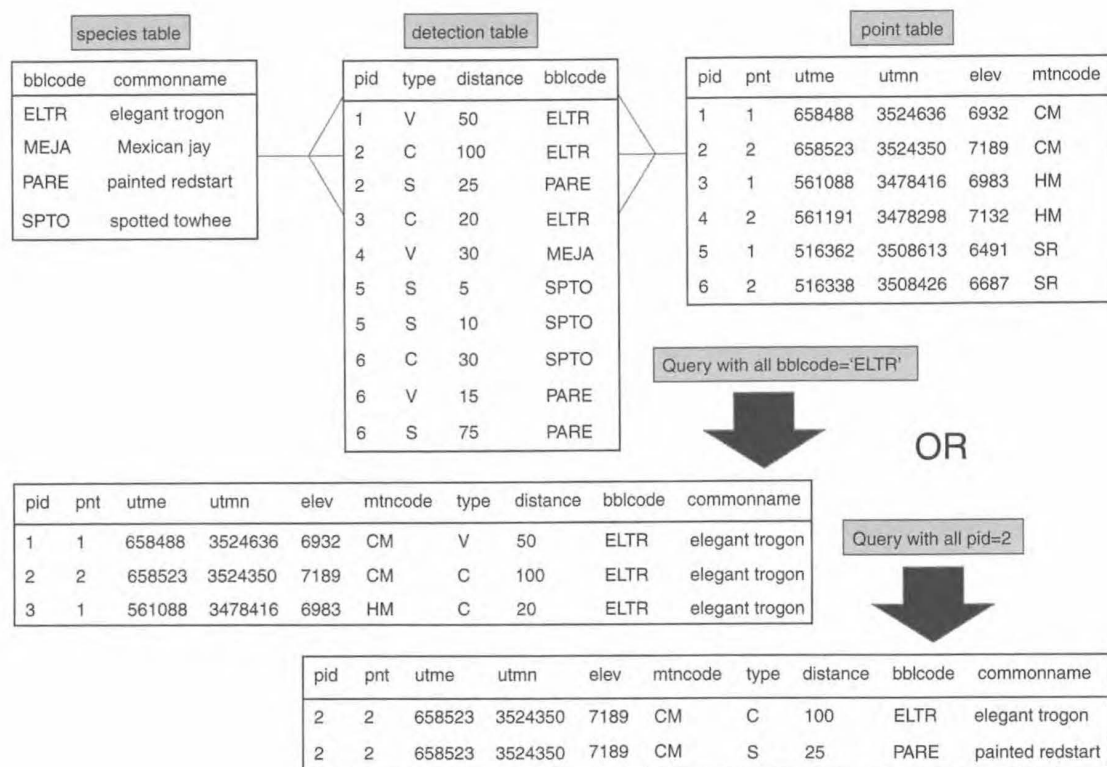


Fig. 8.3. Bird monitoring example of many-to-many relationship. We illustrate two queries whereby a species Elegant trogon (*Trogon elegans*) can be detected at many point count stations, and a point count station (point count station identity [pid] 2) can have many species detected there. Data are stored more efficiently for access and queries in three tables than in one large table.

point count surveys is recording a wrong letter with a species' Breeding Bird Laboratory mnemonic code; therefore, one can query all codes that are not in the species' code table for efficient corrections. Quick report summaries are also possible. For example, with a bird monitoring data set one could be interested in number of different species detected by year and sampling location. Accurate and efficient summaries are accomplished with queries (Watson 2004 provides query examples).

Data Archive

Another critical aspect of data integrity is archiving cleaned data, both physically and electronically. Essential considerations are security and preservation;

hence issues ranging from tampering to future availability and back-up procedures need to be addressed. The primary data archive is the personal data archive, ensuring consistency in future data use. The secondary data archive could include several choices depending on data types (i.e., Dryad [<http://datadryad.org>] or GenBank [<https://www.ncbi.nlm.nih.gov/genbank>]). Journals are starting to require (except with funding agency restrictions and private lands access restrictions) data availability with published studies and are providing archiving capabilities. A data archive must ensure that complete metadata (what, where, why, and how data were collected; data reliability; known data issues) are included with data sets so that information necessary for future analyses will be available.

Analytical Methods

Analysis method choice depends on study design, state variables, and vital rates, which correspond to monitoring objectives. Sometimes the analysis method may depend on the species of interest (Thompson et al. 1998). A few examples include band-recovery methods for survival (Brownie et al. 1978; Brownie and Pollock 1985; Barker 1997), which are more common with birds; removal estimators (e.g., White et al. 1982) for abundance, which tend to be used more with fisheries and small mammal trapping; and nest survival methods (i.e., Dinsmore et al. 2002), which are frequently used with birds. We describe several state variables and vital rates and their most commonly associated analysis methods, analysis programs, and sampling considerations (Table 8.1). In Table 8.1 we also distinguish between two approaches to monitoring—namely, repeated inventories versus change metrics. Our list is not meant to be exhaustive, but it does provide an overview of the methods and programs for state variables and vital rates most commonly associated with monitoring animal populations. Depending on monitoring data availability, novel methods with integrated population models (i.e., Schaub and Abadi 2011) allow multiple state variables and vital rates to be monitored simultaneously (i.e., Tempel et al. 2014).

State Variables and Vital Rates

ABUNDANCE, DENSITY, AND FINITE RATE OF INCREASE

The most common monitoring state variables are abundance (number of individuals in the sampled population), density (number of individuals in the population per unit area), and finite rate of increase (λ ; change in population abundance or density over a unit of time). The most common abundance and density sampling methods include: capture-mark-recapture (CMR), distance-based methods (Buckland et al. 2001), and spatially-explicit capture recapture methods (SECR; Royle and Young 2008). The

most common λ methods and monitoring approaches include: metrics based on multiple inventories to estimate abundance or density, which are then used to extract trends, and change metrics based on matrix models for λ (Caswell 2001). Capture-mark-recapture can be categorized into three types, depending on whether the population is closed to population changes from births, deaths, immigration, and/or emigration (Table 8.1).

In general, abundance estimates are more precise with closed versus open models (Thompson et al. 1998; Williams et al. 2002). From a sampling perspective, however, it is more difficult to maintain closure from movement or demographics. Open models (Jolly 1965; Seber 1965; Schwarz and Arnanon 1996) and temporal symmetry models (Nichols 2016) permit survival, reproduction, and movement estimation, which is more informative regarding population trajectory than abundance. Robust design models (models based on sampling that occurs during primary sessions [population is open] and secondary sessions [population is closed]) are more advantageous than open models because abundance estimates are less biased (Pollock et al. 1993). However, a robust design requires additional sampling effort (compared to open models) and hence more time and money for secondary sampling sessions.

Whereas abundance and density are important, they are not necessarily good surrogates for λ , survival, or reproduction. There is insufficient information to address possible monitoring objectives using only abundance estimates. A population size of 100 with high survival and reproduction rates will have a very different trajectory than another population of size 100 with low survival and reproduction rates. It is important to note, however, that abundance could be the primary monitoring objective and thus survival or reproduction may not be of interest. In these cases, the most efficient way to measure change would be to monitor abundance changes. An advantageous monitoring objective would assess the “why” of abundance changes (assuming minimal additional costs), rather than just monitoring abundance. A

good example of monitoring using λ , in combination with apparent survival and fecundity, is with the northern spotted owl (*Strix occidentalis caurina*) in the Pacific Northwest, a species with which contentious conservation issues are associated because of its association with old forests (Anthony et al. 2006). Monitoring studies often use several vital rates, as in this example, to understand why a population has a certain trajectory. The main study objective of Anthony et al. (2006) was to determine if owl populations were stationary ($\lambda = 1$), increasing ($\lambda > 1$), or declining ($\lambda < 1$). They concluded that populations were declining in nine study areas and stationary in four.

OCCUPANCY

Occupancy probability (MacKenzie et al. 2006), or probability of species presence, is becoming more prevalent in monitoring endeavors (i.e., MacKenzie and Nichols 2004), given a perceived benefit of reduced effort. Occupancy provides more opportunity to monitor changes in rare species compared to CMR or distance-based methods for which it is difficult to obtain adequate sample sizes. But whereas less effort may be needed for occupancy than abundance monitoring, it is not as effective for gaining information about population status.

Occupancy is based on species presence, and does not indicate abundance, unless assumptions about the relationship between detection and population size have been made (Royle and Nichols 2003). If a species is present, occupancy models do not distinguish between 2 individuals versus 100, which may be critical with monitoring. Although occupancy provides less potential information than abundance (or other state variables), it is better to quantify occupancy well than to do a poor job of estimating abundance. As with the abundance and λ relationship for detecting monitoring trends, the change metrics of interest with occupancy would be local extinction and colonization probabilities.

Ganey et al. (2004) used a pilot study of Mexican spotted owls (*S. o. lucida*) to assess abundance mon-

itoring feasibility, but determined it was cost-prohibitive, and thus recommended occupancy monitoring as a population size index because plot size (1 km²) was assumed to have one individual if present. The U.S. Fish and Wildlife Service Mexican Spotted Owl Recovery Team (2012) then used this information about detection probabilities, occupancy rates, and habitat variables to design an occupancy monitoring program with sufficient sampling effort (number of call stations per survey plot, number of visits per plot, numbers of plots).

DIVERSITY, SPECIES RICHNESS, SPECIES TURNOVER, SPECIES EVENNESS

Multi-species monitoring is also becoming more frequent (i.e., DeWan and Zipkin 2010; Noon et al. 2012) using multi-species occupancy models (Dorazio et al. 2006; MacKenzie et al. 2006). The multi-species occupancy model extends the single-species occupancy model (MacKenzie et al. 2006) and allows estimation of unknown species richness (number of species in an area) and species turnover (local extinction and colonization), while accounting for imperfect detection probabilities (Royle and Dorazio 2008). This is an area of rapid statistical method growth, and holds vast potential for including detection probability in diversity measures (number of species and abundance of each species) and community dynamics (Iknayan et al. 2014).

There are, however, limitations to adopting a multiple-species approach. An optimal sampling design will differ for rare and for common or abundant species (Sanderlin et al. 2014), and maximizing the number and range of species that are adequately detected can be challenging (Manly et al. 2004). Still, monitoring multiple species simultaneously, may be preferable to a single-species approach, especially for a study with limited resources. A single-species approach to monitoring as representative of the community runs risks of not representing other species in the community, having weak environmental relationships with management actions, being poor future community indicators, or having so

much uncertainty in single-species responses that community response interpretations are not possible (Manly et al. 2004).

Similar to abundance, occupancy probability and species richness are valuable to monitoring objectives, but do not give species' trajectories, such as local colonization and extinction probabilities. Thus, from a monitoring perspective, more information about persistence is available from local colonization and extinction probabilities compared to occupancy probability. Russell et al. (2009) used a BACI (before-after-control-impact) design to evaluate effects of prescribed fire on avian communities in a ponderosa pine (*Pinus ponderosa*) forest using multi-species occupancy models to estimate species richness, species turnover, and extinction. One advantage of using these methods is that in addition to obtaining information about fire impacts on common species, it was possible to obtain this information for rare or elusive species, which is important for land management agencies with limited budgets. Although Russell et al. (2009) concluded that prescribed fire treatments had little to no short-term effect on the avian community, this did not preclude the possibility that longer-term effects were present. Multi-species occupancy models allow long-term monitoring of turnover and extinction trends.

SURVIVAL AND REPRODUCTION

Many analysis methods for detecting vital rate trends of survival and reproduction or recruitment are based on CMR sampling methodology or radio-telemetry (Table 8.1), although recent advances in noninvasive genetic sampling have elevated the potential in monitoring survival and reproduction change, (Schwarz et al. 2007). Sampling effort is similar to that of abundance methods and requires multiple sample occasions across years (CMR) or days to years (radio-telemetry).

Returning to the northern spotted owl example, the other study objectives were to identify reasons for owl population changes by quantifying temporal and age-specific survival and fecundity rate trends (An-

thony et al. 2006). The researchers found that 6 of the 14 study areas had declining fecundity rates, while 5 study areas had declining and 9 had stable survival rates. Study results suggested fluctuations in fecundity and survival related to weather or prey abundance, which helped guide future monitoring recommendations and identified possible reasons for population trajectories.

MOVEMENT

There are different sampling methods (and thus analysis approaches) for estimating movement trends over time: multi-strata CMR (Arnason 1972, 1973; Brownie et al. 1993; Schwarz et al. 1993), gene flow via population substructure (Hedrick 2005), genetic assignment tests (Waser and Strobeck 1998), and radio and global positioning systems (GPS) telemetry with geographic information systems (GIS) analyses (White and Garrott 1990; Adriaensen et al. 2003). CMR methods, which involve sampling at discrete points in time, are often costly and yield low recapture or resighting probabilities, especially for migratory animals such as birds (Webster et al. 2002). Satellite telemetry can provide valuable movement path information; however, sample sizes (thus power to detect change) are often limited due to high costs, and telemetry methods are often more suitable for larger species due to technological limitations (Hebblewhite and Haydon 2010).

Indirect methods with genetic monitoring and stable isotopes may be more cost-effective and provide more movement information with higher sample sizes or information from individuals that dispersed and reproduced. For example, although Coulon et al. (2008) concluded that dispersal and gene flow between Florida scrub-jay (*Aphelocoma coerulescens*) metapopulations were similar on the basis of separate analyses of demographics and genetics, dispersal and genetic grouping results would have more closely matched if all jays were sampled with the demographic analysis. In this example, jays that dispersed longer distances were missing from the demographic analysis.

RANGE DISTRIBUTION

Species distribution models (SDMs) rely on correlations between species occurrence data and spatial environmental data, resulting from multiple modeling approaches: presence-only data (i.e., maximum entropy modeling; Phillips et al. 2006), presence-absence data (occupancy models; MacKenzie et al. 2006), abundance or density models (detailed above), or abundance indices. In a monitoring context, range distribution trends are quantified by expansions or contractions in species' ranges. Many assumptions (e.g., constant sampling and detection probability with respect to environmental covariates that determine occupancy) of presence-only data are difficult to meet in practice (Yackulic et al. 2013). In an eight-year Swiss breeding bird study monitoring European crossbill (*Loxia curvirostra*), Kéry et al. (2013) illustrated how detection probability was an important source of variation in space and time; had they not included it in their dynamic occupancy models, SDMs would have been biased.

GENETIC MEASURES

There are several analysis methods available to detect trends in genetic measures of hybridization, geographic range, genetic variation, effective population size, and population substructure (i.e., Raymond and Rousset 1995; Pritchard et al. 2000; Schneider et al. 2000; Guillot et al. 2005). Genetic monitoring applications are relatively new, compared to the other methods described above, and show great promise (Schwartz et al. 2007), especially for monitoring adaptive responses to environmental changes such as climate change (Hansen et al. 2012) and for monitoring rare or elusive species (Waits 2004). Genetic monitoring can be more cost-effective than traditional methods, although costs of accounting for and reducing genotyping errors should be considered (Bonin et al. 2004). For example, Beacham et al. (2008) demonstrated that population genetic assignment of Chinook salmon (*Oncorhynchus tshawytscha*) from the Yukon River was both accurate and more cost-efficient than traditional methods of de-

termining population origin. This approach also allowed managers to determine harvest limits or quotas at specific locations more efficiently—an important consideration in a management context. Data preprocessing and quality control steps sometimes differ based on the genotyping technologies employed due to the amount of data generated (i.e., approaches with microsatellites or mitochondrial DNA have fewer loci than next-generation technologies, which could produce millions of single nucleotide polymorphisms or the whole genome of an organism). Massive data sets can create bioinformatics challenges, but also have potentially more information and power to detect population changes.

Environmental DNA (eDNA) monitoring using trace amounts of DNA from many different species in water or soil, for example, is also a novel approach to genetic monitoring (Bohmann et al. 2014). The data collection phase is efficient and cost-effective, yet still poses challenges in the laboratory (e.g., false positives or negatives) and for data analysis (e.g., efficiently handle large amounts of data) challenges. There are questions of how accurate the genetic information is with eDNA technologies (i.e., representative sample of target populations, detection probability biases, false positives due to study design) and whether it could be useful for determining not only presence-absence, but also relative abundance, effective population size, and in combination with other traditional sampling approaches (Bohmann et al. 2014). In a monitoring context, eDNA can be used to detect trends in occupancy (e.g., local extinction and colonization), and possibly changes in relative abundance and effective population size over time.

Analysis Programs

There is a suite of analysis tools available to evaluate monitoring data sets (Table 8.1). Many of these tools can be used with simulation studies (i.e., Field et al. 2005) to evaluate whether there is sufficient power to answer monitoring questions with a given effect size by using estimated quantities (i.e., detection

probability, sample size) from pilot studies, previous studies on or near the study area, or simulated values based on similar studies. It is important to consider the analysis method, animal distribution and spatial scale, and costs when evaluating monitoring sampling designs (Thompson et al. 1998). There are also programs that allow users to evaluate different study designs (sample size), effect size, and associated power for abundance (Program Monitor [Gibbs and Ene 2010]) or occupancy (GENPRES [Bailey et al. 2007]; SPACE [Ellis et al. 2014]).

We illustrate the interactions of sample size, effect size, and power using a fictitious small mammal data set (Fig. 8.4). As sampling effort increases, power to detect a non-zero trend increases. In this example, ability to detect a trend (percentage change in abundance) is different with effect size: there is more power with a bigger effect size. Although this

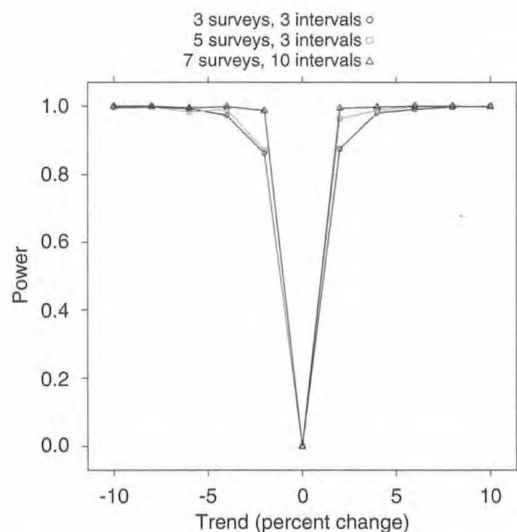


Fig. 8.4. Monitoring data example of the power to detect a trend with different sampling effort amounts. Data were created to be similar to a small mammal abundance study consisting of five plots using program Monitor (Gibbs and Ene 2010). Data were simulated for 10 years, 1,000 iterations, with 2 tails, with rounding, and truncation with counts < 0 . The survey design consisted of monitoring for 10 intervals (all years) or 3 intervals (years 0, 4, 9) with route regression and the log-normal measure type.

example is not exhaustive, one can see potential for sampling efficiencies with monitoring. The population may not need to be monitored all years and/or at the same sampling intensity to achieve a desirable power, and thus design optimization is valuable. Additionally, it is valuable to evaluate sensitivity (Williams et al. 2002) of state variables and vital rates for persistence (e.g., identify which state variables and vital rates are the greatest contributors to persistence; persistence would show the most variation with perturbations of these state variables and vital rates) and to determine appropriate state variables and vital rates for monitoring.

Different packages and programming languages may be needed, depending on state variables and vital rates, as well as problem complexity. Some monitoring questions may be answered with analysis packages (Table 8.1), while other questions are more complex, have a broader scope, or occur over larger scales, and require tailored analyses (i.e., Bayesian approaches) using programming languages like R (R Development Core Team 2016) or Python (van Rossum et al. Python Software Foundation, <https://www.python.org/>). For example, single or two-species occupancy models can be analyzed with PRESENCE (Hines 2006), but Bayesian approaches are necessary with multi-species occupancy models. Although custom-designs can be advantageous, analysis and output time is typically longer due to complexity and to ensuring accurate parameter estimation. Computational time may be critical in time-sensitive monitoring analyses (i.e., setting harvest regulations).

Conclusions

Advances in statistical methods, software, and computational ability have provided some improvement in our ability to collect and analyze high-quality monitoring data sets, yet important challenges remain. We do not always follow the steps described above, especially those concerned with gathering preliminary data and conducting power analyses to determine if objectives can be met with available budgets.

Critical evaluation of cost-effectiveness and efficiencies is needed when deciding on sampling and analysis methods for detecting population changes. Analysis and method choices depend on study design, state variables and vital rates corresponding to monitoring objectives, and species of interest. Selecting appropriate methods in a cost-efficient manner is essential to effective monitoring.

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