



Third Edition

Methods in Stream Ecology

Volume 1: Ecosystem Structure

Edited by
F. Richard Hauer
Gary A. Lamberti



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Amphibians and Reptiles

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17.1 INTRODUCTION

Herpetofauna are a polyphyletic group including amphibians and reptiles. Carolus Linnaeus originally classified these organisms together from the Greek *herpeton* meaning “to creep.” These clades have continued to be studied together due to similar physiological and ecological characteristics (Pough, 1980; Vitt and Caldwell, 2013). The class Amphibia, from *amphibios* meaning “both kinds of life,” include the orders Salientia (frogs and toads), Caecilians, and Caudata (salamanders and newts, Fig. 17.1). The paraphyletic class Reptilia includes orders Testudines (turtles and tortoises), Sphenodontia (tuataras), Squamata (snakes, amphisbaenia, and lizards), and Crocodylia (alligators, crocodiles, and gavials, Fig. 17.1). A wide variety of both amphibians and reptiles rely on and occupy lotic systems.

The traditional model of amphibian life histories includes an aquatic larval stage before metamorphosis into semi-aquatic adults. Different amphibian species have adapted this model to have long and short larval stages, some eliminating them entirely (Petranka, 1998). Likewise, adults can be entirely terrestrial to entirely aquatic, yet all maintain permeable skin that allows gas diffusion and exchange. Cutaneous respiration necessitates moist microclimates to prevent water loss (Spotila, 1972; Feder, 1983; Feder and Burggren, 1992; Hillman et al., 2008). Amphibians occupying lotic systems occur in the temperate and tropical zones around the world and have a variety of adaptations for lotic systems (Lytle and Poff, 2004). Some amphibians, including stream-breeding Plethodontids, have larval periods that match the temporal stability of their preferred habitat (Petranka, 1998; Bruce, 2011). Because most stream-breeding Plethodontids prefer headwater streams, larval periods can range from only a few weeks to over a few years, depending on the permanency of water flow (Petranka, 1998). Some *Desmognathus* sp. prefer wet drainages and seeps—their larvae cannot have larval periods on the scale of years because their larval habitat would disappear (Bruce, 1989, 1996, 2007). Larger *Desmognathus* sp. and those from the Hemidactyliini lineages occur in perennial streams where larvae can take much longer to mature (Petranka, 1998; Bruce, 1972, 1985, 2007). In the western United States, there are even populations of species in the genus *Dicamptodon* that have paedomorphic adults, or adults that display larval traits like gills and tail fans (Nussbaum and Clothier, 1973). Alternately, species that occur in highly ephemeral systems often exhibit long adult periods thought to buffer against years of no recruitment due to the absence of water (Boulton, 2003; Lake, 2003; Price et al., 2012a). Some adults that require aquatic habitat can even develop water-resistant cocoons to withstand periods of no water (Baker, 1954; Clinton et al., 1996).

Another challenge for amphibians in lotic systems is effective egg fertilization. In frogs and some salamanders, fertilization occurs externally, and in running water, sperm may be flushed downstream before fertilization. For salamanders with external fertilization (e.g., hellbenders, *Cryptobranchus alleganiensis*), courtship behavior often takes place beneath large rocks where the flow is minimized (Nickerson and Mays, 1973; Nickerson and Tohulka, 1986). Otherwise, most salamanders exhibit internal fertilization and terrestrial courtship and deposition of spermatophores (Houck and Verrell, 1993). Some frogs display adaptations such as laying eggs on the undersides of leaves above the stream (Wells, 2007), creating foam nests that trap sperm (Byrne and Whiting, 2008), or even developing an external appendage for sperm transfer in the highly aquatic Leopelmatidae and Ascaphidae (Sever et al., 2001). Another challenge for frogs is mate attraction. Frogs typically employ acoustic signals to attract mates, but running water can interfere with transmission of acoustic information.



FIGURE 17.1 Representatives of (A–C) amphibian (A. Frog, B. Salamander, C. Caecilian) and (D–G) reptile (D. Turtle, E. Snake, F. Lizard, G. Alligator) groups. Photos by Todd Pierson.

Some frogs, such as *Atelopus zeteki*, have diminished vocal calls and instead use visual cues (waving) to attract mates (Lindquist and Hetherington, 1996). Alternatively, most mate cues in salamanders are chemical (Houck, 2009).

Finally, amphibians have many behavioral and morphological adaptations for running water, such as upstream-biased dispersal and occasional terrestrial dispersal (Lowe, 2003; Cecala et al., 2009; Grant et al., 2010), but we will focus the rest of this discussion on morphological adaptations that facilitate maintenance within upstream reaches. Few lotic amphibians are free swimming—most crawl along and among benthic substrates. They accomplish this by having wedge-shaped heads that use water flow to drive their bodies to the bottom of streams and rivers (Petranka, 1998). Some salamanders have

developed keratinized toe-tips that may help them grasp the substrate to prevent downstream displacement. This adaptation is also seen in the highly aquatic frog *Barbourula kalimantanensis* (Bickford et al., 2008). Although some tropical frogs may not breed in streams, their tadpoles must have adaptations to avoid downstream displacement to less suitable habitat. These tadpoles are known to have mouth or ventral morphology that allows them to remain “suctioned” onto benthic substrate (Gradwell, 1971; Wells, 2007). Finally, lunglessness appears to be an adaptation for aquatic life in all major groups of amphibians, including caecilians (Nussbaum and Wilkinson, 1995; Petranka, 1998; Bickford et al., 2008). Lunglessness may have been an adaptation to achieve negative buoyancy in well-oxygenated aquatic habitats (Ruben and Boucot, 1989; Beachy and Bruce, 1992). Species that maintain lungs have developed adaptations to increase surface area for gas exchange, which minimize surfacing behaviors. For example, mudpuppies and sirens maintain external gills as adults, and hellbenders have external fleshy folds that increases skin surface area (Petranka, 1998; Wells, 2007).

Unlike amphibians, reptiles can withstand longer periods of time away from water because their scales minimize desiccation (Vitt and Caldwell, 2013). However, like amphibians, reptiles use lotic systems in a variety of ways, including as primary habitat (e.g., order Crocodylia and many turtles), for refuge (e.g., basilisks and iguanas), and for foraging (e.g., natracine snakes). Regardless of the extent of aquatic habitat use, all reptiles have amniotic eggs that must be laid outside of an aquatic habitat (Vitt and Caldwell, 2013), except for the northern snake-necked turtle of Australia, which lays its eggs under water and embryonic development is arrested until the water recedes (Kennett et al., 1993). For some species, particularly large reptiles like crocodilians and large aquatic turtles, egg-laying ventures represent the only times they will exit aquatic habitat. These species, that rarely leave water, exhibit morphological and physiological adaptations to facilitate their persistence in aquatic habitat. First, reptiles exhibit a diversity of adaptations that facilitate movement in water. These include front flippers in the Fly River turtle (*Carettochelys insculpta*), webbed feet in snapping and map turtles as well as basilisks (facilitates running on water, Laerm, 1973), long nails that facilitate crawling on river bottoms such as in musk turtles, and dorsolaterally compressed tails in crocodilians and some lizards, such as iguanas (Fish, 1984). Except for the Fly River turtle, which primarily uses its front flippers for propulsion, turtles move in water by paddling all four legs. Crocodilians and lizards rarely use their limbs for locomotion in water; instead, they use a serpentine movement similar to snakes. As ectotherms that typically prefer operating temperatures above that of their freshwater habitats, aquatic reptiles often exhibit basking behaviors (Seebacher and Franklin, 2005).

Other physiological adaptations allow reptiles to remain underwater for prolonged periods of time for either overwintering or diving. Turtles and snakes have an incomplete septum between the left and right ventricle that facilitates pumping mixed oxygenated and deoxygenated blood to the systemic circuit (Vitt and Caldwell, 2013). Crocodilians have a complete four-chambered heart, but the foramen of Panizza connects the left and right aorta, allowing deoxygenated blood to bypass the pulmonary circuit. Both of these morphological varieties allow individuals to spend extended time underwater by shunting blood from the pulmonary circuit not in use underwater to the systemic circuit (Vitt and Caldwell, 2013). As ectotherms, these animals also have low metabolic rates and slow heart rates that maximize dive length (Pough, 1980). Aquatic reptiles can increase blood oxygenation through dense capillary networks at the mucosal layers of the mouth, throat, and cloaca (Wang et al., 1989). These regions can allow for cutaneous gas exchange while the reptile is underwater.

Numerous studies have documented the vital role of amphibians and reptiles in freshwater ecosystems. Both amphibians and reptiles are often embedded in a myriad of relationships within stream food webs (Davic and Welsh, 2004). Both taxonomic groups can act as predators or prey depending on the context. For example, stream salamanders from the family Plethodontidae (*Gyrinophilus*, *Pseudotriton*, and *Desmognathus*) can be top predators in headwater streams where fish are not present (Hairston, 1987). As top predators, stream salamanders are a driving force in determining the distribution and abundance of aquatic invertebrates within these systems (Huang and Sih, 1991; Parker, 1994; Lowe and Likens, 2005). In addition, stream salamanders have made an excellent system for studying intraguild predation because many interactions are size-dependent (Beachy, 1994; Rudolf, 2008). Smaller species will partition resources spatially and temporally to avoid interactions with other species or larger conspecifics (Hairston, 1980, 1986).

Many stream salamanders are significant prey for fish (Davic and Welsh, 2004). Indeed, trout (rainbow and brook) often limit the distribution and abundance of salamanders in the headwater streams of the Appalachians (Resetarits, 1991, 1995; Lowe et al., 2004). While less is known about larger salamanders in the higher order streams and rivers, it is highly probable that they serve essential roles in structuring those communities as well (Petranka, 1998). Indeed, one larger salamander species (*Necturus maculosus*) serves as the only non-fish host for the mussel species *Simpsonaias ambigua* (Watters, 1995). As *N. maculosus* populations are susceptible to declines, so too are the populations of the salamander mussel (McDaniel et al., 2009). Hellbenders may play an important role in structuring crayfish communities due to the preponderance of crayfish prey in diets (Swanson, 1948). Tadpoles are also key herbivores in neotropical stream systems (Wells, 2007; Whiles et al., 2013; Connelly et al., 2014). As some amphibian species have disappeared or declined due to

disease, researchers have noted dramatic differences in ecosystem structure and function (Whiles et al., 2013). With reduced tadpole biomass, standing stocks of epilithion have doubled despite increases of grazing and shredding macro-invertebrates (Connelly et al., 2014; Rantala et al., 2015). This research has indicated that no compensation has occurred for the loss of the tadpole grazers, and a time-lag shift is occurring as nutrient cycling changes in these stream systems (Colón-Gaud et al., 2010; Rantala et al., 2015).

Reptiles are also major components of lotic system food webs. Riverine turtles are especially adapted for fulfilling trophic roles as either herbivores, omnivores, or carnivores (Ernst and Lovich, 2009). Many are generalist predators that have diets varying according to ontogeny, sexual dimorphism, geography, and microhabitat usage (Moll and Moll, 2004). Given the extent of generalist diets, it is not surprising that studies on the direct impacts of freshwater turtles on prey are scarce (Jackson, 1996). Instead, many studies have focused on documenting the diversity of prey in turtle diets and the range of morphological variation within and across species (see Moll and Moll, 2004; Ernst and Lovich, 2009 for reviews). Given this variation in both diet and morphology, many species likely have an impact at multiple trophic levels. For example, river terrapins will eat invertebrates, fish, plant material, and carrion (Moll, 1980). One species, the alligator snapping turtle, actually lures in prey with a worm-like tongue (Pritchard, 1989). Predacious fish make up a significant total of alligator snapping turtle diets (Harrell and Stringer, 1997). One other major aspect of food webs to which turtles are integral includes scavenging (Moll and Moll, 2004). Carrion can compose approximately 20% of diets for side-necked turtles in the Murray River of Australia (Thompson, 1993). Thompson (1993) estimated that turtles in that system could remove up to 430 metric tons of carrion daily. Therefore, it is safe to assume that turtles play a significant role in energy flow and nutrient cycling in lotic systems (Moll and Moll, 2004).

In addition to serving as dominant predators and herbivores in lotic systems, turtles are also important prey species. Most of the mortality as prey occurs at the egg and hatchling stage by mammalian predators (Moll and Moll, 2004). This high predation rate on turtle eggs aids in the redistributing of energy from the aquatic to the terrestrial environments (Congdon and Gibbons, 1989). Avian and other reptiles (crocodilians and other turtles) and can also serve as predators on turtles (Ernst and Lovich, 2009). However, invertebrates (dipteran maggots) have also been implicated as sources of mortality (Vogt, 1981).

Aside from the previously mentioned role of amphibians and reptiles in food webs, other major motives exist for their study in lotic systems. First, the sheer biomass of both amphibians and reptiles is astounding in comparison to other taxonomic groups. Stream salamanders can reach remarkable biomasses (ranging from 1.7 to 99.3 kg/ha) in small headwater streams (Davic, 1983; Hairston, 1987; Peterman et al., 2008). This rivals biomass estimates for larger vertebrates like birds and mammals in the surrounding upland ecosystems (Burton and Likens, 1975; Semlitsch et al., 2014). Similarly, turtles in medium to large lotic systems can also reach substantial biomasses with up to 137, 255–345, and 877.3 kg/ha for western pond turtles (Bury, 1972; Iverson, 1982), Geoffrey's side-necked turtles (Souza and Abe, 1997), and pond sliders (Congdon et al., 1986), respectively.

Second, both groups are indicators of water quality and environmental stressors (Sparling et al., 2010). Salamanders have served as an excellent bellwether species for watershed protection and management (Welsh and Ollivier, 1998; Willson and Dorcas, 2003). Most species require cool, well-oxygenated water with low sediment loads and conductivity (Petranka, 1998; Davic and Welsh, 2004). If these parameters are compromised, then salamander diversity, density, and occupancy generally decline. This has been noted in stream systems where canopy cover has been reduced due to urbanization and logging, leading to higher stream temperatures and higher sediment loads (Barrett et al., 2010; Price et al., 2012b). Higher sediments have been connected to egg and larvae mortality in eastern hellbenders (Dundee, 1971).

Many riverine turtles are long-lived (with some species living >20 years in the wild; Gibbons, 1987) and can accumulate biological pollutants over time (Sparling et al., 2010). Mercury contamination in streams and rivers has exposed many aquatic organisms to the deleterious effects of mercury (Hopkins et al., 2013a). Recently, riverine turtles (e.g., *Chelydra serpentina*, snapping turtle) have been documented with shocking levels of mercury (Hopkins et al., 2013b). The effects of mercury exposure are less understood, but trade-offs likely exist for adult and offspring (Hopkins et al., 2013c). Due to their longevity and biomass and the current state of many lotic systems, research with turtles and pollutants will likely be a very fruitful avenue in conservation research. As specialized predators, some aquatic herpetofauna may also be among the first species to decline following watershed disturbance (e.g., crayfish snakes prey exclusively on molted crayfish).

Finally, ecological and evolutionary questions revolve around the central theme of understanding what factors influence the distribution and abundance of organisms. Herpetofauna biodiversity can be exceptionally high in lotic ecosystems, which makes for an excellent system to consider what facilitated this diversity and how it is maintained. For example, lotic systems of the southeastern US are prime areas to investigate these types of questions. Turtle and watersnake diversity is highest in the lowland regions, and stream salamander diversity is highest in low-order streams of the upland regions

(Petranka, 1998; Gibbons and Dorcas, 2004; Buhlmann et al., 2009). Recent biogeographic work by Angielczyk et al. (2015) has identified several key factors explaining variation in North American freshwater turtle biodiversity, including various precipitation and temperature variables. Indeed, subtle differences in climatic conditions of montane and lowland regions of North America may be responsible for the documented salamander species' richness (Kozak and Wiens, 2005, 2010). Both of these aforementioned studies indicate the importance of abiotic factors and the potential susceptibility of herpetofauna to climate change.

The sensitivity of herpetofauna to environmental change and their role in lotic ecosystems suggest that they are a group in need of additional research. One challenge to collecting data on herpetofauna is the ability to detect individuals of a variety of species. The physiology and ecology of these organisms requires that they spend much time where they are unavailable for capture: underwater, in the substrate, underground, or out of the river systems. These behaviors increase the likelihood that researchers will detect false absences—that is, not detect individuals or species that are, in fact, present. The objective of this chapter is to describe capture methods and strategies that may be used to observe select groups of amphibians and reptiles for measurements of population demographics, diversity, or other individual traits. These methods explore different methods for evaluating detection or capture probabilities for two groups of herpetofauna to ensure that researchers can recognize situations in which detection or capture biases may influence the results of their study. We explore simple and complex ways to evaluate these rates. We encourage researchers to explore these methods in more detail using the useful references we have provided.

17.2 GENERAL DESIGN

17.2.1 Study Design Considerations

The process of designing a study begins with specifying clear objectives or hypotheses to be tested. The ecology of focal species should be carefully considered to ensure that research questions are interesting and the approach is tractable. Sometimes, people weigh the costs and benefits of “intensive” or “extensive” sampling when considering the study designs. Intensive approaches may involve describing few populations in detail, whereas an extensive sampling regime may describe few details about a larger number of populations. While it is true that certain techniques are labor-intensive, saving time is pointless if it means failing to collect data that are needed to address research questions. It may be more productive to consider whether one is interested in understanding processes within a single population or community, or if one is interested in making broader inferences about a species across entire landscapes. A few examples of this would be estimating demographic rates within a population (Cecala et al., 2013), quantifying patterns of abundance or occupancy across a landscape (Price et al., 2012b), or describing traits within a population (Lowe et al., 2004).

If study objectives include examining the effects of larger spatial patterns on stream organisms, then analyses of landscape structure should be done to inform the selection of study sites. While random sampling is helpful for making broader inferences, different strata may be useful, especially if focal species are not found throughout watersheds. Moderate-to-high resolution spatial data for stream networks can be downloaded for many places within the US (<https://nationalmap.gov>), and elevation data are available for most places on the planet (<http://www2.jpl.nasa.gov/srtm/cbanddataproducs.html>). Most geographic information systems' software contain packages for delineating stream networks, and GRASS GIS has packages for quantifying the spatial structure of stream networks and the position of sampling sites within stream networks (Jasiewicz and Metz, 2011). This can help ensure that researchers select study sites representative of their study organism's requirements. Alternatively, researchers may be interested in controlling for the effect of land use on aquatic organisms. If this is the case, then spatial analyses are conducted prior to field sampling, which provides a good opportunity to create a project database that will facilitate the integration of field survey data and spatial data in later analyses.

For studies that seek to understand the distribution and abundance of amphibians and reptiles, hierarchical models provide a very useful analytical framework. Although explicitly specifying a model for the distribution or abundance of a species may sound complicated, identifying a formal model of the abundance or presence of a species is an excellent way to clearly articulate hypotheses about a system. Kéry and Schaub (2012) provide an accessible introduction to the use of hierarchical models in ecology, and these methods can be applied to amphibians and reptiles in lotic environments. Hierarchical models treat survey data as the result of (1) ecological processes that govern the distribution or abundance of a species and (2) of observation processes that can include factors responsible for imperfect detection. In some cases, the proportion of a population that is available to be sampled may also change over time (Grant, 2015). Stream salamanders are likely to move below the ground during periods of drought (Price et al., 2012a). Likewise,

hierarchical models may be designed to account for reduced spatial variation associated with multiple sites located within a subwatershed.

In order to account for the observation process, some form of repeated sampling is usually used. This can take a variety of forms, from temporary removal sampling, double observer sampling, or repeated visits to sampling sites (Williams et al., 2002). Mark-recapture methods also provide a means for accounting for detection probability. Some have resisted the use of these methods by arguing that models carry assumptions. However, this critique fails to acknowledge that the use of other methods that ignore imperfect detection depend upon the implicit assumption of perfect detection (Mazerolle et al., 2007). For example, if individuals are trap-shy and less likely to be recaptured, results that do not incorporate detection probabilities will suggest that the population is declining (Cecala et al., 2013).

In general, herpetofauna are notoriously difficult to efficiently sample (Heyer et al., 1994; Mazerolle et al., 2007; McDiarmid et al., 2012; Tesche and Hodges, 2015) because many species are fossorial, sedentary, and cryptic. Additionally, abiotic factors, such as temperature, humidity, and precipitation can dramatically influence behavior patterns and therefore impact the detectability and sampling of this group (Connette et al., 2015). Even with the diversity of sampling techniques developed and utilized for this group, obtaining unbiased estimates (Tesche and Hodges, 2015), detection probabilities (Sterrett et al., 2010), and demography estimates (e.g., sex ratio and size-class distribution; Ream and Ream, 1966; Koper and Brooks, 1998; Gamble, 2006; Willson et al., 2008) for reptiles and amphibians are often still difficult. These difficulties are often because of low and variable rates of capture (Bluett et al., 2011), and the ability of some species or one sex within a species to avoid capture (Frazer et al., 1990; Willson et al., 2005; Brown et al., 2011). Even at the community level (e.g., diversity indices), capture methodology can create biases because interspecific behavioral differences among species influence the detection and capture (see Browne and Hecnar, 2005; Gamble, 2006). For example, basking traps will be inefficient to capture turtle species, such as snapping turtles, that rarely bask out of water. To lessen the effect of these biases on statistical results, researchers should carefully consider study design and, in some instances, should utilize several capture methods within their study design when working with these groups—in particular with turtles (see Tesche and Hodges, 2015; Riedle et al., 2015). It can be useful to simulate data and consult a statistician to better assess the utility of a proposed study design.

17.2.2 Site Selection

17.2.2.1 Stream-Breeding Salamanders

The selection of sites for salamander surveys is dependent on the type of question and species of interest for your question. Smaller stream salamanders of the families Plethodontidae, Rhycotritonidae, and Dicamptodontidae are found primarily in first- to third-order streams (Petranka, 1998). These streams are typically sloped to facilitate well-oxygenated water. This is essential for survival because most species in lotic systems rely on cutaneous respiration (Petranka, 1998). In addition to well-oxygenated water, stream salamanders are most often associated with many of the following types of abiotic parameters: low conductivity, cool temperatures, moderate to fast velocity in stream flow, shallow-intermediate water depths, small- to medium-sized rock substrates, and dense canopy cover (Petranka, 1998; Welsh and Ollivier, 1998). However, some species may be more sensitive or specific to one of the aforementioned parameters. For example, Oklahoma salamanders (*Eurycea taylori*) are associated with slow-moving (<10 cm/s), shallow (<10 mm) water with medium-sized rocks (65–256 mm in diameter; Tumblison et al., 1990). Evidence is also accumulating that some species may resist movements across light gaps in stretches of streams where canopy cover is present, but minimal (Cecala et al., 2014). One major contributing factor for site selection is the presence of fish. Stream salamander ensembles differ in composition and abundance above and below a barrier (waterfall) for brook trout (*Salvelinus fontinalis*, Resetarits, 1997). Larger salamanders (*Necturus* and *Cryptobranchus*) are typically found in second- to fourth-order rivers and streams (Petranka, 1998). Larvae of both genera can still be found in lower order streams (Petranka, 1998; Dodd, 2004). As with the smaller stream salamanders, hellbenders require good water quality, well-oxygenated water, and rocky substrates. Hellbenders tend to be found with medium- to large-sized boulders—an important habitat component for rearing offspring (Nickerson et al., 2002). *Necturus* salamanders are more tolerant of slow-moving water and can be found in larger streams with sandy/muddy substrates (Petranka, 1998). In order to increase your chances of encountering your focal species, it is vital that you summarize the literature and museum records for site-specific locality information.

17.2.2.2 Turtles

Site selection for turtle surveys will depend strongly on the size of the stream and the collection method you want to utilize. In slow moving waters, most trapping techniques (e.g., hoop nets, trammel nets, basking traps, and fyke nets) and

hand-capturing techniques (e.g., dip-netting) can be utilized; however, trapping with nets and traps become extremely difficult in higher velocity, shallow, and/or small-order streams. Often in small-order streams, traps and nets are limited to areas deep enough to submerge the throat of the trap and open areas for basking traps. In general, the most effective methods for capturing turtles in small-order streams are direct ones, particularly snorkeling and dip-netting around specific habitats. In streams large enough for indirect methods, traps are usually set in areas with particular habitats, and site selection of the trap will depend on your target species. For example, setting traps near basking sites will inevitably capture more basking turtle species (e.g., map turtles; see [Vogt, 1980](#)) than nonbasking species. Setting baited hoop nets and fyke nets in areas with submerged woody debris, underwater structure (e.g., root masses, fallen trees, cypress knees, aquatic trees, and log jams), and cut banks will result in more captures of ambush predators (e.g., snapping turtles) and other bottom-crawling species (e.g., musk turtles).

17.2.2.3 *Special Considerations for Working With Amphibians and Reptiles*

We caution readers that while working with amphibians and reptiles is fun and important, they must consider the regulations surrounding working with vertebrates and rare, threatened, or endangered species. First, because amphibians and reptiles are vertebrates, any studies involving them must be approved by an oversight board [e.g., Institutional Animal Care and Use Committees (IACUC) in the United States]. Secondly, most countries have oversight organizations and require permits for work with wildlife (including amphibians and reptiles). Please consult a local government agency to obtain any necessary permits to handle wildlife. Finally, it is your responsibility to know how to identify local species and understand the legal restrictions for working with rare, threatened, or endangered species.

As with any animal or plant species, individuals can be sensitive to the capture and restraining process. Ensure that amphibians and reptiles are restrained appropriately based on their identity and that overheating is prevented. Similarly, we encourage researchers to remember that these are wild animals with adaptations to defend themselves from predators. All animals are capable of biting, and we encourage researchers to avoid bites by large turtles and venomous snakes. Bites by large turtles may be avoided by handling the turtle by the back of the shell (and never the tail alone). Bites by venomous snakes can be prevented by avoiding venomous species. Far more nonvenomous species exist than venomous species, and we encourage any researcher working in the field to learn the appearance of local venomous snakes.

Because of their physiological needs, appropriate restraining techniques and trap-setting protocols must be followed. Prevent salamander overheating by keeping salamanders in a cooler or in the stream channel in ziplock bags containing native stream water. Avoid releasing salamanders into an area through which researchers will walk to exit the site. Although turtles are capable of extracting oxygen from water, during warm periods, they require access to air. Do not set turtle traps fully submerged. Be sure to tie traps to a terrestrial object to prevent captured animals from pulling the trap into deeper water. Finally, traps should be checked daily or every 48 h to prevent additional stress and even mortality of captured animals.

7.3 SPECIFIC METHODS

7.3.1 Basic Method 1: Estimating Detection Probabilities

This exercise will examine the impact that incomplete detection may have on inferences about ecological patterns and processes involving stream-breeding salamanders. Surveys to determine where a species does or does not occur can be used to evaluate habitat associations, distributions, and anthropogenic impacts. Two states can be observed for each site. If you observe the species, the site is considered occupied. Alternatively, if you do not observe the species, the species is either absent from the site or it is present but undetected. Over a range of sites, you can assess the probability that a site is occupied. Detection probability is simply the probability that a species is detected given that it is present at a site. More complex models can be developed that allow detection probabilities to vary by location, time, or other covariates. Similarly, occupancy probabilities can be modeled by a variety of predictors. These joint probabilities can be estimated using programs such as PRESENCE, MARK, and WinBUGS, along with their associated R packages, and we recommend that researchers interested in pursuing these methods consult a series of well-developed documentation for these models ([MacKenzie et al., 2002, 2005](#)).

Falsely concluding that a species does not occupy a site can cause underestimates in distribution and can potentially bias field survey results. For example, if it is more challenging to detect a species in high-quality habitat relative to low-quality habitat, occupancy models uncorrected for detection may suggest that the study species is more likely to occupy low-quality habitat. A recent study demonstrated that environmental conditions that affect salamander detection probability may bias inferences about community composition or population structure ([Connette et al., 2015](#)). Likewise, previous

research using estimated detection probabilities predicted that over 15 surveys would need to be conducted to provide 95% confidence in the absence of a stream-breeding salamander (*Desmognathus auriculatus*; Maerz et al., 2016). Completing this many surveys at a single site is logistically challenging, so researchers should consider the use of hierarchical models that model the probability of finding an individual of a species and the probability of a species occupying a site.

17.3.1.1 Field Data Collection

1. Using geospatial data, identify at least five watersheds for study that have relatively similar watershed-scale land-use (e.g., forest cover, development).
2. Once at the first site, designate at least five 10-m transects for surveying. In these transects, use a dip net with $<1/4''$ mesh to sample the entire width of the stream for the length of the transect. Survey the stream by dip-netting areas with silt and leaf litter. To effectively dip-net, quickly scoop up organic material. After each scoop, sift through the material to search for any salamanders. Some salamander larvae are small, so search carefully, separating leaves and moving material around. Replace the substrate back in the stream corridor. Survey all cover objects within the stream by placing a net downstream of a cover object, flip the rock or wood, and scoop underneath. Be sure to replace all cover objects back into the stream in a similar arrangement as you found them. Also survey leaf litter and cover objects within 2 m of the stream edge. These surveys can be completed by hand. Temporarily house all captured salamanders until surveys of the transects are complete. Do not house salamanders of different sizes with one another. You may want to mark bags with transect meters to ensure that all species are released close to their capture locations.
3. Identify all captured salamanders to species and record that information by transect. Presumably, if a species is detected in one transect, it is present throughout the site.
4. Repeat this process at each watershed.
5. Calculate the detection probability for each species using the formula below:

$$\frac{\text{\#Transects Species Found}}{\text{\#Transects Surveyed}} = \text{Raw Detection Probability} \quad (17.1)$$

6. Calculate the number of surveys necessary to conclude with 95% certainty (i.e., global detection rate = 0.95) that each species does not occur using the following formula:

$$\text{Global Detection Rate} = 1 - (1 - p)^k \quad (17.2)$$

where p = detection probability; k = number of transects surveyed.

17.3.2 Basic Method 2: Estimating Occupancy Probabilities When Detection is Less Than One

Conditions are rarely such that a species is detected with a probability of 1. Therefore, naïve occupancy analyses that do not consider detection will underestimate the true occupancy status of a species. Estimating detection probabilities will require spatial or temporal replication of sampling efforts to develop detection histories for each site of interest. Typically, researchers use “1” to denote presence and “0” to denote absence. Therefore, if surveys of three transects find a species in the first two transects but not in the third, the detection history for the site would be “110”. This would correspond to the following probability of finding this capture history:

$$p(110) = \psi^* p_1^* p_2^* (1 - p_3) \quad (17.3)$$

where ψ = probability that a site is occupied; p_1 = probability of detection in transect 1; p_2 = probability of detection in transect 2; and p_3 = probability of detection in transect 3.

By developing a collection of capture histories for a variety of sites, maximum likelihood methods can be used to estimate detection probabilities and unbiased occupancy rates (MacKenzie et al., 2005).

Single-season, single-species occupancy models have several assumptions (see MacKenzie et al., 2005 for more details). First, they assume that the state of a site cannot change within the survey period. That is, an occupied site cannot become unoccupied or vice versa during the study period. Second, detection at one site is independent of detection at another. The default models assume constant occupancy and detection rates among sites unless covariates are collected and included to describe variability in these probabilities.

Below, we describe a stream salamander survey with estimation of detection probabilities and regional occupancy probabilities. We recommend using the program PRESENCE (MacKenzie et al., 2005). PRESENCE is a Windows-based

software that can be downloaded from the Patuxent Software Site (<http://www.mbr-pwrc.usgs.gov/software.html>). It can fit both predefined models used in this exercise, or it can incorporate site covariates or other custom models. This program will provide maximum likelihood estimates of parameters and their associated standard errors as well as assess the model fit given your data.

Model fit results from PRESENCE will use Akaike's Information Criterion (AIC, [Akaike, 1973](#)) to evaluate model fit given the log likelihood obtained from maximum likelihood procedures. Although the absolute value of the AIC values is not important, the relative difference among AIC values will inform researchers of the relative fit of the models to your data. Based on the difference in AIC values from the top-ranked model (lowest AIC value), model weights will be calculated for each model that are represented by values between 0 and 1 that sum to 1. Relative to other models, the AIC weight demonstrates the probability of the model being correct given the data ([Burnham and Anderson, 2002](#)).

17.3.2.1 Field Data Collection

1. Using procedures identified in Basic Method 1, select 5–10 watersheds for surveys. In selecting sites, researchers may choose to survey a range of sites to develop occupancy probability estimates for a region. Alternatively, researchers may select sites that represent similar disturbance categories to assess occupancy probabilities within one type of watershed.
2. At each site, designate and sample five 10-m transects using methods identified in Basic Method 1.

17.3.2.2 Data Analysis

1. Download and install the program PRESENCE from the software archive of the Patuxent Wildlife Research Center of the US Geological Survey (See book Website).
2. Data may be entered directly from your datasheets into the program PRESENCE ([Box 17.1](#)).
3. To begin a new analysis, select “File/New Project” from the menu. Enter in a title, the number of sites surveyed, the number of transects surveyed (in No. Occasions), and enter that same number in the No. Occasions/season field.
4. Select the Input Data Form. This is where you may enter the presence-absence data collected from your field observations. If you are missing any datapoints, simply enter “-”. You may correct any errors on the initial entry form in the data input form. Select “Save As” before closing this form with your entered data. Select “No” when a pop-up asks if you would like to use the last column of data as frequency. Return to the opening New Project page and enter “OK” to create a folder for your input file and all the model outputs.
5. You will now advance to a Model Results Screen. From the drop-down menu under “Run,” select “Analysis:Single Season.”
6. For this exercise, you will run 2 predefined models by selecting “PreDefined” in the Model box. We first will run the “1 group, Constant P” model by highlighting it and clicking “Ok to Run.” This model indicates that detection probability is constant across each survey.
7. When a box pops up asking you if you want to append the results, select “OK”.
8. Repeat this process for the “1 group, Survey-specific P” model. This model indicates that detection probability varied among sampling events due to factors such as weather, personnel, etc.
9. You will assess model fit by evaluating the AIC weight. More likely models will have higher AIC weights.
10. Using the best-fitting model, right click on the model and select “View model output”.
11. At the bottom of the file that will open, estimates of detection probability can be found under “Individual site estimates of <p1>”. An estimate of group occupancy probability will be found under “Individual site estimates of <psi>”. Finally, you will find site-specific occupancy corrected for detection probabilities below “Derived parameter – Psi conditional = [Pr(occ|detection history)]” (see [Box 17.1](#) for an example run-through of this procedure with simulated data).

17.3.3 Advanced Method 1: Estimating Survival, Sex Ratios, and Abundance Using Capture-Mark-Recapture Protocols

In this exercise, we will examine population dynamics of turtles by estimating population size and sex ratios using capture-mark-and-recapture techniques. We use turtles for these exercises because they are easy to permanently mark without expensive equipment and sex is easily determined. [Cagle \(1939\)](#) devised a simple, inexpensive way to individually mark turtles by “notching” a combination of marginal scutes of the carapace and/or plastron scutes ([Fig. 17.2](#)). However, most researchers agree that marginal scutes (usually 4–7) associated with the bridge should not be notched so that the integrity

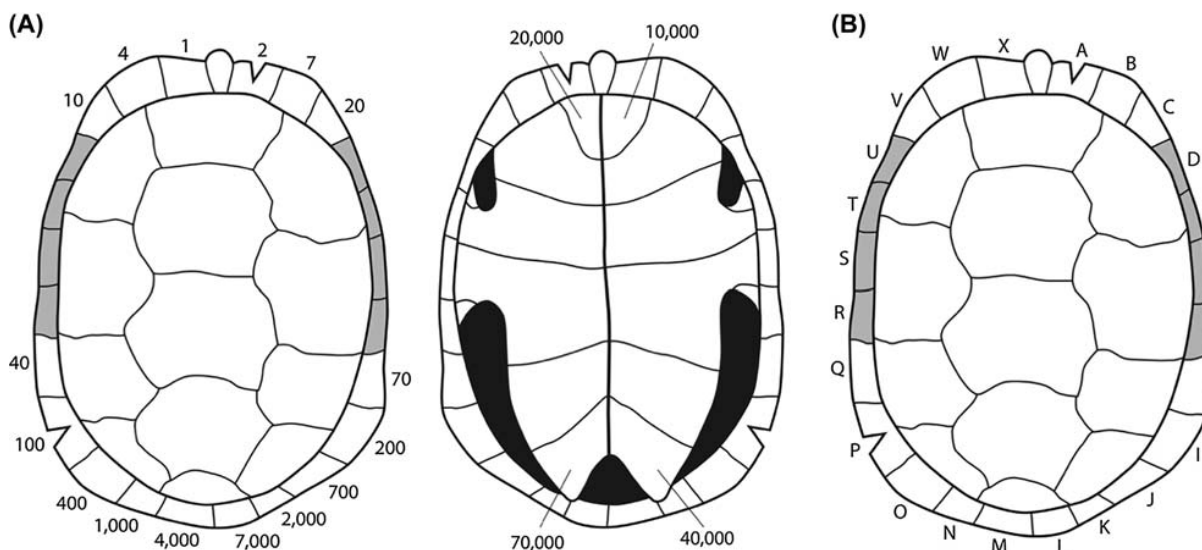


FIGURE 17.2 There are various methods of coding individual turtles within a population. (A) Numerical coding systems that includes carapace (left) and plastron (right); and (B) alphabetical coding system. The shaded (gray) marginal scutes are associated with bridge and are usually not marked by turtle researchers. The codes represented here are (A) “20,102”, and (B) “AP”.

of the bridge remains intact. “Notching” can entail filing, grinding, cutting, or drilling into the marginal scutes, and several coding schematics have been utilized by researchers (Fig. 17.2). For example, in Fig. 17.2, the turtle is marked as 102 and AP in the numerical and alphabetical coding system, respectively. Although “notching” is the most simple and inexpensive approach, marginal scutes are often naturally damaged; therefore, researchers run the risk of violating the population model assumption that marks are permanent and cannot be lost. If funds are available, most researchers would prefer using passive integrated transponder (PIT) tags, which are inserted into the body cavity or tail of the turtle.

The Lincoln–Petersen formula has been used to estimate population size in ecology for decades. It a simple approach to estimate population size:

$$N = \frac{M \times C}{R} \quad (17.4)$$

where N is the estimated population size, M is the number of originally marked individuals, C is the number of individuals captured during the second interval, and R is the number of recaptures in the second interval. There are several assumptions of the Lincoln–Petersen method: (1) the population is closed; (2) all individuals have the same probability of being captured; (3) marking individuals do not affect catchability, and (4) no tags or markings were lost.

Many species of turtles exhibit sexual dimorphism, in particularly size dimorphism, which helps identify the sex of an individual. For example, mature female map turtles (genus *Graptemys*) are often twice the size of mature males. Other sexually dimorphic traits include elongated forelimb claws [e.g., sliders (*Trachemys*) and cooters (*Pseudemys*)] and an enlarged tail with the cloacal opening extending past the carapace edge in mature males (e.g., most stream turtles; Fig. 17.3).

Chi-squared tests have been used for decades to test if there is a significant difference between the expected frequencies and the observed frequencies of the sexes within a turtle population. Essentially, a chi-square test used in this context specifically tests if there is a deviation from an equitable sex ratio (e.g., 1:1 or 0.5 for each sex):

$$\chi^2 = \sum_{i=1}^2 \frac{(\text{obs}_i - \text{exp}_i)^2}{\text{exp}_i} \quad (17.5)$$

where the expected value (exp) will be equal to half of the total population of a turtle species sampled, and the observed value (obs) will be the number of captured individuals of each sex. Once you have calculated the test statistic (χ^2), use the CHIDIST function in Microsoft Excel to calculate a p -value. You will need to input the test statistic (χ^2) and degrees of freedom ($df = n - 1$).

Open population models (e.g., Cormack–Jolly–Seber [CJS]) allow scientists to estimate the following parameters between sampling periods: apparent survival, recruitment, capture probability, and population size. However, the CJS model is a more simplistic version of open population models and can only estimate apparent survival and capture probability. Open

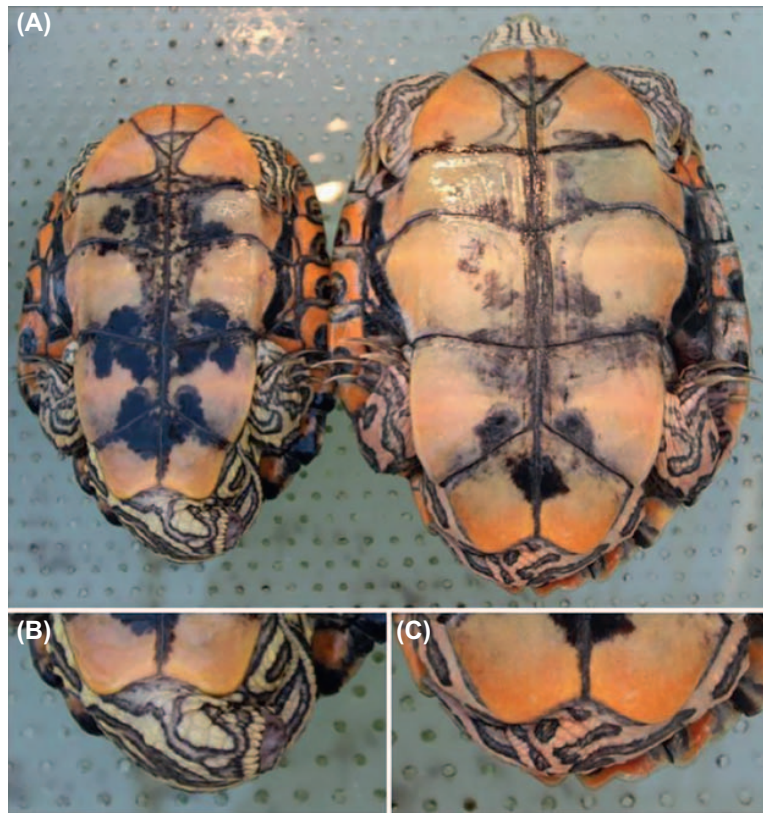


FIGURE 17.3 Many species of stream turtles are sexually dimorphic in body size and secondary sex characteristics. In *Trachemys gaigeae*, (A) males (left) are generally smaller with a larger tails. Enlarged images of the tails of a male (B) and female (C) *T. gaigeae*. Photo by Bernie Kuhajda.

population models assume: (1) all marked individuals are representative of the populations, (2) all marking is accurate without loss or misidentification, and (3) marking periods are short relative to the intervals between sampling periods.

17.3.3.1 Field Collection

1. Within a defined section of the stream (e.g., 1 km), identify the various habitats that would be important for your target species, such as nesting beaches, basking sites, emergent structures (e.g., vegetation or woody debris), submerged habitats (e.g., woody debris) near the bank, and undercut banks.
2. Starting at zero (km), place one hoop net several meters from an identified habitat from Step 1. Place these every 200 m within this 1-km section of stream. Place the hoop net in an area where the net rests on the bottom and leave air space within hoop net to allow captured turtles to breathe. Many researchers use PVC (or metal conduit) pipe to stretch out the individual hoop nets. Essentially, you use two pieces of small-diameter PVC that are equal to the length of your hoop nets. Next, you should notch grooves at both ends of the PVC pipes. These grooves are large enough for the front and rear frame of the hoop net to fit firmly. Finally, fit the front frame of the hoop net in one groove and then stretch the hoop net so that the rear frame fits into the opposite groove of the same PVC pipe. This step should be repeated on opposite sides of the hoop net.
3. The 1-km section should be trapped for a period of time (e.g., at least 3 days), which we will consider trapping interval 1. Each hoop net has an end, which is opposite of the funnel, that can be untied to retrieve captured turtles. All captured individuals should be sexed, marked, and released at the point of capture. Additionally, it is important to note “captures” and “no captures” by trap number or ID.
4. After the conclusion of trapping interval 1, wait several days (at least 7 days) before beginning trapping interval 2. Repeat steps 1–3, but record whether individuals were recaptures and, if so, which individual the recapture was. Fig. 17.4 demonstrates an example datasheet for these sampling methods.

17.3.3.2 Data Analysis

1. To evaluate sex ratios of your population, use the chi-square analysis described above.
2. If only two time intervals were used, assumptions of a closed population are likely to be met, and population size can be estimated using the Lincoln-Petersen method described above.
3. To estimate abundance using three or more time intervals, estimates of abundance may be analyzed using an open population model to assess survival (Cormack-Jolly-Seber model in Program MARK; [White and Burnham, 1999](#); [Box 17.2](#)).

Date _____	LAT _____
	LONG _____
Observers _____	
Site/Location _____	
Trap ID _____	Trap Type _____

Site Description/General Weather:

Water Temp _____	Air Temp _____
------------------	----------------

Measurements

CL _____	CH _____	PW _____
PL _____	CW _____	Mass _____

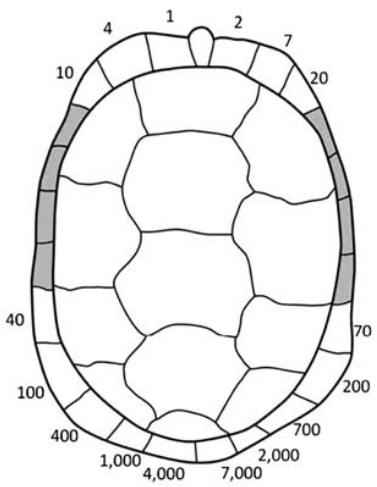
General Information

Recaptured? _____

ID _____

PIT #: _____

Habitat Description:



Notes:

FIGURE 17.4 A basic datasheet for turtle research that can easily be modified for more complex study designs. Abbreviations are defined as per the following: carapace length (CL), carapace height (CH), carapace width (CW), plastron length (PL), plastron width (PW), and passive integrated transponder tags (PIT).

4. To download Program MARK, go to the phidog.org forum and find Program MARK under software. The Local Page for Program MARK will provide access to download the Windows-based program and provide instructions for installation.
5. Data will need to be formatted properly for Program MARK. Capture strings should be created in Excel for each individual, consisting of “0” for nondetection and “1” for detections. Under “Format Cells” in the “Number” tab, the Custom selection will allow you to format the cells so that you can have leading 0s. To do this, select the option “0000”. In the “Type” field, you can enter as many zeros as you have sampling occasions.
6. Once the datafile is completely formatted, save the file as a Tab-Delimited Text file. Change the file type in the file name from “.txt” to “.inp”.
7. Open Program MARK. Immediately, a screen to define a new data file will appear. Define a title for the dataset and input your datafile. Below, enter the specific information for your model. Enter the number of sampling occasions in the “Encounter Occasions” space. Unless you have grouped the data or collected covariates, you will leave the “Attribute groups” at “1” and the “Individual covariates” at “0”.
8. Program MARK’s default model is a CJS model that should be selected on the left. Enter “OK.”
9. To run predefined models in Program MARK, select “PreDefined Models” from the Run menu. In the pop-up menu, click on “Select Models.” To run the four defined models, select (.) and (t) for both Phi (ϕ) and p . This indicates that you wish to evaluate models that do and do not allow survival and capture probability to vary with time. Select “Yes” on the pop-up asking to use an identity design matrix. Select “Yes” to append the model output to the database.
10. Using AIC_c (AIC incorporating a small-sample bias adjustment; [Hurvich and Tsai, 1989](#)) weights to evaluate model fit, identify the model with the largest AIC_c weight. This is the model that is most likely to fit the data. Right click on that model, and select “Real Estimates.” This text file will provide an estimate of the capture probability for each sampling occasion (p) and survival between trapping occasions (ϕ , ϕ ; see [Box 17.2](#) for an example of this procedure).

17.3.4 Advanced Method 2: Estimating Stream Salamander Abundance From Count Data

This exercise explores how Bayesian analysis of count data can be used with data collected from unmarked individuals. Exercises one and two illustrate how to estimate the probability of detecting a species and the proportion of sites that it occupies, and this is frequently of interest to ecologists. However, estimating the abundance may be of more interest in cases where individuals occupy a high proportion of sites within a study area. When survey data are carefully collected with analytical assumptions in mind, it is possible to estimate abundance instead of occupancy, even when data are collected without marking individuals in a population.

In order to consider how abundance can be estimated from a population of unmarked individuals, first consider the demographic processes that result in changes in population size: immigration, emigration, survival, and recruitment. This is the fundamental population equation that one frequently encounters in basic ecology textbooks:

$$N = S + F - E + I \quad (17.6)$$

Many mark-recapture analyses, like the previous example with the Lincoln–Petersen estimator, assume that a population is “closed,” or not changing in size. However, if we incorporate some of these processes into a model, we can relax the assumption of population closure.

One recent advancement in this area comes from the work of [Dail and Madsen \(2011\)](#), who relaxed the closure assumption for count data from populations. Their model begins by assuming that the initial abundance of individuals within a population at some time follows a distribution. The new population size in a subsequent time period is then represented as the sum of the individuals that have survived and remained in the population (S) and the number of new individuals that have been introduced into the population through recruitment or immigration (G):

$$N = S + G \quad (17.7)$$

It is important to note how these relate to the fundamental population equation above. S is often referred to as *apparent survival* because it reflects the outcome of both the survival and emigration processes. In a similar manner, the gains (G) to the population result from a combination of the recruitment and immigration processes.

We can gain further insight into this by explicitly considering the processes that result in S and G ([Kanno et al., 2014](#)). First, S , the number of individuals that survived between two sampling occasions, can be assumed to follow a binomial process as

$$S_i \approx \text{Binomial}(N_{i,t}, \omega_i) \quad (17.8)$$

where ω_i is the apparent survival probability for all individuals and $N_{i,l}$ represent the number of individuals, i , at location l . This can be thought of as flipping a coin for each individual in a population. The coin lands heads up with a probability of ω_i , which represents the probability that an individual has survived from the first to the second sampling period and remained in the population.

As ecologists, we might have some intuition about environmental factors that affect apparent survival. This can be tested by incorporating covariates to model ω_i with the logit link (Kanno et al., 2014):

$$\text{logit}(\omega_i) = \alpha + \beta X_i \quad (17.9)$$

where we denote an intercept term with α , β represents the effect of a covariate on apparent survival, and X_i represents a covariate (e.g., stream flow, stream gradient, number of cover objects, etc.)

This exercise will utilize count data of unmarked salamander populations to estimate abundance and apparent survival. Here we illustrate this method through simulated data that is used to fit a Bayesian hierarchical model using Markov chain Monte Carlo (MCMC) techniques. This method requires a recent version of the R language as well as a recent version of JAGS (<http://mcmc-jags.sourceforge.net>) and a library that allows R to run Bayesian analyses using JAGS (rjags or jagsUI). Use of an integrated development environment like RStudio is optional, but it can make it easier to run and debug R programs.

Mark-recapture techniques provide a wide range of tools for the estimation of population size and other vital rates of interest to ecologists. Unfortunately, the act of marking individuals can present significant logistical challenges because marking techniques may be difficult to perform in the field or involve significant costs for equipment. Counts of unmarked individuals within a population are sometimes the only data that are feasible to collect, but incorporating count data that is unadjusted for detection probability can provide misleading insights into the status of populations (Kéry et al., 2009).

However, several analytical techniques for dealing with data from sampling protocols for mark-recapture techniques provide a useful framework for thinking about how to deal with counts of unmarked individuals. Detection probability and abundance can be estimated through removal sampling, distance sampling, or capture-recapture techniques (Buckland et al., 2001; Royle and Dorazio, 2008). These data are often obtained from a population that is assumed to be closed (e.g., no births or deaths occur), but these methods can be extended to open populations to provide estimates of abundance and apparent survival.

There are several papers that provide more context on this approach, including some with examples of count data for stream fauna (Royle, 2004; Dail and Madsen, 2011; Zipkin et al., 2014; Kanno et al., 2014, 2015). Here, we provide a brief overview of the model based on the one used by Zipkin et al. (2014) before illustrating its application to simulated data that reflects population dynamics of a salamander population.

Consider a population that occupies a set of j sites, with the number of individuals at each site represented by N_j . The change in population size at a site can be considered to be a result of two processes: the number of individuals that survive from one time period to the next and remain in that site, and the number of individuals that were gained from one time period to the next through local recruitment or immigration. These processes can be expressed mathematically (Dail and Madsen, 2011; Zipkin et al., 2014):

$$N_j \approx \text{Poisson}(\lambda) \quad (17.10)$$

$$S_{j,t} \approx \text{Binomial}(N_{j,t-1}, \omega) \quad (17.11)$$

$$G_{j,t} \approx \text{Poisson}(\gamma N_{j,t-1}) \quad (17.12)$$

Because the survival process for a site does not reflect the process of emigration, it is referred to as apparent survival. Here the number of new individuals gained, $G_{j,t}$, is a function of the population size at a site and the rate at which new individuals are added to a site through local recruitment and immigration, γ . Note that other formulations could be used to account for processes like apparent survival that is affected by density dependence, or the effect of environmental covariates on these parameters, but that is beyond the scope of this example.

17.3.4.1 Data Analysis

1. Download the file `openpopmodel.r` from the book's Website, and open it in RStudio or R. The first section loads the library that has wrappers that allow R to execute code using JAGS, and it specifies the model file that will be run in JAGS. Execute lines 1–89 to do this.

2. Once the model is specified, several other pieces of data need to be specified for JAGS to be able to run the analysis. First, there are settings that need to be set to determine how MCMC methods are implemented. These include the number of iterations in the chains, the burn in period, the number of separate chains, and the degree to which chains are thinned. Markov chains develop values that approximate the posterior distribution of a parameter that are conditional upon the previous value. Running multiple chains allows for evaluation of convergence on a posterior distribution. Similarly, because each iteration is conditional on the previous iteration, we run large numbers of iterations and discard a subset of the initial iterations to reduce the effect of instability in the chain on the final posterior distribution. Increasing the thinning parameter will also reduce autocorrelation among values within a chain. More information about fitting models with MCMC may be found in [Kéry and Schaub \(2012\)](#) and [Royle and Dorazio \(2008\)](#). Lines 92–95 do this:

```
nc <- 3      # number of chains
ni <- 50,000 # number of iterations
nb <- 10,000 # burnin
nt <- 1      # thinning parameter
```

3. After the MCMC settings are specified, the data used to fit the model are compiled. Here, we pass JAGS the simulated counts from spatially replicated counts of the population. If we were modeling parameters as a function of environmental covariates, we would include that environmental data as part of this list. We then identify a list of parameters for JAGS to keep track of, before giving JAGS a function to generate a set of initial values to use in starting the sampler. Lines 98–104 do this:

```
jags.data <- list(N=N, nSites=sites, nStages=stages)
parameters <- c("")
inits <- function(){} 
```

4. After all of this is specified, we pass this to JAGS to run the analysis:

```
jags.data <- list(N=N, nSites=sites, nStages=stages)
parameters <- c("")
inits <- function(){}
model1 <- jags(jags.data, parameters, "model.txt", inits, n.thin=nt, n.burnin=nb,
n.chains=nc, n.iter=ni)
```

5. After the model is finished running, we can view a summary of the estimated model parameters:

```
summary(model1)
```

6. This summary function prints several helpful pieces of information about the object that JAGS returned. First, it shows the MCMC settings that were used and the time it took to run the model. This is followed by a table that has estimates for the mean, standard error, and quantiles of parameters that were modeled. The overlap 0 column indicates whether the 95% credible interval for a parameter includes 0. Here, we see the credible interval for apparent survival, ω , does not overlap 0. The Rhat column reflects whether convergence was achieved for a parameter. By convention, Rhat values under 1.1 are generally considered to be satisfactory. [Kéry and Schaub \(2012\)](#) and [Kéry and Royle \(2016\)](#) provide a more thorough overview of Bayesian models for ecology.

17.4 QUESTIONS

1. Did you detect every species in all surveyed transects? What are some factors that may have caused you not to detect a species? Are there methods you could use to improve your detection rates?
2. Why is it important to assess detection probabilities? In what ways could species traits or ecological factors cause detection to vary? How might your results have been biased if you did not account for detection probabilities?
3. If the marking on the animal has a high probability of being misidentified or overlooked, what is the effect on R , $M * C$, and therefore N if you are using a Lincoln-Petersen equation to estimate abundance?
4. If the population is evaluated using an open population framework, how would that influence R , $M * C$, and ultimately N ?
5. Was the sex ratio of turtles equal? If not, what environmental factors could contribute to nonequal sex ratios?

6. Based on your surveys, what are some environmental changes that could negatively impact detection or capture probabilities?
7. What are some environmental changes that could negatively impact the occupancy probabilities or abundance of amphibians and reptiles in lotic systems?

17.5 MATERIALS AND SUPPLIES

Clipboard
 File
 Fine mesh aquarium dip nets
 Fyke net
 Hoop net traps
 Permanent marker
 Plastic bags (sealable)
 Wire brush
 Species identification guides including:
 Altig and McDiarmid (2015)—Larval salamanders
 Ernst and Lovich (2009)—Turtles
 Petranka (1998)—Adult salamanders

SUPPLEMENTAL INFORMATION

Download Program PRESENCE: <http://www.mbr-pwrc.usgs.gov/software/presence.html>

- Website also includes a worked example

Download Program MARK: <http://www.phidot.org/software/mark/downloads/>

- MARK Online Book: <http://www.phidot.org/software/mark/docs/book/>

Download Program R: <https://www.r-project.org>

Download JAGS: <http://mcmc-jags.sourceforge.net>

Resources for high resolution spatial data:

<https://nationalmap.gov>

<http://www2.jpl.nasa.gov/srtm/cbanddataproducts.html>

GRASS — <https://grass.osgeo.org>.

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BOX 17.1 Example results using Basic Method 2 to assess amphibian occupancy probabilities. Shown here is an example of data output. Data file format can be downloaded from the book website.

Transects					
Sites	1	2	3	4	5
1	0	1	0	0	1
2	0	1	0	0	0
3	0	1	0	0	1
4	0	0	0	0	0
5	1	1	1	0	1
6	0	0	0	0	0
7	0	1	0	0	1
8	1	1	1	0	1
9	1	1	1	0	1
10	0	1	0	0	0


```

***** Input Data summary *****
Number of sites                = 10
Number of sampling occasions = 5
Number of missing observations = 0
Data checksum = 7558
-----
-2log(likelihood)              = 40.1754
AIC                             = 52.1754
=====

Individual Site estimates of <psi>
Site      estimate Std.err  95% conf. interval
psi  1 site 1      : 0.8000  0.1265  0.4593 - 0.9496
=====

Individual Site estimates of <p1>
Site      estimate Std.err  95% conf. interval
p1  1 site 1      : 0.3750  0.1712  0.1254 - 0.7152
p2  1 site 1      : 1.0000  0.0000  0.0000 - 1.0000
p3  1 site 1      : 0.3750  0.1712  0.1254 - 0.7152
p4  1 site 1      : 0.0000  0.0000  0.0000 - 1.0000
p5  1 site 1      : 0.7500  0.1531  0.3771 - 0.9370
=====

DERIVED parameter - Psi-conditional = [Pr(occ | detection history)]

Site      psi-cond Std.err  95% conf. interval
1 site 1  1.0000  0.0000  1.0000 - 1.0000
2 site 2  1.0000  0.0000  1.0000 - 1.0000
3 site 3  1.0000  0.0000  1.0000 - 1.0000
4 site 4  0.0000 112.7608  0.0000 - 1.0000
5 site 5  1.0000  0.0000  1.0000 - 1.0000
6 site 6  0.0000  0.0000  0.0000 - 0.0000
7 site 7  1.0000  0.0000  1.0000 - 1.0000
8 site 8  1.0000  0.0000  1.0000 - 1.0000
9 site 9  1.0000  0.0000  1.0000 - 1.0000
10 site 10 1.0000  0.0000  1.0000 - 1.0000
=====

```

After implementing the default models in Program PRESENCE, this analysis revealed that the best fitting model was the survey-specific P model with an AIC value of 52.18 and AIC weight (AIC wtg) was 0.9998. Asking the program to view model output will provide an output text file. Below, we have included excerpts from the output file. The output file includes metadata on the input file (# sites, sampling occasions and missing observations), AIC, an estimate of the regional occupancy probability (0.80 ± 0.13), site-specific estimates of detection probabilities ("Individual Site estimates of <p1>"), and site specific estimates of occupancy probabilities given the estimated detection probability for each site ("DERIVED parameter - Psi-conditional = [Pr(occ | detection history)]").

