

CHAPTER 10

Multi-state models...

Many of the preceding chapters in this book focussed on ‘typical’ open population mark-recapture models, where the probability of an individual being seen was defined by 2 parameters: for example, in a live encounter study, the probability the animal survived and remained in the sample area (ϕ), and the probability that the animal was encountered (p), conditional on being alive and in the sample area.

In this chapter, we extend this simpler paradigm by (in effect) considering a third parameter – a ‘movement’ parameter (ψ). We’ll defer formal definition of this parameter for a moment, since the definition changes somewhat depending on one or more assumptions. However, to foreshadow, let ψ represent the probability of moving between ‘states’ in which the marked individual may potentially be encountered, conditional on being alive and in that state. The fact that there may be more than a single state (i.e., more than one location, or condition, or state) is what leads to the models we describe in this chapter being referred to generally as *multi-state models*.

Most of this chapter is a synthesis of the key ideas behind multi-state models, with particular focus on how to implement them in **MARK**. The key concepts are based on seminal work by Neil Arnason, Carl Schwarz, Cavell Brownie, Ken Pollock, Bill Kendall, Jim Hines, Roger Pradel, Jean-Dominique Lebreton, and Jim Nichols. Critical in this early evolution was the advent of software to fit multi-state models, most notably program **MS-SURVIV**, created by Jim Hines. More recently, the development of programs **M-SURGE** and **E-SURGE** by Rémi Choquet, Roger Pradel, and Jean-Dominique Lebreton. Multi-state models have been shown to be an extremely rich class of models, with broad application to many important questions in evolutionary ecology, population dynamics (especially metapopulation dynamics), and conservation biology and management. At best, we hope to provide you with the essence of multi-state models as implemented in **MARK**, sufficient to convince you of the importance of more careful study of this class of models.

So what are multi-state models? A simple example – suppose you are conducting a study of some seabird that breeds on any one of three discrete islands far offshore from any large land mass. Here, the islands represent the different ‘states’. Let the islands have the less-than-inspired names of island **A**, island **B**, and island **C**. Each individual bird, given that it is alive and breeding, will do so on one of these three islands. You are fortunate enough to find sufficient funding so that you are able to mount capture (or resight) operations on all three islands simultaneously (a *critical* assumption – sampling in each state must be done at the same time). On each occasion (say, each year at the end of the breeding season), you capture, mark and release unmarked individuals, and record recaptures of previously marked individuals. On each occasion, you record the fact that the marked individual was reencountered, and on which island (i.e., the ‘state’).

Let’s consider what factors will define the probability of encounter. In the ‘typical’ mark-recapture context, with one sampling location, the probability of encountering the individual in the sample was

defined by the probability that it was alive and in the sampling area (φ), and the probability of encounter conditional on being alive and in the sample area (p).

In our ‘island’ example, though, we have more than one sampling state – we have 3 islands (A, B and C). Suppose you are working on island B. You capture an unmarked individual, individually mark and release it. You come back next year, and look for this individual. What determines whether or not you will detect it? In effect, a re-reading of the definitions of the parameters for the single-state model provides a clue – the marked individual might be encountered on island B, conditional on (a) it surviving to the next occasion, and (b) it not moving to either of the other two islands. As originally described by Arnason (1972, 1973), and later by Brownie *et al.* (1993) and Schwarz *et al.* (1993), the transition probabilities (i.e., making the transition from live to dead, or from one island to another) represent what is known as a *first-order Markov process*. Such a process is defined as one in which the probability of making a given transition between occasion (i) and ($i + 1$) is dependent only on the state at time (i).

Under this assumption, we can now define the parameters which jointly define the probability of encountering a marked individual in a given state on a given occasion:

φ_i^{rs} = the probability that an animal alive in state r at time (i) is alive and in state (s) at time ($i + 1$)

p_i^s = the probability that a marked animal alive in state (s) at time (i) is recaptured or resighted at time (i)

As written, φ reflects the *joint probability* of both surviving *and* making a transition. Let’s consider this schematically. In Fig. (10.1), we show the 3 islands, with arrows indicating the possible transitions:

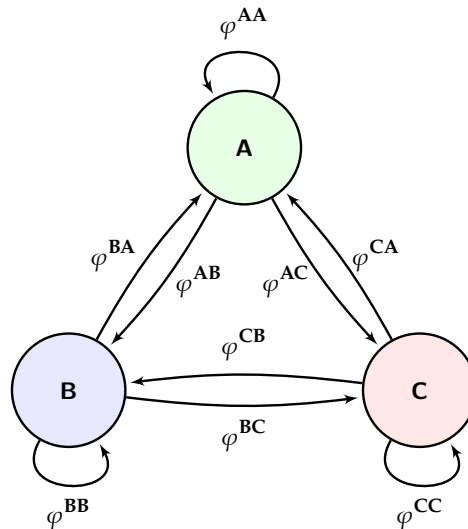


Figure 10.1: Schematic representing a typical multi-state model. Here, there are 3 states (A, B and C), with the arrows indicating directional movement between states over a given time interval. The probability of moving, conditional on surviving, from state $i \rightarrow j$ over the time interval is specified by parameter φ^{ij}

Remember, the φ values are the probabilities of *both* surviving *and* moving. Now, at this point some of you are probably already leaping ahead to the question ‘...is there any way to separate these two probabilities – survival and movement?’. We’ll address that in a moment. For now, let’s stick with these 2 parameters (φ and p), as defined above. What do our capture (or encounter) histories look like,

and what are the associated probability statements? In fact, as discussed briefly in Chapter 2 ('Data Formatting'), the format of the encounter history for multi-state models is qualitatively identical to the 'normal' mark-recapture history – a contiguous series of variables indicating whether or not the marked individual was encountered on a particular sampling occasion. For 'normal' mark-recapture, this is typically a contiguous series of '1's and '0's.

For multi-state models, instead of '1's to indicate an encounter, we use variables (letters or numbers*) which reflect the particular state in which the individual was encountered. We continue to use '0's to indicate if the individual wasn't encountered in any of the states on a particular occasion.

For example, given islands **A**, **B** and **C** (Fig. 10.1):

<i>encounter history</i>	<i>interpretation</i>
AAB0CC	marked on A at occasion 1, seen again on A at occasion 2, seen on B at occasion 3, not seen on any of the islands on occasion 4, seen on C at occasion 5 and occasion 6
BABA00	marked on B at occasion 1, seen on A at occasion 2, returned to B on occasion 3, back to A on occasion 4, and not seen on any island at either occasion 5 or occasion 6
ACAAAA	seen on A on occasion 1, moved to C on occasion 2, then back to A and seen on all subsequent occasions in the study

Of course, as we've seen from earlier chapters, each of these encounter histories reflects a particular realization of a probabilistic series of events. It is the relative frequency of each history in the data set which provides the basis for parameter estimation.

Consider a simpler case, with only 2 states: **A** and **B**. What does the encounter history 'AAB' tell us? In this case, the individual was marked and released on island **A**, seen again on **A** on the next occasion, and then seen on **B** on the final occasion. What is the corresponding probability expression? Clearly, the organism survived from occasion 1 to occasion 2, and remained on **A**. It also survived from occasion 2 to occasion 3, but in the process, moved from **A** to **B**. Thus, for the encounter history 'AAB', the corresponding probability expression is $\varphi^{AA} p^A \varphi^{AB} p^B$ (note that for convenience we do not show the subscripts corresponding to the occasions – normally we would do so. The absence of subscripting normally would indicate that the probabilities do not change through time).

What about something slightly more complex – like 'A0B'? In this case, the individual was marked in state **A** on occasion 1, released, not seen in either state **A** or **B** on the second occasion, and then seen again on the third occasion in state **B**. What would the corresponding probability statement look like? In this case, the trick is to realize that there are 2 different 'probability paths' by which this encounter history could occur:

<i>encounter history</i>	<i>interpretation</i>
$\varphi^{AA} (1 - p^A) \varphi^{AB} p^B$	survived and stayed in state A , but not seen in A on occasion 2, survived and moved from A to B and seen in B on occasion 3
$\varphi^{AB} (1 - p^B) \varphi^{BB} p^B$	survived and moved from A to B during first interval, not seen in B at occasion 2, stayed in state B and seen in B on occasion 3

* We hope it is obvious to you that '0' (zero) is not a valid variable to use to indicate a particular state. We hope the reason why is also sufficiently obvious.

The trick is to realize that (i) the individual survives from occasion 1 to occasion 3 – it is simply ‘missed’ (not encountered) at occasion 2 in either state, and (ii) since we don’t know where the individual was at occasion 2 (i.e., in which state), we must accommodate both possibilities – that it either stayed in state **A** (where it was originally marked), or that it moved from **A** to **B** during the first interval. As such, the expected frequency of individuals with encounter history ‘A0B’ would be:

$$R_1^A [\varphi_1^{AA} (1 - p_2^A) \varphi_2^{AB} p_3^B + \varphi_1^{AB} (1 - p_2^B) \varphi_2^{BB} p_3^B],$$

where R_1^A is the number marked and released in state **A** on sampling occasion 1.

10.1. Separating survival and movement

Now, while the ability to estimate the combined probability of surviving and moving is useful for some purposes, it is ultimately limiting for others. For example, suppose that the states don’t consist of physical locations (like islands), but breeding states (say, ‘breeder’ and ‘non-breeder’). There is no shortage of literature on whether or not mortality selection operates on individuals as a function of their breeding status (does ‘cost of reproduction’ ring a bell, or two?). In a typical analysis of the cost of reproduction, we might want to know (1) is survival dependent upon breeding state, and (2) given that the individual survives, is breeding state at time (i) a significant determinant of breeding state at time ($i + 1$)?

So, can we in fact separate ‘survival’ from ‘movement’? The answer is a qualified ‘yes’ – qualified, because the separation of ‘survival’ and ‘movement’ requires making a particular assumption:

If we assume that survival from time (i) to ($i + 1$) does not depend on state at time ($i + 1$), then we can write

$$\varphi_i^{rs} = S_i^r \psi_i^{rs},$$

where S_i^r is the probability of survival from time (i) to ($i + 1$), given that the individual is in state r at time (i), and ψ^{rs} is the conditional probability that an animal in state r at time (i) is in state s at time ($i + 1$), given that the animal is alive at ($i + 1$).

Read it again – carefully. The basic idea is to ‘separate’ the two events in time – survival, and moving. Think of it this way – the individual is in state **A**. It survives from (i) to ($i + 1$) with probability S^A based solely on the fact that it was in state **A** at time (i). Then, immediately before ($i + 1$), it either moves to another state, or stays, with probability ψ^{Ax} (where $x = \mathbf{A}, \mathbf{B}$, or \mathbf{C} in our example). In other words, first flip the ‘survive or not’ coin, and then conditional on survival, flip the ‘move or not’ coin. If the independence assumption is met (i.e., two separate coins – one for survival, another one for movement), then the ordering here (survive and move, or move and survive) is arbitrary.

Now, if we make these assumptions, then the sum of the joint survival/transition probabilities for a given state is equal to the survival probability for that state. In other words,

$$\sum_s \varphi_i^{r-} = S_i^r.$$

Consider the following example – assume there are just two states: s and r . Since $\varphi^{rs} = S^r \psi^{rs}$ and since $\varphi^{rr} = S^r \psi^{rr}$, then $\sum \varphi^{r-} = S^r \psi^{rr} + S^r \psi^{rs} = S^r (\psi^{rr} + \psi^{rs})$. Since $(\psi^{rr} + \psi^{rs}) = 1$, then $\sum \varphi^{r-} = S^r (\psi^{rr} + \psi^{rs}) = S^r (1) = S^r$. The same logic is true (obviously) for $\sum \varphi^{s-} = S^s$.

In the following (Fig. 10.2), we re-draw the early multi-state figure (10.1), decomposing φ into the survival (S) and movement (ψ) parameters:

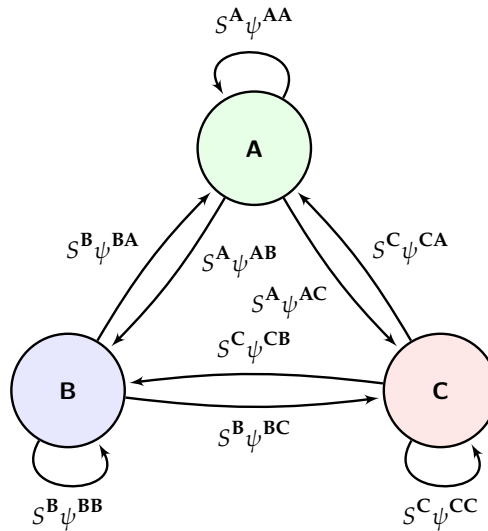


Figure 10.2: Re-parametrization of Fig. (10.1), where φ^{ij} is partitioned as the product of survival in state i (S^i) and movement from state $i \rightarrow j$ (ψ^{ij}).

If you've followed the earlier chapters on standard mark-recapture approaches, you might be thinking that 'while this is a neat trick, the parameters are probably not separately identifiable'. In fact, they are, because of the constraint that $\sum \psi_i^r = 1$. In other words, the transition (movement) parameters ψ_i^r are conditional on survival – and hence, on being present in the study area. The effect of this constraint is that animals that move out of all the states in the study, i.e., move outside the study area, cause the estimates of survival to be biased in the same sense that 'apparent survival' is estimated. That is, emigration off (or, out of) all the states in the study results in 'apparent survival' being 'true survival' times the probability that the animal remains on the study area.

A simple example will make this clearer. Assume that 3 states are sampled: **A**, **B**, and **C**. As noted earlier, the encounter histories must include the information indicating which state an animal was encountered in. For 5 encounter occasions, a history such as 'BCACC' could result. That is, the animal was initially captured in state **B**, captured in state **C** on the second sampling occasion, captured in state **A** on the third occasion, captured in state **C** on the fourth occasion, and then again in state **C** on the fifth occasion. The cell probability describing this encounter history is

$$[S_1^B \psi_1^{BC} p_2^C] \times [S_2^C \psi_2^{CA} p_3^A] \times [S_3^A \psi_3^{AC} p_4^C] \times [S_4^C (1 - \psi_4^{CA} - \psi_4^{CB}) p_5^C],$$

where encounter occasions are separated within the square brackets. Note that for the fourth interval, the probability of *remaining* in state **C** is just 1 minus the sum of the probabilities of *leaving* state **C**.

This cell probability demonstrates a key assumption of this model: survival is modeled with the survival probability for the state *where the animal was captured*, and *then* movement to a new state takes place. That is, as implemented in **MARK**, *all mortality takes place before movement*. An animal cannot move to a new state where a different survival probability applies, and then die. If it dies, it must do so on (or, as a function of) the current state. If it lives, then it can move to a new state. This assumption is critical if survival probabilities are different between the states. If survival is constant across states, then the assumption is not important. Biologically, this assumption may not always be reasonable.

begin sidebar

Another assumption for MS models...

Previously, we noted one of the key assumptions which we need to make in order to partition φ into subcomponents S and ψ . Specifically, that survival from time (i) to ($i + 1$) does not depend on the state at time ($i + 1$). Obviously, if this assumption is not met, then the estimates of S and ψ may be strongly biased.

Although the preceding assumption is well-known (and usually mentioned at least once in most papers using MS approaches), there is another assumption which has not received as much attention:

MS models assume that all individuals make the transitions at the same time (relative to the start or end of the time interval), or if not, that the distribution of the transition times is known.

The consequences of violating this assumption are addressed in Joe & Pollock (2002).

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10.2. A worked example: cost of breeding analysis

Consider the following example. You are studying a single cohort of individually marked adult deer, for 8 years (i.e., you mark a sample of deer on the first occasion, and then simply follow them for 7 more years). On each occasion, the breeding status of the deer can be determined without error (all individuals can be assigned either breeder or non-breeder status). You want to examine the possibility that survival is influenced by breeding status.

The conceptual premise for this example is very similar to a paper published by Nichols *et al.* (1994) on estimating breeding proportions and costs of reproduction with capture-recapture data. Normally, we might consider breeding status as a ‘trait’, but clearly this is an annually variable phenotypic trait for most organisms. As such, the classic approach of subdividing the sample along trait-lines and looking for differences among the trait groups will not work here. We need another approach. In fact, multi-state models are just such an approach – we model the movement between breeding states just as we would model movement among physically discrete states.

To demonstrate the point without the complications of ‘messy real world data’, we’ve simulated a data set for this ‘virtual deer’ population (**deer.inp**), using the parameter values tabulated at the top of the next page. There are 500 total individuals to start in the simulated data – 250 in the breeding state, and 250 in the non-breeding state. We assume that both states are ‘observable’ – meaning, that $p > 0$ in either state (although the detection probability might differ between the states). The assumption that both states are observable is an important one we consider later in this chapter.

If you look carefully at the parameter values (tabulated at the top of the next page), you’ll see we’re simulating a data set where it is ‘costly’ to breed – the survival from time (i) to ($i + 1$) for individuals in the breeding state at time (i) is somewhat lower than for non-breeders at time (i). However, the probability of switching states (moving from one state to the opposite state) is higher for non-breeders than for breeders (i.e., individuals aren’t likely to stay non-breeders for very long).

Begin a new project in **MARK**. For the multi-state analysis of the ‘virtual deer’, we want to select ‘**Multi-strata Recaptures only**’ (about half-way down the list of different data types). Once you select the multi-strata option, you may have noticed that the option to ‘**Enter State Names**’ has now become active (lower-right corner of the specification window). This will become important in a minute.

parameter	value
$S^{breeder}$	0.7
$S^{non-breeder}$	0.8
$\psi^{breeder \rightarrow non-breeder}$	0.4
$\psi^{non-breeder \rightarrow breeder}$	0.8
$p^{breeder}$	0.7
$p^{non-breeder}$	0.7

Next, enter a title for the project (say, 'Analysis of virtual deer'), and then select the file (**deer.inp**). Note that the encounter histories in **deer.inp** look virtually identical to the histories we used for typical mark-recapture analysis – a contiguous string 8 characters long (i.e., 8 occasions), followed by the frequency of individuals having that particular history.

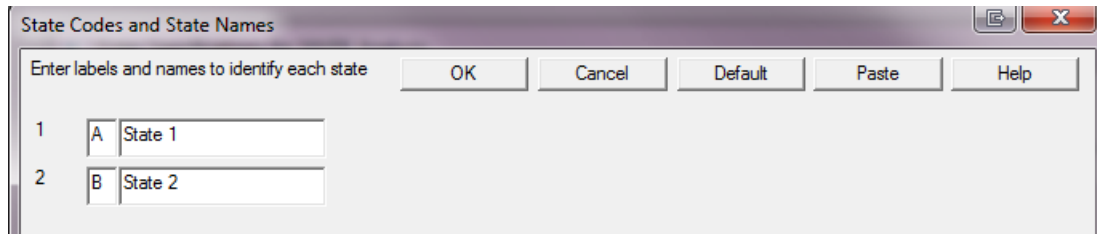
But remember – rather than '1's and '0's, we now have 'N's, 'B's and '0's. In this case, the 'N' value represents individuals in the non-breeding state at a particular occasion, and the 'B' values are for breeding individuals. The '0's always represent occasions when the individual was not encountered.

Thus, the history 'NBNN0BB' represents an individual marked as a non-breeder on the first occasion, seen as a breeder on the second occasion, seen as a non-breeder on occasions 3 to 4, not seen at all on occasion 5, and then seen as a breeder for the final two occasions. The use of 'N' and 'B' in this example is entirely arbitrary – you can use any non-zero value you want to indicate state (i.e., numbers 1 → 9, upper- or lower-case letters). The only condition is that it can be only one character wide (e.g., 'N' for non-breeders, say, not 'NB').

Next, we tell **MARK** that **deer.inp** has 8 occasions.* Finally, we need to tell **MARK** how the states are coded in the input file. To do this, click on the 'Enter State Names' button we referred to earlier (**MARK** defaults to 2 states, so we don't need to change anything there).

This will cause **MARK** to spawn a new window (shown at the top of the next page) which lets you set the labels (codes) for the different states, and their respective names.

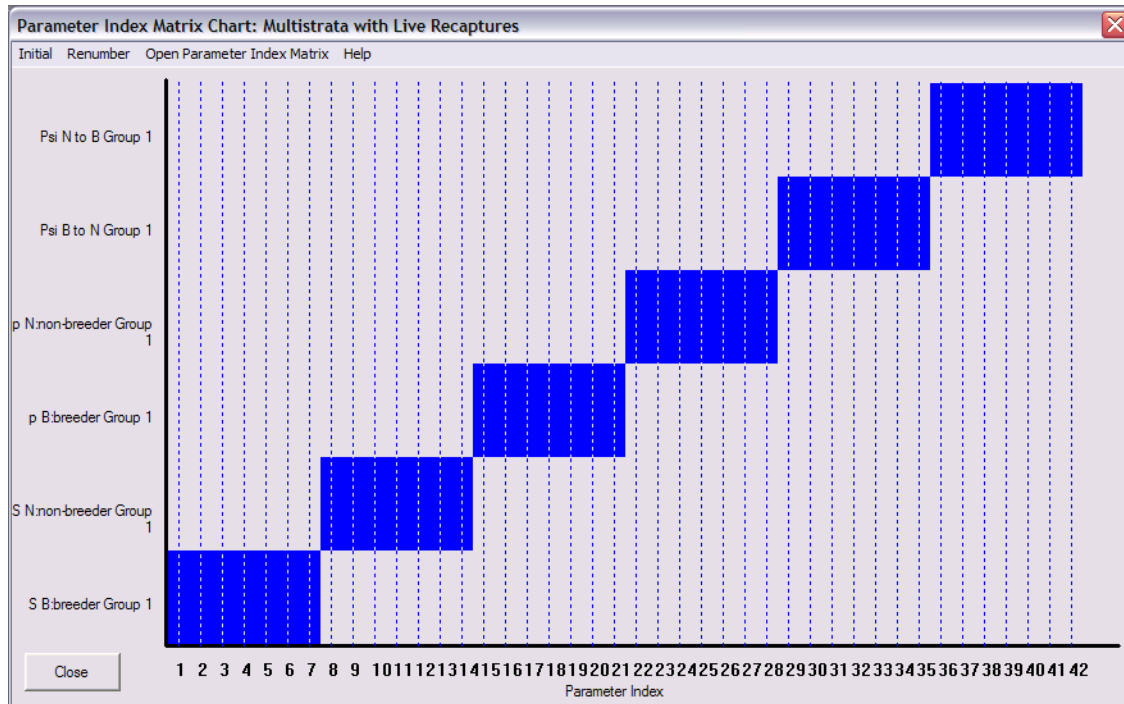
* Here, time intervals are assumed to be equal, 1.0. However, if you have unequal intervals in a multi-state analysis, you need to be very careful on how you proceed. See section 10.6.



Once you've entered the appropriate codes (for this example, 'N' and 'B'), and state names ('non-breeder' and 'breeder', respectively), click '**OK**', which will bring you back to the Specification window. Once you're sure everything in this window is correct, click '**OK**'.

As with our standard mark-recapture analysis in **MARK**, what you'll see first is the PIM for the survival parameters for Group 1 (in this example, we have only one group). But, within a group, you might have 2 or more states. If you look at the PIM chart, you should recognize that the PIM reflects a time-dependent structure for survival for individuals in breeding state.

To get a quick sense of the way **MARK** lays out the parameters for this model, let's look at the PIM chart (by clicking the '**PIM Chart**' button in the PIM itself):



There are 6 parameters involved for each state. Right away this should tell you something. Six parameters means that **MARK** is making the assumption that survival is dependent only on the state at occasion (i), and is not influenced by the state entered at occasion ($i + 1$). In other words, we're using the identity we introduced earlier:

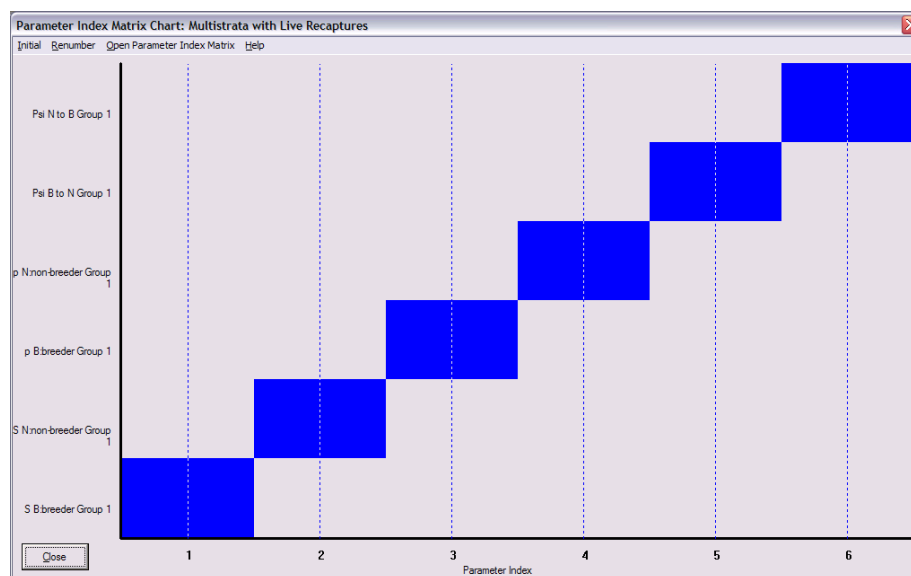
$$\phi_i^{rs} = S_i^r \psi_i^{rs}.$$

Recall that this identity is true only under this stated assumption. The fact that **MARK** defaults to this assumption becomes important later on. Thus, each of the 'blue boxes' in the PIM chart refers to (respectively, going from the lower-left to the upper-right) S^B , S^N , p^B , p^N , ψ^{BN} and ψ^{NB} . Examination of the horizontal axis of the PIM chart shows that the current model has time-dependence for each parameter, and that there are 42 total parameters. Even though we know that for these simulated data the parameters are constant through time (no time-dependence), let's pretend we're approaching these data naïvely, and go ahead and run this model (call it ' $S(g, t)p(g, t)\psi(g, t)$ ', where the 'g' refers to group – or state, breeder or non-breeder in this case).

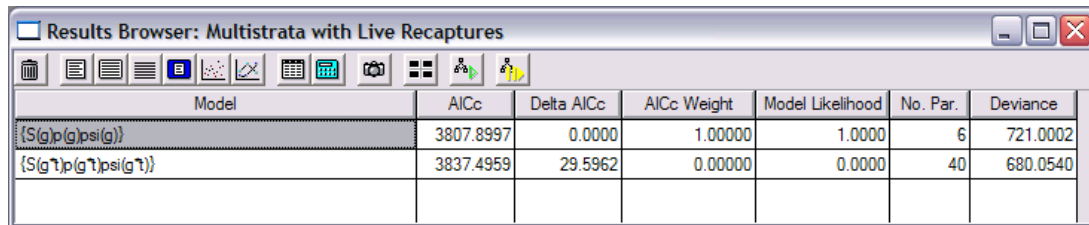
The first thing you might notice, especially if you're using a computer of 'average' processing power, is how much longer this model takes to run than analysis of typical mark-recapture data. The reason is fairly straightforward – the more parameters, the longer it takes to reach the solution (although the increase in time taken does not scale as a simple linear function of the number of parameters). We have 3 parameters (S , p and ψ), so it takes longer than models with only 2 (say, ϕ and p). Once the estimation is complete, add the results to the browser.

Before we look at the results of this analysis, let's run another model – ' $S(g)p(g)\psi(g)$ ' – constancy for all parameters, but allowing for possible differences among groups (breeding states). Obviously, the first thing we need to do is modify the parameter structure. As you may have gathered from earlier chapters, this is most easily done using the PIM chart. Recall from earlier chapters that we could modify the parameter structure from within the PIM chart (at least for certain models) by simply right clicking on each of the 'blue boxes' on the PIM chart. In this case, you could move the cursor over each of the 'blue boxes' and right-click with the mouse. This causes a menu to pop up which lets you select among various parameter structures. One of the options is '**Constant**'. By selecting the '**Constant**' option for each blue box in turn, we could build our model. Then, to eliminate the 'gaps' between the 'blue boxes' (i.e., to make the parameter index values contiguous), you could either drag each box manually, or right-click anywhere in the PIM chart, and select '**Renumber no overlap**'. This will cause the PIM chart to reformat without any gaps between any of the blue boxes.

While this works, in this case, for this particular model (where the structure is the same for all 6 blue boxes), there is a much faster way – simply select the '**Initial | All | Constant**' menu option from within the PIM chart. If you do this, your PIM chart will be quickly reformatted to the model we're after, which looks like the following:

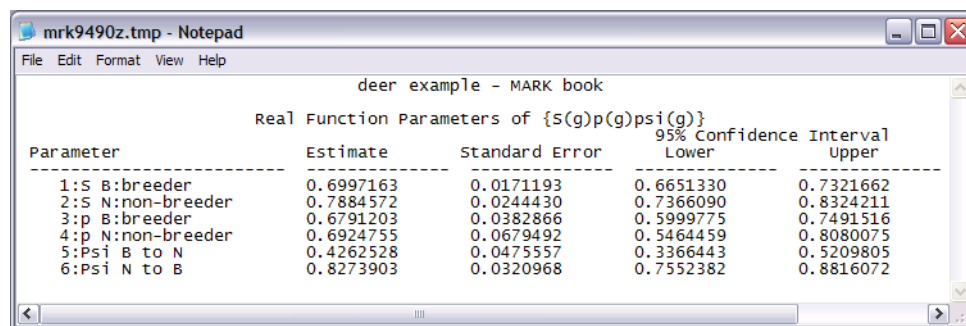


Note that, superficially, this looks identical to the PIM chart we saw for the fully time-dependent model discussed earlier, but if you look carefully at the horizontal axis, you'll see it now has many fewer parameters – 6 (instead of 42). Go ahead and run this model, and add the results to the browser.



Model	AICc	Delta AICc	AICc Weight	Model Likelihood	No. Par.	Deviance
$\{S(g)p(g)\psi(g)\}$	3807.8997	0.0000	1.00000	1.0000	6	721.0002
$\{S(g)p(g)\psi(g)\}$	3837.4959	29.5962	0.00000	0.0000	40	680.0540

Inspecting the results browser shows us immediately that the model with constant parameter values is a much more parsimonious model of these data than is the fully time-dependent model. Before we go much further, let's have a look at the real parameter estimates for the constant model – ' $S(g)p(g)\psi(g)$ ' – more formally, model $\{S^g p^g \psi^g\}$.



Parameter	Estimate	Standard Error	95% Confidence Interval	
			Lower	Upper
1:S B:breeder	0.6997163	0.0171193	0.6651330	0.7321662
2:S N:non-breeder	0.7884572	0.0244430	0.7366090	0.8324211
3:p B:breeder	0.6791203	0.0382866	0.5999775	0.7491516
4:p N:non-breeder	0.6924755	0.0679492	0.5464459	0.8080075
5:Psi B to N	0.4262528	0.0475557	0.3366443	0.5209805
6:Psi N to B	0.8273903	0.0320968	0.7552382	0.8816072

We can see that the estimates are quite close to the parameters used to simulate the data set. Since the constant model is much better supported than the fully-time-dependent model, let's delete the time-dependent results from the browser (by highlighting the time-dependent model and then clicking on the trash can icon in the toolbar of the browser window). We will use the constant model $\{S^g p^g \psi^g\}$ as the general model in our candidate model set. We're interested in examining two questions: (1) is there a difference in survival among breeders and non-breeders, and (2) does the probability of transition between breeding states depend on breeding state at occasion (i)?

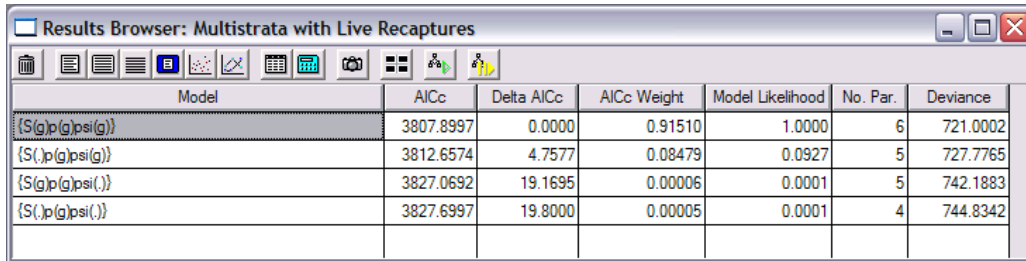
Let the following represent the candidate model set:

$$\{S^g p^g \psi^g\}, \{S. p^g \psi^g\}, \{S^g p^g \psi.\}, \{S. p^g \psi.\}.$$

In other words, (1) constant over time, but with group (g ; breeding state) differences for all parameters, (2) equal survival between breeding states, but differences in recapture and movement, (3) differences in survival and recapture, but no differences in transitions probabilities between breeding states, and (4) differences in recapture probability among breeding states only.

At this point, you should be able to run the 3 new models fairly easily – it should take you only a few seconds to construct each model using the PIM chart approach. The results for all 4 models in the candidate model set are shown at the top of the next page. We see that the model with differences in both survival and movement rates between breeders and non-breeders is 10-times better supported

by the data than the next best model, where survival is the same between breeding states, and both recapture and movement probability differ ($0.915/0.085 = 10.8$).



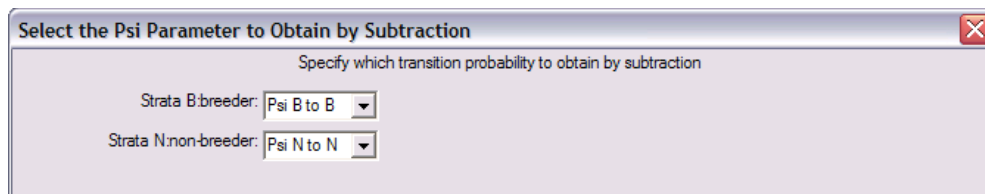
Model	AICc	Delta AICc	AICc Weight	Model Likelihood	No. Par.	Deviance
{S(g)p(g)psi(g)}	3807.8997	0.0000	0.91510	1.0000	6	721.0002
{S(.)p(g)psi(g)}	3812.6574	4.7577	0.08479	0.0927	5	727.7765
{S(g)p(g)psi(.)}	3827.0692	19.1695	0.00006	0.0001	5	742.1883
{S(.)p(g)psi(.)}	3827.6997	19.8000	0.00005	0.0001	4	744.8342

Let's re-examine the estimates from our best model, $\{S^g p^g \psi^g\}$. While survival is clearly estimated for each state separately, the question is, which 'movement' parameter gets estimated? For example, among individuals in breeding state (**B**) at time (*i*), they can either move to the other state (**N**, with probability ψ^{BN}), or stay in the breeding state (ψ^{BB}). Which one do we estimate?

Well, at this point, we take advantage of the logical necessity that the sum of ψ^{BN} and ψ^{BB} must equal 1.0 (i.e., an animal in a given state, must either remain in that state or move to another state, conditional on remaining alive). As such, one of the movement parameters is redundant (if you know the value of one, you know the other as 1 minus the first one). As such, any one of the movement parameters for a given state could be omitted. For example, our estimate for $\psi^{NB} = 0.8274$. Thus, ψ^{NN} is estimated as $\hat{\psi}^{NN} = (1 - 0.8274) = 0.1726$, which is fairly close to the parameter used in the simulation (0.2).

Fortunately, **MARK** gives you some flexibility as to what movement parameters are estimated – the default is to estimate the probability of moving from one state to another (i.e., ψ^{ij} ; probability of moving from state *i* to state *j*). However, you might instead want to estimate the probability of remaining within a state (ψ^{ii} ; probability of moving from state *i* to state *i*). You can force **MARK** to estimate ψ^{ii} , instead of ψ^{ij} , simply by changing the definition of the PIM. Returning back to our previous deer example, we can simply retrieve a model from the browser, and then select 'Change PIM definition' from the PIM menu, and run it (or you can change the PIM structure before running the model).

Go ahead and try it – doing so will bring up a window showing you the non-default transitions that are available – in this case, there is only one other possibility (i.e., the non-default ψ^{ii}):



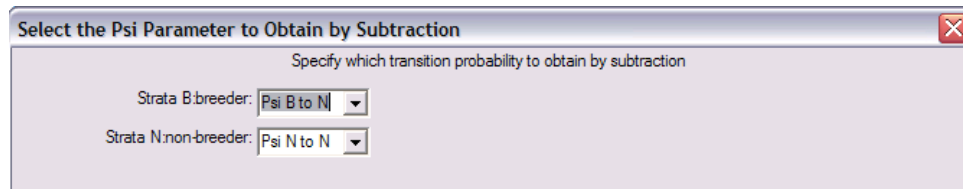
Select the Psi Parameter to Obtain by Subtraction

Specify which transition probability to obtain by subtraction

Strata B breeder: Psi B to B

Strata N non-breeder: Psi N to N

Now, you need to be a bit careful here – read the text at the top of this window carefully. It's asking you to tell **MARK** which of the transitions you want to estimate *by subtraction*. For example, **MARK** defaults to estimating the transition ψ^{ij} . So, you'd normally (by default) have to derive ψ^{ii} by subtraction. So, if you want **MARK** to estimate ψ^{ii} , you need to tell it you want to estimate ψ^{ij} by subtraction. So, in our example, with two states (**N** and **B**), **MARK** defaults to estimating ψ^{NB} and ψ^{BN} . So, if you want **MARK** to estimate (for example) ψ^{BB} , you need to tell **MARK** you want to estimate ψ^{BN} by subtraction, as shown at the top of the next page:



If you run this model, you'll see that it gives you the estimate of ψ^{BB} you want. And, changing the specification of which transitions are estimated does not (and should not) change anything else about fitting the model – the model deviance, and AIC value, should be unchanged.

There are several potential advantages to being able to specify which transition parameters are estimated. First, the optimization routine in **MARK** is known to work better if the parameters are not close to the boundaries (i.e., not close to 0.0 or 1.0). Second, you are likely not to want estimates of the estimated parameters to be 'too big', because if their sum is > 1 , then the remaining probability is estimated as < 0 . The idea, then, is to pick transition probabilities that are likely to be small, giving you the best chance that the remainder transition probability will be > 0 (although as we will see, we can circumvent this particular problem by specifying a different link function – the *multinomial logit* link).

Third, and perhaps most importantly, being able to specify which movement parameter you want to use gives you the ability to build specific constrained models. For example, suppose you are working with a 3-island system, and wanted to assess whether the probability of returning to a given island (i.e., philopatry) was equal for the various islands, but did not want to assume that the probabilities of movement to other islands was also equal. You could do this by constraining the probability of remaining on a given island. Note that for a 2-state model, setting the probabilities of leaving for the other state equal is also setting the probability of remaining equal. With > 2 states, this is not true.

However, it is important to remember that you can change the PIM definition only in terms of the 'recipient' state. The 'donor' state at the time of the transition is fixed, whereas the 'recipient' state is dynamic, since it is the outcome of a probabilistic process determined by the parameter ψ . You have one ψ parameter for movements *from* each state, not movements *to* a given state. So, for our 2 state 'breeder' (B) or 'non-breeder' (N) example, we could change the PIM definitions to (say) ψ^{NB} and ψ^{BB} , or ψ^{BN} and ψ^{NN} . In either case, we're estimating the probabilities of moving into a common 'recipient state', each as a function of the different 'donor' states. Note that the sum of $\psi^{NB} + \psi^{BB}$ (for example) does not necessarily equal 1. In contrast, $\psi^{BN} + \psi^{BB} = 1$. As noted earlier, since the movement is conditional on survival, then the sum of all movement probabilities from a given state must equal 1 (if you're alive at the end of the interval, you must be in one of the available states, with probability 1).

Why is this distinction important? It is important because being aware of it gives you some additional flexibility to test various hypotheses. For example, suppose for our 'cost of breeding' analysis we wanted to test a model where the probability of breeding next time step is potentially a function of whether or not you breed this time step. In other words, you might be interested in constructing a null model where $\psi^{BN} = \psi^{BB}$ – i.e., a model where the probability of breeding next year is random with respect to breeding state this year.

The problem is, the two parameters are constructed based on a common 'donor' state (breeder, B), which is not possible to construct by simply changing the PIM definition. But, if you remember that $\psi^{BN} + \psi^{BB} = 1$, then if $\psi^{BN} = \psi^{BB}$, then $\psi^{BN} = \psi^{BB} = 0.5$. Which of course is the expected probability for either transition if the movement is strictly random. So, you simply need to build a model where you first fix the estimate of either ψ^{BN} or ψ^{BB} (whichever one you've defined in your PIM) to be 0.5.

Alternatively, you might be interested in whether or not breeding next year is a function of not breeding this year. You apply exactly the same logic – you build a model where you first fix the estimate of either

ψ^{NN} or ψ^{NB} to be 0.5. As noted above, for a 2-state model, setting the probabilities of leaving for the other state equal is also setting the probability of remaining equal. Also as noted, this is not true with > 2 states, at which point, things get somewhat more complicated.

What about φ^{rs} ? Recall that as originally described, the multi-state models focussed on estimation of the ‘combined’ probability of survival and movement. **MARK** assumes that survival is dependent only on state at time (i) – this allows **MARK** to separate φ into its component parts S and ψ . Can we estimate φ using **MARK**? Yes, but only by hand. Consider the results of our analysis so far. ψ^{BN} is estimated as 0.4263. S^B is estimated as 0.6997. Thus, φ^{BN} is estimated as $\hat{\varphi}^{BN} = \hat{S}^B \hat{\psi}^{BN} = 0.2983$. Given the standard errors for both S^B and ψ^{BN} from **MARK**, it is possible to derive standard errors for $\hat{\varphi}^{BN}$ using the Delta method, or by using the sample chains from an MCMC analysis (Appendix B).

Are there further limitations imposed by **MARK**? In fact, there may be one more, stemming from the underlying ‘assumption’ **MARK** defaults to – the assumption that survival depends only on state at time (i). While this is perhaps reasonable in many ‘real world’ situations, what if it isn’t? Nichols and colleagues have extensively explored models where the transition probabilities depend on state both at time (i) and ($i - 1$). While the recapture parameters remain the same, they introduced a new transition parameter:

$$\varphi_{i-1,i}^{rst} = \text{the probability that an animal alive in state } r \text{ at time } (i - 1) \text{ and state } s \text{ at time } (i) \text{ is in state } t \text{ at time } (i + 1).$$

They referred to this as a ‘memory model’ (technically, it is a second order Markov model), suggesting that the ‘history’ of events experienced by the marked individual leading up to its state at time (i) might influence the transition probability between (i) and ($i + 1$). These ‘memory’ models were coded into program **MS-SURVIV**^{*}, and allow for testing hypotheses that the transition φ is first-order Markovian (i.e., dependent only on state at time i) versus those in which the transition φ is dependent on the state at both (i) and ($i - 1$) (i.e., second-order Markovian).

At present, **MARK** is unable to handle ‘memory’ models, in part since they clearly violate the assumption **MARK** makes that survival is dependent only on state at time (i). These models may prove increasingly important tools to explore questions concerning life-history decisions over the lifetime of the organism. Much theory exists suggesting that the optimal decisions at age x (e.g., breed or not, emigrate or not) are likely to reflect the sequence of decisions experienced (or made) at age $< x$. However, such memory models are extremely ‘data hungry’, and much work remains to be done to develop extensions of such models to relevant biological questions.

But while this is a limitation of **MARK** when compared to **MS-SURVIV**, for Markovian models, **MARK** adds significant flexibility for many models, particularly through use of the design matrix. In the next section, we shall explore examples showing how we can use the design matrix to constrain the estimates of survival and movement.

10.3. States as ‘groups’ – multi-state models and the DM

In the preceding, we fit a series of ‘dot’ models to the data – there was no need to build a design matrix (DM) for the models in our candidate model set. But, it is important to understand how the DM is built for multi-state models. It is really not much different from what you’ve already seen – all you need to do is remember that states are, in effect, treated like groups. But, with a catch you need to be aware of.

Consider the deer data we just analyzed, and consider fitting a fully time-dependent model, for all parameters (S , p and ψ). If we set the PIM structure to $\{S_t^g p_t^g \psi_t^g\}$, and then pull up the design matrix

^{*} Program **MS-SURVIV** was developed and is maintained by Jim Hines, USGS-Patuxent Wildlife Research Center.

using ‘Design matrix | Full’, this is what we see (if we ‘zoom in’ in on the part of the DM coding for variation survival, S):

Design Matrix Specification (B = Beta)													
B1: S B breeder Int	B2: S B breeder t1	B3: S B breeder t2	B4: S B breeder t3	B5: S B breeder t4	B6: S B breeder t5	B7: S B breeder t6	B8: S N non-breeder Int	B9: S N non-breeder t1	B10: S N non-breeder t2	B11: S N non-breeder t3	B12: S N non-breeder t4	B13: S N non-breeder t5	B14: S N non-breeder t6
1	1	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	0	0	0	0	0	0	0	0	0	0	0
1	0	0	1	0	0	0	0	0	0	0	0	0	0
1	0	0	0	1	0	0	0	0	0	0	0	0	0
1	0	0	0	0	1	0	0	0	0	0	0	0	0
1	0	0	0	0	0	1	0	0	0	0	0	0	0
1	0	0	0	0	0	0	1	0	0	0	0	0	0
0	0	0	0	0	0	0	1	1	0	0	0	0	0
0	0	0	0	0	0	0	1	0	1	0	0	0	0
0	0	0	0	0	0	0	1	0	0	1	0	0	0
0	0	0	0	0	0	0	1	0	0	0	1	0	0
0	0	0	0	0	0	0	1	0	0	0	0	1	0
0	0	0	0	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0

If you look closely, you’ll see that columns 1 → 7 correspond to survival for *breeding* individuals, while columns 8 → 14 correspond to survival for *non-breeding* individuals. What is important to note here is that each parameter has a separate intercept – meaning, **MARK** is treating the same parameter (S) for different levels of the state (breeding, non-breeding) as if they were separate parameters.

While there is nothing wrong with this in terms of the reconstituted parameter values, it does limit the models you can build. For example, you would not be able to construct an additive model in any obvious way, since there are no *explicit* interaction columns. In fact, the interaction is *implicit* in the fact that the two parameters do not share a common intercept. So, in order to have more flexibility, we generally choose to re-code the DM such that parameters share a common intercept across levels of the state variable. To demonstrate this, we first go ahead and run this model (using the default ‘fully time-dependent’ DM with a separate intercept for each parameter/state combination. The reported model deviance is 680.054.

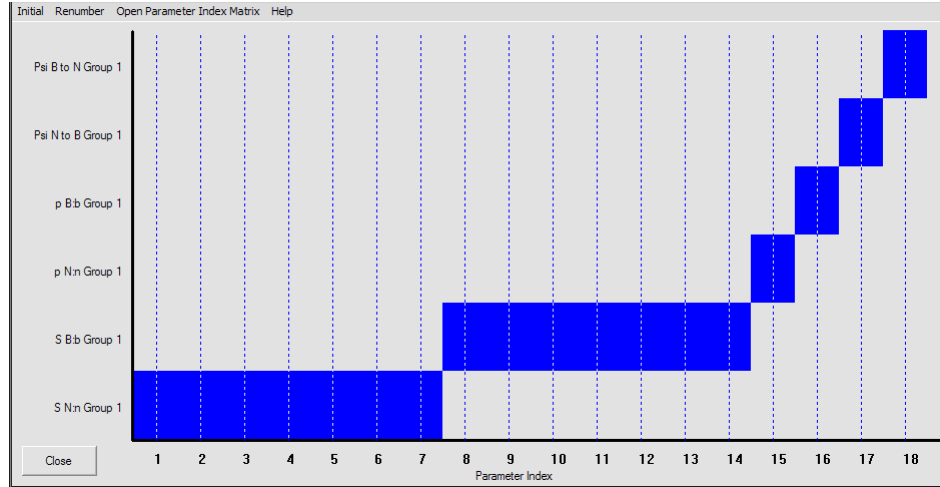
Now, how would we modify the DM with a common intercept? Simple:

B1 S intercept	B2 State	B3 t1	B4 t2	B5 t3	B6 t4	B7 t5	B8 t6	B9 state*t1	B10 state*t2	B11 state*t3	B12 state*t4	B13 state*t5	B14 state*t6	Parm
1	1	1	0	0	0	0	0	1	0	0	0	0	0	1: S B breeder
1	1	0	1	0	0	0	0	0	1	0	0	0	0	2: S B breeder
1	1	0	0	1	0	0	0	0	0	1	0	0	0	3: S B breeder
1	1	0	0	0	1	0	0	0	0	0	1	0	0	4: S B breeder
1	1	0	0	0	0	1	0	0	0	0	0	1	0	5: S B breeder
1	1	0	0	0	0	0	1	0	0	0	0	0	1	6: S B breeder
1	1	0	0	0	0	0	0	0	0	0	0	0	0	7: S B breeder
1	0	1	0	0	0	0	0	0	0	0	0	0	0	8: S N non-breeder
1	0	0	1	0	0	0	0	0	0	0	0	0	0	9: S N non-breeder
1	0	0	0	1	0	0	0	0	0	0	0	0	0	10: S N non-breeder
1	0	0	0	0	1	0	0	0	0	0	0	0	0	11: S N non-breeder
1	0	0	0	0	0	1	0	0	0	0	0	0	0	12: S N non-breeder
1	0	0	0	0	0	0	1	0	0	0	0	0	0	13: S N non-breeder
1	0	0	0	0	0	0	0	0	0	0	0	0	0	14: S N non-breeder

Here, we have a column for the common intercept, a single column for state (since there are 2 states, we need only a single column), and then 6 columns for time, and 6 additional columns for state.time interactions (for a total of 14 columns, identical to the number of columns in the original DM, and equal

to the number of parameters specified in the PIMs for survival, S). If you run this modified DM (shown below), the resulting deviance is 680.054, identical to the value reported for the original DM.

Here is another DM example, again using the deer data. Suppose we decided to fit model $\{S_t^g, p_t^g, \psi_t^g\}$ – in other words, time varying survival as a function of breeding state (g), with constant encounter and movement probabilities which differ between breeding states. First, build the model using PIMs – here is the PIM chart corresponding to our model:



Run this model, and add the results to the browser. Now, let’s build this same model using a design matrix approach. Based on the PIM chart, we see that we have 18 structural parameters in the model. We select ‘**Design | Reduced**’, and specify 18 covariate columns in the design matrix. We will follow the convention introduced above, and treat ‘state’ as a grouping or classification factor. In other words, we’ll use a common intercept for modeling differences in survival among states. In this example, we have 2 levels of ‘state’, so we need one column to code for it.

Here is the design matrix corresponding to our model:

Design Matrix Specification (B = Beta)																		
B1 int	B2 strata	B3 t1	B4 t2	B5 t3	B6 t4	B7 t5	B8 t6	B9 st11	B10 st12	B11 st13	B12 st14	B13 st15	B14 st16	Parm	B15 pn	B16 pb	B17 psi(N-B)	B18 psi(B-N)
1	1	1	0	0	0	0	0	1	0	0	0	0	0	1:S N:n	0	0	0	0
1	1	0	1	0	0	0	0	0	1	0	0	0	0	2:S N:n	0	0	0	0
1	1	0	0	1	0	0	0	0	0	1	0	0	0	3:S N:n	0	0	0	0
1	1	0	0	0	1	0	0	0	0	0	1	0	0	4:S N:n	0	0	0	0
1	1	0	0	0	0	1	0	0	0	0	0	1	0	5:S N:n	0	0	0	0
1	1	0	0	0	0	0	1	0	0	0	0	0	1	6:S N:n	0	0	0	0
1	1	0	0	0	0	0	0	0	0	0	0	0	0	7:S N:n	0	0	0	0
1	0	1	0	0	0	0	0	0	0	0	0	0	0	8:S B:b	0	0	0	0
1	0	0	1	0	0	0	0	0	0	0	0	0	0	9:S B:b	0	0	0	0
1	0	0	0	1	0	0	0	0	0	0	0	0	0	10:S B:b	0	0	0	0
1	0	0	0	0	1	0	0	0	0	0	0	0	0	11:S B:b	0	0	0	0
1	0	0	0	0	0	1	0	0	0	0	0	0	0	12:S B:b	0	0	0	0
1	0	0	0	0	0	0	1	0	0	0	0	0	0	13:S B:b	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	14:S B:b	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	15p N:n	1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	16p B:b	0	1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	17:Psi N to B	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	18:Psi B to N	0	0	0	1

Again, this structure is *identical* to what you have seen before for a single classification factor with 2 levels of the factor. Run this model (label it with 'DM'), and add the results to the browser:

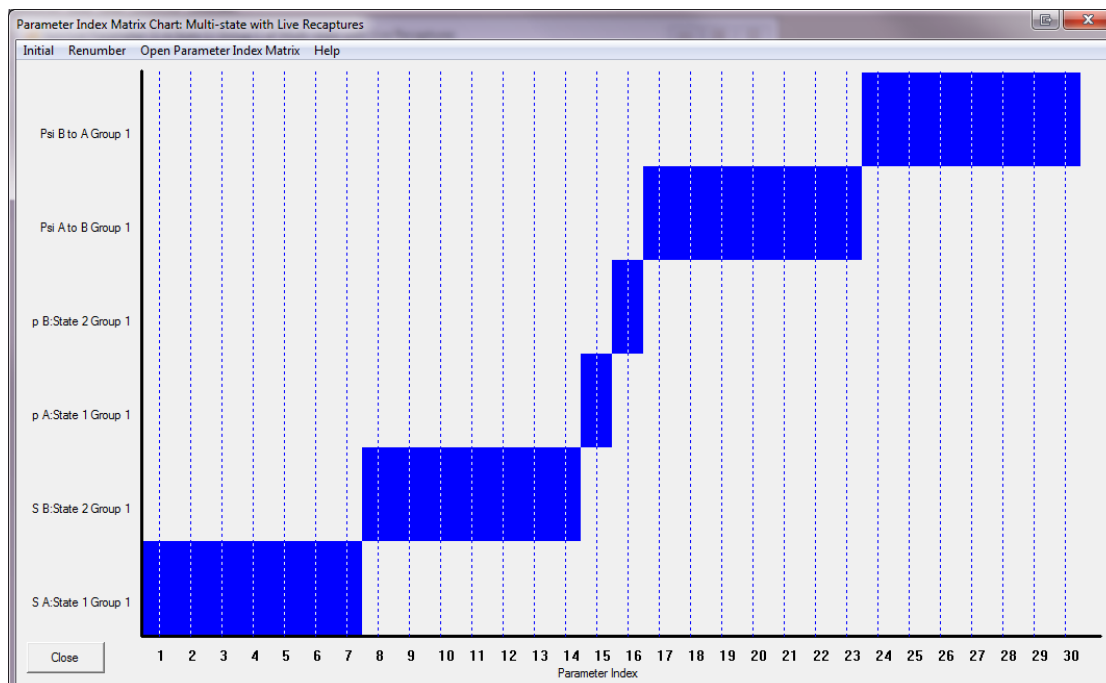
Model	AICc	Delta AICc	AICc Weight	Model Likelihood	No. Par.	Deviance	-2Log(L)
{S(g)p(g)psi(g) - DM}	3819.0683	0.0000	0.73659	1.0000	17	709.7560	3784.5905
{S(g)p(g)psi(g) - PIM}	3821.1249	2.0566	0.26341	0.3576	18	709.7560	3784.5905

Note that the models have different AIC_c values. Is our design matrix wrong? No! Look at the deviances. Note that they are exactly the same. If the deviances are the same, then the models are the same.

So, why the difference in the AIC_c values? Remember (Chapter 4), the AIC is calculated as a function of the fit (deviance), and the number of parameters. If the AIC values differ, but the fit is the same (i.e., same model deviances), then it is the number of estimated parameters which differ. You see in the browser that this is indeed the case – the model built with the PIM chart (which defaults to using the sin link function) shows 18 estimated parameters, whereas the model we just built using the DM (which defaults to the logit link function) reports only 17 parameters. This explains why the two models have different AIC_c values. You can confirm this was indeed the problem by re-running the model you built with PIMs, but first specifying the logit link, instead of the default sin link. If you do so, you'll see that the PIM model run using the logit link reports 17 parameters. Meaning, the problem (difference) is due to the link function, not 'errors' in your DM.

What about time-varying movement parameters, ψ_i ? Let's consider model $\{S_t^g p_t^g \psi_t^g\}$ – time variation in survival and movement, but constant encounter probability.

Here is the PIM chart corresponding to this model:



What is the structure of the design matrix corresponding this parameter structure?

We covered the construction of the DM for the survival and encounter parameters for a multi-state design earlier. The DM for these 2 parameters should look like:

Design Matrix Specification (B = Beta)																
B1 S-int	B2 S-state	B3 t1	B4 t2	B5 t3	B6 t4	B7 t5	B8 t6	B9 S*t1	B10 S*t2	B11 S*t3	B12 S*t4	B13 S*t5	B14 S*t6	B15 p(B)	B16 P(N)	Parm
1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1:S B:breeding
1	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0	2:S B:breeding
1	1	0	0	1	0	0	0	0	0	1	0	0	0	0	0	3:S B:breeding
1	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	4:S B:breeding
1	1	0	0	0	0	1	0	0	0	0	0	1	0	0	0	5:S B:breeding
1	1	0	0	0	0	0	1	0	0	0	0	0	1	0	0	6:S B:breeding
1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7:S B:breeding
1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	8:S N:nonbreeding
1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	9:S N:nonbreeding
1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	10:S N:nonbreeding
1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	11:S N:nonbreeding
1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	12:S N:nonbreeding
1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	13:S N:nonbreeding
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	14:S N:nonbreeding
0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	15:p B:breeding
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	16:p N:nonbreeding

For the movement parameters, ψ , the structure is essentially the same as what we used for the survival parameter:

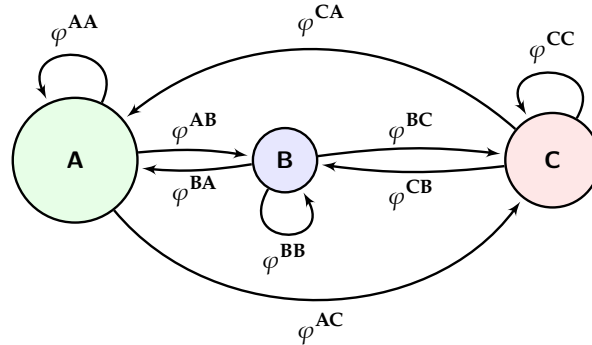
17:Psi B to N	1	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0
18:Psi B to N	1	1	0	1	0	0	0	0	0	0	1	0	0	0	0	0
19:Psi B to N	1	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0
20:Psi B to N	1	1	0	0	0	1	0	0	0	0	0	0	1	0	0	0
21:Psi B to N	1	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0
22:Psi B to N	1	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0
23:Psi B to N	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24:Psi N to B	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
25:Psi N to B	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
26:Psi N to B	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
27:Psi N to B	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
28:Psi N to B	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
29:Psi N to B	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
30:Psi N to B	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Note that it is not necessary to use a common intercept, but it can be convenient to do so for models where you may want to create a structural relationship between the parameters.

10.3.1. A simple metapopulation model – size, distance & quality

In this example, we go back to the hypothetical model we considered right at the beginning – 3 islands with colonies of a particular species of sea-bird, with the potential for exchange among some or all of the islands. For this example, we'll add some complexity to the model, by introducing a number of factors which might potentially influence any of the 3 parameters, either individually or together –

factors which are fairly representative of ‘real-world’ data.* In our example, we’ll vary 2 main factors: (1) the size of individual islands, and (2) the spacing (distance) among the islands. Here is a graphical representation of our ‘island system’:



We see clearly that the islands are not equally spaced: as drawn, island **B** is closer to island **A** than it is to island **C**. And, the islands are not the same size: island **A** is the largest, followed by island **C**, with island **B** the smallest. The islands might differ in terms of some characteristic (say, some limiting resource). Sometimes this might scale with the size of the island. For our example, we’ll simplify somewhat: we’ll assume that island **A** has the highest ‘quality’, while island **B** and island **C** have equivalent quality. As indicated, all transitions among islands are possible. The question we have then is – are there differences in survival, movement probability or recapture probability among the 3 islands? Further, might any differences correlate with differences in spacing, size or quality of the islands?

Based on this ‘metapopulation structure’, we simulated a 6 occasion study, with capture, mark and release occurring simultaneously on all three islands in all years. In other words, in this example, we’re not simply following a single marked cohort through time, but are releasing recaptures and newly marked birds on each occasion. We simulated 250 newly marked individuals on each island at each occasion. The encounter data are contained in the file **island.inp**.

Rather than tell you *a priori* what the parameter values were in the simulation, let’s see how well we can do by building a candidate model set, and using Akaike weights to select the best model. Based on our description of the system, we have good reason to expect that island quality might influence survival. Further, distance among islands, and differences in island size, might influence movement probabilities.

Of course, we might also hypothesize that island size could influence both survival and movement if we invoked density-dependent effects (which will tend to lead to departures from the ideal free distribution based on simple differences in quality). For now, let’s say that, based on earlier studies of this species, we have no evidence for density-dependent effects.

Next, assume there is a fixed number of investigators on each island capturing and releasing the birds. Assume also that, all other things being equal, colony size is proportional to the size of the island. Thus, since island **A** is the largest, you might anticipate that for a constant level of capture effort, that recapture probability should be smaller on island **A** than on (say) island **B**, which is the smallest of the three islands.

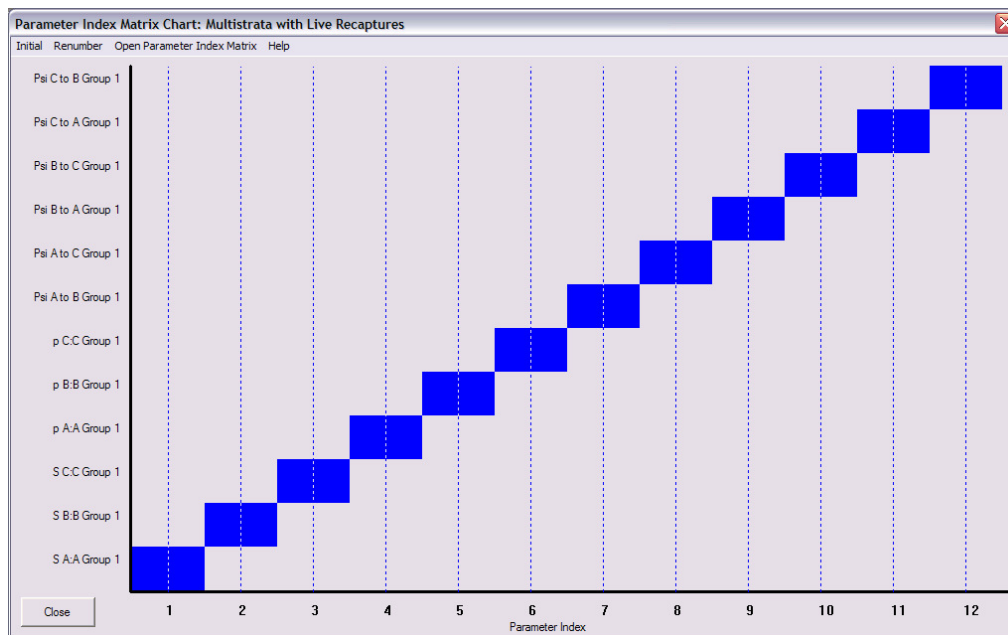
Finally, we assume that environmental conditions during the 6 years of the study have been near-constant.

* In fact, the structure of our example is qualitatively similar to the classic study by Spendelov *et al.* (1995) of a metapopulation of roseate terns.

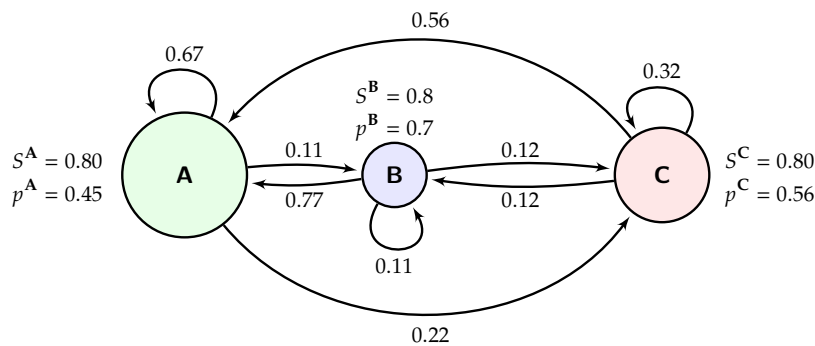
Based on these *a priori* hypotheses, we construct our candidate model set (shown below). Given the detail of our background knowledge, and our insight about these birds, we might start with a general model which allows for ‘group’ differences (i.e., differences among islands), but one that is constant over time. We include several plausible reduced parameter models starting from this general model.

<i>model</i>	<i>description</i>
$S^g p^g \psi^g$	general model – all groups (states) different – constant over time
$S p^g \psi^g$	constant survival – group difference in recapture and movement
$S^g p \psi^g$	constant recapture – group differences in survival and movement
$S^g p^g \psi$	constant movement (inter-island all equal) – group differences in survival and recapture
$S^{quality} p^g \psi^g$	survival constrained to be a function of island quality – group differences in recapture and movement
$S^g p^{size} \psi^g$	recapture constrained as a function of island size – group differences in survival and movement
$S^g p^g \psi^{distance}$	inter-island movement a function of inter-island distance – group differences in survival and recapture
$S p^{size} \psi^{distance}$	recapture a function of island size, movement a function of inter-island distance – constant survival
$S^{quality} p^{size} \psi^{distance}$	survival a function of island quality, recapture a function of island size, and inter-island movement a function of inter-island distance

Open up the PIM chart, and change the default (time-dependent) parameter structure to one that has group (i.e., island) differences, but that is constant over time for each parameter, as shown below:



Go ahead and run the model, and add the results to the results browser. The AIC_c for this model is 19703.54, with 12 estimated parameters. Since this is our general model, let's have a preliminary look at the parameter values. To make it easier to relate the estimates to the model, we'll add them to our 'model diagram', shown below:



Clearly, there is some heterogeneity among islands for recapture and movement probability, but not survival. The question is, are the apparent differences in recapture or movement significant, and does the pattern of variation correlate with one or more of the covariates in our model(s)? Since the 2nd through 4th models in the model set (preceding page) are straightforward (hopefully!), we'll skip the mechanics of setting them up and running them, and go ahead and consider the results:

Results Browser: Multistrata with Live Recaptures						
Model	AICc	Delta AICc	AICc Weight	Model Likelihood	No. Par.	Deviance
$\{S(.p(g)psi(g))\}$	19700.1861	0.0000	0.49366	1.0000	10	1605.7806
$\{S(g)p(.psi(g))\}$	19700.5381	0.3520	0.41399	0.8386	10	1606.1323
$\{S(g)p(g)psi(g)\}$	19703.5388	3.3527	0.09234	0.1871	12	1605.1185
$\{S(g)p(g)psi(.)\}$	19781.7919	81.6058	0.00000	0.0000	7	1693.4039

The best model $\{S.p^g.\psi^g.\}$ is not much better supported by the data than is the next best model $\{S^g.p.\psi^g.\}$. As such, we could only say that these two models are probably equally likely. So, our tentative conclusion at this point is that there is some evidence of equivalence (in some senses) of survival among islands. The movement probabilities clearly differ. This would seem to be concordant with our casual inspection of the estimates from the most general model (shown in the schematic diagram, above).

What about GOF (goodness of fit)? Normally, at this stage, we'd be thinking about fit of our general model – in part for the purposes of deriving an estimate of \hat{c} . We discuss GOF testing for multi-state models at the end of this chapter – for this example, we'll assume the general model fits the data, and leave \hat{c} at the default value of 1.0.

Can we improve our understanding by constraining the general model to be a function of one or more of the 'potentially relevant' covariates? At this point we need to modify the design matrix to constrain the general model. Click once on model $\{S^g.p^g.\psi^g.\}$ in the browser – to make it the active model. Then, right-click this model, and select the **Retrieve** option. Since we want to constrain model $\{S^g.p^g.\psi^g.\}$, we want the design matrix to initially reflect its parameter structure.

Before we actually look at the design matrix, what would the linear model look like for the model you just retrieved? Remember, the retrieved model was $\{S^g.p^g.\psi^g.\}$. Since 'group' = 'island', then there are 3 levels of group (i.e., 3 islands). Thus, we need $(3 - 1) = 2$ columns, plus a column for the intercept, to code for the various group effects for survival and recapture. The structure of the design matrix for the

S and p parameters is (hopefully) straightforward – a column for the intercept, followed by 2 columns of dummy variables, '1 0' for island **A**, '0 1' for island **B**, and '0 0' for island **C**. For this model, we'll use the same basic linear structure for both parameters (S and p). Remember, these codings are arbitrary – we could have just as easily used '1 0' for **A**, '1 1' for **B**, and '0 1' for **C**. The important point is that what is required is 2 columns for the coding, and that the coding is based on 0 or 1 dummy variables.

What about the ψ (movement) parameters? A little trickier, since there are several equivalent coding schemes which would accomplish the same thing. Note that there are 3 groups of movement parameters – those involving movements from island **A**, those involving movements from island **B**, and those involving movements from island **C** – 2 parameters for each group. Thus, following the standard linear models paradigm, we could also use 1 intercept column, and 1 column to indicate which of the 2 transitions within each of the 3 movement groups. For example, as shown below, for the parameters ψ^{AB} and ψ^{AC} , we could have a column of intercept, followed by a column with a '0' indicating movement from **A** to **B**, and a '1' indicating the **A** to **C** movement.

The design matrix for all 3 parameters is shown below:

B1	B2	B3	B4	B5	B6	Pam	B7	B8	B9	B10	B11	B12
1	1	0	0	0	0	1:S A:A	0	0	0	0	0	0
1	0	1	0	0	0	2:S B:B	0	0	0	0	0	0
1	0	0	0	0	0	3:S C:C	0	0	0	0	0	0
0	0	0	1	1	0	4:p A:A	0	0	0	0	0	0
0	0	0	1	0	1	5:p B:B	0	0	0	0	0	0
0	0	0	1	0	0	6:p C:C	0	0	0	0	0	0
0	0	0	0	0	0	7:Psi A to B	1	0	0	0	0	0
0	0	0	0	0	0	8:Psi A to C	1	1	0	0	0	0
0	0	0	0	0	0	9:Psi B to A	0	0	1	0	0	0
0	0	0	0	0	0	10:Psi B to C	0	0	1	1	0	0
0	0	0	0	0	0	11:Psi C to A	0	0	0	0	1	0
0	0	0	0	0	0	12:Psi C to B	0	0	0	0	1	1

Try running this design matrix – the estimates are identical to the estimates for the model you created initially simply by modifying the PIMs.

Now that we have built our general model using the design matrix, let's build the next model in the set, model $\{S^{quality} p^g \psi^g\}$. For model $\{S^{quality} p^g \psi^g\}$, we want to constrain survival to be a function of island 'quality'. Recall that in this example, island **A** is believed to be of better quality than island **B** or **C**, but that island **B** and **C** are believed to be of equal quality. Thus, we need a single column for the intercept, and a single column coding for quality. We'll let '1' represent 'good quality', and '0' represent 'poor quality'.

Thus, the design matrix corresponding to the survival parameters would look like:

Design Matr	
B1	B2
intcpt	quality
1	1
1	0
1	0

Go ahead and run this model, and add the results to the browser. Before we examine the results

of this model, let's go ahead and fit the next 2 models in the list – model $\{S^g p^{size} \psi^g\}$ and model $\{S^g p^g \psi^{distance}\}$.

Since we need some 'numbers' to represent island size and inter-island distance, we used the following values for each, respectively:

island	size	island	A	B	C
A	10	A	0	5	12
B	3	B		0	7
C	6	C			0

Since models $\{S^g p^{size} \psi^g\}$ and $\{S^g p^g \psi^{distance}\}$ are both structurally similar to model $\{S^{quality} p^g \psi^g\}$, you should be able to quickly see how to modify the design matrix (basically, as we just did, but for different parameters).

For example, consider model $\{S^g p^{size} \psi^g\}$, where we want to constrain the probability of recapture to be a function of the size of the island (where it might be reasonable to assume that the bigger the island, the lower the recapture probability for a given marked individual, all other things being equal). To fit this model, you simply need to modify the part of the design matrix corresponding to the recapture probabilities.

Given the 'island size data' in the preceding table, here is the design matrix for model $\{S^g p^{size} \psi^g\}$ (only that part of the design matrix corresponding to the survival and recapture parameters is shown).

B1	B2	B3	B4	B5	Pam
1	1	0	0	0	1:S A:A
1	0	1	0	0	2:S B:B
1	0	0	0	0	3:S C:C
0	0	0	1	10	4:p A:A
0	0	0	1	3	5:p B:B
0	0	0	1	6	6:p C:C

Pretty straightforward. Potentially the only tricky one is model $\{S^g p^g \psi^{distance}\}$. Again, the key is to look closely at the coding for the movement parameters, ψ . If you're constraining ψ to be a function of the distance, then you would replace the '1' and '0' dummy variables in the design matrix with the actual distance values themselves (remember: the '0' and '1' coding treated islands as levels of a classification factor, while using the distances directly is considering them as linear covariates). Sounds reasonable.

However, this is a good example of a problem that is in fact a bit trickier than it might seem at first. For example, you need to decide if you want the probability of moving from A to C (ψ^{AC}) to be the same as the probability of moving from C to A (ψ^{CA}), since clearly the distance is the same between the same two islands, regardless of the direction you're moving. Is this a reasonable constraint?

Let's assume we want to allow the movement probabilities to differ, even among 'complementary' transitions (i.e., we'll let ψ^{AC} differ from ψ^{CA}). How would we set that up? Well, the most flexible way would be to categorize each of the movement transitions according to the donor island. For example, treating movements from island A as one group, from island B as one group, and so on. Since there

are 3 island groups, then 1 intercept column, and 2 columns of dummy variables to code for island. Then, a single covariate column coding for the linear distance among islands. Finally, 2 columns for the interaction of ‘island group’ with linear distance.

The relevant portion of the design matrix we need for this model is shown below. The values of the covariates are the inter-island distance values listed in the table at the top of this page:

7:Psi A to B	1	1	1	5	5	5
8:Psi A to C	1	1	1	12	12	12
9:Psi B to A	1	1	0	5	5	0
10:Psi B to C	1	1	0	7	7	0
11:Psi C to A	1	0	1	12	0	12
12:Psi C to B	1	0	1	7	0	7

Now, it is important here to understand what we’ve done in the design matrix. The intercept is in the first column, the dummy variables for ‘island grouping’ are in columns two and three, and the linear covariate (distances among islands) is in column four. The interaction of ‘island’ and ‘distance’ is shown in columns five and six. Remember, the interaction means that the estimate of movement rate varies as a unique function of island and distance among islands. Go ahead and run the model corresponding to this design matrix, and add the results to the browser. See if you can build all the candidate models listed earlier at the start of this example.

[begin sidebar](#)

The multinomial logit link and MS models

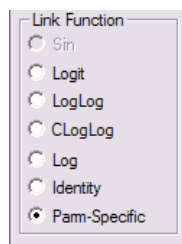
Logically, the transitions from a given state must logically sum to 1.0. However, for reasons related to how **MARK** numerically calculates the estimates of the various parameters, this logical constraint isn’t always met – in other words, the sum is occasionally > 1 , which is clearly not logically feasible. This tends to happen (if it happens at all) if some of the transitions are close to the $[0, 1]$ boundaries.

One solution is to change the link function **MARK** uses – from the sin or logit link, to what is known as the *multinomial logit link* function (MLogit). We will introduce the MLogit link here with respect to multi-state models, but it is also frequently used in POPAN (J-S) models (Chapter 12), multi-state Jolly-Seber models (Chapter 13) and ‘open robust design’ models (Chapter 16).

The multinomial logit works as follows. Assume that each of the transition parameters from state **A** have their own β value, so that **A** to **B** is β_1 , **A** to **C** is β_2 , and **A** to **D** is β_3 . To constrain these 3 parameters to sum to ≤ 1 , the multinomial logit link works as follows:

$$\psi^{AB} = \frac{e^{\beta_1}}{1 + e^{\beta_1} + e^{\beta_2} + e^{\beta_3}} \quad \psi^{AC} = \frac{e^{\beta_2}}{1 + e^{\beta_1} + e^{\beta_2} + e^{\beta_3}} \quad \psi^{AD} = \frac{e^{\beta_3}}{1 + e^{\beta_1} + e^{\beta_2} + e^{\beta_3}}$$

To create this set of links, you need to tell **MARK** to use a Mlogit link. You do this by first selecting the ‘**Parm-Specific**’ link function from list of link options on the ‘**Run**’ window:



When you hit the ‘OK to run’ button, you’re presented with a second window, which allows you to specify the link function for each parameter in your model (this window was first described in Chapter 6 when we introduced the cumulative logit link).

For example, in the deer example, for model $\{S^{\delta} p^{\delta} \psi^{\delta}\}$ you have 6 parameters, so the relevant part of the window looks like:

1.S B breeder	Logit
2.S N non-breeder	Logit
3.p B breeder	Logit
4.p N non-breeder	Logit
5.Psi B to N	MLogit(1)
6.Psi N to B	MLogit(2)

Here, we’ve selected **MLogit(1)** for ‘Psi B to N’, and **MLogit(2)** for ‘Psi N to B’. The number inside the parentheses is a simple indexing for state (2 states – index 1 and index 2). So, if we had 3 states (A, B and C), we’d need 3 levels of indexing. Thus, for example, if we use **MLogit(1)** for all of the A state transitions, we might use **MLogit(2)** for state B transitions, and **MLogit(3)** for state C transitions. For each set of parameters where you want the constraint that the parameters sum to ≤ 1 , you must specify a **MLogit(x)** function, where ‘x’ represents the set number of the MLogit link function.

Here is an example involving > 2 states – based on the example input file `mssurv.inp`, with 4 occasions and 3 states (A, B and C). For a model with full time-dependence in all parameters (including the movement parameters ψ^{ij}), we would use the following MLogit specification:

11:Psi A to B	MLogit(1)	21:Psi B to C	MLogit(5)
12:Psi A to B	MLogit(2)	22:Psi B to C	MLogit(6)
13:Psi A to B	MLogit(3)	23:Psi C to A	MLogit(7)
14:Psi A to C	MLogit(1)	24:Psi C to A	MLogit(8)
15:Psi A to C	MLogit(2)	25:Psi C to A	MLogit(9)
16:Psi A to C	MLogit(3)	26:Psi C to B	MLogit(7)
17:Psi B to A	MLogit(4)	27:Psi C to B	MLogit(8)
18:Psi B to A	MLogit(5)	28:Psi C to B	MLogit(9)
19:Psi B to A	MLogit(6)		
20:Psi B to C	MLogit(4)		

It is important to understand the ‘pattern’. For 4 occasions, there are 3 intervals. So, there would be 3 parameters for ψ^{AB} (i.e., ψ_1^{AB} , ψ_2^{AB} , and ψ_3^{AB}). Same for ψ^{AC} , ψ^{BA} , and so on. Consider state A for occasion 1. Given 3 states, then there are 3 possible state transitions: $A \rightarrow A$, $A \rightarrow B$, and $A \rightarrow C$. Since the default in **MARK** is to estimate the probability of remaining in a state by subtraction (i.e., $\hat{\psi}^{AA} = 1 - \hat{\psi}^{AB} - \hat{\psi}^{AC}$), then there are only 2 parameters for individuals in state A at occasion 1. We apply the same MLogit link (**MLogit(1)**) to those two parameters. For occasion 2 for state A, we use **MLogit(2)**, and so on. The key is (1) remembering that the index x in **MLogit(x)** refers to a set of parameters that you want to constrain, and (2) for time-dependent models, you need to keep track of which sets of parameters correspond to which sampling intervals.

Still not clear? Here is a final demonstration, unrelated to MS models, but using the familiar male Dipper data. Recall that there are 7 sample occasions for the Dipper data – so 6 intervals. Suppose for some reason you wanted the sum of the estimates $(\varphi_1 + \varphi_2) = 1$, $(\varphi_3 + \varphi_4) = 1$, and $(\varphi_5 + \varphi_6) = 1$.

All you need to do to enforce these constraints using the MLogit is start with a model where apparent survival (φ) is time-dependent, then specify the ‘**Parm-Specific**’ option from the ‘**Setup Numerical Estimation Run**’ window. Since there are 3 sets of parameters we want to constraint (i.e., φ_1 and φ_2 , φ_3 and φ_4 and φ_5 and φ_6), then we use indexing $1 \rightarrow 3$ when we specify the MLogit link for each successive pair of parameters (**MLogit(1)** for φ_1 and φ_2 , **MLogit(2)** for φ_3 and φ_4 , and **MLogit(3)** for φ_5 and φ_6):

Specify Link Values

Specify Parameter-Specific Link Function Values for {phi(t)p(t)} - MLogit constraint

1:Phi	MLogit(1)	11:p	Logit
2:Phi	MLogit(1)	12:p	Logit
3:Phi	MLogit(2)		
4:Phi	MLogit(2)		
5:Phi	MLogit(3)		
6:Phi	MLogit(3)		
7:p	Logit		
8:p	Logit		
9:p	Logit		
10:p	Logit		

OK Cancel Default Reset All Paste Help

Looking at the reconstituted estimates on the real probability scale

Real Function Parameters of {phi(t)p(t)} - MLogit constraint				
Parameter	Estimate	Standard Error	95% Confidence Lower	Interval Upper
1:Phi	0.5949028	0.0872560	0.4193647	0.7491199
2:Phi	0.4050961	0.0872554	0.2508800	0.5806332
3:Phi	0.4438275	0.0613644	0.3289607	0.5650306
4:Phi	0.5561725	0.0613644	0.4349694	0.6710393
5:Phi	0.4892534	0.0532551	0.3868184	0.5925990
6:Phi	0.5107465	0.0532551	0.4074010	0.6131815

we see that $(\hat{\varphi}_1 + \hat{\varphi}_2) = (0.5949 + 0.4051) = 1.0000$, $(\hat{\varphi}_3 + \hat{\varphi}_4) = (0.4438 + 0.5562) = 1.0000$, and $(\hat{\varphi}_5 + \hat{\varphi}_6) = (0.4893 + 0.5107) = 1.0000$, as expected.

While constructing the MLogit link is straightforward, you need to be careful. Consider the following set of parameters in a PIM for the survival probability for the male Dipper data:

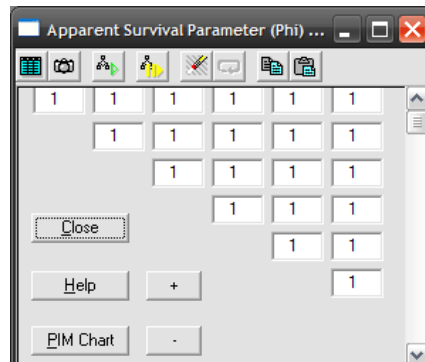
Apparent Survival Parameter (Phi) ...

1	2	3	4	5	6
	2	3	4	5	6
		3	4	5	6
			4	5	6
				5	6
					6

Close Help + PIM Chart -

The parameter-specific link would be selected in the ‘Setup Numerical Estimation Run’ window, and the **MLogit(1)** link would be applied to parameters 1 → 6 to force these 6 estimates to sum to ≤ 1 .

But suppose that instead you wanted to force *all* of the 6 survival probabilities to be the same, and have the sum of all 6 be ≤ 1 ? You might be tempted to specify a PIM such as



(i.e., simply use the same index value for all the parameters in the PIM, which would result in the same estimate for each interval), and apply the MLogit link to parameter 1, but that would be incorrect. Changing the PIM and selecting the MLogit link for parameter 1 would result in parameter 1 alone summing to ≤ 1 (i.e., just like a logit link), but would *not* force the sum of the 6 values of parameter 1 to sum to ≤ 1 . Go ahead and try it for yourself – you’ll see that whether or not you use the MLogit or logit link, parameter 1 is estimated (for a model with time-varying encounter probability) as 0.5561. Clearly, $(6 \times 0.5561) \gg 1$.

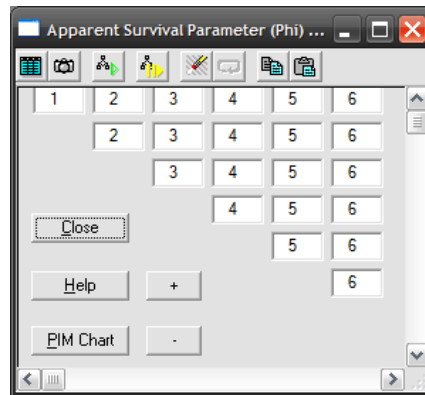
But, what if you want the sum of the 6 estimates to be 1.0? To implement such a model, the PIM should not be changed from a time-dependent PIM (i.e., it should maintain the indexing from 1 → 6); instead, the *design matrix* should be used to force the same estimate for parameters 1 → 6. Then the **MLogit(1)** link should be specified for all 6 parameters for apparent survival, 1 → 6. The result is that now all 6 parameters have the same value ($\hat{\phi} = 0.1\dot{6}$ for the model specified in this DM – with time-dependent encounter probability), where $(6 \times 0.1\dot{6}) = 1$.

Another example – suppose you wanted parameters 1 and 4 → 6 (non-flood years) to be the same value, and parameters 2 and 3 (flood years) to be the same value. Obviously, there are multiple ways to implement such a model in **MARK** – the approach you use will be determined by what constraints you want to implement. If you want to have a separate estimate of apparent survival for flood and non-flood years, and (i) have the same estimate for all flood and non-flood years, and (ii) have the estimates within a flood-type sum to 1.0, then you need to use the design matrix, and apply the MLogit link function to the appropriate parameters. If we apply **MLogit(1)** to flood years (parameters 1, 4 → 6), and **MLogit(2)** to non-flood years (parameters 2 and 3), we end up with estimates of apparent survival of 0.25 for each of the 4 flood years ($4 \times 0.25 = 1.0$), and 0.4965 for each of the 2 flood years ($2 \times 0.4965 = 0.9930 \leq 1.0$).

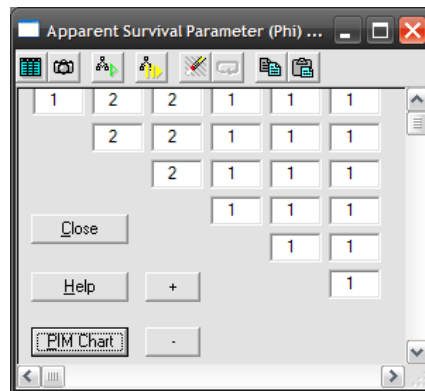
What happens if we apply a single MLogit constraint to all 6 parameters (i.e., **MLogit(1)** to parameters 1 → 6)? As you might expect, applying this constraint will still yield separate estimates of apparent survival for all flood and non-flood years, but now, the sum of estimates over all 6 parameters will be ≤ 1 . What we see if we run this model, with **MLogit(1)** applied to parameters 1 → 6 is $\hat{\phi}_{flood} = 0.1857$, and $\hat{\phi}_{non-flood} = 0.1286$. Summing over all estimates, $(4 \times 0.1857) + (2 \times 0.1286) = 1.0$.

Now, final test – what if you want to have a single separate estimate for flood and non-flood years, and have them sum to 1.0? In other words, instead of generating an estimate for each year subject to the constraint, you want to generate an estimate for each flood type subject to the constraint (so, 2 estimates, not 6, with the sum of the estimates ≤ 1).

With a bit of thought, you should realize that to fit this particular model, you do, in fact, need to first modify the PIM (shown at the top of the next page), which ultimately controls the number of estimated parameters – and then apply the Mlogit constraint to the 2 parameters specified in the PIM.



Here is the modified PIM – parameter 1 indicating the flood years, and parameter 2 indicating the non-flood years:



If we run this model without applying the MLogit constraint, using instead the standard logit link, we see that we obtain estimates of $\hat{\phi}_{flood} = 0.5970$, and $\hat{\phi}_{non-flood} = 0.4725$. Note that the sum of these estimates ($0.5970 + 0.4725$) = $1.07 > 1.0$.

Now, if we re-run the analysis, but apply the MLogit constraint to both parameters (i.e., $MLogit(1)$ for both parameters 1 and 2), we obtain estimates of $\hat{\phi}_{flood} = 0.5728$, and $\hat{\phi}_{non-flood} = 0.4272$ – the sum of these constrained estimates is ($0.5728 + 0.4272$) = 1.0 , as expected.

The key point with these examples is that the PIM *cannot* be used to constrain parameters if you want the entire set of parameters (i.e., over all intervals) to sum to ≤ 1 . Rather, the design matrix has to be used to make the constraints, with each of the entries in the PIM given the same **MLogit(x)** link.

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10.4. Multi-state models as a unifying framework

Multi-state models offer great potential to increase our understanding of complex, structured systems – systems with multiple states, and stochastic (or probabilistic) transitions among states. **MARK** makes it fairly straightforward to fit some relatively complex models to the underlying multi-state structure.

This point was first noted in a paper by Lebreton, Almeras & Pradel (1999), who demonstrated that

multi-state modeling does, in fact, have the potential to be a common, unified ‘framework’ under which a large variety of models can be fit – including those combining information from multiple sources. Using data from multiple types will be discussed in a later chapter – for the moment, we’ll introduce the conceptual framework described by Lebreton *et al.*, to give you the sense of ‘how it is done’, and (with a bit of thought) how easy it is to implement.

10.4.1. Simple example (1) – live mark-recapture as a MS problem

We’ll start by considering a simple (CJS) mark-recapture analysis, based on live-encounter data. While we already have plenty of tools to handle these sorts of data, the simplicity of this data type, and your familiarity with it, make it a good starting point. First, keep in mind that the multi-state approach considers multiple states. In a mark-recapture analysis (or any simple survival analysis), there are 2 states of interest: live, and dead.

As noted by Lebreton *et al.*, the interesting ‘paradoxical’ issue with mark-recapture analysis is that the information on survival (or, equivalently, mortality) is not based on observations of dead animals. Some animals are in fact in the ‘dead’ state, but are never seen. So, if a ‘dead’ state animal is never seen, then clearly, the recapture probability for this state is 0. This leads quite logically to a fairly straightforward representation of the CJS model as a 2-state multi-state model (with states Alive=1, Dead=2), with a 0 probability of capture in the second state (i.e., when dead, or state 2, $p = 0$).

As such, we can define the following transition probabilities. Let φ_i = probability of surviving from time (i) to ($i + 1$). Thus, the probability of surviving and moving from state 1 to 1 (i.e., from live \rightarrow live) is clearly φ . The probability of moving from state 1 to 2 (live \rightarrow dead) is $(1 - \varphi)$. The probability of moving from dead to live is clearly 0. And the probability of moving from dead to dead is 1 (i.e., if you’re already dead, then you will be dead at the next occasion also). Now, if you’re in state 1 (live), the recapture probability is p , while if you’re in state 2 (dead), the recapture probability is 0.

We can express these transitions in a 2-state transition matrix Ψ , and the recapture probabilities in a 2-state vector, \mathbf{p} :

$$\Psi = \begin{matrix} & \begin{matrix} 1 & 2 \end{matrix} \\ \begin{matrix} 1 \\ 2 \end{matrix} & \begin{bmatrix} \varphi & 0 \\ 1 - \varphi & 1 \end{bmatrix} \end{matrix} \quad \mathbf{p} = \begin{matrix} 1 \\ 2 \end{matrix} \begin{bmatrix} p \\ 0 \end{bmatrix}$$

For the transition matrix Ψ , the rows correspond to the state at time ($i + 1$) (live and dead for rows 1 and 2), and the columns correspond to the state at time i (live and dead for columns 1 and 2). Note that the matrix must be constrained to have the sum of each column be equal to 1. Using ‘Alive’ = state 1, and ‘Dead’ = state 2, a typical capture history might be ‘00110100’. No ‘2’ ever appears since that state is never observed.

To demonstrate this analysis, we simulated a CJS data set (**cjs_ms.inp**) – 8 occasions, big sample sizes, with the following parameter values:

	occasion						
	1	2	3	4	5	6	7
φ	0.5	0.85	0.85	0.65	0.50	0.60	0.85
p	0.45	0.45	0.55	0.75	0.75	0.45	0.55

So, time dependence in both survival and recapture probability – model $\{\varphi_i p_i\}$.

Estimates from fitting this model to the data using a live-encounter CJS approach are shown below:

Real Function Parameters of $\{\phi(t)p(t)\}$				
Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:Phi	0.4924350	0.0134292	0.4661590	0.5187528
2:Phi	0.8373917	0.0123089	0.8118035	0.8601003
3:Phi	0.8574654	0.0116202	0.8331397	0.8787609
4:Phi	0.6528416	0.0096733	0.6336476	0.6715512
5:Phi	0.5018881	0.0087432	0.4847559	0.5190158
6:Phi	0.6045285	0.0126119	0.5795616	0.6289620
7:Phi	0.6824350	57.774503	0.2553029E-226	1.0000000
8:p	0.4198697	0.0164394	0.3880324	0.4523881
9:p	0.4447301	0.0106304	0.4240035	0.4656508
10:p	0.5606805	0.0095834	0.5418188	0.5793685
11:p	0.7510784	0.0097206	0.7315430	0.7696398
12:p	0.7608846	0.0109886	0.7386873	0.7817535
13:p	0.4555198	0.0114734	0.4331374	0.4780832
14:p	0.6821416	57.749647	0.4130439E-226	1.0000000

Now let's analyze these data using a multi-state approach. Start **MARK**, and select the '**multi-state data type**'. Specify 8 occasions, and 2 states – the .INP file uses classic '0' or '1' coding for a recapture data set, so change state **A** to 1, and label it 'live', and state **B** to 2, and label it 'dead':

Enter labels and names to identify each stratum

1	1	live
2	2	dead

Now, the only potentially 'tricky' part of the analysis. Open up the PIM chart. You'll see that there are the 6 blue boxes – 2 for survival, 2 for recapture, and 2 for movement, for the 2 states, respectively.

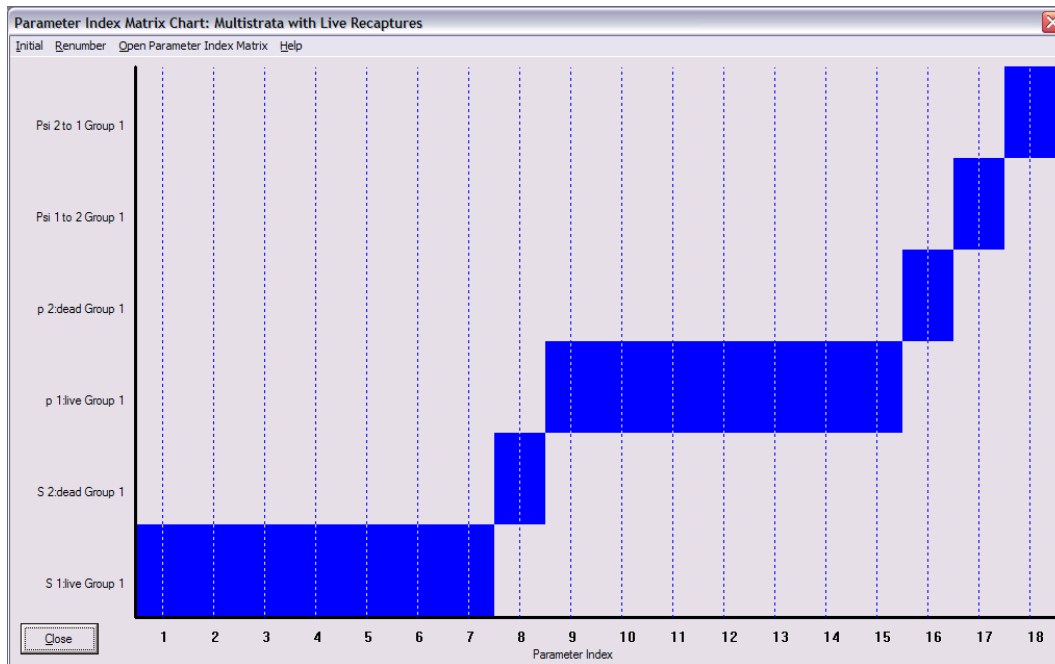
Now, some thinking. Based on the preceding page, we know that recapture probability for dead individuals (state 2) is 0 (in other words, we assume that we never see dead individuals. In effect, we're modeling movement into an 'unobservable state'). So, right click the blue box corresponding to recapture probability for that state, and set it 'constant' – we will fix the parameter value later, during the numerical estimation run. Renumber it with (or without) overlap – doesn't much matter in this case.

Next, we know that the probability of moving from dead to live is 0. So, we set this transition (from state 2 to state 1) constant – again, we will fix the value of this parameter to be 0 during the numerical estimation run. We also need to consider the survival probability of state 2 individuals (i.e., dead individuals) constant – once dead, always dead, so the probability of surviving and staying in this state is clearly 1. So, you could in fact set this parameter to 1. In fact, since there is no information from 'dead' individuals, then 'survival of the dead state' (as a parameter) doesn't enter the likelihood. And as such, you could fix this parameter to any value, or not fix it at all. It won't make any difference. Go ahead and modify the PIM chart, followed by renumbering to eliminate the 'spaces' between the blue boxes (alternatively, you can manually drag the boxes so they are effectively contiguous).

Now, for the last step – and one you might have to think about for a minute. What about the movement parameter from state 1 to 2 (i.e., 'live' to 'dead')? Clearly this movement (from 'live' to 'dead') is a logical complement to the probability of dying, which is defined as $(1 - \phi)$. So, in order for an individual to enter state 2, it must die. State 2 is clearly an 'absorbing state' – once entered, it can't be left. Thus, the

probability of moving from state 1 to state 2, conditional on surviving from (i) to $(i + 1)$ (which is the assumption we're making throughout) is clearly 0 in this case. If you survive from (i) to $(i + 1)$, then you clearly can't move from state 1 ('live') to state 2 ('dead')! Read this section again – a couple of times if needed – to make sure you have the logic down. Once you've gotten a good grip on the idea, simply modify the PIM chart accordingly – set the parameter structure for the movement probability from state 1 ('live') to state 2 ('dead') to be constant.

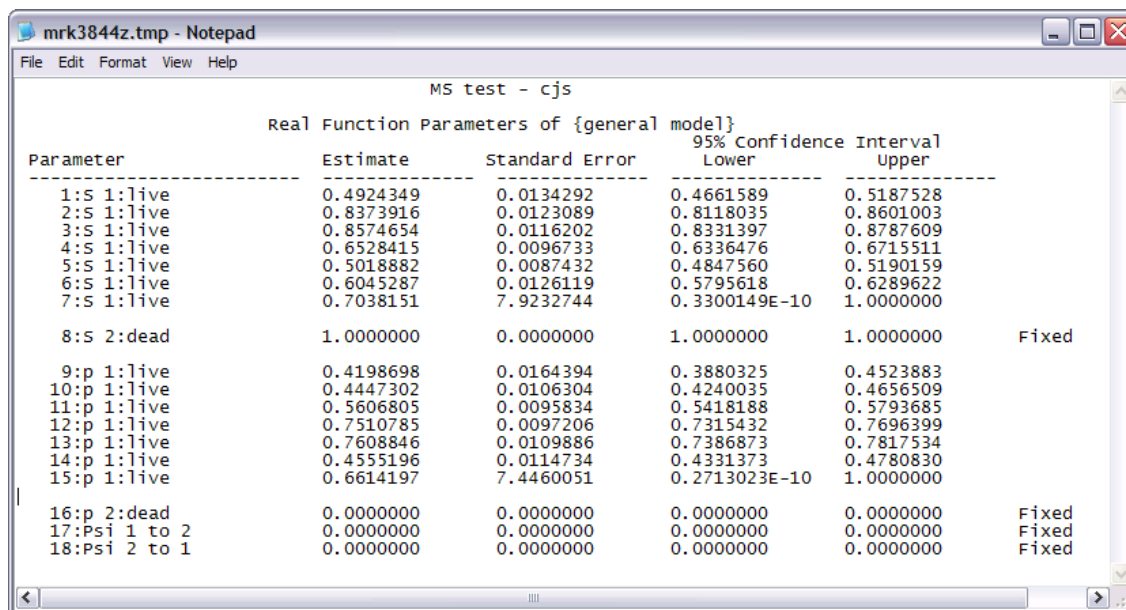
The modified PIM chart is shown below:



That's about it. Now, the only thing we need to do is fix some of the parameters. From the PIM chart, we want to set parameters 16, 17, and 18 (the encounter probability for dead individuals, and the movement probabilities – which are conditional on survival) to be 0. To do this, click the **'Fix Parameters'** button, and set the parameter to the desired value (on the real probability scale):

Parameter	Value
1:S 1:live	
2:S 1:live	
3:S 1:live	
4:S 1:live	
5:S 1:live	
6:S 1:live	
7:S 1:live	
8:S 2:dead	
9:p 1:live	
10:p 1:live	
11:p 1:live	
12:p 1:live	
13:p 1:live	
14:p 1:live	
15:p 1:live	
16:p 2:dead	0
17:Psi 1 to 2	0
18:Psi 2 to 1	0

Go ahead, run the model, and look at the reconstituted estimates:



Parameter	Estimate	Standard Error	95% Confidence Interval Lower	95% Confidence Interval Upper	
1:S 1:live	0.4924349	0.0134292	0.4661589	0.5187528	
2:S 1:live	0.8373916	0.0123089	0.8118035	0.8601003	
3:S 1:live	0.8574654	0.0116202	0.8331397	0.8787609	
4:S 1:live	0.6528415	0.0096733	0.6336476	0.6715511	
5:S 1:live	0.5018882	0.0087432	0.4847560	0.5190159	
6:S 1:live	0.6045287	0.0126119	0.5795618	0.6289622	
7:S 1:live	0.7038151	7.9232744	0.3300149E-10	1.0000000	
8:S 2:dead	1.0000000	0.0000000	1.0000000	1.0000000	Fixed
9:p 1:live	0.4198698	0.0164394	0.3880325	0.4523883	
10:p 1:live	0.4447302	0.0106304	0.4240035	0.4656509	
11:p 1:live	0.5606805	0.0095834	0.5418188	0.5793685	
12:p 1:live	0.7510785	0.0097206	0.7315432	0.7696399	
13:p 1:live	0.7608846	0.0109886	0.7386873	0.7817534	
14:p 1:live	0.4555196	0.0114734	0.4331373	0.4780830	
15:p 1:live	0.6614197	7.4460051	0.2713023E-10	1.0000000	
16:p 2:dead	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
17:Psi 1 to 2	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
18:Psi 2 to 1	0.0000000	0.0000000	0.0000000	0.0000000	Fixed

The estimates for survival and recapture probability are identical to what we observed earlier, using a 'normal' CJS approach to this analysis.

Again, at this point, you might be asking yourself – why bother with a multi-state approach to this analysis, when we could have just as easily done it (in fact, more easily) using the standard 'recapture' analysis? The reason is – if you understand this multi-state approach in this simple case, then it won't be too difficult to see how it can be applied to other data types – for example, dead recovery data, our next example.

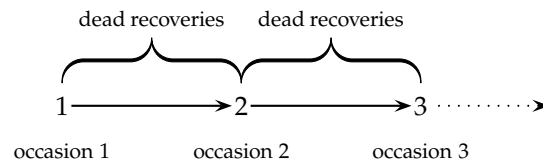
10.4.2. Simple example (2) – dead-recovery analysis as a MS problem

Lebreton, Almeras & Pradel (1999) showed that analysis of dead recoveries can be naturally reframed as multi-state capture-recapture models with two discrete states (live and dead). When framing recovery models as multi-state models, death (mortality) is represented by the transition between 'live' and 'dead', where the 'dead' state is then an 'absorbing state' (meaning, entry into the 'dead' state is permanent). The main challenges in implementing them in **MARK** are to some degree 'conceptual', and 'mechanical' (in particular, the re-formatting of the .INP file that will be required).

In multi-state models, animals move and are potentially detected ('encountered' in the broad sense) in one of N possible states. They are parameterized in terms of an $(N \times N)$ transition matrix Ψ , an $(N \times 1)$ vector \mathbf{p} of capture probabilities, and a $(N \times 1)$ vector \mathbf{S} of survival probabilities. This is the $(\mathbf{S}, \Psi, \mathbf{p})$ parametrization. This framework can be used for band-recovery models if one defines 2 discrete states: newly marked (say, 'banded') alive (state **B**) and newly-dead (state **N**).

However, for multi-state analysis of dead recovery data, building encounter histories takes a bit of thought. While marking and live re-encounters occur during discrete, short periods (i.e., at discrete 'encounter occasions'), dead recoveries occur throughout the interval between discrete live marking/encounter occasions. of the interval between two occasions.

In the following, dead recoveries occur *between* discrete sampling occasions (1, 2, 3...).



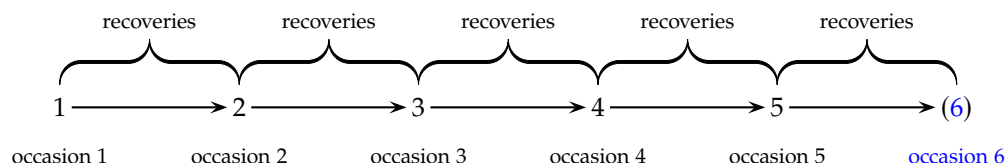
Since MS models are used to estimate transition probabilities among discrete states, then we clearly need to ‘discretize’ time of entry into the ‘newly dead’ state. To do this, individuals recovered dead between live sampling occasion (i) and ($i + 1$) will be coded as entering the state ‘newly-dead’ (N) at the discrete occasion ($i + 1$). For instance, with a study of 4 occasions, the capture history for an animal marked and released alive at occasion 1 and recovered dead between time 2 and 3 would then be ‘A0N0’. Note that if we were using standard LDLD coding (chapter 2, chapter 8), then this individual history would be coded ‘10000100’. And, in fact, this is the first challenge in using a MS approach to analyze dead recovery data in **MARK** – you first need to reformat your data such that dead recoveries are coded as entering the new state (in this case, the newly dead state N) at the end of the interval during which they were recovered. If you have some ‘programming skills’, this isn’t too difficult. But, it is necessary.

To give you a sense of what is required, consider the first few lines of a data set (**recovery-LDLD.inp**) coded in standard LDLD format: the data consists of 5 occasions of mark and release, and 5 intervals during which dead recoveries can occur.

```
1000000000 1649;
1001000000 74;
1000010000 61;
1100000000 134;
1000000001 40;
1000000100 42;
```

So, how do we ‘transform’ these LDLD encounter histories to MS format? The first thing we have to remember is that individuals recovered between occasion (i) and ($i + 1$) will be coded as entering the state ‘newly-dead’ (N) at the discrete occasion ($i + 1$). Sounds straightforward, but what about the final occasion/interval?

In fact, with 5 mark and release occasions, we will need to restructure our MS encounter histories to have 6 occasions: 5 true mark and release occasions ($1 \rightarrow 5$), and one ‘virtual’ occasion (6) which represents the ‘occasion’ on which the newly dead and recovered during the interval following sampling occasion 5 are tabulated (as entering the newly dead state N):



Once you grasp the basic idea, the next steps needed to re-format the encounter history data are relatively easy. Take, for example, the encounter history ‘1001000000’. For this history, there are 5 LD pairs (‘10 01 00 00 00’) – live marked and released at the first sampling occasion, dead recovery over the second interval, and then never encountered again. How do we transform this to the MS format?

The key step is to remember that we're discretizing the interval over which dead recoveries occur, such that a dead recovery occurring over the interval $(i) \rightarrow (i + 1)$ is coded as entering the 'newly dead' state (N) at $(i + 1)$. The trick, then, is to correctly assign events for a given 'LD' pair to the appropriate single occasion in the encounter history reformatted for a multi-state analysis.

One way to 'get events lined up' with the correct discrete occasion is to re-write the contiguous encounter history by first separating the initial 1 from the rest of the history – recall that for any history the first '1' will always represent the newly marked individuals.

So, for example,

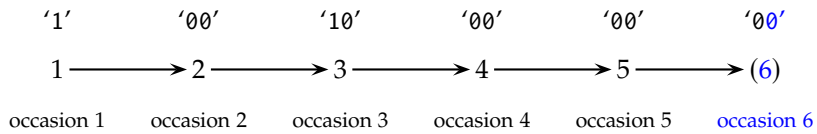
$$'1001000000' \rightarrow '1 \ 001000000'.$$

Next, split the contiguous part of the history into consecutive pairs:

$$'1 \ 001000000' \rightarrow '1 \ 00 \ 10 \ 00 \ 00 \ 00'.$$

Now, here is the key – each of these 'pairs' represent events that occur at a particular discrete occasion, with the final '0' representing a virtual occasion 6 (to allow for dead recoveries after the final marking event at occasion 5 – we simply add a '0' to complete the 'pair' at occasion 6).

So, the initial '1' is the initial mark and release event at occasion 1, the first pair, '00', refers to events that will be coded as if they occurred at occasion 2, then the next pair, '10', refers to events that will be coded as if they occurred at occasion 3, and so on. The basic idea is represented in the following:



What next? Well, the initial '1' for any history will always represent the newly marked individuals – so, we simply change the initial '1' to 'B':

$$'1 \ 00 \ 10 \ 00 \ 00 \ 00' \rightarrow 'B \ 00 \ 10 \ 00 \ 00 \ 00'$$

Next, for a 'dead recovery' study, (i) the dead recovery only occurs once, and (ii) there can only be one event at a given occasion – and, other than the release occasion that event is the transition to 'newly dead' (N).

Thus, a '00' pair indicates 'no event' (0), whereas a '10' pair indicates 'newly dead' (N), and our encounter history would be rewritten as

$$'B \ 00 \ 10 \ 00 \ 00 \ 00' \rightarrow 'B \ 0 \ N \ 0 \ 0 \ 0'$$

which, after removing the spaces, yields

$$'B \ 0 \ N \ 0 \ 0 \ 0' \rightarrow 'B0N000'$$

Let's try another one: consider the encounter history '1100000000'. Here, we have both the 'live marking event' and the 'dead recovery event' occur in the same LD pair. But, the key is remembering that we associate the dead recovery with sampling occasion 2.

Thus, the transformation would go

$$'1100000000' \rightarrow '1 \ 10 \ 00 \ 00 \ 00 \ 00' \rightarrow 'B \ N \ 0 \ 0 \ 0 \ 0' \rightarrow 'BN0000'$$

Finally, what about '1000000001'? For this history, we have a dead recovery in the final LD pair, of the 5 LD pairs in the history. But, as noted earlier, since a 'dead recovery event' over interval $(i) \rightarrow (i + 1)$ is associated with occasion $(i + 1)$, then we need to add a 6th occasion (even though it didn't really exist in our data).

Here, the transformation would go

$$'1000000001' \rightarrow '1 \ 00 \ 00 \ 00 \ 00 \ 10' \rightarrow 'B \ 0 \ 0 \ 0 \ 0 \ N' \rightarrow 'B0000N'$$

So, here (below) are the first few lines of the transformed input file (**recovery-MS.inp**). Make sure you see the connection between each of these transformed encounter histories and the same lines for the corresponding history in LDLD format shown a few pages back:

```
B00000 1649;
B0N000 74;
B00N00 61;
BN0000 134;
B0000N 40;
B000N0 42;
```

OK – now that we have our 'transformed' data file ready, what next? Well, now we move from a 'mechanical' consideration (data formatting) to a 'conceptual' one.

Here is the 2-state transition matrix Ψ , and the 2-state survival and encounter vectors, \mathbf{S} and \mathbf{p} :

$$\Psi = \begin{matrix} & \begin{matrix} B & N \end{matrix} \\ \begin{matrix} B \\ N \end{matrix} & \begin{bmatrix} \psi^{11} & 1 - \psi^{11} \\ 0 & 1 \end{bmatrix} \end{matrix} \quad \mathbf{S} = \begin{matrix} B \\ N \end{matrix} \begin{bmatrix} 1 \\ 0 \end{bmatrix} \quad \mathbf{p} = \begin{matrix} B \\ N \end{matrix} \begin{bmatrix} 0 \\ r \end{bmatrix}$$

By fixing the first entry of the \mathbf{S} vector to 1, then the elements of the first row of Ψ represent survival S (element ψ^{11}) and mortality $1 - S$ (element $1 - \psi^{11}$), respectively. In the second row of the matrix, the transition from state $\mathbf{N} \rightarrow \mathbf{B}$ is logically fixed to 0, and thus its complement (i.e., the transition from state $\mathbf{N} \rightarrow \mathbf{N}$) is by default 1.

Now, a subtle point. In theory, a third state (which we might call 'permanently dead') is needed because an animal can be recovered only once in the \mathbf{N} state (i.e., the year it dies). Failing to consider such a 'permanently dead' state would mean that an individual entering the \mathbf{N} state could be recovered forever, which is clearly a logical impossibility. However, because such a 'permanently dead' state to which individuals move immediately after death contributes no information (i.e., it is never encountered and transitions to this state are all fixed), it can be ignored. We simply need to fix the survival of the state \mathbf{N} to 0 in the \mathbf{S} matrix.

Now, we're ready to proceed with the analysis. First, for purposes of comparison, we'll start with a 'classical' dead recovery analysis of these data, using the Seber parameterization. We'll fit the default time-dependent model $\{S_t, r_t\}$ to these data. The model deviance was 5.8316. Parameter estimates are shown at the top of the next page.

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File Edit Format View Help

dead recovery analysis - standard Seber

Real Function Parameters of $\{S(t)r(t)\}$

Parameter	Estimate	Standard Error	95% Confidence Interval	
			Lower	Upper
1:S	0.6516521	0.0529857	0.5421037	0.7472132
2:S	0.8628893	0.0715949	0.6577818	0.9537161
3:S	0.6543631	0.0599772	0.5295937	0.7609753
4:S	0.8308025	0.0932623	0.5722274	0.9474349
5:S	0.3005045	21.677160	0.7092337E-088	1.0000000
6:r	0.1923365	0.0323149	0.1367413	0.2636324
7:r	0.4150861	0.2224813	0.1053605	0.8104713
8:r	0.1497192	0.0309655	0.0985394	0.2209651
9:r	0.3506915	0.2016190	0.0869508	0.7538858
10:r	0.0957834	2.9683088	0.7106176E-030	1.0000000

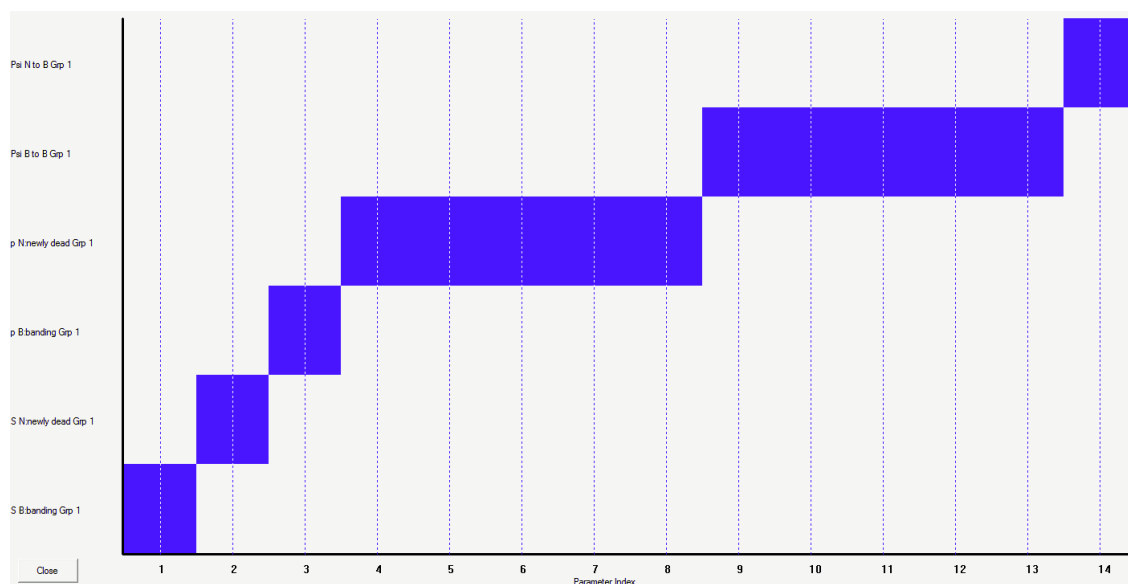
As expected for a fully time-dependent model, the final estimates of S and r are confounded.

Now, let's fit these data using a MS approach. We have to start a new project in **MARK**, specifying a multi-state data type with 2 states (**B** and **N**), and 6 occasions. Since we want to estimate survival (and not mortality), we want to change the default PIM definition so that ψ^{BD} is estimated by subtraction.

Next, we need to modify the PIM structure to represent the transition structure for the 3 parameters in our model. Recall that the model we're trying to fit is $\{S_t r_t\}$.

$$\Psi = \begin{matrix} & \begin{matrix} \text{B} & \text{N} \end{matrix} \\ \begin{matrix} \text{B} \\ \text{N} \end{matrix} & \begin{bmatrix} \psi^{11} & 1 - \psi^{11} \\ 0 & 1 \end{bmatrix} \end{matrix} \quad S = \begin{matrix} \text{B} \\ \text{N} \end{matrix} \begin{bmatrix} 1 \\ 0 \end{bmatrix} \quad p = \begin{matrix} \text{B} \\ \text{N} \end{matrix} \begin{bmatrix} 0 \\ r \end{bmatrix}$$

The multi-state PIM structure for this model (given these transitions) is shown at below:



As a check, notice that the PIM structure has only 2 time-dependent parameters (ψ^{BB} , representing survival, and p^N , represent the recovery probability r) – all the other parameters are fixed constants. This makes sense, since the model we’re trying to fit $\{S_t, r_t\}$ clearly has only two parameters, both time-dependent.

Before running the model, we need to fix some parameters. From the transition structures on the preceding page, we see that we fix survival for the newly banded individuals in state **B** (i.e., parameter 1) to 1, and the survival for newly dead individual in state **N** (i.e., parameter 2) to 0. Clearly, the encounter probability for the newly banded individuals (i.e., parameter 3) is fixed to 0.

Finally, the probability of moving from state **N** to **B** (i.e., from dead to live; parameter 14) is fixed to 0. After fixing the parameters, we run the model. Model deviance is reported as 5.8316, which is identical to the deviance reported for the same model using the classical dead recovery analysis.

The parameter estimates from the MS analysis are shown below:

MS analysis of dead recovery data (Seber)					
Real Function Parameters of $\{S(t)r(t)\}$ -- MS formulation					
Parameter	Estimate	Standard Error	95% Confidence Interval		
			Lower	Upper	
1:S B:banded	1.0000000	0.0000000	1.0000000	1.0000000	Fixed
2:S D:newly dead	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:p B:banded	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
4:p D:newly dead	0.1923365	0.0323147	0.1367416	0.2636318	
5:p D:newly dead	0.4150901	0.2224773	0.1053656	0.8104681	
6:p D:newly dead	0.1497187	0.0309650	0.0985396	0.2209634	
7:p D:newly dead	0.3506943	0.2016258	0.0869476	0.7538978	
8:p D:newly dead	0.0950922	0.0000000	0.0950922	0.0950922	
9:Psi B to B	0.6516522	0.0529853	0.5421047	0.7472126	
10:Psi B to B	0.8628908	0.0715922	0.6577921	0.9537151	
11:Psi B to B	0.6543624	0.0599768	0.5295938	0.7609741	
12:Psi B to B	0.8308038	0.0932641	0.5722217	0.9474370	
13:Psi B to B	0.2954209	0.0000000	0.2954209	0.2954209	
14:Psi D to B	0.0000000	0.0000000	0.0000000	0.0000000	Fixed

If you compare these estimates to those from the classical dead recovery analysis (on the preceding page), you’ll see they are identical (at least for the non-confounded parameters).

Pretty slick, eh? We’ll leave it to you to figure out how to extend this approach to a joint live encounter-dead recovery analysis (see Lebreton *et al.* 1999 and Lebreton & Pradel 2002 for details).

10.4.3. A more complex example – recruitment probability

To really make the flexibility of the ‘omnibus MS’ approach clear, we’ll now consider an example related to the earlier question concerning different breeding states (breeding, and non-breeding), but with a twist – here we’re going to look at ‘recruitment’, which we’ll define as the probability of moving between a non-breeder to a first time breeder. Unlike the analysis of breeding state we presented earlier, but analogous to the multi-state approach to live recapture analysis we just completed, we’re interested here in a ‘permanent’ state transition. In the recapture analysis, we were interested in the transition from ‘live’ to ‘dead’. The various constraints we imposed during the numerical estimation reflect the fact that the transition is permanent (once dead, always dead). In this example, we’re also considering a permanent state transition – from ‘non-breeder’, defined as an individual which has *never* bred, to a ‘breeder’, or (perhaps more accurately, a ‘recruit’) – an individual which has become a breeder (i.e., has bred at least once). Now, once an individual is a breeder, it is always a breeder (i.e., a permanent state transition). It may not breed in every year following first breeding, but it is always a breeder.

This question, and various approaches to estimation of the probability of making this transition from non-breeder to recruit, have been discussed at length by Pradel & Lebreton (1999), and references therein. Our purpose here is merely to point out again how the multi-state approach can be used to deal with situations where there is a non-observable state. What is the non-observable state? In this case, it is the non-breeding (pre-recruitment) state (which we'll call **NB**). In many species, only breeding individuals are encountered. Thus, we need to separate the effects of being a **NB** (non-breeding, pre-recruitment) individual (for which $p = 0$) from death. A multi-state approach is one way to tackle this problem.

Consider the following situation (as described by Pradel & Lebreton). The probability of making the permanent transition from non-breeding to breeding (i.e., the probability of recruiting) is governed by the parameter a . Formally, let a_i be the probability that an as yet inexperienced individual of age (i) starts to breed at that age. An individual is marked as a newborn, and then each year, you go out to look for that individual. If you encounter the individual, then it has both survived, and recruited. If you don't encounter the individual, it is either because it hasn't survived, or that it hasn't recruited (and is thus non-observable).

Take the encounter history '2011', where '2' denotes the birth date (time of initial marking), and '1' denotes 'breeding' or 'recruited'. So, state '2' represents 'pre-breeders' (**PB**), and state '1' represents recruited 'breeders' (**B**). Assume there are only 2 age-specific survival probabilities (φ_j and φ_a), a constant recapture probability p , and age-specific probabilities of recruitment (a_1 , a_2 and a_3). Thus, the associated probability of this encounter history is $\varphi_j[(1 - a_1)a_2 + a_1(1 - p)]\varphi_a p \cdot \varphi_a p \cdot$.

Pradel & Lebreton then simulated a data set of consisting of a single cohort of 5,000 individuals, setting $\varphi_j = 0.4$, $\varphi_a = 0.8$, $p = 0.5$. They assumed that survival did not differ among pre-recruits (non-breeders) and recruits. For age-specific recruitment probabilities, they used $a_1 = 0.2$, $a_2 = 0.375$, and $a_3 = 1.0$. Here are the simulated encounter histories:

<i>history</i>	<i>frequency</i>	<i>history</i>	<i>frequency</i>
2111	32	2011	128
2110	48	2010	192
2101	32	2001	448
2100	88	2000	4,032

Let's analyze these data using **MARK**. The transition matrices governing these data are:

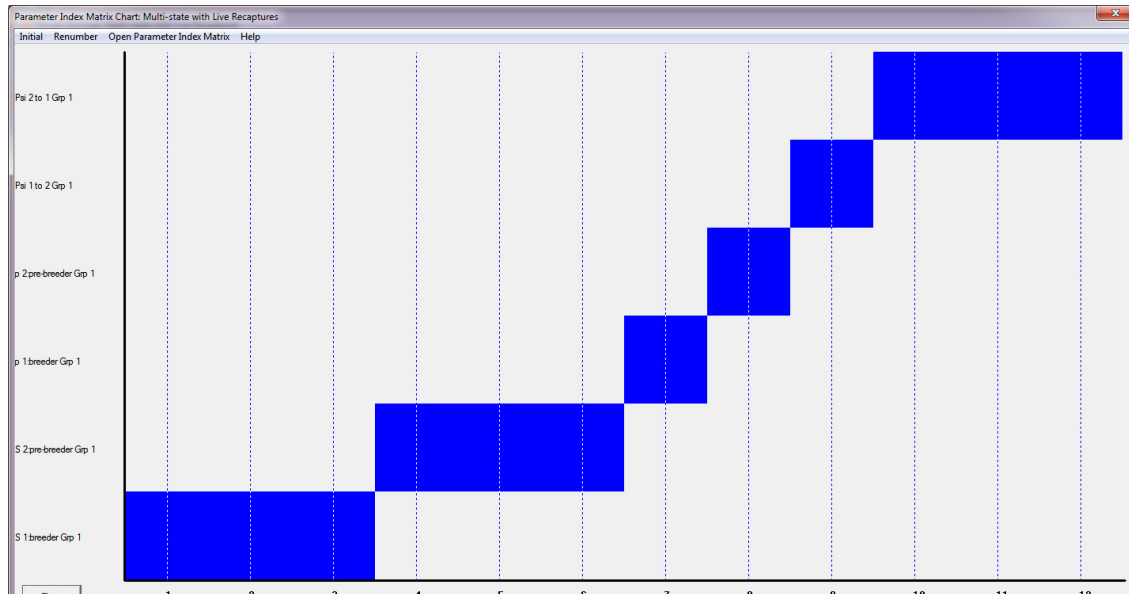
$$\Psi = \begin{matrix} & \text{PB} & \text{B} \\ \begin{matrix} \text{PB} \\ \text{B} \end{matrix} & \begin{bmatrix} 1 - a_i & 0 \\ a_i & 1 \end{bmatrix} \end{matrix} \quad \mathbf{S} = \begin{matrix} \text{PB} \\ \text{B} \end{matrix} \begin{bmatrix} \varphi_i \\ \varphi_i \end{bmatrix} \quad \mathbf{P} = \begin{matrix} \text{PB} \\ \text{B} \end{matrix} \begin{bmatrix} 0 \\ p_i \end{bmatrix}$$

The procedure for analyzing these data using **MARK** is mechanically similar to what we just did when using the multi-state approach to analyze live recapture data. The only difference in this case is that we have to impose different constraints. The challenge is to determine constraints to impose, and whether or not they make 'biological' sense (as opposed to constraints that are needed out of structural necessity to make one or more parameters identifiable).

We 'know' from the simulated data that recapture probability is constant, so we'll modify the PIM chart to reflect this. We also know that the probability of capturing a non-breeding pre-recruit is 0, so we set recapture probability for non-breeders to be a constant (we'll fix it to 0 just before the numerical estimation run). We also know the probability of moving from breeder to non-breeder is 0, so we will set that parameter to be 0 before the numerical estimation. Finally, the ' a ' parameter we're really interested in – this corresponds to the probability of moving from non-breeder to breeder. We 'believe' that

this is likely to be age-specific, so we use a simple time-specific parameterizations for this probability (remember, ‘age = time within cohort’, and here, we’re dealing with a single cohort).

Here is the resulting PIM chart:



and the corresponding DM:

B1: S: int	B2: state	B3: t1	B4: t2	B5: state.t1	B6: state.t2	Parm	B7: p-B	B8: p-NB	B9: psiBN	B10: psiNB1	B11: psiNB2	B12: psiNB3
1	1	1	0	1	0	1: S 1 breeder	0	0	0	0	0	0
1	1	0	1	0	1	2: S 1 breeder	0	0	0	0	0	0
1	1	0	0	0	0	3: S 1 breeder	0	0	0	0	0	0
1	0	1	0	0	0	4: S 2 pre-breeder	0	0	0	0	0	0
1	0	0	1	0	0	5: S 2 pre-breeder	0	0	0	0	0	0
1	0	0	0	0	0	6: S 2 pre-breeder	0	0	0	0	0	0
0	0	0	0	0	0	7: p 1 breeder	1	0	0	0	0	0
0	0	0	0	0	0	8: p 2 pre-breeder	0	1	0	0	0	0
0	0	0	0	0	0	9: Psi 1 to 2	0	0	1	0	0	0
0	0	0	0	0	0	10: Psi 2 to 1	0	0	0	1	0	0
0	0	0	0	0	0	11: Psi 2 to 1	0	0	0	0	1	0
0	0	0	0	0	0	12: Psi 2 to 1	0	0	0	0	0	1

We proceed to run the numerical estimation, first fixing both the recapture probability for non-breeders (parameter 8 in the PIM chart), and the probability of moving from breeder back to non-breeder (parameter 9 in the PIM chart) to 0.

But, what about the probability of moving from non-breeder to breeder (parameter a)? It might seem *a priori* there is no need to fix any of these parameters, since these are the parameters we’re interested in estimating in the first place. Anything we need to do with the survival parameters? Perhaps nothing immediately obvious.

However, once we run this model, and look at the estimates (top of the next page), we see quickly that fixing only parameters 8 and 9 as described leads to several problems. Although numerical convergence

Chapter 10 - recruitment analysis as MS problem

Real Function Parameters of {S(state*time)p(.)psi(time) - DM - SA}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper	
1:S 1:breeder	0.7660211	54.141834	0.2416491E-256	1.0000000	
2:S 1:breeder	0.7999998	0.0663322	0.6396220	0.9001473	
3:S 1:breeder	0.7999983	0.0871764	0.5789292	0.9208672	
4:S 2:pre-breeder	0.6298578	0.0000000	0.6298578	0.6298578	
5:S 2:pre-breeder	0.6298578	0.0000000	0.6298578	0.6298578	
6:S 2:pre-breeder	0.6298578	0.0000000	0.6298578	0.6298578	
7:p 1:breeder	0.5000009	0.0544857	0.3948037	0.6051980	
8:p 2:pre-breeder	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
9:Psi 1 to 2	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
10:Psi 2 to 1	0.1270126	0.0000000	0.1270126	0.1270126	
11:Psi 2 to 1	0.2771902	0.0000000	0.2771902	0.2771902	
12:Psi 2 to 1	0.8118027	0.0000000	0.8118027	0.8118027	

is reached, the estimates for virtually all of the parameters are clearly wrong – anything estimated with a standard error of 0 or a 95% CI from 0 \rightarrow 1 is clearly wrong (even with simulated data!).

Nonetheless, note that the estimates themselves ‘seem’ to approximate the ‘true’ values used in the simulation rather well, except for φ_j , and the final recruitment probability a_3 . This sort of thing often implies that one (or more) parameters are not identifiable under the given set of constraints – either because the constraints are incorrect, or because you haven’t constrained enough parameters. In this case, it turns out that the latter is the cause of the problems here.*

What other constraint(s) do we need? Well, as it turns out, we need to impose 2 further constraints. First, consider the survival parameter. How can we estimate the survival probability of individuals we don’t see (i.e., the pre-breeders)? The answer is – we can’t. We need to apply a constraint, wherein we need to assume that survival of pre-breeders and breeders is the same for a given interval.[†] We can do that simply by deleting the ‘state’ and ‘state.time’ interaction columns from the design matrix.

In addition, we also need to assume that there is some age (in this example, age 3) by which all individuals in the population that are still alive will have recruited (in other words, this involves setting $\psi_3^{N \rightarrow B} = 1$, by fixing parameter 12 to 1.0 in the numerical estimation). [Note: the data were simulated assuming $a_3 = 1.0$ in the first place.] This second assumption is explained in detail in the Pradel & Lebreton paper. If we re-run the analysis, fixing parameter 8 and parameter 9 to 0, and also fixing parameter 12 to 1, we see that our estimates (shown below) are now ‘correct’:

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper	
1:S 1:breeder	0.4007452	0.0312549	0.3413123	0.4632488	
2:S 1:breeder	0.7987880	0.0660386	0.6395511	0.8988086	
3:S 1:breeder	0.7966122	0.0858095	0.5810780	0.9170791	
4:S 2:pre-breeder	0.4007452	0.0312549	0.3413123	0.4632488	
5:S 2:pre-breeder	0.7987880	0.0660386	0.6395511	0.8988086	
6:S 2:pre-breeder	0.7966122	0.0858095	0.5810780	0.9170791	
7:p 1:breeder	0.5017766	0.0541075	0.3972104	0.6061876	
8:p 2:pre-breeder	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
9:Psi 1 to 2	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
10:Psi 2 to 1	0.1989184	0.0340053	0.1404772	0.2739240	
11:Psi 2 to 1	0.3736612	0.0442597	0.2916873	0.4635944	
12:Psi 2 to 1	1.0000000	0.0000000	1.0000000	1.0000000	Fixed

* The identification of parameters that are not estimable given the structure of the model is discussed in Appendix F.

[†] This ‘equality of survival’ assumption (which is very common when trying to model ‘unobservable states’), and its implications, is discussed in some detail in Cam *et al.* (2005).

Now, clearly, the key step was assuming that there was an age after which all individuals were recruited, conditional on still being alive. This is a strong assumption, and one that makes application of this approach somewhat problematic – see Pradel & Lebreton for a full discussion. However, the point here is to demonstrate the methodology, and not to provide a full treatment of this complex problem. As noted by Pradel & Lebreton, the multi-state approach may have utility for this particular analysis, given some assumptions. But, more importantly, we again see how useful the multi-state approach can be in dealing with states which are not observable.

[begin sidebar](#)

Optimization challenges: multi-state models + local minima – approaches and solutions

In the preceding example, our estimates were ‘wonky’ (nonsensical) until we applied the appropriate and necessary logical constraints to the model. However, this is not always the case. Sometimes, multi-state models have ‘problems’ converging to global maxima. In fact, the multi-state model can display some heinous behavior when there are > 2 states, most notably multiple optima in the likelihood function (Lebreton & Pradel 2002). That is, depending on the starting values used to maximize the likelihood function, the numerical solution can vary. Most of the models we have explored so far have a single maximum, and so this behavior is not encountered.

There are several approaches to handling the potential problem of multiple optima in the multi-state likelihood function, which we describe here. First, for multi-state models in particular, it is not a bad idea to first build a simple, time-constant ‘dot’ model containing all the factors of interest. We will use this model to generate ‘good starting values’ for the more general model. Note that previously, we advocated first building the most general model in your candidate model set, for which you will then estimate \hat{c} (see chapter 5). In general, this works fine. But for multi-state models in particular, and other data types where you might be having some ‘numerical estimation problems’ for your general model, using starting values from a simpler model often helps you avoid some problems.

In some cases, even very simple models will have problems. A second approach is to make use of a different link function. In some cases, a different link function may ‘do better’ at navigating what might be a multi-modal likelihood surface. In fact, if you find fitting a given model to a data set using different link functions yields very different model deviances, then this is a reasonable indicator that you might be having problems finding the global minima with some link functions.

Finally, you might try using an alternative optimization procedure available in **MARK**. This procedure, based on *simulated annealing*, is selected by clicking the ‘**alternate optimization**’ checkbox on the right-hand side of the ‘**run numerical estimation**’ window. Simulated annealing (Goffe & Ferrier 1994) is less computationally efficient than the default optimization algorithm in finding the maximum of the function, typically requiring many more evaluations of the likelihood to reach a solution. However, the reason for this ‘inefficiency’ is why simulated annealing is provided in **MARK**; periodically, the simulated annealing algorithm makes a random ‘jump’ to a new parameter value, and this characteristic is what allows the algorithm more flexibility in finding the global maximum (instead of getting stuck at a local maximum).

We will demonstrate the various approaches to handling ‘estimation problems’ using an example multi-state data set with a known local minimum: 2 states (1 and 2), 7 occasions (this example was extracted from an example from Jerome Dupuis, used in a paper by Gimenez *et al.* 2005). Here are the encounter histories:

2021202 4;	1110101 4;
2020201 4;	1010101 4;
2020202 4;	1010102 4;
2201021 4;	2102011 4;

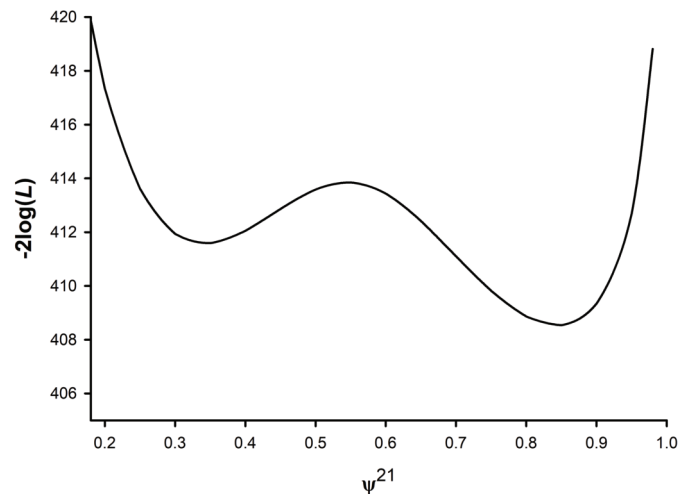
The true parameter values are $S = 1.0$ (constant over time, and the same for both states), $p = 0.6$ (constant over time, and the same for both states), $\psi^{12} = 0.60$ (constant over time), and $\psi^{21} = 0.85$ (constant over time). If you fit model $\{S, p, \psi^s\}$ (which is the true model) to the data in **MARK**, using

the default numerical optimization routine with a sin link, we get the following estimates. We see clearly that **MARK** has had some problems coming up with estimates for $\hat{\psi}^s$ that are even remotely close to the true values.

MS - local minima

Parameter	Real Function Parameters of {true - default}			
	Estimate	Standard Error	95% Confidence Interval Lower	95% Confidence Interval Upper
1:S 1:1	1.0000000	0.0000000	1.0000000	1.0000000
2:p 1:1	0.5833333	0.0355797	0.5123869	0.6509884
3:Psi 1 to 2	0.2480010	0.0666486	0.1406682	0.3991871
4:Psi 2 to 1	0.3419952	0.0753735	0.2123359	0.5005178

What has happened? Well, take a look at the likelihood profile for values of ψ^{21} from 0.2 \rightarrow 1.0, shown below:



We see from the likelihood profile that there are in fact two local minima: one at approximately 0.35, and another at approximately 0.85. Now, look back at our estimate for ψ^{21} generated using the default numerical optimization routine – we see that $\hat{\psi}^{21} = 0.342$, which is roughly where the first local (non-global) minima occurs. In this case, it was a case of ‘bad luck’ that **MARK** converged to this local minima – the bad luck owing to the starting values **MARK** defaults to.

If we use a starting value of 0.85 for ψ^{21} , and try again, we see that now **MARK** ‘correctly’ gives us the ‘right’ parameter estimates:

MS - local minima

Parameter	Real Function Parameters of {true - default}			
	Estimate	Standard Error	95% Confidence Interval Lower	95% Confidence Interval Upper
1:S 1:1	1.0000000	0.0000000	1.0000000	1.0000000
2:p 1:1	0.5833333	0.0355797	0.5123869	0.6509884
3:Psi 1 to 2	0.5993209	0.0738200	0.4501940	0.7320718
4:Psi 2 to 1	0.8441960	0.0705638	0.6543620	0.9394203

Of course, in practice, we won’t be able to ‘cheat’ by using starting values close to the true values – since we won’t know what the true parameter values are (obviously)!

Moreover, for this particular problem, it turns out the estimates are also strongly influenced by the choice of the link function. In the preceding, we used the default sin link. What happens if instead we'd selected the logit link? In fact, for these example data, parameter estimates using the logit link (below) are very close to the true parameter values under which they data were simulated.

multiple local minima

Real Function Parameters of {s(.)p(.).psi(g) - s fixed - logit link}

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:S 1:1	1.0000000	0.0000000	1.0000000	1.0000000
2:p 1:1	0.5833333	0.0355797	0.5123869	0.6509884
3:Psi 1 to 2	0.5993209	0.0738200	0.4501939	0.7320718
4:Psi 2 to 1	0.8441960	0.0705638	0.6543620	0.9394203

So, estimates for MS models may depend on choices of starting values, and link functions. This is clearly disconcerting. What can we do?

Well, if you're willing to get your computer to do a bit of work for you, you can either (i) try a variety of different starting values and/or link functions, and see if there is convergence in your answers, or (ii) make use of the alternate optimization capability in **MARK** – based on simulated annealing. Recall that the simulated annealing algorithm makes a periodic 'random jump' to a new parameter value (i.e., jumps to a different part of the likelihood surface). It is this characteristic that allows the annealing algorithm to be more likely to find the global maximum instead of a local maximum.

For our example, when we run the simulated annealing algorithm, we see that **MARK** gives us the correct estimates – even using the default starting values:

MS - local minima

Real Function Parameters of {true - simulated annealing}

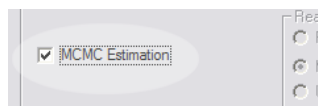
Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper
1:S 1:1	1.0000000	0.2748396E-06	0.9999995	1.0000005
2:p 1:1	0.5833360	0.0355796	0.5123896	0.6509910
3:Psi 1 to 2	0.5993190	0.0738203	0.4501917	0.7320706
4:Psi 2 to 1	0.8441935	0.0705648	0.6543575	0.9394193

However, as noted earlier, simulated annealing is typically **much** slower than the standard numerical optimization routine **MARK** uses. But, if you have a strong suspicion that one or more of your parameter estimates are at the boundary, then there is some chance you might have a local minima (or several, especially if you have > 2 states), and simulated annealing might be an option.

Is there any way you can 'predict' when you might have such local minima? Unfortunately, at present there is no known diagnostic you can apply *a priori* (although there does seem to be some evidence that such local minima are more likely to occur for time-dependent models with > 2 states).

However, by making use of a numerically intensive approach known as *Markov chain Monte Carlo* (MCMC), we can evaluate the *posterior distribution* to determine whether or not there may be local minima in the likelihood for a given parameter (if the notion of MCMC, and posterior distributions, are new to you, no need to worry – these are covered in detail in Appendix E). Here, we will simply demonstrate the mechanics of using MCMC in **MARK**, using the preceding example where we have already determined there to be local minima in the likelihood.

To use MCMC estimation in **MARK** you first need to check the '**MCMC Estimation**' check-box in the '**numerical estimation run**' window:



Once you've clicked 'OK to run', you'll be prompted to specify the MCMC parameters:

Markov Chain Monte Carlo Parameters

Random Number Seed: 0

Number of 'tuning' samples: 4000

Number of 'burn in' samples: 1000

Number of samples to store: 10000

Name of binary file to store samples: MCMC.BIN

Default SD of normal proposal distribution: 0.5

Hyperdistribution Specification

Number of hyperdistributions: 0

☐ Hyperdistribution means modeled with a design matrix of 2 columns

☐ Variance-covariance matrix specified

Prior Distributions for Parameters not Included in Hyperdistributions

☐ No Prior - Prior Ratio

☒ Default Prior: Mean 0.0 Sigma 1.75

☐ Specify Priors Individually

Convergence Diagnostics

☐ Estimate sample sizes using gibbsit procedure

☒ Single chain, with no convergence diagnostics

☐ More than 1 series, using convergence of Markov chain

Number of chains: 10

Help Cancel OK

For the moment, we'll simply accept the defaults (the details of the various MCMC parameters are covered in Appendix E) – these are *usually* sufficient to give us 'a reasonable' look at the posterior, from which we can often determine the presence of local minima in the likelihood for a given parameter. Note that the default file where the MCMC samples will be stored is the file `MCMC.BIN` (we need these samples to construct the posterior). The `MCMC.BIN` file is created in whatever directory contains, the `.INP`, `.DBF`, and `.FPT` files associated with the data set you're working with.

Once you click the 'OK' button, **MARK** will spawn a numerical estimation window – you can 'watch' as **MARK** iterates through the MCMC samples (where the number of iterations is equal to the number of burn in samples (1,000, by default), plus the number of 'tuning' samples (4,000, by default), plus the number of post-burn and post-tuning samples (10,000, by default) – so, accepting the default parameters, 15,000 total samples (iterations of the Markov chain).

Once **MARK** has finished, it will spawn a window showing various summary statistics calculated from the posterior distribution for each of your parameters. These summary statistics (shown at the top of the next page) are presented for both the parameter estimates on the transformed scale (*note*: for MCMC estimation in **MARK**, the default settings for the priors assume you're using the logit link. If you change to another link function, you'll probably want to modify the priors as well), followed by the same summary statistics for the parameters transformed back to the real probability scale. The summary statistics for the 4 parameters for our example problem are shown at the top of the next page.

Of particular interest are the mean, median and modes of the posterior distributions, and the 2.5th and 97.5th percentiles of the posterior (from which we derive the 95% 'credibility interval' for our various parameters). Look closely at the mean, mode, and median statistics for the various parameters. Start with the encounter parameter p (we ignore survival S , here, since it was fixed to 1.0). Note that for p , the mean, median and mode are all very close to each other.

However, this is obviously not the case for parameters ψ^{12} and ψ^{21} . For ψ^{12} , for example, the mean is 0.535, the median is 0.572, and the mode is 0.600. Similarly, for ψ^{21} , the mean is 0.737, the median is 0.803, and the mode is 0.834. Recall that the 'true' parameter values were $\psi^{12} = 0.60$, and $\psi^{21} = 0.85$.


```
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```

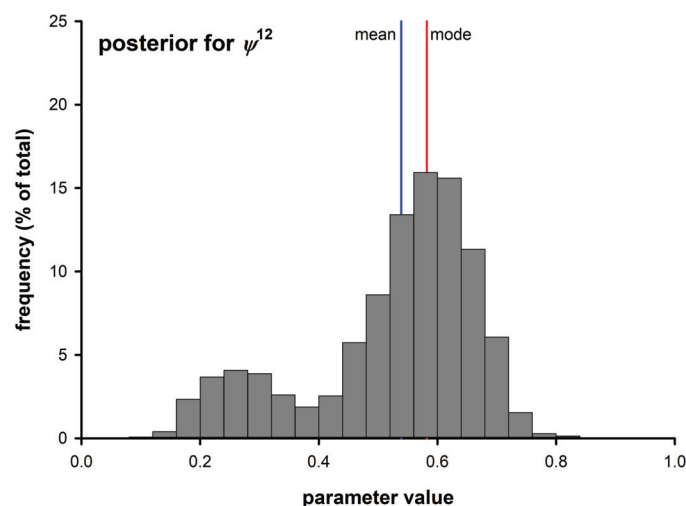
Real Function Parameters of {S(.)p(.)psi(.)}				
Parameter	Mean	Standard Dev.	Median	Mode
-----	-----	-----	-----	-----
1:S 1:1	1.0000000	0.0000000	1.0000000	1.0000000
2:p 1:1	0.5816763	0.0355879	0.5832833	0.5856200
3:Psi 1 to 2	0.5354289	0.1395439	0.5716242	0.6004277
4:Psi 2 to 1	0.7371661	0.1836224	0.8027127	0.8337389
-----	-----	-----	-----	-----
Parameter	2.5th Percentile	5th Percentile	10th Percentile	20th Percentile
-----	-----	-----	-----	-----
1:S 1:1	1.0000000	1.0000000	1.0000000	1.0000000
2:p 1:1	0.5111651	0.5207171	0.5350718	0.5503562
3:Psi 1 to 2	0.1992024	0.2262820	0.2817665	0.4525208
4:Psi 2 to 1	0.2739837	0.3183161	0.3789612	0.6456372
-----	-----	-----	-----	-----
Parameter	80th Percentile	90th Percentile	95th Percentile	97.5th Percentile
-----	-----	-----	-----	-----
1:S 1:1	1.0000000	1.0000000	1.0000000	1.0000000
2:p 1:1	0.6116886	0.6264250	0.6382888	0.6482099
3:Psi 1 to 2	0.6438906	0.6806330	0.7047624	0.7235685
4:Psi 2 to 1	0.8717621	0.8992822	0.9165888	0.9285783
-----	-----	-----	-----	-----

```
=====
```

Clearly, both the mean and median are not particularly robust estimators of either parameter – in both cases, the mode is the better statistic.*

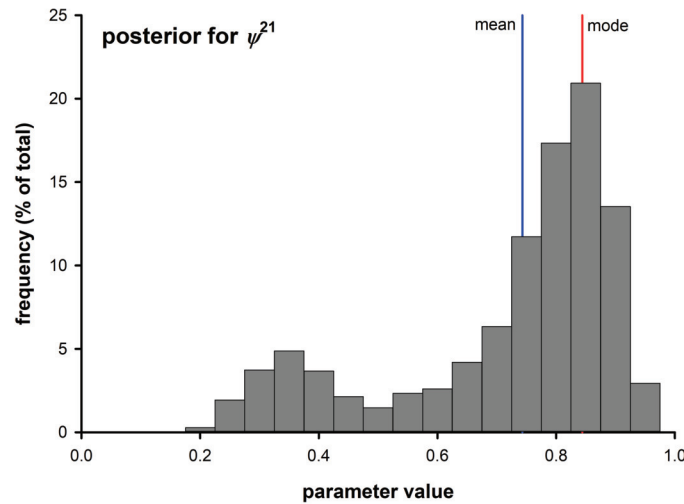
What do these differences among mean, median and mode suggest? Well, simplistically, they ‘hint’ at the possibility there may be ‘problems’ with the likelihood – specifically, multiple local minima. We can confirm our suspicion by considering two different ‘plots’ derived from the MCMC samples. First, consider a frequency histogram plotting the frequency (expressed as a percentage of the total) with which a particular parameter value was ‘visited’ during the iteration of the Markov chain.

Here is the frequency histogram for the posterior chain for ψ^{12} (note: for a variety of reasons, the chain was ‘thinned’ by extracting every tenth value, prior to deriving the frequency histograms. This is commonly done to minimize the effects of serial autocorrelation in the Markov chains, although there is some debate as to whether or not this is really necessary).



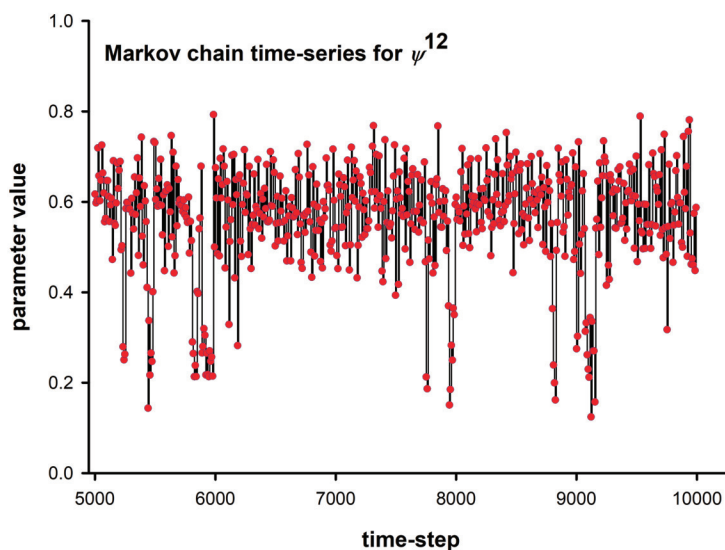
* But we know this only because here we know the true parameter values. In fact, what we’ve just demonstrated is that MCMC is not necessarily a generally robust solution to deriving point parameter estimates.

Here is the equivalent histogram for ψ^{21} :



We see clearly that the posterior distributions for both ψ^{12} and ψ^{21} are bimodal. These plots help us understand why **MARK** converged on the local minimum. For example, note that the smaller, left-hand modal point for ψ^{21} occurs at approximately 0.34 – 0.35, which is roughly what **MARK** reported (incorrectly) as the MLE for this parameter. The default starting value used by **MARK** (0.45) was closer to this local minimum than the global minimum for ψ^{21} (which occurs at 0.85). The same explanation holds for ψ^{12} as well. So, multi-modal frequency distributions of ‘visits by the Markov chain’ to parts of the parameter space indicates local minima, which **MARK** may (or may not) converge to (depending on the relative proximity of the starting value to a local minima).

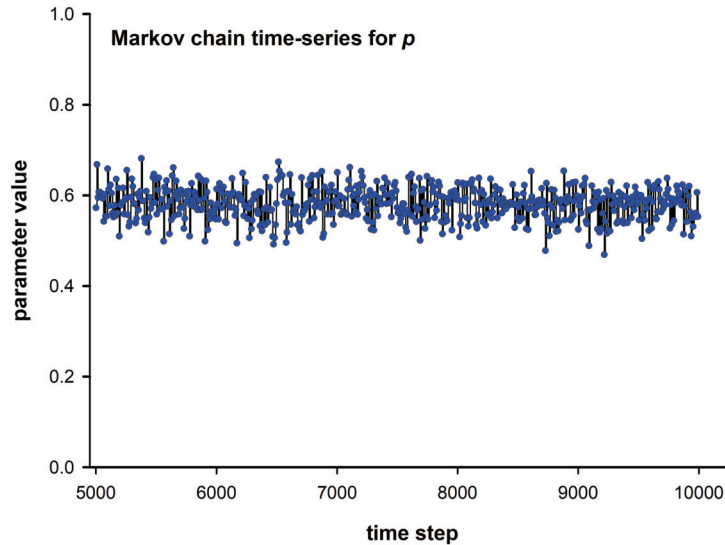
We can also find evidence for local minima by examining the time-series of iterations of the Markov chain. Here is a plot of part of the time-series (first 5,000 iterations after burn-in and tuning) for ψ^{12} :



We see clearly that the chain periodically ‘jumps’ to a region of the parameter space between 0.1

and 0.4, corresponding to the smaller, left-hand mode shown on the frequency histogram for ψ^{12} .

Contrast this Markov chain with that generated for parameter p :



For p , we see that the Markov chain is very ‘tight’ – indicating that the parameter will be estimated with good precision. In fact, the profile likelihood CI for p , estimated using the simulated annealing approach to estimating the likelihood, shows the 95% CI for p to be $[0.513, -0.652]$, which is remarkably close to the MCMC-based 95% ‘credibility interval’, $[0.511, -0.648]$.

From the preceding, we can draw several conclusions:

1. > 1 minima in the likelihood for a given parameter are possible for multi-state models, especially for fully time-dependent models where there are numerous states. This can cause problems, if **MARK** converges on one of these local minima (thus yielding the ‘wrong’ estimate for that parameter). **MARK** will give you **no** warning when this occurs.
2. you can often test for the possibility of local minima by examining the posterior distribution for a given parameter, generated using the Markov Chain Monte Carlo (MCMC) option in **MARK**. Doing so for the various parameters in your general model may be a good first step prior to fitting other models.

But, be warned – MCMC estimation on all of the parameters of a ‘large’ general model (i.e., time-dependence, many states) can take a *long* time. Moreover, there are a number of options in using the MCMC estimation routines in **MARK** that you may have to ‘tweak’ in the process (these are described in Appendix E), adding to the overall time it might take to fully explore the posterior distributions for various parameters.

3. an alternative approach is to either (i) try various different starting values – if they all result in convergence to the same parameter values, then you may be fortunate and not have local minima to concern yourself with. Or, alternatively, you could (ii) use the optimization routines based on simulated annealing, which are generally likely to converge – *eventually* – to the true local minima. Again – we emphasize the word ‘eventually’, since simulated annealing can take a *long* time to converge.

end sidebar

10.5. GOF testing and multi-state models

What about GOF (goodness of fit)? By now, you should realize that one of the first steps in any analysis is assessing the fit of the most general model in your candidate model set to the data (introduced in Chapter 5). As part of this process, we make an estimate of \hat{c} (a measure of the lack of fit of the model to the data), and use this \hat{c} to 'adjust' the criterion we use for model selection. Here, we will describe 2 approaches to GOF testing for multi-state models.

10.5.1. Program U-CARE and GOF for multi-state models

Some years ago, Roger Pradel and colleagues (Pradel *et al.* 2003) have described a method for assessing the fit of a fully time-dependent MS model to data. Although the specific details are somewhat complex, the rationale for the tests proposed by Pradel and colleagues are very similar to those underlying program **RELEASE**, as applied to 'normal' CJS data: the proposed tests essentially consider the fates of individuals seen before, or not, and whether (and when) they are seen again – but, in this case, conditional on the state in which they were previously observed.

The GOF test proposed by Pradel *et al.* is relevant for what they refer to as the 'Arnason-Schwarz' (AS) model (the AS model is in fact what we've been discussing in this chapter). To test the GOF of the AS model to multi-state data, Pradel *et al.* first describe a fully efficient goodness of fit test to what they refer to as a '**Jolly Move**' model (JMV). Any fully efficient GOF test is based on the property that all animals present at any given time behave in the same way. This is the basic point underlying the use of program **RELEASE**: in **Test 3**, we test the assumption of 'equivalent behaviors' whatever their past capture history, while in **Test 2**, we test the 'equivalence' assumption whether they are currently captured or not. The same logic underlies the GOF test for the JMV model.

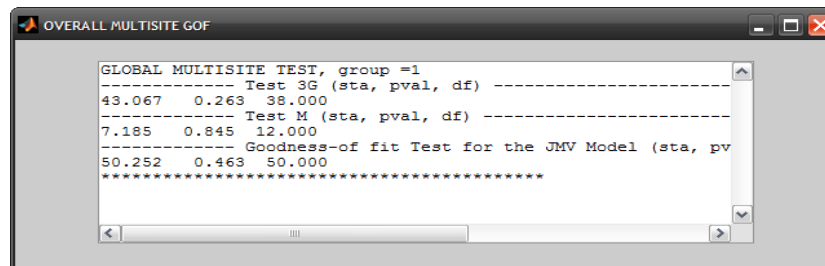
What is this JMV model, and how does it relate to the AS model? The JMV model (Brownie *et al.* 1993) differs from the typical AS model in that it permits the capture probability for time $(i + 1)$ to depend on the state at periods (i) and $(i + 1)$ (whereas the AS model permits the encounter probability to depend only on current state, and time). Thus, the AS model is in fact a special (reduced) case of the more general JMV model. As with program **RELEASE**, a fully efficient GOF test for the JMV model is based on the property that all animals present at any given time on the same site behave the same.

Pradel *et al.* introduce 2 general tests of this multi-state 'equivalence' assumption: **Test 3G**, which assumes 'behavioral equivalence' of individuals released together regardless of their past capture history, and **Test M**, which tests 'equivalence' among those individuals that are eventually recaptured (on a subsequent occasion) conditional on whether or not they are encountered at the present occasion. (There are also 2 possible subcomponents testing for transience, and memory models, but we will not discuss those here). See Pradel *et al.* for full details – for now, we'll focus on the basic ideas and mechanics.

The first step in the GOF test proposed by Pradel *et al.* is to assess the fit of the fully time-dependent JMV model to the data. In many cases, the JMV model is unlikely to show significantly greater fit to the data than the AS model (since the dependence of the capture probability at time $(i + 1)$ to depend on both (i) and $(i + 1)$ is unlikely to be observed in practice very often). As such, the GOF test for the JMV model may be a generally valid test of fit for the AS model as well. Here's how you implement a GOF test to the general JMV model.

First, you need a recent build of the program **U-CARE** (first described in Chapter 5). Then, you might need to modify your **MARK** input file – slightly. The only thing you need to do is make sure that all of your 'state coding' is numeric (e.g., if you use 'B' and 'N' in your input file, for example, you'll need to change them to numbers, say 1 for 'N', and 2 for 'B'...**U-CARE** cannot currently handle letters for state coding in the input file).

We'll demonstrate the use of **U-CARE** for multi-state GOF testing using simulated data (**MS_GOF.inp**). These data, consisting of 2 states, 8 occasions, were simulated under the true model $\{S_{g+t} p_{g+t} \psi_g\}$ – so additive time variation between the two states for survival, and encounter probability, but constant state differences in transition probability over time. We start **U-CARE**, and read in the input file. **U-CARE** will ask you to confirm a few things about the file (e.g., presence or absence of covariates). Once you've answered those questions, all you need to do is pull down the '**Goodness-of-Fit for Multi-state**' menu, and select '**Sum of multi-site tests**'. Selecting this option will cause **U-CARE** to fit the component tests (**3G** and **M**) and the JMV to the data. Once finished, **U-CARE** will spawn another window, giving the results of the various tests.



We see that **U-CARE** reports the 2 individual component tests (**3G** and **M**). For these simulated data, **U-CARE** reports that both tests are accepted (**Test 3G**: $\chi^2 = 33.464$, $df = 25$, $P = 0.120$, **Test M**: $\chi^2 = 5.838$, $df = 10$, $P = 0.829$).

The next line is the key. It reports the overall test of the JMV model to the data (basically, the sum of the 2 component tests **3G** and **M**). In this case, **U-CARE** reports that the $\chi^2 = 50.252$, with $df = 50$. The P -value is 0.463. Thus, our estimate of \hat{c} would be $(50.252/50) = 1.00$, which is very close to 1.0.

10.5.2. MS models and the median- \hat{c} test

What about the median- \hat{c} test introduced in Chapter 5 – can it be used for MS data? Yes, although there is limited experience with it to date. For purposes of comparison with the results from **U-CARE**, start **MARK**, and run the fully time-dependent model on these same, simulated data. Then, run the median- \hat{c} test – since we know these data are simulated under a reduced parameter AS model, we'll save ourselves some time and use lower bound of 1.0, and an upper bound of 2.5 for our analysis (if you don't remember the details of the median- \hat{c} GOF test, go back and look at Chapter 5). We'll use 5 design points, with 10 replicates at each point. Using these values, **MARK** reported an estimate of \hat{c} of 0.99, which is effectively 1.0. Again, although there is little experience to date with the median \hat{c} and GOF testing of MS models, preliminary results look promising. For the moment, we suggest using **U-CARE** for GOF testing, especially if your general model is the fully time-dependent model. For reduced parameter general models, it is probably worth trying the median \hat{c} approach.

However, be advised that running a median- \hat{c} test for multi-state models with a large number of occasions, and states, can take a **lot** of computer time (especially if you decide to use the simulated annealing algorithm – as described earlier in this chapter). For f fully time-dependent models, **U-CARE** is much faster. However, if your most general model which adequately fits the data is not time-dependent, then your only real option is to run the median- \hat{c} GOF test. The good news (relatively speaking) is that you need only assess GOF for the most general model in your candidate model set – so you need only do it once.

10.6. multi-state models & unequal time intervals

Various data types in **MARK** involve state transitions – clearly, the multi-state data type that is presented in this chapter, but they also arise in robust designs (Chapter 16), Barker models (Chapter 9), and multi-season occupancy models (Chapter 22). Any data type with state transitions potentially suffers from the same problem when the intervals between occasions are unequal (how **MARK** handles unequal intervals in general was introduced earlier in Chapter 4). You may recall that ‘unequal intervals’ can reflect either of two different but superficially similar situations – (i) a ‘missing’ sampling occasion (where $p = 0$ for the missed occasion), or (ii) a truly unequal sampling interval, but one where the probability of encounter at each sampling occasion is potentially >0 .

Consider first the situation with a ‘missing’ sampling occasion. Suppose we have a 3 occasion study (2 transition intervals), with two states (**A** and **B**), which generates the following multi-state encounter history ‘A.A’, with occasions all 1 time unit apart. Here, the missing occasion is shown as a ‘dot’. To explain this ‘dot’, two possible ‘encounter probability expressions’ exist for this encounter history, namely:

$$(i) S_1^A \psi_1^{AA} (1 - p_2^A) S_2^A \psi_1^{AA} p_3^A \quad \text{and} \quad (ii) S_1^A \psi_1^{AB} (1 - p_2^B) S_2^B \psi_2^{BA} p_3^A.$$

In other words, the ‘dot’ could represent one of two scenarios: (i) survive the interval from occasion 1 \rightarrow 2 and *stay* in state **A** (with probability $S_1^A \psi_1^{AA}$), but not be observed in state **A** at occasion 2 (with probability $1 - p_2^A$), or (ii) survive the interval from occasion 1 \rightarrow 2 and *move* from state **A** to **B** (with probability $S_1^A \psi_1^{AB}$), but not be observed in state **B** at occasion 2 (with probability $1 - p_2^B$).

However, suppose that you coded the data with the ‘dot’ left out, so the encounter history is now ‘AA’, and set the time interval to ‘2’. That is, only 2 sampling occasions (occasion 1, and occasion 3, occasion 2 ‘missed’) are considered instead of 3 – so the interval from sampling occasion 1 \rightarrow 3 is 2. Unfortunately, this approach of adjusting the interval length is going to give *very* different results from the proper parametrization (using the ‘dot’ approach) outlined above. **MARK** does not generate the probabilities for the possible transition from state **A** to state **B** with this parametrization. The probability of surviving from sampling occasion 1 to occasion 2 would now be $(S_1^S)^2$, with no consideration that the animal could have moved to state **B** during the missing occasion. So, even the survival estimates S will be incorrect. The ψ parameters for the first interval are not comparable to the ψ parameters for the second and third intervals because they represent different time scales.

For the situation with no missing samples, but with truly unequal intervals between samples, it is important to remember that the critical assumption of the multi-state models is that all transitions take place *at the end of the time interval*. Under this assumption, it doesn’t matter how long the interval is – the ψ parameter will not be affected. The reason for this assumption is that the survival probabilities in the 2 states where the transition is taking place can be different. For example, if state **A** survival is $S^A = 0.9$ and state **B** survival is $S^B = 0.8$, then timing of the transition between state **A** and state **B** affects the survival across the interval. Hence, the requirement that all transitions take place at the end of the interval, so that only one survival rate applies to the interval.

Here is a simple numerical experiment to demonstrate what **MARK** does (and does not do) in terms of adjusting MS parameters for uneven interval lengths. We simulated a situation with 2 observable states (**A** and **B**) over 5 sampling occasions, with 10,000 individuals released at occasion 1 in state **A** only. The simulation assumed (i) that state **B** is ‘absorbing’ (i.e., $\psi^{BB} = 1.0$, $\psi^{BA} = 0$), and (ii) that the probability of making the state transition from state **A** \rightarrow **B** was constant over time ($\psi^{AB} = 0.8$), except over intervals 2 \rightarrow 3 \rightarrow 4. All other parameters were held constant. The structure and true values for all transition parameters used in the simulation are shown in Fig. 10.3 (top of the next page). To simplify our analysis, we assumed perfect detectability in both states ($p = 1$).

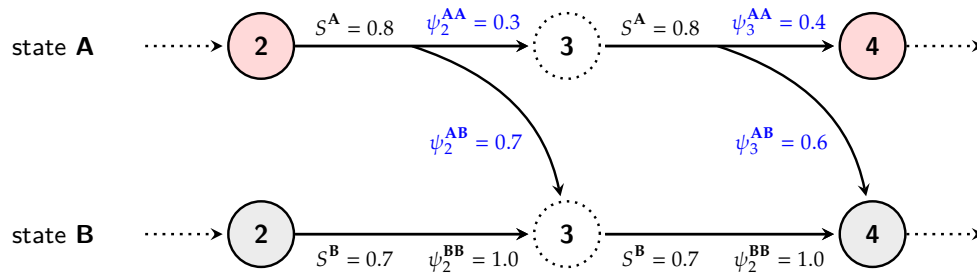


Figure 10.3: Example of a multi-state model with a ‘missing’ sampling occasion. Here, the third sampling occasion is missing for both states (indicated by the dashed circle). The true survival (S) and state transition (ψ) probabilities are indicated. It is important to remember that (i) with a missing sampling occasion 3, any state transition that occurs over the interval from occasion 2 \rightarrow 3, or 3 \rightarrow 4, is unobserved, and that (ii) the state transitions are conditional on having survived the interval. All parameters used to simulate the data are constant over time ($S^A = 0.8$, $S^B = 0.7$, $\psi^{AB} = 0.8$, $\psi^{BA} = 0$, $p = 1$), with the exception of the probability of state transition from state A \rightarrow B over the intervals from 2 \rightarrow 3 ($\psi_2^{AB} = 0.7$) and 3 \rightarrow 4 ($\psi_3^{AB} = 0.6$).

Using the same approach for handling ‘missing occasions’ introduced in Chapter 4 for a simple live-encounter mark-recapture context (CJS), we generated 3 different versions of the .INP file containing the stimulated encounter data: (i) one (our ‘control’) with the full MS data (for all 5 sampling occasions, assuming that sampling occasion 3 was not missed), (ii) one where we deleted the column for sampling occasion 2 (as if it were ‘missed’), then manually setting the interval from 2 \rightarrow 4 as ‘2’, and (iii) one where the ‘missing’ sampling occasion 3 was entered as a ‘dot’ (i.e., we converted all occasion 3 data in the original file to a ‘dot’). Our interest concerns what **MARK** estimates for the ‘interval parameters’ \hat{S}_2^A , \hat{S}_3^A , $\hat{\psi}_2^{AB}$ and $\hat{\psi}_3^{AB}$, for each of the modified .INP files.

Here are the estimates from fitting the true model to the full history data, assuming no missing sampling occasions. Note that because simulated individuals were entered into the population in state **A** only (and on occasion1 only), and given that state **B** is an absorbing state, that some parameters were logically fixed to 0 (as shown). [We also fixed $p = 1$, since we ‘knew’ that to be true for these simulated data.] The remaining parameter estimates are all very close to the true parameter values (Fig.10.3).

Parameter	Estimate	Standard Error	95% Confidence Interval		
			Lower	Upper	
1:S A:Strata 1	0.7999173	0.0011501	0.7976536	0.8021621	
2:S B:Strata 2	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
3:S B:Strata 2	0.6998938	0.0011558	0.6976235	0.7021543	
4:p A:Strata 1	1.0000000	0.0000000	1.0000000	1.0000000	Fixed
5:Psi A to B	0.8007949	0.0014120	0.7980129	0.8035481	
6:Psi A to B	0.6997566	0.0040620	0.6917352	0.7076574	
7:Psi A to B	0.5990904	0.0088336	0.5816597	0.6162740	
8:Psi A to B	0.8035161	0.0127776	0.7772631	0.8273620	
9:Psi B to A	0.0000000	0.0000000	0.0000000	0.0000000	Fixed

Next, we considered the modified version of the encounter data where encounters on the third occasion were deleted, which reduced the number of sampling occasions from 5 to 4. The sampling interval from occasion 2 \rightarrow 4 was manually adjusted to ‘2’ during the specification of the data type.

Because there are no individuals in state **B** at occasion 2, S_1^B is not estimable – in which case, **MARK** would normally return the default value used to start the optimization (0.45). We modified the PIM to allow us to set this parameter to 0 (although this isn't really necessary, it 'looks better'). Here are the parameter estimates:

Parameter	Estimate	Standard Error	95% Confidence Interval		
			Lower	Upper	
1:S A:Strata 1	0.8000800	0.0012647	0.7975896	0.8025473	
2:S A:Strata 1	0.7627282	0.0025613	0.7576714	0.7677118	
3:S A:Strata 1	0.7836305	0.0117218	0.7597753	0.8057224	
4:S B:Strata 2	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
5:S B:Strata 2	0.7001883	0.0012035	0.6978241	0.7025419	
6:p A:Strata 1	1.0000000	0.0000000	1.0000000	1.0000000	Fixed
7:Psi A to B	0.8007949	0.0014120	0.7980129	0.8035481	
8:Psi A to B	0.8669111	0.0035275	0.8598439	0.8736744	
9:Psi A to B	0.8035161	0.0127775	0.7772631	0.8273620	
10:Psi B to A	0.0000000	0.0000000	0.0000000	0.0000000	Fixed

Our particular focus is on parameter estimates $\hat{S}_2^A = 0.7627$ (representing survival over the interval from $2 \rightarrow 4$), and $\hat{\psi}_2^{AB} = 0.8669$, representing the transition from state **A** to **B** over the same interval. How do we interpret these estimates?

a. survival parameters

We'll start with the estimate $\hat{S}_2^A = 0.7627$. The true survival probabilities for the intervals from $2 \rightarrow 3 \rightarrow 4$ are $S_2^A = S_3^A = 0.8$. In a simple, single-state (CJS) context, expected survival from $2 \rightarrow 4$ would then simply be the product: $(0.8 \times 0.8) = 0.64$. But, here, we have 2 states – neither of which are observed on the third occasion (since sampling occasion 3 is 'missing'). So, given that an individual could survive and make an unobserved transition to state **B** over interval $2 \rightarrow 3$, and survive with state-specific probability $S_3^B = 0.7$, what does the value of the estimate $\hat{S}_2^A = 0.7627$ represent?

A key conceptual starting point to interpreting $\hat{S}_2^A = 0.7627$ is to recall from Chapter 4 that for a simple CJS model (single state), the value for survival over an interval of l time steps is given by **MARK** as the l th root of the probability of surviving over the interval from $(i) \rightarrow (i + l)$. For example, if true $\varphi_1 = 0.6$ and $\varphi_2 = 0.8$, then the probability of surviving over the interval from $1 \rightarrow 3$ is simply $(\varphi_1 \times \varphi_2) = (0.6 \times 0.8) = 0.48$. So, if occasion 2 is missing, then **MARK** would report $\sqrt[2]{0.48} = 0.6928$ as the estimate of survival for each time step over this interval. This value of 0.6928 is the average (technically, the *geometric* average) of 0.6 and 0.8. Since there is a missing occasion, the best that **MARK** can do is report the average survival for those intervals.

OK – so what **MARK** reports for the single state CJS example is an 'average'. In fact, the value $\hat{S}_2^A = 0.7627$ from our two state system is also an average, but one that takes into account that some of the individuals surviving from one time step to the next might have 'switched states'. Since the two states in this example have different survival probabilities, then the average survival is in fact a *weighted* average over the different states, based on the relative frequency of individuals surviving in each state at each time step.

There are a couple of ways you can work out what this weighted average should be. Here's a starting point making use of the fact that the state transitions in a multi-state model involve state-specific survival, and possible movement between states, conditional on survival.

We'll start by constructing the general transition matrix M_i for interval (i) to $(i + 1)$:

$$M_i = \begin{matrix} & \mathbf{A} & \mathbf{B} \\ \begin{matrix} \mathbf{A} \\ \mathbf{B} \end{matrix} & \begin{bmatrix} S_i^{\mathbf{A}}(1 - \psi_i^{\mathbf{AB}}) & 0 \\ S_i^{\mathbf{A}}\psi_i^{\mathbf{AB}} & S_i^{\mathbf{B}} \end{bmatrix} \end{matrix}.$$

This transition matrix represents:

- The probability of staying in state **A**, conditional on surviving: $S_i^{\mathbf{A}}(1 - \psi_i^{\mathbf{AB}})$
- The probability of moving from state **A** to **B**, conditional on surviving: $S_i^{\mathbf{A}}\psi_i^{\mathbf{AB}}$
- The probability of staying in state **B**: $S_i^{\mathbf{B}}$ (since $\psi_i^{\mathbf{BB}} = 1$)
- The probability of moving from state **B** to **A**, conditional on surviving: 0 (for our example, **B** is an absorbing state, so transition out of **B** to **A** is not possible)

Since our interest concerns the interval from occasion 2 \rightarrow 4, let's assume that the population vector at occasion 2 consists of a single individual in state **A** (subscript 0 for n_0 indicates initial condition at occasion 2):

$$n_0 = \begin{bmatrix} 1 \\ 0 \end{bmatrix}.$$

All we need to do next is 'project' the population structure two time-steps forward (i.e., from occasion 2 \rightarrow 4). We first show the symbolic matrix multiplication (below) before we evaluate it numerically. This will be useful to refer to in a moment:

$$\begin{aligned} n_2 &= M_1 M_2 n_0 \\ &= \begin{bmatrix} S^{\mathbf{A}}(1 - \psi_2^{\mathbf{AB}}) & 0 \\ S^{\mathbf{A}}\psi_2^{\mathbf{AB}} & S^{\mathbf{B}} \end{bmatrix} \begin{bmatrix} S^{\mathbf{A}}(1 - \psi_3^{\mathbf{AB}}) & 0 \\ S^{\mathbf{A}}\psi_3^{\mathbf{AB}} & S^{\mathbf{B}} \end{bmatrix} \begin{bmatrix} 1 \\ 0 \end{bmatrix} \\ &= \begin{bmatrix} (S^{\mathbf{A}})^2(1 - \psi_2^{\mathbf{AB}})(1 - \psi_3^{\mathbf{AB}}) \\ S^{\mathbf{A}}(1 - \psi_2^{\mathbf{AB}})S^{\mathbf{A}}(1 - \psi_3^{\mathbf{AB}}) + S^{\mathbf{A}}(1 - \psi_2^{\mathbf{AB}})S^{\mathbf{A}}\psi_3^{\mathbf{AB}} + S^{\mathbf{A}}\psi_2^{\mathbf{AB}}S^{\mathbf{B}} \end{bmatrix}. \end{aligned}$$

We can evaluate this expression numerically by substituting the true parameter values ($S^{\mathbf{A}} = 0.8$, $S^{\mathbf{B}} = 0.7$, $\psi_1^{\mathbf{AB}} = 0.7$ and $\psi_2^{\mathbf{AB}} = 0.6$):

$$\begin{aligned} n_2 &= M_1 M_2 n_0 \\ &= \begin{bmatrix} 0.0768 \\ 0.5072 \end{bmatrix}. \end{aligned}$$

So, after 2 time steps, the probability of the single starting individual being alive and in state **A** is $P_2^{\mathbf{A}} = 0.0768$, while the probability of being alive and in state **B** is $P_2^{\mathbf{B}} = 0.5072$. The expected survival probability over both time steps (i.e., from 2 \rightarrow 4) is the sum of these probabilities:

$$\begin{aligned} S_2^{\mathbf{A}} &= P_2^{\mathbf{A}} + P_2^{\mathbf{B}} \\ &= 0.0768 + 0.5072 = 0.584. \end{aligned}$$

So, if the length of the interval from occasion 2 \rightarrow 4 is $l = 2$, then what do you think the l th root of 0.584 is? Can you guess, based on the single-state CJS example introduced earlier? In fact, $\sqrt[2]{0.584} = 0.7642$, which is *very* close to the estimate $\hat{S}_2^A = 0.7627$ that **MARK** reported for our simulated data.

OK, but how is this a *weighted* average, as was suggested earlier? Recall that we define: P_T^A as the probability that an individual starting in state **A** is in state **A** after T time steps, P_T^B is the probability that an individual starting in state **A** is in state **B** after T time steps, and S_T^A is the overall survival probability after T time steps for an individual starting in state **A**.

From above, the overall survival probability is the sum of probabilities of being in either state:

$$S_T^A = P_T^A + P_T^B.$$

Recall that the probability of surviving both intervals for an individual starting in state **A** (S_2^A) could reflect realizations of either

- (i) (**A** \rightarrow **A** \rightarrow **A**) – surviving and staying in state **A** for both intervals with a probability of $S^A(1 - \psi_2^{AB})S^A(1 - \psi_3^{AB})$, or
- (ii) (**A** \rightarrow **B** \rightarrow **B**) – starting in state **A**, surviving and then moving to state **B** after the first interval, and surviving in state **B** to the final occasion and remaining in state **B**, with probability $S^A\psi_2^{AB}S^B$ (recall that in our simulated data, $\psi^{BB} = 1$, since **B** is an absorbing state), or
- (iii) (**A** \rightarrow **A** \rightarrow **B**) – starting in state **A**, surviving and remaining in state **A** over the first interval, surviving the final interval and then moving to state **B**, with probability $S^A(1 - \psi_2^{AB})S^A\psi_3^{AB}$.

Survival over the interval from 2 \rightarrow 4 (S_2^A) is simply the sum of the probability expressions for each of these pathways:

$$S_2^A = [S^A(1 - \psi_2^{AB})S^A(1 - \psi_3^{AB})] + [S^A\psi_2^{AB}S^B] + [S^A(1 - \psi_2^{AB})S^A\psi_3^{AB}].$$

Note: If you look closely, you'll see that the first term on the RHS of this expression is the same as the first element of the vector for n_2 generated by the symbolic matrix multiplication on the previous page, representing the probability of surviving and remaining state **A**. Similarly the second two terms together is the second element of that vector, representing the probability of surviving and ending up in state **B**.

If we factor out S^A from each term

$$S_2^A = S^A \cdot [S^A(1 - \psi_2^{AB})(1 - \psi_3^{AB})] + [\psi_2^{AB}S^B] + [(1 - \psi_2^{AB})S^A\psi_3^{AB}],$$

This expresses S_2^A as the product of:

- S^A : survival probability for state **A**,
- $[S^A(1 - \psi_2^{AB})(1 - \psi_3^{AB})] + [\psi_2^{AB}S^B] + [(1 - \psi_2^{AB})S^A\psi_3^{AB}]$: a *weighted* average of conditional survival probabilities for the second interval, with weights given by the probabilities of being in each state after the first interval.

Substituting the given values of the various parameters yields:

$$\begin{aligned} S_2^A &= 0.8 \cdot [0.8(1 - 0.7)(1 - 0.6) + 0.7(0.7) + 0.8(0.6)(0.3)] \\ &= 0.584, \end{aligned}$$

which of course is the same value we derived previously using the matrix projection approach.

b. state transition parameters

For our simulated data, **MARK** reported $\hat{\psi}_2^{AB} = 0.8669$. What does this value actually represent?

The *realized* transition probability from state **A** to state **B** after T time steps, which we will denote as R_T^{AB} , is defined as the probability of being in state **B** at time T , given that the individual has survived until time T , and started in state **A**:

$$R_T^{AB} = \frac{P_T^B}{P_T^A + P_T^B}.$$

In other words, the ratio of the probability of surviving and being in state **B** (numerator), given that you survived at all (denominator).

From the projection matrix approach introduced earlier, we know that $P_2^A = 0.0768$, and $P_2^B = 0.5072$. Thus,

$$R_2^{AB} = \frac{P_2^B}{P_2^A + P_2^B} = \frac{0.5072}{0.0768 + 0.5072} \approx 0.8685,$$

which is *very* close (at least to within Monte Carlo error) to $\hat{\psi}^{AB} = 0.8669$ reported by **MARK**.

So, to summarize, if you manually adjust the interval for a MS model in **MARK**, then

- the reported parameter estimates for survival (S) represent the l th root of the weighted average survival over the interval of length l ,
- whereas the reported state transition parameters (ψ) over the same interval are simply the realized proportions making the transition, conditional on survival. Because in **MARK** transitions are always estimated conditional on surviving, they are not adjusted in any way for the length of the interval.

dot models?

What about the situation where instead of manually adjusting the time interval to account for missing occasion 3, we coded the ‘missing’ data for occasion 3 using a ‘dot’ in the encounter history file?

Here are the estimates from analyzing those re-coded data:

Parameter	Estimate	Standard Error	95% Confidence Interval		
			Lower	Upper	
1:S A:Strata 1	0.8000800	0.0012647	0.7975896	0.8025473	
2:S A:Strata 1	0.8507429	1.7317732	0.1402091E-10	1.0000000	
3:S A:Strata 1	0.5941432	7.8051032	0.4105766E-27	1.0000000	
4:S A:Strata 1	0.7836305	0.0117218	0.7597754	0.8057225	
5:S B:Strata 2	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
6:S B:Strata 2	0.7001883	0.0012035	0.6978241	0.7025419	
7:p A:Strata 1	1.0000000	0.0000000	1.0000000	1.0000000	Fixed
8:Psi A to B	0.8007949	0.0014120	0.7980129	0.8035481	
9:Psi A to B	0.8456398	1.8696873	0.3517761E-11	1.0000000	
10:Psi A to B	0.0076692	4.3669159	0.4299080E-310	1.0000000	
11:Psi A to B	0.8035161	0.0127775	0.7772631	0.8273620	
12:Psi B to A	0.0000000	0.0000000	0.0000000	0.0000000	Fixed

Here again, our interest is in estimates for \hat{S}_2^A , \hat{S}_3^A , $\hat{\psi}_2^{AB}$ and $\hat{\psi}_3^{AB}$. Although **MARK** appears to generate separate estimates for all 4 parameters, we should intuitively understand that in the absence of ‘observations’ at occasion 3, **MARK** has no information on which to estimate *time-specific* transitions over the interval from $2 \rightarrow 3 \rightarrow 4$. This is reflected in the impossible estimates of the SE for all 4 parameters. The SE (and the estimates themselves) are meaningless, because we haven’t imposed any sort of constraint on the survival estimates for the ‘two pieces’ of the interval from occasion $2 \rightarrow 4$ (i.e., φ_3, φ_4). As such, **MARK** has no way of estimating the covariance between the two reported values.

If, however, we modified the survival and state-transition PIMs, setting the estimates for the intervals from occasion $3 \rightarrow 4$ and from $4 \rightarrow 5$ equal to each other, then we appear to get ‘sensible estimates’ (well, sort of...):

Parameter	Estimate	Standard Error	95% Confidence Interval		
			Lower	Upper	
1:S A:Strata 1	0.8000800	0.0012647	0.7975896	0.8025473	
2:S A:Strata 1	0.7672455	0.0000000	0.7672455	0.7672455	
3:S A:Strata 1	0.7836303	0.0117219	0.7597752	0.8057223	
4:S B:Strata 2	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
5:S B:Strata 2	0.7001883	0.0012035	0.6978241	0.7025419	
6:p A:Strata 1	1.0000000	0.0000000	1.0000000	1.0000000	Fixed
7:Psi A to B	0.8007949	0.0014120	0.7980129	0.8035481	
8:Psi A to B	0.1343327	0.0000000	0.1343327	0.1343327	
9:Psi A to B	0.8480636	0.0000000	0.8480636	0.8480636	
10:Psi A to B	0.8035159	0.0127776	0.7772630	0.8273619	
11:Psi B to A	0.0000000	0.0000000	0.0000000	0.0000000	Fixed

In fact, what we have done here is estimate the square-root of the product of the two, non-estimable time-specific survival probabilities. Which is what you are doing when you delete occasion 3 and set the interval to 2 (as in our first approach), or keeping occasion 3, but translating the encounter data to ‘dots’ and setting the 2 two time-specific probabilities that form the product equal to each other, as we just did here.*

Superficially, our present analysis where we set the two time-specific survival probabilities over the interval equal to each other seems reasonable. From above, the estimate $\hat{S}_2^A = 0.7672$ is very close to the value for $\hat{S}_2^A = 0.7627$ estimated for the case where we had deleted occasion 3 from the history file and manually adjusted the interval. And, both are very close to the true expected value of 0.7642, which is the square-root of the expected weighted survival (0.584) over the interval from $2 \rightarrow 4$.

But, note (above) that there is no SE estimated for $\hat{S}_2^A = 0.7672$ in our analysis of the ‘dot’ encoded history file. Further, the estimates for $\psi_2^A = 0.1343$ and $\psi_3^A = 0.8481$ are also reported without SE, and are not connected in any obvious way to the expected realized transition probability (0.8685) from state **A** \rightarrow **B** over the interval from $2 \rightarrow 4$.

Why is the ‘dot’ approach not working as might be expected? The answer lies in the fact that MS models in **MARK** are parameterized assuming the movement (state transitions) are conditional on surviving (i.e., ‘survive, then move’). But, you might ask, isn’t this also true for the ‘interval’ approach,

* If this were a single-state model with a ‘dot’, you can estimate the product over the interval $2 \rightarrow 4$ by fixing one of the survival probabilities to 1 (does not matter which one) – the remaining ‘free’ estimate will be the product. However, for multi-state problems, we demonstrated that the product is in fact a weighted average over the various states, and the value returned by **MARK** if you fix one of the two survival probabilities to 1 doesn’t have any obvious connection to this average.

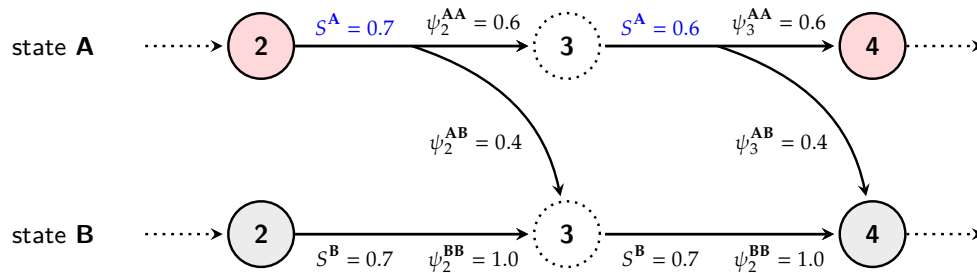


Figure 10.4: As in Fig. 10.3, the third sampling occasion is missing for both states (again, indicated by the dashed circle). Here, however, survival for individuals in state A varies over time during the interval from occasion 2 \rightarrow 4 ($S_2^A = 0.7$, $S_3^A = 0.6$), whereas the probability of transition from state A \rightarrow B is constant over time ($\psi^{AB} = 0.4$). All other parameters used to simulate the data are constant over time ($S_1^A = S_4^A = 0.8$, $S^B = 0.7$, $\psi^{BA} = 0$, $p = 1$).

which seems to yield interpretable estimates for both S and ψ ? A clue to why one approach seems to work, but not the other, is obtained if we ‘flip’ the logic for the simulated data. Instead of having ‘constant survival, but time varying transition probabilities’ over the interval (as in the first case – Fig. 10.3), let’s consider the case where survival varies over time, but the transition probabilities are constant. This situation is shown in Fig. 10.4 (above).

As in the previous example, we simulated a situation with 2 observable states (A and B) over 5 sampling occasions, with 10,000 individuals released at occasion 1 in state A only. Again, our simulation assumed that state B was ‘absorbing’ (i.e., $\psi^{BB} = 1.0$, $\psi^{BA} = 0$). Here, though, we assumed probability of making the state transition from state A \rightarrow B was constant over time for all intervals ($\psi^{AB} = 0.4$), whereas survival in state A varied over time during the interval from occasion 2 \rightarrow 4 ($S_2^A = 0.7$, $S_3^A = 0.6$). The structure and true values for all transition parameters used in the simulation are shown in Fig. 10.4 (above). Again, to simplify our analysis, we assumed perfect detectability in both states ($p = 1$).

Our modeling approach was similar to that used in the preceding example. Here are the results of fitting the full model to the simulated data (which included encounter data for occasion 3):

Parameter	Estimate	Standard Error	95% Confidence Interval Lower	Upper	
1:S A:Strata 1	0.8000880	0.7998680E-03	0.7985156	0.8016511	
2:S A:Strata 1	0.7026983	0.0068705	0.6890587	0.7159861	
3:S A:Strata 1	0.5917789	0.0095960	0.5728450	0.6104442	
4:S A:Strata 1	0.7980395	0.0029962	0.7921032	0.8038482	
5:S B:Strata 2	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
6:S B:Strata 2	0.7006269	0.0010074	0.6986487	0.7025977	
7:p A:Strata 1	1.0000000	0.0000000	1.0000000	1.0000000	Fixed
8:Psi A to B	0.4000933	0.0010582	0.3980211	0.4021691	
9:Psi B to A	0.0000000	0.0000000	0.0000000	0.0000000	Fixed

We see that the estimates are virtually identical to the true underlying parameter values we used in to simulate the encounter data (Fig. 10.4).

Next, we considered the modified version of the encounter data where encounters on the third occasion were deleted, which reduced the number of sampling occasions from 5 to 4. The sampling interval from occasion 2 \rightarrow 4 was manually adjusted to ‘2’ during the specification of the data type.

Parameter	Estimate	Standard Error	95% Confidence Interval		
			Lower	Upper	
1:S A:Strata 1	0.8000880	0.7998680E-03	0.7985156	0.8016511	
2:S A:Strata 1	0.6681647	0.0010740	0.6660562	0.6702664	
3:S A:Strata 1	0.7980394	0.0029962	0.7921032	0.8038482	
4:S B:Strata 2	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
5:S B:Strata 2	0.7006269	0.0010074	0.6986487	0.7025976	
6:p A:Strata 1	1.0000000	0.0000000	1.0000000	1.0000000	Fixed
7:Psi A to B	0.4530083	0.9617225E-03	0.4511240	0.4548939	
8:Psi B to A	0.0000000	0.0000000	0.0000000	0.0000000	Fixed

The estimate for $\hat{\psi}^{AB} = 0.4530$ over the interval from $2 \rightarrow 4$ is clearly nonsense (the SE is essentially 0, and the reported estimate is basically just the default starting value). But, what about $\hat{S}^A = 0.6682$?

Using the same ‘matrix projection’ approach used in the previous example, with a starting vector of

$$n_0 = \begin{bmatrix} 1 \\ 0 \end{bmatrix}.$$

and substituting in the true parameter values ($S_2^A = 0.7$, $S_3^A = 0.6$, $S^B = 0.7$, $\psi^{AB} = 0.4$) we can calculate the probability of a single starting individual being alive and in state **A** or **B** as

$$\begin{aligned}
 n_2 &= M_1 M_2 n_0 \\
 &= \begin{bmatrix} S_2^A(1 - \psi^{AB}) & 0 \\ S_2^A \psi^{AB} & S^B \end{bmatrix} \begin{bmatrix} S_3^A(1 - \psi^{AB}) & 0 \\ S_3^A \psi^{AB} & S^B \end{bmatrix} \begin{bmatrix} 1 \\ 0 \end{bmatrix} \\
 &= \begin{bmatrix} 0.1512 \\ 0.2968 \end{bmatrix}.
 \end{aligned}$$

So, after 2 time steps, the probability of the single starting individual being alive and in state **A** is $P_2^A = 0.1512$, while the probability of being alive and in state **B** is $P_2^B = 0.2968$. The expected survival probability over both time steps (i.e., from $2 \rightarrow 4$) is the sum of these probabilities (0.448). The square-root of $\sqrt{0.448} = 0.6693$, which is virtually identical to the estimate $\hat{S}^A = 0.6682$ that **MARK** reported for our simulated data.

So, to summarize, if you manually adjust the interval for a MS model in **MARK**, for the situation where survival varies over time, and but the transition probabilities are constant,

- the reported parameter estimates for survival (S) still represents the l th root of the weighted average survival over the interval of length l ,
- whereas the reported state transition parameters (ψ) over the same interval are not interpretable.

Finally, what about the situation where instead of manually adjusting the time interval to account for missing occasion 3, we coded the ‘missing’ data for occasion 3 using a ‘dot’ in the encounter history file?

Here are the estimates from analyzing those re-coded data:

Parameter	Estimate	Standard Error	95% Confidence Interval		
			Lower	Upper	
1:S A:Strata 1	0.8000880	0.7998680E-03	0.7985156	0.8016511	
2:S A:Strata 1	0.7026983	0.0068705	0.6890587	0.7159861	
3:S A:Strata 1	0.5917789	0.0095960	0.5728450	0.6104442	
4:S A:Strata 1	0.7980395	0.0029962	0.7921032	0.8038482	
5:S B:Strata 2	0.0000000	0.0000000	0.0000000	0.0000000	Fixed
6:S B:Strata 2	0.7006269	0.0010074	0.6986487	0.7025977	
7:p A:Strata 1	1.0000000	0.0000000	1.0000000	1.0000000	Fixed
8:Psi A to B	0.4000933	0.0010582	0.3980211	0.4021691	
9:Psi B to A	0.0000000	0.0000000	0.0000000	0.0000000	Fixed

Here, we see that the estimates for $\hat{S}_2^A = 0.702$ and $\hat{S}_3^A = 0.5917$ are very close to the true parameter values of 0.7 and 0.6, respectively. Moreover, $\hat{\psi}^{AB} = 0.4001$ is a close match to the true parameter value (0.4).

Overarching conclusions \Rightarrow From the two preceding examples, we see that what can, and cannot, be estimated for a MS model with uneven intervals (in the extreme, a completely missing occasion), may depend strongly on whether you assume time-variation (or not) in S , or ψ , or both. This is not uncommon – in the absence of ‘data’ in some context, you might occasionally need to constrain some parameters in some fashion to allow the others to be estimated. This is always a ‘compromise’ to full reality, which assumes you have all the data you need. What constraints you might impose in this ‘compromise’ will depend potentially on what parameters are most important to your question(s). For example, you might prefer time varying S and constant ψ models (as in the last example), even if holding ψ constant might not be what you actually believe to be true, because you might be more interested in decent estimates of survival than transition.

Overarching recommendations \Rightarrow Simply put, don’t have uneven sampling intervals, or missing occasions in a multi-state sampling design! Either/both will complicate a lot of things for you (as the previous few pages have no doubt demonstrated). This would be doubly true if say the pattern of sampling differed between states (e.g., two states **A** and **B**, and on occasion 3, you managed to sample state **A**, but not state **B**). It is important to understand, though, that our focus in the preceding has been on the parameter estimates themselves. The various approaches you might take for handling uneven sampling intervals will generally not impact model selection (i.e., model likelihood and AIC values will not change). But, multi-model inference ultimately focusses on parameter estimates averaged over the model set, and so having to consider just what is being averaged is an unavoidable complication.

10.7. Summary

In this chapter, we have considerably expanded the range of ‘underlying’ models we can fit to mark-recapture data. In particular, we’ve added a ‘movement’ parameter. We have also seen how to apply constraints to these models as we did with CJS models. In fact, we’ve seen how we can apply movement models to other data types (live encounters, dead recoveries...), which highlights one of the singular strengths of MS models – the ability to combine sources of information in a natural and relatively intuitive framework. In fact, if a particular ‘data type’ you’re after isn’t already coded into **MARK**, then you might be able to ‘build it for yourself’, by considering the model from a multi-state perspective.

10.8. References

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