FISH 621 Estimation of Fish Abundance: 8: Jolly-Seber Model for Open Populations

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Schnabel Experimental Design

Path of animals that are captured

Path of animals that are *not* captured

start of survey occasion

Captures: n_i Recaptures: m_i Total marks: M_i

Survey 1 Survey 2 Survey 3 Survey 4+ $U_t = N_1$ U_2 U_3 U_4 $U_1 - u_1$ $U_2 - u_2$ $U_3 - u_3$ **Unmarked: New Marks:** u_4 u_1 u_2 u_3 $u_i = n_i - m_i$ $M_2 - m_2$ $M_3 - m_3$ $M_4 - m_4$ M_3 M_4 Marked: M_2 m_2 m_3 m_{4} **M**_s Marked individuals at

Example of Mean Petersen and Schnabel Captures: n_i

Data

- s = 10 sampling periods take place, in each of which ...
 - Number of captures recorded: n_i
 - Number of marked individuals are recorded: m_i
 - All unmarked individuals $u_i = n_i m_i$ are marked
 - All captures are released back into the population N

Period (i)	Captures (n_i)	Recaptures (m_i)	New Marks (u_i)	Total Marks (M_i)	$n_i M_i$
1	20	0	20	0	0
2	20	4	16	20	400
3	20	3	17	36	720
4	20	2	18	53	1,060
5	20	4	16	71	1,420
6	20	3	17	87	1,740
7	20	3	17	104	2,080
8	20	5	15	121	2,420
9	20	4	16	136	2,720
10	20	3	17	152	3,040
Total		31			15,600

Schnabel

$$N' = \frac{\sum n_i M_i}{\sum m_i}$$

Recaptures: m_i

Total marks: M_i

$$N' = \frac{15600}{31} \approx 503$$

3. Schumacher-Eschmeyer Regression Method

- Let $y_i = m_i/n_i$ and assume y_i has a binomial distribution
 - With expected value: $\tilde{p}_i = M_i/N$
 - And variance: $\sigma_i^2 = \tilde{p}_i (1 \tilde{p}_i)/n_i$
- A standard linear regression-through-the-origin model can be written
 - $y_i = \beta M_i + e_i$, where...
 - $\beta = 1/N$
 - $e_i \sim Normal(0, \sigma_i^2)$
- Because variance is not constant (across i = 2, ..., s)
 - Weighted least squares should be used, leading to

•
$$\tilde{\beta} = \frac{1}{\tilde{N}} = \frac{\sum_{i=2}^{S} w_i y_i M_i}{\sum_{i=2}^{S} w_i M_i^2}$$
, with $w_i \propto \frac{1}{\sigma_i^2}$

- Since N is unknown and $\tilde{p}_i(1-\tilde{p}_i)$ varies little
 - For \tilde{p}_i between 0.2 and 0.8

• Choosing
$$w_i$$
 to be sample size (i.e. $w_i = n_i$) often works well
• $\tilde{\beta} = \frac{1}{\tilde{N}} = \frac{\sum_{i=2}^{S} n_i y_i M_i}{\sum_{i=2}^{S} n_i M_i^2} = \frac{\sum_{i=2}^{S} m_i M_i}{\sum_{i=2}^{S} n_i M_i^2}$

3. Schumacher-Eschmeyer Regression Method

Captures: n_i Recaptures: m_i Total marks: M_i

- Regression through the origin
 - $y_i = \beta M_i + e_i$, where...
 - $y_i = m_i/n_i$
 - $\beta = 1/N$
 - $e_i \sim Normal(0, \sigma_i^2)$
 - $\tilde{\beta} = \frac{1}{\tilde{N}} = \frac{\sum_{i=2}^{S} m_i M_i}{\sum_{i=2}^{S} n_i M_i^2}$, therefore $\tilde{N} = \frac{1}{B}$

	•	_			
Period (i)	Captures (n_i)	Recaptures (m_i)	New Marks (u_i)	Total Marks (M_i)	Mark Fraction $(m_i/\mathrm{n_i})$
1	20	0	20	0	0.00
2	20	4	16	20	0.20
3	20	3	17	36	0.15
4	20	2	18	53	0.10
5	20	4	16	71	0.20
6	20	3	17	87	0.15
7	20	3	17	104	0.15
8	20	5	15	121	0.25
9	20	4	16	136	0.20
10	20	3	17	152	0.15

3. Schumacher-Eschmeyer Regression Method

Captures: n_i Recaptures: m_i Total marks: M_i

Regression through the origin

•
$$y_i = \beta M_i + e_i$$
, where...

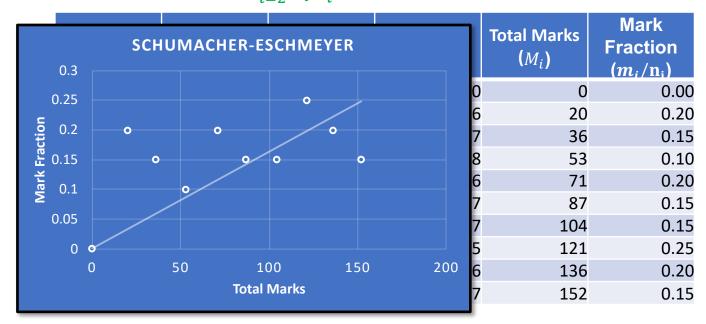
•
$$y_i = m_i/n_i$$

•
$$\beta = 1/N$$

•
$$e_i \sim Normal(0, \sigma_i^2)$$

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$$e_i \sim Normal(0, \sigma_i^2)$$

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Captures: n_i Recaptures: m_i Total marks: M_i

- Regression through the origin
 - $y_i = \beta M_i + e_i$, where...
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1	20	0	20	0	0	0
2	20	4	16	20	400	8,000
3	20	3	17	36	720	25,920
4	20	2	18	53	1,060	56,180
5	20	4	16	71	1,420	100,820
6	20	3	17	87	1,740	151,380
7	20	3	17	104	2,080	216,320
8	20	5	15	121	2,420	292,820
9	20	4	16	136	2,720	369,920
10	20	3	17	152	3,040	462,080
Total		31			15,600	1,683,440

$$\tilde{\beta} = \frac{\sum_{i=2}^{s} m_i M_i}{\sum_{i=2}^{s} n_i M_i^2}$$

$$\tilde{\beta} = \frac{15,600}{1,683,440}$$

$$\tilde{\beta} = 0.009267$$

$$\tilde{N} = \frac{1}{\tilde{\beta}} = 107.9$$

3. Schumacher-Eschmeyer Regression Method

Captures: n_i Recaptures: m_i

Total marks: M_i

- Regression through the origin
 - $y_i = \beta M_i + e_i$, where...
 - $y_i = m_i/n_i$
 - $\beta = 1/N$

• $e_i \sim Normal(0, \sigma_i^2)$

• $\tilde{\beta} = \frac{1}{\tilde{N}} = \frac{\sum_{i=2}^{S} m_i M_i}{\sum_{i=2}^{S} n_i M_i^2}$, therefore $\tilde{N} = \frac{1}{B}$

WRONG!!!	W	RO	N	G!	!!
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Period (i)	Captures (n_i)	Recaptures (m_i)	New Marks (u_i)	Total Marks (M_i)	$n_i M_i$	$n_i M_i^2$
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Total		31			15,600	1,683,440

$$\tilde{\beta} = \frac{\sum_{i=2}^{s} m_i M_i}{\sum_{i=2}^{s} n_i M_i^2}$$

$$\tilde{\beta} = \frac{15,600}{1,683,440}$$

$$\tilde{\beta} = 0.009267$$

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3. Schumacher-Eschmeyer Regression Method

Captures: n_i Recaptures: m_i Total marks: M_i

- Regression through the origin
 - $y_i = \beta M_i + e_i$, where...
 - $y_i = m_i/n_i$
 - $\beta = 1/N$

• $e_i \sim Normal(0, \sigma_i^2)$

• $\widetilde{\beta} = \frac{1}{\widetilde{N}} = \frac{\sum_{i=2}^{S} m_i M_i}{\sum_{i=2}^{S} n_i M_i^2}$, therefore $\widetilde{N} = \frac{1}{B}$

Correct!!!	

Period (i)	Captures	Recaptures	New Marks	Total Marks	m M	$n_i M_i^2$
renou (t)	(n_i)	(m_i)	(u_i)	(M_i)	$m_i M_i$	$n_{i}m_{i}$
1	20	0	20	0	0	0
2	20	4	16	20	80	8,000
3	20	3	17	36	108	25,920
4	20	2	18	53	106	56,180
5	20	4	16	71	284	100,820
6	20	3	17	87	261	151,380
7	20	3	17	104	312	216,320
8	20	5	15	121	605	292,820
9	20	4	16	136	544	369,920
10	20	3	17	152	456	462,080
Total		31			2,756	1,683,440

$$\tilde{\beta} = \frac{\sum_{i=2}^{S} m_i M_i}{\sum_{i=2}^{S} n_i M_i^2}$$

$$\tilde{\beta} = \frac{2,756}{1,683,440}$$

$$\tilde{\beta} = 0.001637$$

$$\tilde{N} = \frac{1}{\tilde{\beta}} = 610.8$$

Jolly-Seber Background

References

- Seber (1982), Chapter 5
 - General and concise description of Jolly-Seber methods
- Brownie et al. (1986)
 - Presented modifications of the Jolly-Seber model for capturerecapture data, which assume constant survival and/or capture rates.
 - Where appropriate, because of the reduced number of parameters, these models lead to more efficient estimators than the Jolly-Seber model.
- Hightower and Gilbert (1984)
- Arnason and Mills (1981)
- Arnason et al. (1982)

Jolly-Seber Background

- Methodology extends the Schnabel experimental design
 - To open populations that have
 - Mortality, recruitment, immigration, and/or permanent emigration
- The Schnabel experimental design is *followed*, except
 - Some individuals need not be returned to the population after capture
 - Animals must receive a recognizable mark or tag
 - That allows the occasion of capture to be determined (individual ID will work)
- Complications of sampling without replacement
 - Will be ignored for now
 - So likelihoods are based on binomial or multinomial distributions

Jolly-Seber Notation

- We will use the same notation we saw for Schnabel estimation
 - With the addition of the following parameters, which will be treated as random variables
 - N_i = number in the population **just prior** to sampling at occasion i at time t_i
 - $U_i = N_i M_i$ =unmarked number in the population
 - ϕ_i = survival (or permanent emigration) from t_i to t_{i+1}
 - B_i = recruitment (or immigration) into the population from t_i to t_{i+1}
 - $N_i(h)$ = members of B_h (cohort) still alive and present at time t_i

Schnabel Experimental Design

Path of animals that are captured

Path of animals that are *not* captured

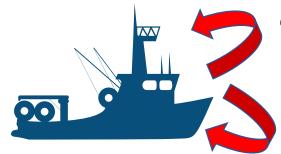
start of survey occasion

Captures: n_i Recaptures: m_i Total marks: M_i

Survey 1 Survey 2 Survey 3 Survey 4+ $U_t = N_1$ U_2 U_3 U_4 $U_1 - u_1$ $U_2 - u_2$ $U_3 - u_3$ **Unmarked: New Marks:** u_4 u_1 u_2 u_3 $u_i = n_i - m_i$ $M_2 - m_2$ $M_3 - m_3$ $M_4 - m_4$ M_3 M_4 Marked: M_2 m_2 m_3 m_{4} **M**_s Marked individuals at

Jolly-Seber Notation

- Additional data variables and parameters
 - $n_i = m_i + u_i = R_i + d_i + d_i'$ is the number sampled, where...
 - R_i = number **returned to the population** from number sampled n_i (including m_i)
 - d_i = number of m_i (recaptures) **not** released
 - d'_i = number of u_i (unmarked) **not** released
 - v_i = probability of a *marked member* being *released*
 - v_i' = probability of an **unmarked** member being **released**
 - χ_i = probability of a release **not** being recaptured



 $d_i = m_i(1 - v_i)$: retained-recap

 R_i : Returns to population

 $d'_i = u_i(1 - v'_i)$: retained-unmarked

Jolly-Seber Notation

- Additional data variables and parameters
 - $n_i = m_i + u_i = R_i + d_i + d_i'$ is the number sampled, where...
- Data
 - m_{hi} = number caught in the *i*th sample
 - Last caught in sample h
 - r_i = number of R_i (releases) later *captured*
 - z_i = number caught **before** sample i
 - Not captured in sample i
 - And captured after i



Jolly-Seber Assumptions

- 1) There is a constant probability of capture
 - $p_i = 1 q_i$ at sampling occasion i
 - i.e. no behavioral or heterogeneity effects
 - Therefore...
 - Expected **total** captures: $E(n_i) = N_i p_i$
 - Expected recaptures: $E(m_i) = M_i p_i$
 - Expected **unmarked** captures: $E(u_i) = U_i p_i$
- 2) To estimate abundance and survival
 - The constant survival ϕ_i for each time period
 - Applies to **marked** members M_i
 - To estimate recruitment
 - Necessary to assume it applies to $\emph{unmarked}$ members as well U_i

Jolly-Seber Assumptions

- 3) Each animal in the marked M_i or unmarked U_i group
 - Has the same probability of being returned to the population
 - Tag bounty ???? But, what about the free hats!
- 4) Other Schnabel assumptions apply:
 - Samples are instantaneous
 - No tag loss (but see below) or non-reporting
- 5) Some releases occur at each period
 - Otherwise some parameters are not estimable!

Jolly-Seber Model

- New population = Survivors from old population + Recruitment
 - $N_{i+1} = \phi_i(N_i n_i + R_i) + B_i = M_{i+1} + U_{i+1}$
- Expected unmarked population
 - $U_{i+1} = \phi_i(U_i u_i) + B_i = U_i\phi_iq_i + B_i$
 - Constant *non-capture* probability: $q_i = 1 p_i$
 - Unmarked population is made up of
 - Surviving unmarked members not caught

Jolly-Seber Model

- New population = Survivors from old population + Recruitment
 - $N_{i+1} = \phi_i(N_i n_i + R_i) + B_i = M_{i+1} + U_{i+1}$
- Expected marked population
 - $M_{i+1} = \phi_i (M_i m_i + R_i)$
 - $M_{i+1} = \phi_i M_i (q_i + p_i v_i) + \phi_i U_i (p_i v_i')$
 - v_i = probability of a **marked member** being **released**
 - v_i' = probability of an **unmarked** member being **released**
 - Surviving marked members
 - Those not caught and those caught and returned to the population after sample
 - And surviving
 - Previously unmarked members that are caught
 - And returned to the population as marked members

- The likelihood follows directly from the Schnabel experiment
 - With one major modification
 - In order to be considered for capture at occasion i, an animal must survive the prior period
- Therefore, the survival term ϕ_i must be added to
 - Capture and non-capture probabilities
 - In the binomial likelihood
- In addition, a captured animal must be re-released back into the population
 - With probability v_i if already marked
 - And probability v_i^\prime if unmarked

Jolly-Seber Cap History

- Example capture histories
 - (10010)
 - $(p_1v_1'\phi_1)(q_2\phi_2)(q_3\phi_3)(p_4v_4\phi_4)(q_5)$
 - (0 1 0 1 0)
 - $(q_1\phi_1)(p_2v_2'\phi_2)(q_3\phi_3)(p_4v_4\phi_4)(q_5)$

- Seber and Brownie et al. show how do do this from capture histories
 - The net result being the likelihood component for marked recaputres
 - Can be expressed in terms of the sufficient statistics (r_i, m_i, z_i)
 - m_{hi} = number caught in the *i*th sample
 - Last caught in sample h
 - r_i = number of R_i (releases) later *captured*
 - z_i = number caught **before** sample i
 - **Not** captured in sample *i*
 - And captured after i

- Sufficient statistics (r_i, m_i, z_i) are calculated from
 - The recapture matrix (m_{hi})
 - Shown below
- Which combined with information on the release process (R_i, d_i, d_i')
 - d_i = number of m_i (recaptures) **not** released
 - d'_i = number of u_i (unmarked) **not** released
 - And the unmarked captures u_i
 - Produces the total likelihood
- The total likelihood L
 - Is the product of three different likelihood components

•
$$L = L_1 L_2 L_3$$

- Likelihood component #1 (L_1)
 - Seber and Brownie et al. have slightly different forms of the likelihood
 - We'll consider the Brownie version:

$$L_{1} = \prod_{i=1}^{s-1} \binom{R_{i}}{r_{i}} (1 - \chi_{i})^{r_{i}} \chi_{i}^{R_{i} - r_{i}} \prod_{i=2}^{s-1} \binom{m_{i} + z_{i}}{m_{i}} \left(\frac{p_{i}}{1 - q_{i} \chi_{i}} \right)^{m_{i}} \left(1 - \frac{p_{i}}{1 - q_{i} \chi_{i}} \right)^{z_{i}}$$

- The number of recaptures from release group R_i
 - Is binomially distributed
- As is the number of recaptures from releases prior to period i
 - Divided into those caught at period i, and those caught after
- This component gives estimates of the parameters ϕ_i and p_i
 - This could be obtained numerically, but there are closed-form solutions

- Likelihood component #2 (L_2)
 - The numbers *not* returned to the population are binomially distributed
 - $d_i \sim Binomial(m_i, 1 v_i)$
 - $d_i' \sim Binomial(u_i, 1 v_i')$
 - Multiplying these together gives the component L_2
 - Providing the estimators for the *release probabilities* (e.g. $\hat{v}_i = 1 d_i/m_i$)
 - But otherwise have no connection to other estimates
 - i.e. nuisance parameters

- Likelihood component #3 (L_3)
 - The number of unmarked captures u_i is binomially distributed
 - $L_3(u_i) \sim \prod_{i=1}^s Binomial(U_i, p_i)$
 - This provides estimators for the unmarked population at each time period
 - E.g. $\widehat{U}_i = u_i/\hat{p}_i$
 - With a connection to the first component (L_1)
 - Through the probabilities of capture
 - This necessarily assumes that capture probabilities apply equally to marked and unmarked members!

- The first task is to estimate the number of marks M_i in the population prior to sampling
 - Because this is no longer known due to mortality
- The MLE derived from the likelihood equations can be explained intuitively
 - Break M_i into two groups
 - m_i = the number caught
 - $M_i m_i$ = the number **not** caught
 - After sample i, there are two groups
 - $M_i m_i$, of which z_i are caught later
 - R_i , of which r_i are caught later

- By equating the *recapture* proportions
 - The estimated number of marks is found

•
$$\frac{z_i}{M_i - m_i} = \frac{r_i}{R_i} \Longrightarrow \frac{1}{\widehat{M}_i - m_i} = \frac{r_i}{R_i z_i} \Longrightarrow \widehat{M}_i = \frac{R_i z_i}{r_i} + m_i$$

- r_i = number of R_i (releases) later *captured*
- z_i = number caught **before** sample i
 - Not captured in sample i
 - And captured after i
- Or the bias-corrected version

•
$$M_i^* = \frac{R_i + 1}{r_i + 1} z_i + m_i$$

- By equating the *recapture* proportions
 - · The estimated number of marks is found

•
$$\frac{z_i}{M_i - m_i} = \frac{r_i}{R_i} \Longrightarrow \frac{1}{\widehat{M}_i - m_i} = \frac{r_i}{R_i z_i} \Longrightarrow \widehat{M}_i = \frac{R_i z_i}{r_i} + m_i$$

- r_i = number of R_i (releases) later *captured*
- z_i = number caught **before** sample i
 - **Not** captured in sample *i*
 - And *captured* after *i*
- Or the bias-corrected version

•
$$M_i^* = \frac{R_i + 1}{r_i + 1} z_i + m_i$$

Note also that

$$\bullet \ \frac{1}{\widehat{M}_i - m_i + R_i} = \frac{r_i}{R_i(z_i + r_i)}$$

Captures: n_i Recaptures: m_i Total marks: M_i Returns: R_i Recruitment: B_i Survival: ϕ_i

The estimated probability of capture is then

•
$$\hat{p}_i = \frac{m_i}{\widehat{M}_i}$$

From which the unmarked and total population can be estimated from

$$\bullet \ \widehat{U}_i = \frac{u_i}{\widehat{p}_i} = \frac{\widehat{M}_i u_i}{m_i}$$

$$\bullet \ \widehat{N}_i = \frac{n_i}{\widehat{p}_i} = \frac{\widehat{M}_i n_i}{m_i}$$

- Our old friend the Petersen estimators!
- The bias-corrected estimators are:

$$U_i^* = \frac{M_i^*(u_i+1)}{m_i+1}$$

•
$$N_i^* = M_i^* + U_i^* = \frac{M_i^*(n_i+2)}{m_i+1}$$

Captures: n_i Recaptures: m_i Total marks: M_i Returns: R_i Recruitment: B_i Survival: ϕ_i

- Survival is estimated from marked members alone
 - By taking the ratio of the estimated number marked prior to sample $i\,+\,1$
 - And the estimated number marked just after sample i

$$\bullet \ \phi_i^* = \frac{M_{i+1}^*}{\widehat{M}_i - m_i + R_i}$$

• First period: i = 1

•
$$\phi_1^* = \frac{M_2^*}{R_1}$$

- Note that M_i^* is used in the numerator and \widehat{M}_i is used in the denominator
 - To get the least biased estimator

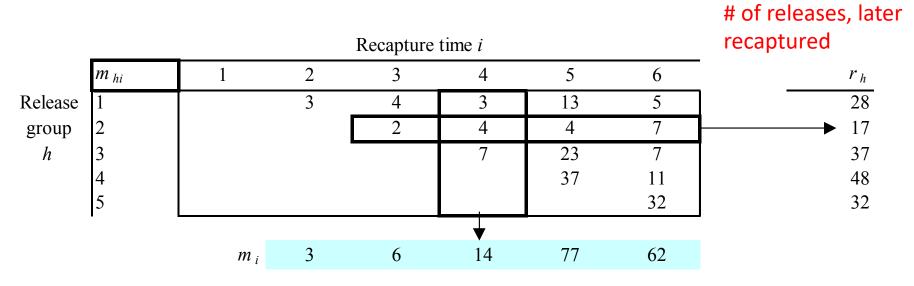
- The proportion of marks in the population $\rho_i = M_i/N_i$
 - Is estimated by: $\rho_i = \frac{M_i}{N_i} = \frac{m_i}{n_i}$
- The estimated probability of not being caught after sample i is
 - $\chi_i = 1 r_i/R_i$
- Recruitment is estimated as
 - $B_i^* = U_{i+1}^* \phi_i^* (U_i^* u_i)$, or as • $B_i^* = U_{i+1}^* - U_i^* \phi_i^* \hat{q}_i$ (less biased)
 - Where $\hat{q}_i = 1 \hat{p}_i$

- Estimates of abundance N_i^* can be made for i = 2, ..., s 1
 - Estimates of survival ϕ_i^* for i=1,...,s-2
 - Estimates of capture probability \hat{p}_i for i=2,...,s-2
 - Estimates of recruitment B_i^* for i=2,...,s-2
- Note that ϕ_S and B_S are undefined beyond the time period of consideration
- However, if there is **no** recruitment for the first period $(B_1 = 0)$
 - And all animals are **released** $(R_1 = n_1)$
 - Then a simple extrapolation is:

•
$$N_1^* = N_2^*/\phi_1^*$$

Captures: n_i Recaptures: m_i Total marks: M_i Returns: R_i Recruitment: B_i Survival: ϕ_i

- 1) Obtain the capture history raw data
 - Summarize in the matrix m_{hi}
 - For release group h (row) the column i gets
 - The number of marked recaptures that were next captured on occasion i



of total recaptures

Captures: n_i Recaptures: m_i Total marks: M_i Returns: R_i Recruitment: B_i

Survival: ϕ_i

- $c_{1i} = m_{1i}$ for release group 1
 - $c_{hi} = c_{h-1,i} + m_{hi}$ for other release groups

Recapture time *i* m_{hi} r_h Release group h m_i Recapture time *i* c_{hi} z_{h+1} Release group h

Captures: n_i Recaptures: m_i Total marks: M_i Returns: R_i Recruitment: B_i Survival: ϕ_i

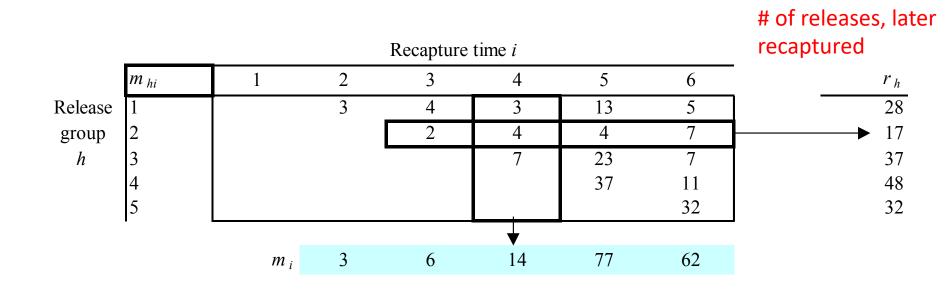
- 3) Get m_i by summing each column of m matrix
 - $m_i = \sum_{h=1}^{i-1} m_{hi}$
 - Should be equal to first diagonal of c_{hi}

				Recapture	time i				
	m_{hi}	1	2	3	4	5	6	•	r_h
Release	1		3	4	3	13	5		28
group	2			2	4	4	7		▶ 17
h	3				7	23	7		37
	4					37	11		48
	5						32		32
					\forall				
		m_i	3	6	14	77	62		

of total recaptures

Captures: n_i Recaptures: m_i Total marks: M_i Returns: R_i Recruitment: B_i Survival: ϕ_i

- 4) Get r_h by summing each row of m matrix
 - $r_h = \sum_{i=h+1}^s m_{hi}$



of total recaptures

Captures: n_i Recaptures: m_i Total marks: M_i Returns: R_i Recruitment: B_i Survival: ϕ_i

- 5) Get z_{h+1} by summing each row of c_{hi} matrix
 - Minus the first element

•
$$z_{h+1} = \sum_{i=h+2}^{s} c_{hi}$$

•
$$z_{h+1} - z_h = r_h - m_{h+1}$$

• Example: h = 2 36-25=17-6

Recapture time i

	C_{hi}	1	2	3	4	5	6	z_{h+1}
Release	1		3	4	3	13	5	25
group	2			6	7	17	12	→ 36
h	3				14	40	19	59
	4					77	30	30
	5						62	

Captures: n_i Recaptures: m_i Total marks: M_i Returns: R_i Recruitment: B_i Survival: ϕ_i

• 6) Get the data n_i and R_i

i	1	2	3	4	5	6
n_i	1015	417	606	789	1906	1151
R_{i}	1015	405	603	789	1880	0

• 7) Calculate all desired estimators using previous equations