Program MARK Parameter Estimation from Marked Animals

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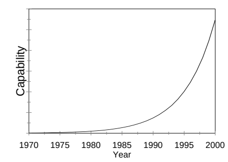
Advances since 1985

- More complex time/space models
- Covariates – more realistic biology
- New models – innovative data collection



- **Standard tags, leg bands, or neck collars**
- **Radios (implants)**
- **PIT tags**
- **Camera “traps”**
- **DNA samples**

Estimable Parameters

- Survival
- Movement
- Emigration/immigration
- Reproduction/recruitment
- Population size
- Rate of population change

Models in MARK

- Live encounters – Cormack, Jolly, Seber
- Dead encounters – Band or ring recovery
- Joint live and dead – Burnham, Barker, Lindberg
- Known fate – radio-tracking
- Closed capture-recapture – likelihood only, including individual heterogeneity
- Robust design – Pollock, Kendall
- Multistrata design – Brownie, Nichols, with dead recoveries – Barker
- Jolly-Seber – POPAN – Pradel – Link-Barker (7 parameterizations)
- Nest success
- Occupancy estimation, with robust design

- **Multiple attribute groups**
- **Time, group and individual covariates**
- **Unequal time intervals**
- **Model management**
- **AIC model selection**
- **Quasi-likelihood**
- **Variance Components**
- **Model Averaging**

- **Windows 95/98/NT/2000/ME/XP**
- **Structure of models**
- **Design matrix and link functions**
- **AIC, model selection**
- **Maximum likelihood estimation**

☞ **Sharp knives cut people**

Data are Required to Gain Reliable Knowledge

A statistician's primary function is to prevent, or at least impede research.

Computer Requirements

- Windows 95/98/NT 4.0/ 2000/ME/XP
- CPU speed to compute estimates in reasonable amount of time
- ≥128 Mb RAM

- Interface written in Computer Associates Visual Objects
- Numerical analysis in 32 bit FORTRAN 95 code
- Communication by files

Basic Data

Encounter Histories

- **LDLDLD...**
  - **Dead recoveries**
  - **Joint live and dead**
  - **Known fate**
- **LLLLLLL...**
  - **Live recaptures**
  - **Closed capture-recapture**
- **Dead recovery matrices**
- **Known fate**

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Likelihood Function

Maximum Likelihood Estimation

Likelihood = Pr(Enc. Hist.)$^{\text{Observed}}$

$\log_e$(Likelihood) = Num. Observed *X* $\log_e$[Pr(Enc. Hist.)]

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- How are encounter histories translated into probabilities that are a function of the parameters of interest?

						Encounter History (LD)
	S	Live				10 *S*
Releases			*r*	Reported		11 (1 - *S*)*r*
	1 - *S*	Dead				
			1 - *r*	Not Reported		10 (1 - *S*)(1 - *r*)

Seber 1970

Brownie et al.: $f_i = (1 - S_i)r_i$

$(1-S_1)r_1$	$S_1(1-S_2)r_2$	$S_1S_2(1-S_3)r_3$	$S_1S_2S_3(1-S_4)r_4$
	$(1-S_2)r_2$	$S_2(1-S_3)r_3$	$S_2S_3(1-S_4)r_4$
		$(1-S_3)r_3$	$S_3(1-S_4)r_4$
			$(1-S_4)r_4$

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Brownie et al. 1985 Model

f_1	S_1f_2	$S_1S_2f_3$	$S_1S_2S_3f_4$
	f_2	S_2f_3	$S_2S_3f_4$
		f_3	S_3f_4
			f_4

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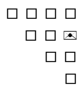
Dead Encounters

00100001

$S_2 S_3 (1 - S_4) r_4$



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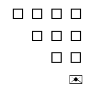
Dead Encounters

00000011

$(1 - S_4) r_4$



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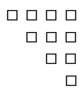

Dead Encounters

Model notation:

$\{S(.)\ r(t)\}$

$S_1 = S_2 = ... = S_t$;

$r_1, r_2, ..., r_t$.

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Dead Encounters

Model notation:

$\{S(t)\ r(.)\}$

$S_1, S_2, ..., S_t$;

$r_1 = r_2 = ... = r_t$.

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Model notation:

$\{S(g^*t)\ r(g^*t)\}$

$S_{11}, S_{12}, ..., S_{1t}$,

$S_{21}, S_{22}, ..., S_{2t}$;

$r_{12}, r_{13}, ..., r_{1t}, r_{22}, r_{23}, ..., r_{2t}$.

Dead Encounters

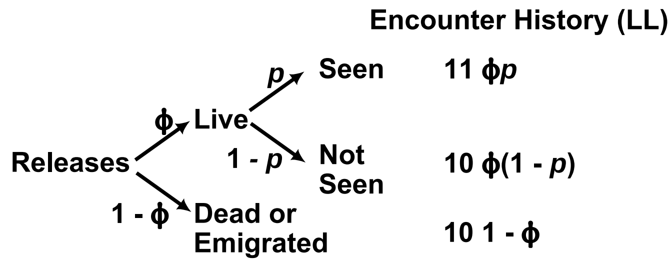
Model notation:

{*S*(*g*) *r*(*g*)}

$S_{1.}, S_{2.}, ..., S_{g.};$

$r_{1.}, r_{2.}, ..., r_{g.}.$

Live Encounters (CJS)



Live Encounters (CJS)

0101

$$\phi_2(1 - p_3)\phi_3 p_4$$

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Live Encounters (CJS)

1110

$$\phi_1 p_2 \phi_2 p_3$$

$$[\phi_3(1 - p_4) + (1 - \phi_3)]$$

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Live Encounters (CJS)

Model notation:

$\{\phi(.)\ p(.)\}$

$\phi_1 = \phi_2 = ... = \phi_{t-1}$;

$p_2 = p_3 = ... = p_t$.

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Live Encounters (CJS)

Model notation:

$\{\phi(t)\ p(.)\}$

$\phi_1, \phi_2, ..., \phi_{t-1}$;

$p_2 = p_3 = ... = p_t$.

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Model notation:

$\{\phi(g*t)\ p(g*t)\}$

$\phi_{11}, \phi_{12}, ..., \phi_{1t-1}$,

$\phi_{21}, \phi_{22}, ..., \phi_{2t-1}$;

$p_{12}, p_{13}, ..., p_{1t}$;

Model notation:

$\{\phi(g)\ p(g)\}$

$\phi_{1.}, \phi_{2.}, ..., \phi_{g.}$;

$p_{1.}, p_{2.}, ..., p_{g.}$.

Extensions to CJS

Extensions allow additional parameters to be estimated.

- **Multi-strata**
- **Jolly-Seber (Pradel, POPAN, Link-Barker)**
- **Robust design**
- **Incorporate dead encounters**

Multi-Strata Model

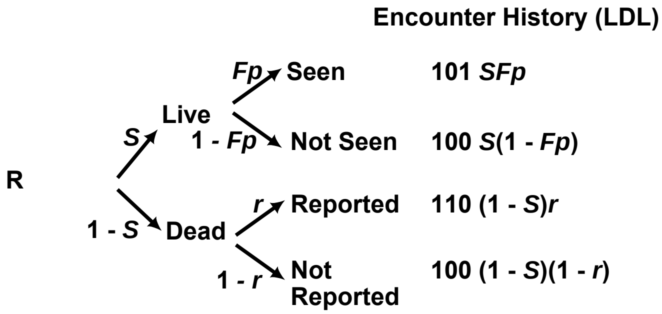
- Allows transitions between categories, e.g.:
  - Life stages
  - Areas (e.g., wintering grounds)
  - Breeding status

- Estimates of ϕ and *p*
- "Leading Zeros" used to estimate:
  - Lambda ($\lambda = N_{t+1}/N_t = \phi + f$)
  - Recruitment ($f = \lambda - \phi$)
  - Seniority (γ)
  - Population size (N_t)

- Multiple trapping occasions close together where no population change is assumed
- Estimates of:
  - Temporary emigration
  - Population size (*N*)

Joint Encounters

Both live and dead encounters



Joint Encounters

4 encounter occasions

LDLDLDLD

***S* - survival prob.**

***r* - reporting prob.**

***p* - capture prob.**

***F* - fidelity prob. ($\phi = SF$)**

Joint Encounters

10101001

$$S_1F_2p_2S_2F_3p_3S_3$$

$$[F_4(1 - p_4) + (1 - F_4)]$$

$$(1 - S_4)r_4$$

Barker Live-Dead Model

- Extension of joint live and dead recoveries model that allows resightings during intervals
- Estimation of survival and fidelity to study area

- Barker model extended to include robust design (also see Lindberg et al. 2001)
- Estimate temporary and permanent emigration, survival, and population size.

- For wildlife applications, this general model could incorporate data from DNA, radios, harvest, and casual resightings of marked animals
- Estimates of survival, temporary and permanent emigration, and population size

Multi-strata with Live and Dead Encounters

- Strata-specific live encounters, dead encounters ignore strata
- Estimation of transition probabilities, true survival, strata-specific live encounter probability, and dead encounter probability

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Joint Encounters: Estimation of Radio Effects

- Group 1: regular live/dead encounters
  - 00100001
- Group 2: known fate data entered as joint live/dead encounter history
  - 00101011
  - *p* = 1
  - *r* = 1
- Compare *S*-hat and *F*-hat for 2 groups

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					Encounter History (LL)
U	*p*	Seen	*c*	Seen	11 *pc*
			1 - *c*	Not Seen	10 *p*(1 - *c*)
	1 - *p*	Not Seen	*p*	Seen	01 (1 - *p*)*p*
			1 - *p*	Not Seen	00 (1 - *p*)(1 - *p*)

Closed Captures

- $N = M_{t+1}/[1 - (1-p_1)(1-p_2)...(1-p_4)]$

Closed Captures

1111

$\boldsymbol{p_1 c_2 c_3 c_4}$

Closed Captures

0100

$$(1 - p_1)p_2(1 - c_3)(1 - c_4)$$

Closed Captures

0000

$$(1 - p_1)(1 - p_2)(1 - p_3)(1 - p_4)$$

- $p_1 = \pi p_a + (1 - \pi)p_b$

where π is probability animal is from mixture distribution *a* which has p_a initial capture probability

- Similarly for remaining p_i and c_i

Closed Captures with Heterogeneity

Model notation with 2 mixtures (*a*, *b*):

$\{\pi\, p_a(t)\, p_b(t)\, c_a(t)\, c_b(t)\, N(.)\}$

π;

$p_{a1}, p_{a2}, \ldots, p_{at}; p_{b1}, p_{b2}, \ldots, p_{bt};$

$c_{a2}, c_{a3}, \ldots, c_{at}; c_{b2}, c_{b3}, \ldots, c_{bt};$

N .

Known Fate

Radio-tracking Data

Fate	Encounter History (LD)
Releases → S → **Live**	**10** S
Releases → $1 - S$ → **Dead**	**11** $(1 - S)$

Known Fate

00101011

$S_2 S_3(1 - S_4)$

Known Fate

10100011

$S_1 S_2(1 - S_4)$

- KM estimate is product of survival estimates for fixed time intervals
- Staggered entry
  - 0000101010
  - 0000101011
- Right censoring or <u>missing</u> intervals
  - 1010<u>0000</u>101000

Advantages of Using MARK Known Fate over Kaplan-Meier

- Alternative models
- Covariates
- Model selection
- Model averaging
- Variance components

Model Building

PIM
↘ **Design Matrix (β)**
↘ **Link Function**
↘ **Real Parameters**

Parameter Index Matrix – PIM

Time-specific apparent survival

Φ_1 Φ_2 Φ_3 Φ_4
1 ➜ 2 ➜ 3 ➜ 4 ➜ 5
Φ_2 Φ_3 Φ_4
2 ➜ 3 ➜ 4 ➜ 5
Φ_3 Φ_4
3 ➜ 4 ➜ 5
Φ_4
4 ➜ 5

```
1 2 3 4
  2 3 4
    3 4
      4
```

Parameter Index Matrix – PIM

Time-specific capture probabilities

1 ➜ 2 ➜ 3 ➜ 4 ➜ 5
p_2 p_3 p_4 p_5
2 ➜ 3 ➜ 4 ➜ 5
p_3 p_4 p_5
3 ➜ 4 ➜ 5
p_4 p_5
4 ➜ 5
p_5

```
5 6 7 8
  6 7 8
    7 8
      8
```

Parameter Index Matrix – PIM

Age-specific apparent survival

$1 \xrightarrow{\Phi_1} 2 \xrightarrow{\Phi_2} 3 \xrightarrow{\Phi_3} 4 \xrightarrow{\Phi_4} 5$

$2 \xrightarrow{\Phi_1} 3 \xrightarrow{\Phi_2} 4 \xrightarrow{\Phi_3} 5$

$3 \xrightarrow{\Phi_1} 4 \xrightarrow{\Phi_2} 5$

$4 \xrightarrow{\Phi_1} 5$

⇨

1	2	3	4
	1	2	3
		1	2
			1

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Parameter Index Matrix – PIM

Age- and time-specific apparent survival, 2 age classes

$1 \xrightarrow{\Phi_1} 2 \xrightarrow{\Phi_5} 3 \xrightarrow{\Phi_6} 4 \xrightarrow{\Phi_7} 5$

$2 \xrightarrow{\Phi_2} 3 \xrightarrow{\Phi_6} 4 \xrightarrow{\Phi_7} 5$

$3 \xrightarrow{\Phi_3} 4 \xrightarrow{\Phi_7} 5$

$4 \xrightarrow{\Phi_4} 5$

⇨

1	5	6	7
	2	6	7
		3	7
			4

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Parameter Index Matrix – PIM

2 Groups, Survival Different, Time-specific Model {*S*(*g***t*)}

Group 1					Group 2				
1	2	3	4	5	6	7	8	9	10
	2	3	4	5		7	8	9	10
		3	4	5			8	9	10
			4	5				9	10
				5					10

Parameter Index Matrix – PIM

2 Groups, Survival Same, Time- specific Model {*S*(*t*)}

Group 1					Group 2				
1	2	3	4	5	1	2	3	4	5
	2	3	4	5		2	3	4	5
		3	4	5			3	4	5
			4	5				4	5
				5					5

Parameter Index Matrix – PIM

2 Groups, Survival Different, Model {*S*(*g*)}

Group 1					Group 2				
1	1	1	1	1	2	2	2	2	2
	1	1	1	1		2	2	2	2
		1	1	1			2	2	2
			1	1				2	2
				1					2

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Parameter Index Matrix – PIM

2 Groups, Survival Same, Model {*S*(.)}

Group 1					Group 2				
1	1	1	1	1	1	1	1	1	1
	1	1	1	1		1	1	1	1
		1	1	1			1	1	1
			1	1				1	1
				1					1

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- Time-specific (current PIM or all)
- Age-specific (current PIM or all)
- Constant (current PIM or all)
- Diagonal, Row, Column changes
- Change a singe cell
- Exchange or copy whole PIMs
- Paste or copy to clipboard
- Renumber (with or without overlap)

- Visually assess PIMs
- Drag boxes to copy PIMs
- Right click to select menu choices

Design Matrix

- **Allows additional constraints not possible using PIMs**
  - **Additive models with parallelism between groups, ages**
- **Covariates, including individual covariates**

Individual Covariates

- **Included in Encounter Histories File**
- **Attached to animal's encounter history**

PIMs for Design Matrix Examples 5 intervals (6 occasions), 3 groups

Group 1	Group 2	Group 3
1 2 3 4 5	6 7 8 9 10	11 12 13 14 15
2 3 4 5	7 8 9 10	12 13 14 15
3 4 5	8 9 10	13 14 15
4 5	9 10	14 15
5	10	15

Group 1	Group 2	Group 3
1 2 3 4 5	6 7 8 9 10	11 12 13 14 15
2 3 4 5	7 8 9 10	12 13 14 15
3 4 5	8 9 10	13 14 15
4 5	9 10	14 15
5	10	15

Model {theta(*g***t*)}

1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 1 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 1 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 1 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 1 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 1 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 1 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 1 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 1 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 1 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 1 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 1 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 1 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 1 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 1

Link Functions

- Sin
- Logit
- Log-Log
- Complementary Log-Log
- Log
- Identity
- Multinomial Logit
- Cumulative Logit

Design Matrix
Identity Link

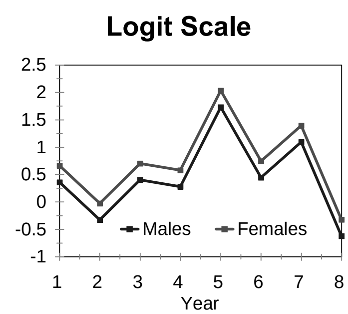
Unbounded

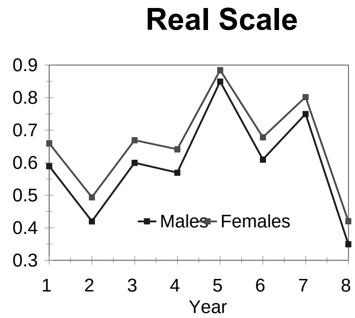
Real Estimate = $X\beta$

Bounded 0-1

Bounded 0-1

Logit vs. Real Parameters

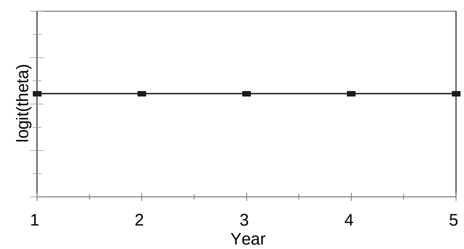




Group 1					Group 2					Group 3				
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	2	3	4	5		7	8	9	10		12	13	14	15
		3	4	5			8	9	10			13	14	15
			4	5				9	10				14	15
				5					10					15

Model {theta(.)}

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1



No variation in theta by time or groups

Group 1					Group 2					Group 3				
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	2	3	4	5		7	8	9	10		12	13	14	15
		3	4	5			8	9	10			13	14	15
			4	5				9	10				14	15
				5					10					15

Model {theta(*g*)}

1	1	0
1	1	0
1	1	0
1	1	0
1	1	0
1	0	1
1	0	1
1	0	1
1	0	1
1	0	1
1	0	0
1	0	0
1	0	0
1	0	0
1	0	0

Group 1					Group 2					Group 3				
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	2	3	4	5		7	8	9	10		12	13	14	15
		3	4	5			8	9	10			13	14	15
			4	5				9	10				14	15
				5					10					15

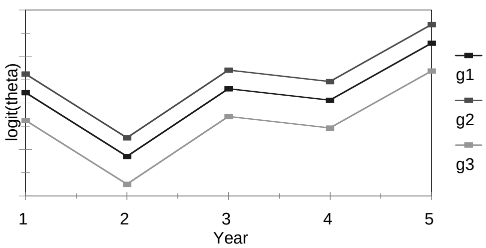
Model {theta(*t*)}

1	1	0	0	0
1	0	1	0	0
1	0	0	1	0
1	0	0	0	1
1	0	0	0	0
1	1	0	0	0
1	0	1	0	0
1	0	0	1	0
1	0	0	0	1
1	0	0	0	0
1	1	0	0	0
1	0	1	0	0
1	0	0	1	0
1	0	0	0	1
1	0	0	0	0

Group 1	Group 2	Group 3
1 2 3 4 5	6 7 8 9 10	11 12 13 14 15
2 3 4 5	7 8 9 10	12 13 14 15
3 4 5	8 9 10	13 14 15
4 5	9 10	14 15
5	10	15

Model {theta(*g* + *t*)}

1 1 0 1 0 0 0
1 1 0 0 1 0 0
1 1 0 0 0 1 0
1 1 0 0 0 0 1
1 1 0 0 0 0 0
1 0 1 1 0 0 0
1 0 1 0 1 0 0
1 0 1 0 0 1 0
1 0 1 0 0 0 1
1 0 1 0 0 0 0
1 0 0 1 0 0 0
1 0 0 0 1 0 0
1 0 0 0 0 1 0
1 0 0 0 0 0 1
1 0 0 0 0 0 0

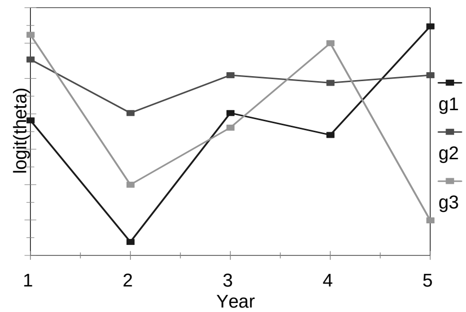


Variation in theta by time and by group
Additive model with no interactions

Group 1	Group 2	Group 3
1 2 3 4 5	6 7 8 9 10	11 12 13 14 15
2 3 4 5	7 8 9 10	12 13 14 15
3 4 5	8 9 10	13 14 15
4 5	9 10	14 15
5	10	15

Model {theta(*g***t*)}

1 1 0 1 0 0 0 1 0 0 0 0 0 0 0
1 1 0 0 1 0 0 0 1 0 0 0 0 0 0
1 1 0 0 0 1 0 0 0 1 0 0 0 0 0
1 1 0 0 0 0 1 0 0 0 1 0 0 0 0
1 1 0 0 0 0 0 0 0 0 0 0 0 0 0
1 0 1 1 0 0 0 0 0 0 0 1 0 0 0
1 0 1 0 1 0 0 0 0 0 0 0 1 0 0
1 0 1 0 0 1 0 0 0 0 0 0 0 1 0
1 0 1 0 0 0 1 0 0 0 0 0 0 0 1
1 0 1 0 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 0
1 0 0 0 1 0 0 0 0 0 0 0 0 0 0
1 0 0 0 0 1 0 0 0 0 0 0 0 0 0
1 0 0 0 0 0 1 0 0 0 0 0 0 0 0
1 0 0 0 0 0 0 0 0 0 0 0 0 0 0



Variation in theta by time and by group

Group 1	Group 2	Group 3
1 2 3 4 5	6 7 8 9 10	11 12 13 14 15
2 3 4 5	7 8 9 10	12 13 14 15
3 4 5	8 9 10	13 14 15
4 5	9 10	14 15
5	10	15

Model {theta(*T*)}

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

Group 1	Group 2	Group 3
1 2 3 4 5	6 7 8 9 10	11 12 13 14 15
2 3 4 5	7 8 9 10	12 13 14 15
3 4 5	8 9 10	13 14 15
4 5	9 10	14 15
5	10	15

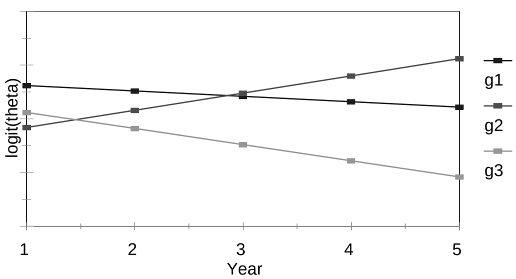
Model {theta(*g* + *T*)}

1 1 0 1
1 1 0 2
1 1 0 3
1 1 0 4
1 1 0 5
1 0 1 1
1 0 1 2
1 0 1 3
1 0 1 4
1 0 1 5
1 0 0 1
1 0 0 2
1 0 0 3
1 0 0 4
1 0 0 5

Group 1					Group 2					Group 3				
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	2	3	4	5		7	8	9	10		12	13	14	15
		3	4	5			8	9	10			13	14	15
			4	5				9	10				14	15
				5					10					15

Model {theta(*g**T*)}

```
1 1 0 1 1 0
1 1 0 2 2 0
1 1 0 3 3 0
1 1 0 4 4 0
1 1 0 5 5 0
1 0 1 1 0 1
1 0 1 2 0 2
1 0 1 3 0 3
1 0 1 4 0 4
1 0 1 5 0 5
1 0 0 1 0 0
1 0 0 2 0 0
1 0 0 3 0 0
1 0 0 4 0 0
1 0 0 5 0 0
```



Time trend in theta by groups
Additive model with interactions

Design Matrix Manipulation

- Add and delete columns
- Products of columns or copy a column
- Intercept or trend covariates
- Identity matrix
- Time or group indicator variables
- Covariates or individual covariate names
- Functions of columns and/or individual covariates
- Copy values or rotate column up/down
- Paste values from clipboard
- Retrieve columns from previous models

- Separate FORTRAN code
- Runs as a separate process in a different thread
- Can be used separately from interface program

- Encounter histories parsed to compute probability as function of parameters
- Numerical optimization of likelihood with quasi-Newton algorithm
- Singular value decomposition of information matrix to obtain VC matrix and rank

Features of Results Browser

- Retrieve PIMs and Design Matrix of models to construct a new model
- Retrieve full output
- Retrieve parameter estimates
- Retrieve variance-covariance matrix
- Output to a NotePad window, to Excel, to the clipboard, or printed directly
- Graphics

Hypothesis Tests

- Likelihood ratio tests
- Analysis of Deviance (ANODEV)

- Program RELEASE
- Programs ESTIMATE/BROWNIE
- Parametric bootstrap with deviance or Pearson chi-square

- Model averaging
- Variance components estimation
- Quasi-likelihood to correct for overdispersion
- Bootstrap procedure

Model Selection
Older Approaches

- Forward selection
- Backward selection
- Best R^2
- All possible models

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Model Selection
Information-Theoretic Approach

- AIC
- Akaike's Information Criterion
- AIC = $-2\log(\mathcal{L}(\beta)) + 2K$
- MARK ranks models based on their AIC values

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Burnham and Anderson (1998)

- AIC = $-2\log(\mathcal{L}(\beta)) + 2K$
- $AIC_c = -2\log(\mathcal{L}(\beta)) + 2K + 2K(K+1)/(n-K-1)$
- $\Delta AIC_c = AIC_c - \min AIC_c$
- $w_i = \exp(-\Delta_i/2)/\sum \exp(-\Delta_j/2)$

Model Averaging

- Incorporate model selection uncertainty into parameter variances
- Obtain proper confidence interval coverage

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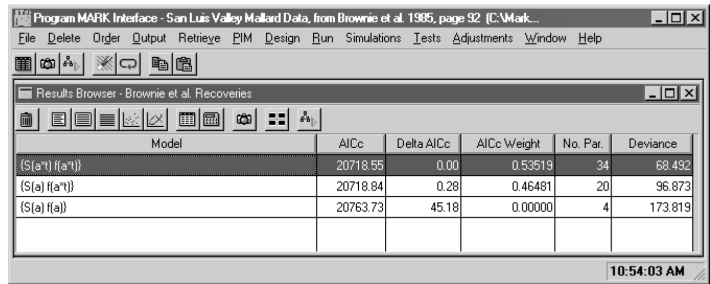
Model Averaging



Model	AICc	Delta AICc	AICc Weight	No. Par.	Deviance
{S(a*t) f(a*t)}	20718.55	0.00	0.53519	34	68.492
{S(a) f(a*t)}	20718.84	0.28	0.46481	20	96.873
{S(a) f(a)}	20763.73	45.18	0.00000	4	173.819

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San Luis Valley Mallard Data, from Brownie et al. 1985, page 92

Survival Parameter (S) Adults Parameter 1

Model	Weight	Estimate	Standard Error
{S(a*t) f(a*t)}	0.53519	0.5790623	0.1140629
{S(a) f(a*t)}	0.46481	0.6522073	0.0120278
Weighted Average		0.6130607	0.0666361
Unconditional SE			**0.0827347**

95% CI for Wgt. Ave. Est. (logit trans.) is 0.4443819 to 0.7583747
Percent of Variation Attributable to Model Variation is 35.13%

Variance Components

- Sampling Variance, e.g., Standard Errors
- Process Variance, e.g., Variance across time
- Sum is Total Variance

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Process Variance σ^2

- Needed for valid Population Viability Analysis
- Forecasting population trends

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Variance Components

- Mean
- Linear Trend
- User-defined linear function

Example

Beta-hat	SE(Beta-hat)
0.362423	0.038221

S-hat	SE(S-hat)	S-tilde	SE(S-tilde)	RMSE(S-tilde)
0.377622	0.164105	0.382632	0.096390	0.096520
0.620369	0.193238	0.493115	0.100578	0.162203
...				
0.097701	0.060745	0.124123	0.051765	0.058118
0.249997	0.169099	0.291019	0.098057	0.106292

Estimate of σ^2 = 0.0135 with 95% CI (0.0027 to 0.0666)

- Animal fates are independent
- Binomial variation
- Violations lead to overdispersion

Quasi-likelihood Estimation

- Correction for overdispersion
- Variance inflation factor $\hat{c}$
- QAIC = -2log(ℒ(β))/$\hat{c}$ + 2*K*
- $QAIC_c$ = -2log(ℒ(β))/$\hat{c}$ + 2*K* + 2*K*(*K* + 1)/(*n* - *K* - 1)
- $SE(\hat{\theta}) = \sqrt{\frac{Var(\hat{\theta})}{\hat{c}}}$

Goodness of Fit

- Estimate of over dispersion, *c*
- Rejection of global model as fitting the data

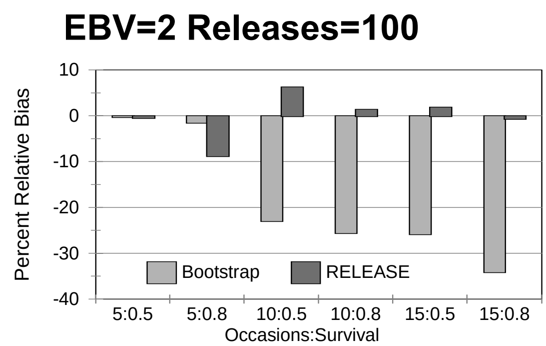
Decide if *c*>1 for global model

- Program RELEASE
- Programs ESTIMATE/BROWNIE
- Deviance
  -2log(ℒ model) - -2log(ℒ saturated)
- Bootstrap procedure

Bootstrap Procedure

- Compute estimates from data
- Compute parametric bootstraps from estimates
- Determine likelihood of observed deviance
- Estimate $\hat{c}$ as observed deviance divided by mean of bootstrap deviances (or Pearson chi-square)

Goodness of Fit – Bootstrap Approach



- Help file
- WWW
  - Gentle introduction
    - Evan Cooch
  - Theory description
    - David Anderson
    - Ken Burnham
- Various other publications

http://www.cnr.colostate.edu/~gwhite

- Single 13Mb zipped setup file
- Nine 1.4Mb zipped setup disks
- Update zip file of executable files

➔ **Includes help file and examples**