# Violations of assumptions in
# INTEGRATED POPULATION MODELS:
# Consequences and Diagnostics

Count data

Reproductive data

Survival data

R

$S_J$  $S_A$

p

y

N

M

C

# INTEGRATED MODELS

**Data type B**                                    **Data  type A**
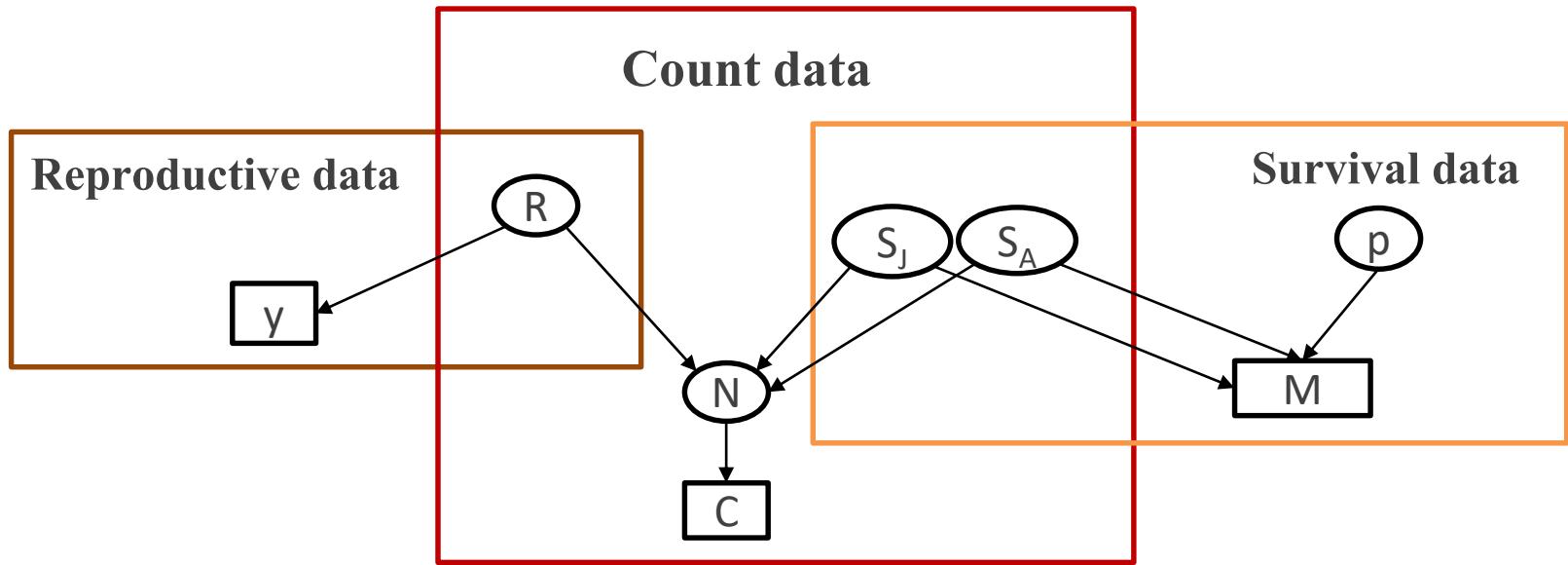


**Likelihood B → P2**                    **Likelihood A → P1**
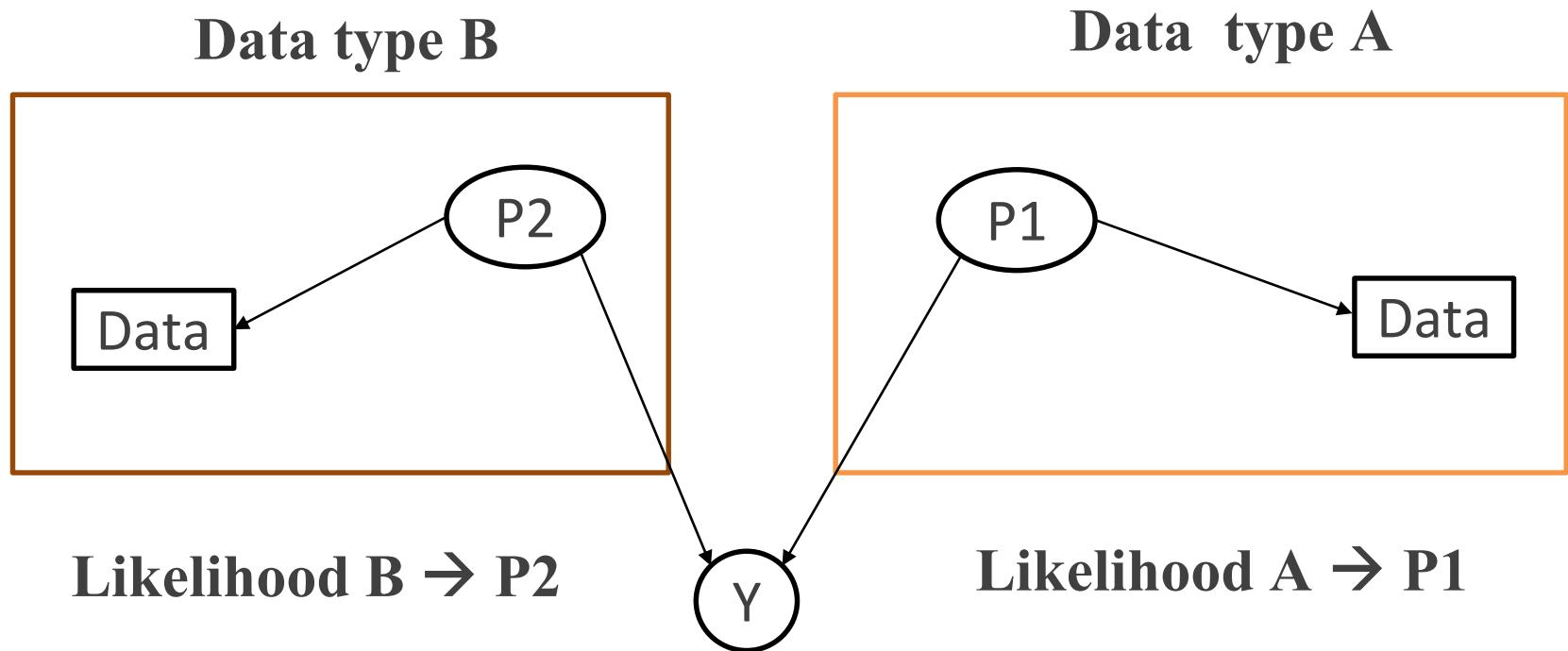
**Likelihood Model** = Likelihood **B** **x** Likelihood **A**

# INTEGRATED MODELS

**Data type B**

**Data type A**



**Likelihood B → P2**

**Likelihood A → P1**

**Data type C**
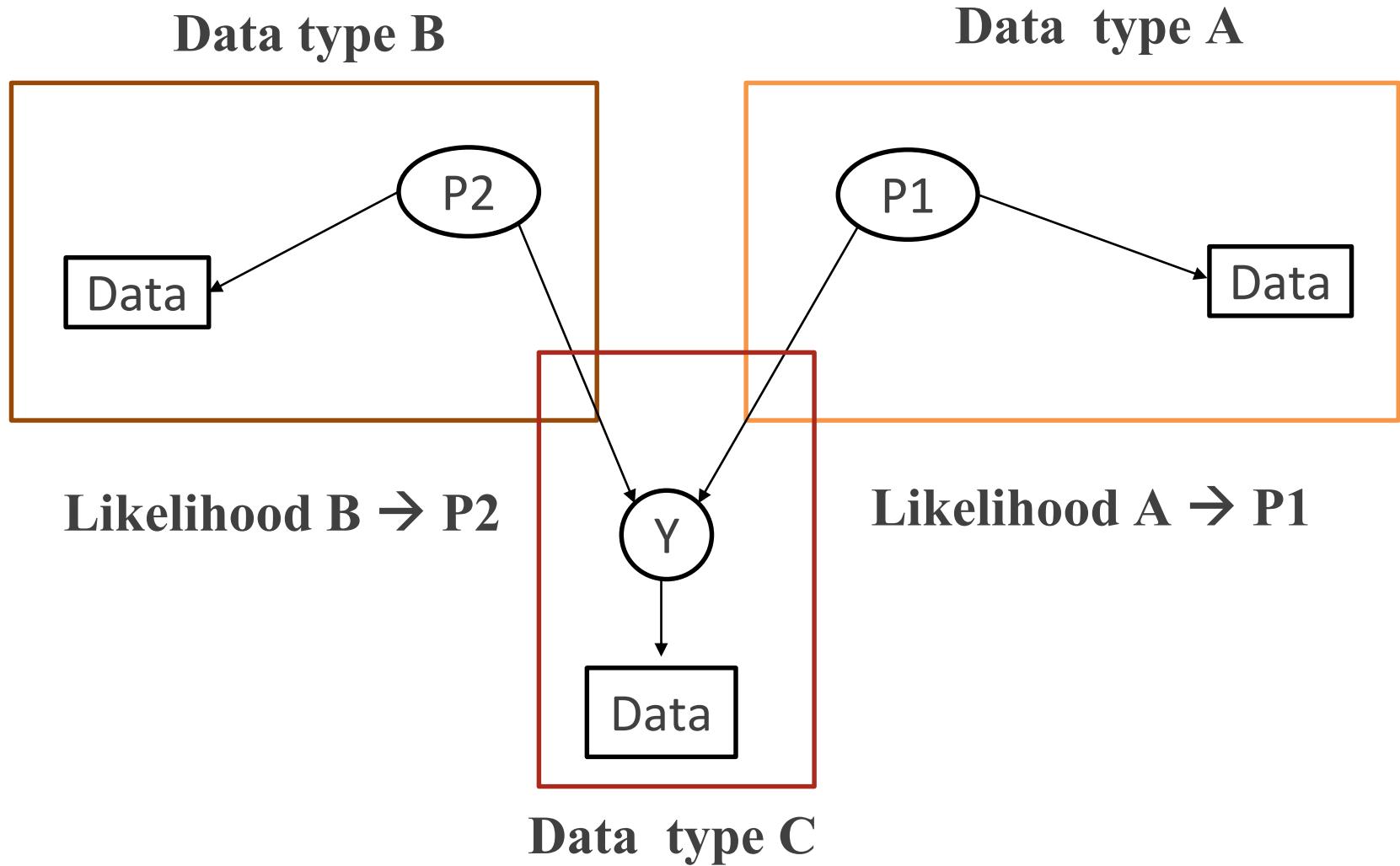
**Likelihood Model** = Likelihood **B** x Likelihood **A** x Likelihood **C**

# THE NEED TO PREDICT POPULATION DYNAMICS
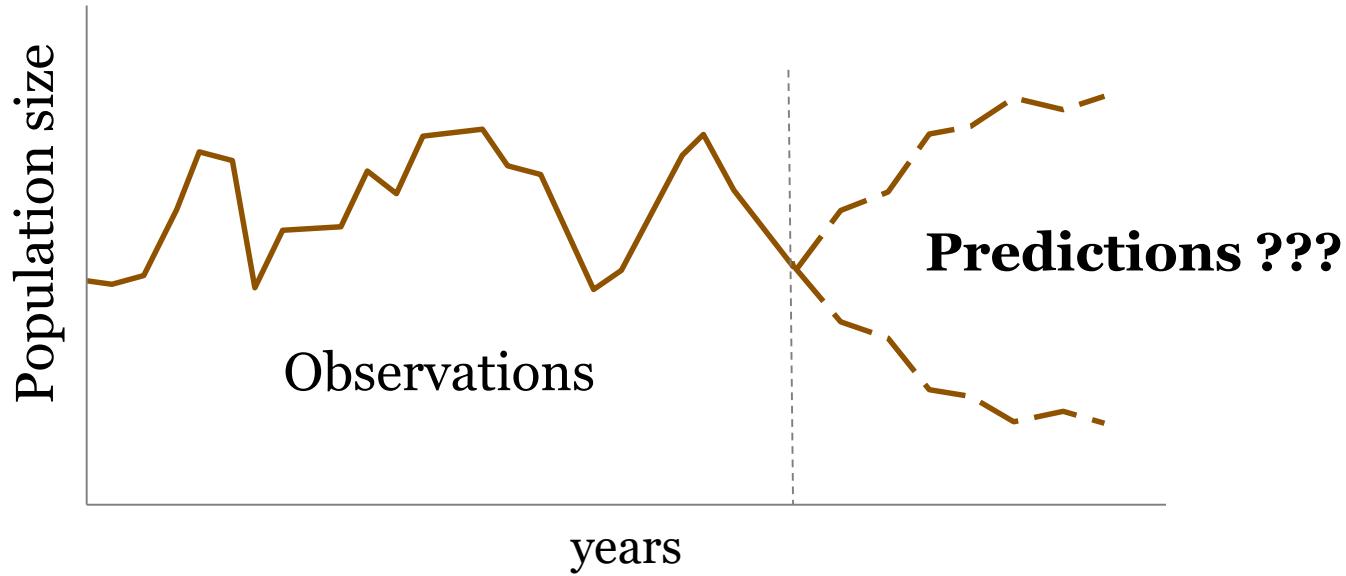


**Conservation**
**Management**
**Fundamental research**

# POPULATION MODELS



$$\text{At } t$$

$$\begin{array}{cc} \text{juvenile} & \text{adult} \end{array}$$

At t+1
$$\begin{array}{c} \text{juvenile} \\ \text{adult} \end{array} \begin{bmatrix} S_J * R & S_A * R \\ \\ S_J & S_A \end{bmatrix}$$
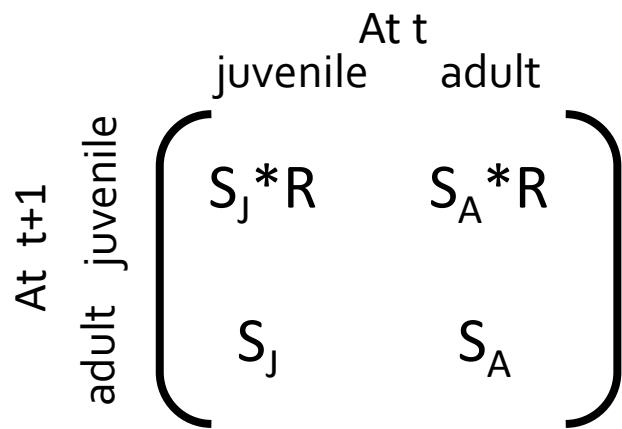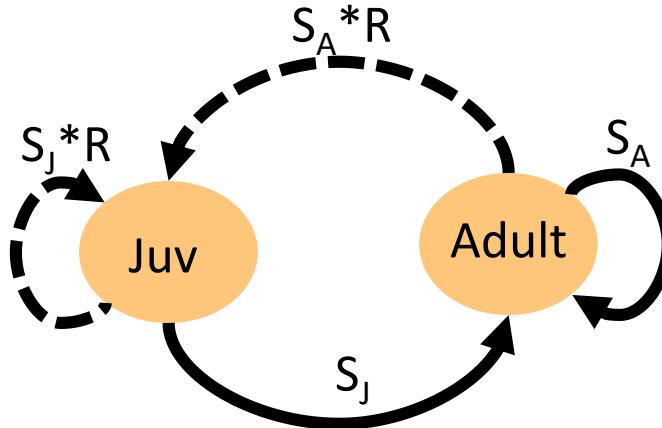
NJuv [t-1]  ~ dpois(R* N[t-1])

Nadj [t]      ~ dbin  (SJ , NJuv[t-1])
Nad [t]       ~ dbin  (SA, N[t-1])

N[t] = Nadj[t] + Nad[t]

# POPULATION MODELS
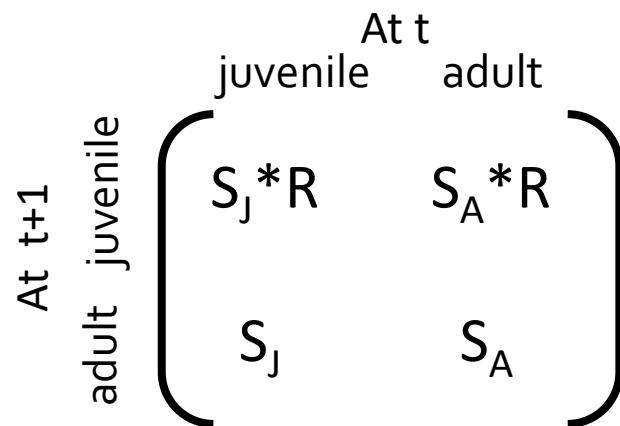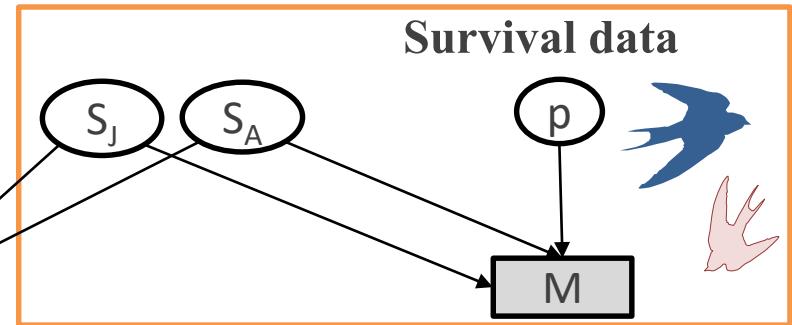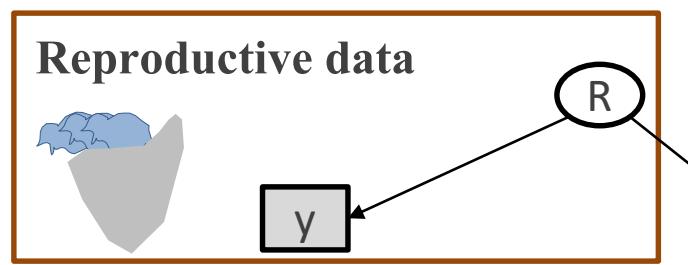




Reproductive data

Survival data

$$\begin{array}{c} \text{At } t \\ \text{juvenile} \quad \text{adult} \\ \begin{pmatrix} S_J * R & S_A * R \\ \\ S_J & S_A \end{pmatrix} \end{array}$$

At t+1   juvenile   adult

NJuv [t-1]   ~ dpois(R* N[t-1])

Nadj [t]      ~  dbin  (SJ , NJuv[t-1])
Nad [t]       ~  dbin  (SA, N[t-1])

N[t] = Nadj[t] + Nad[t]

# INTEGRATED POPULATION MODELS



Count data

Reproductive data

R

y

$S_J$  $S_A$

p

Survival data

N

C

M

At t

juvenile     adult

$$\begin{pmatrix} S_J*R & S_A*R \\ \\ S_J & S_A \end{pmatrix}$$

At t+1    juvenile

adult
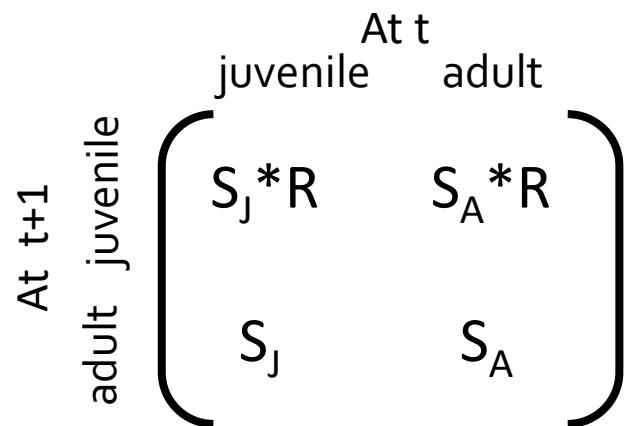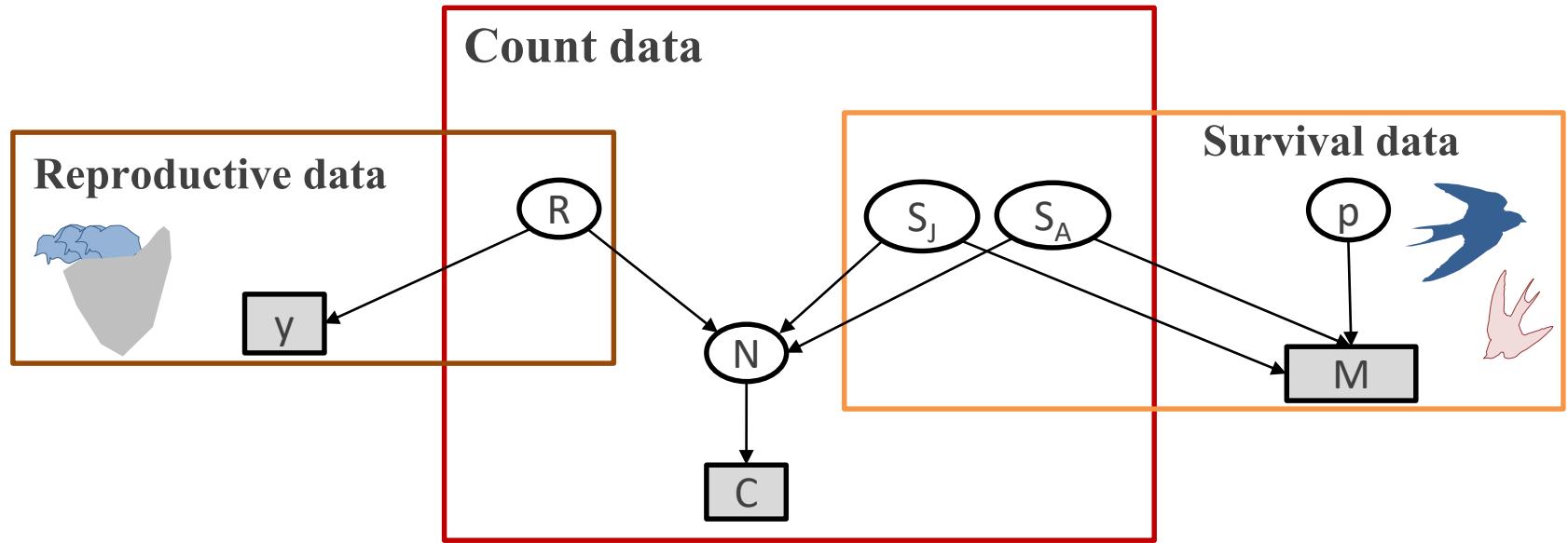
NJuv [t-1]  ~ dpois(R* N[t-1])

Nadj [t]     ~  dbin  (SJ , NJuv[t-1])
Nad [t]      ~  dbin  (SA, N[t-1])

N[t] = Nadj[t] + Nad[t]

# INTEGRATED POPULATION MODELS
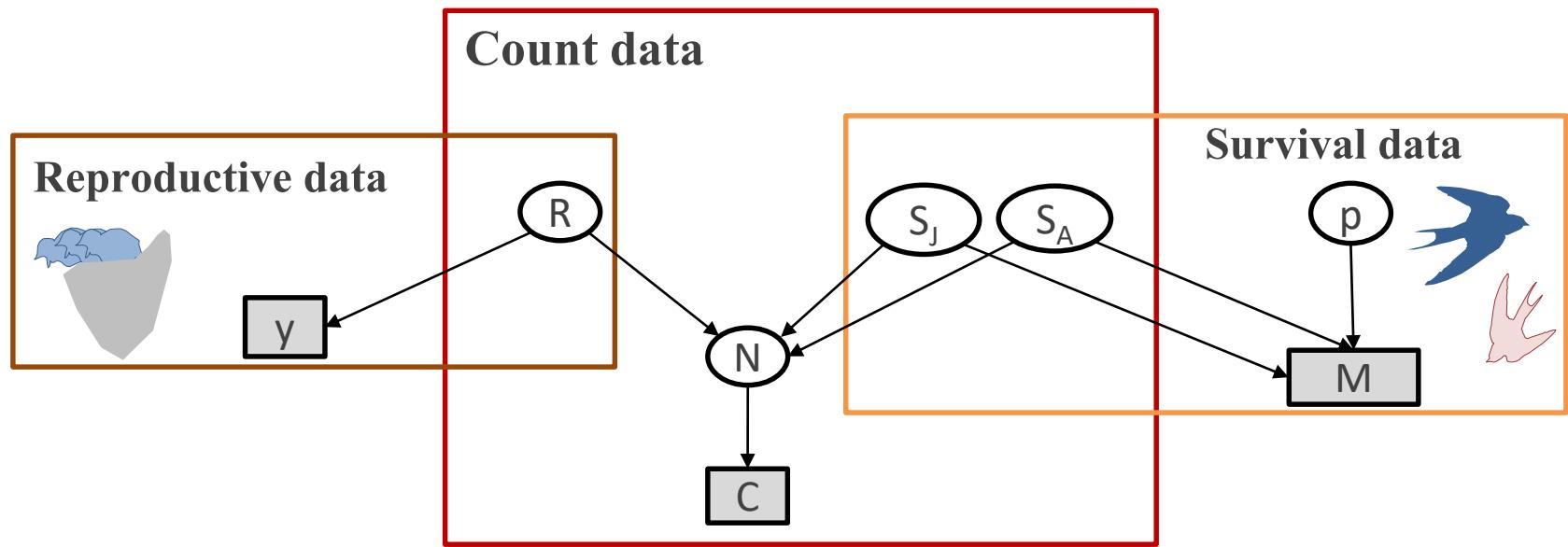


**Integrated models = combine data**

Joint Likelihood = $\prod$ likelihood of different datasets

**If datasets are independent!**

# INTEGRATED POPULATION MODELS



**Integrated models = combine data**
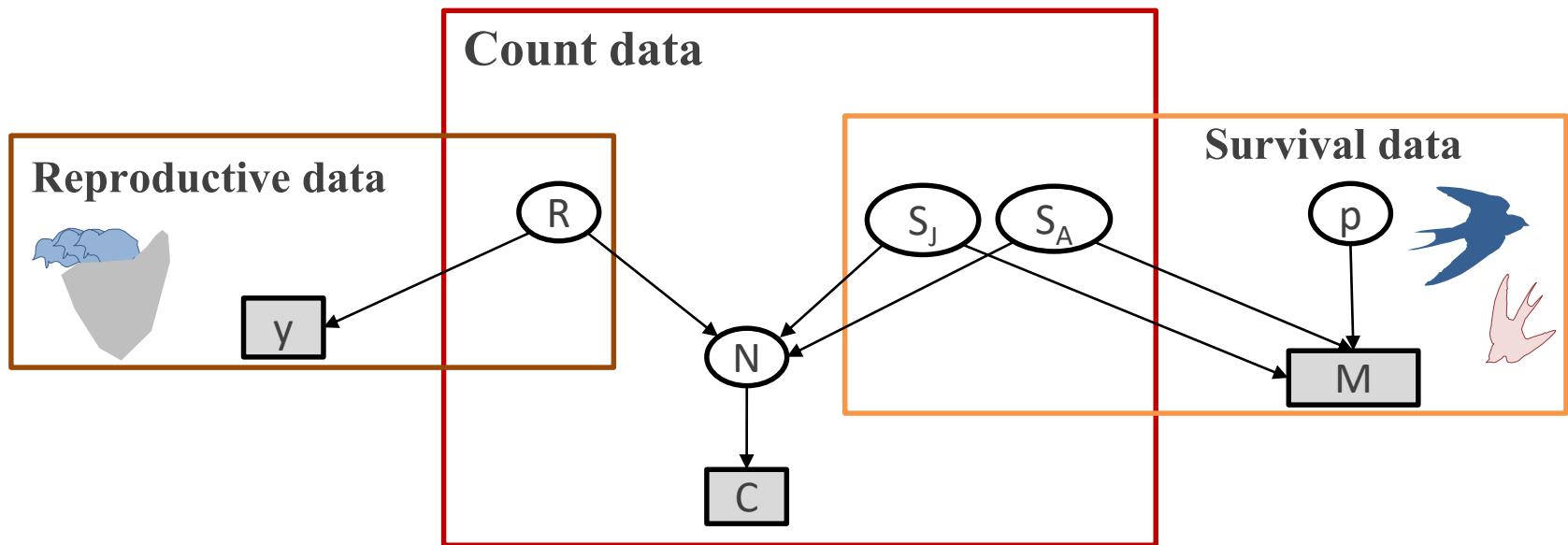
**Advantages:**    - lower uncertainty
                   - estimate supplemental parameter

## Immigration (for instance)

## Immigration (for instance)
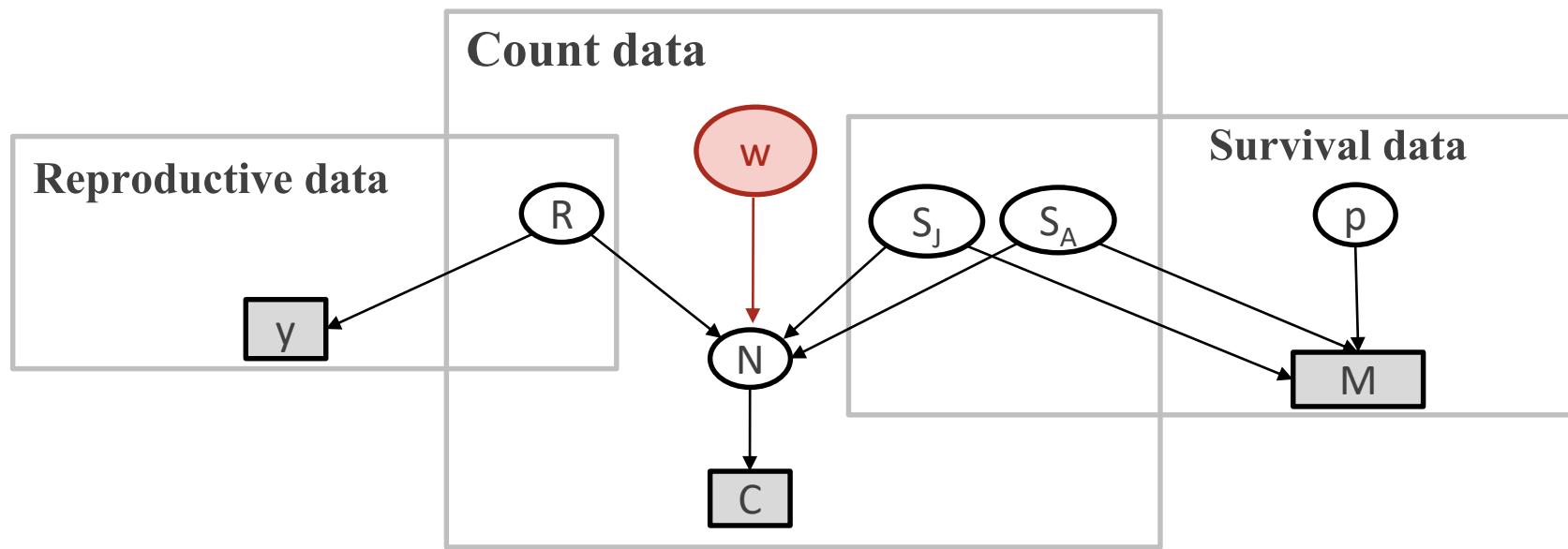


**BUT:   What if there is another mechanism that we do not know about?**

## Immigration (for instance)

Simple Survival model
IPM simple (no immigration)
IPM immigration
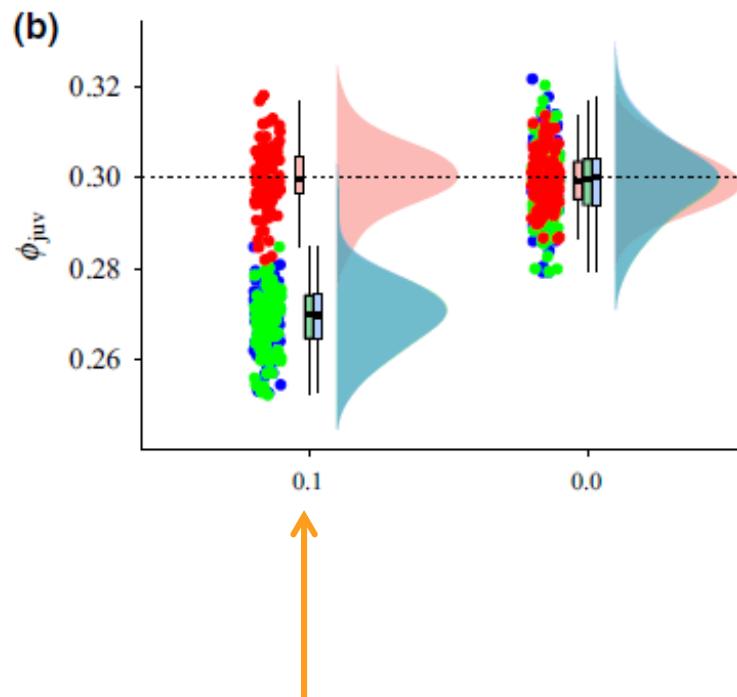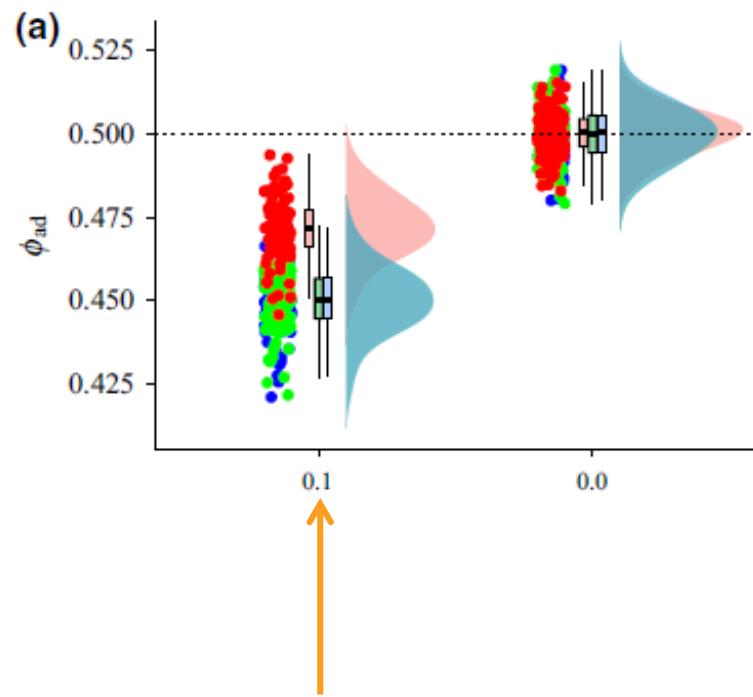


**BUT:   What if there is also mark loss?**

If some assumptions are violated, some parameters
are going to be biaised

If some assumptions are violated, some parameters
are going to be biaised

Assumptions:
- Independance of datasets
- Distributions of parameters
- Heterogeneity in parameters

**We also make many assumptions about the chosen
demographic model**
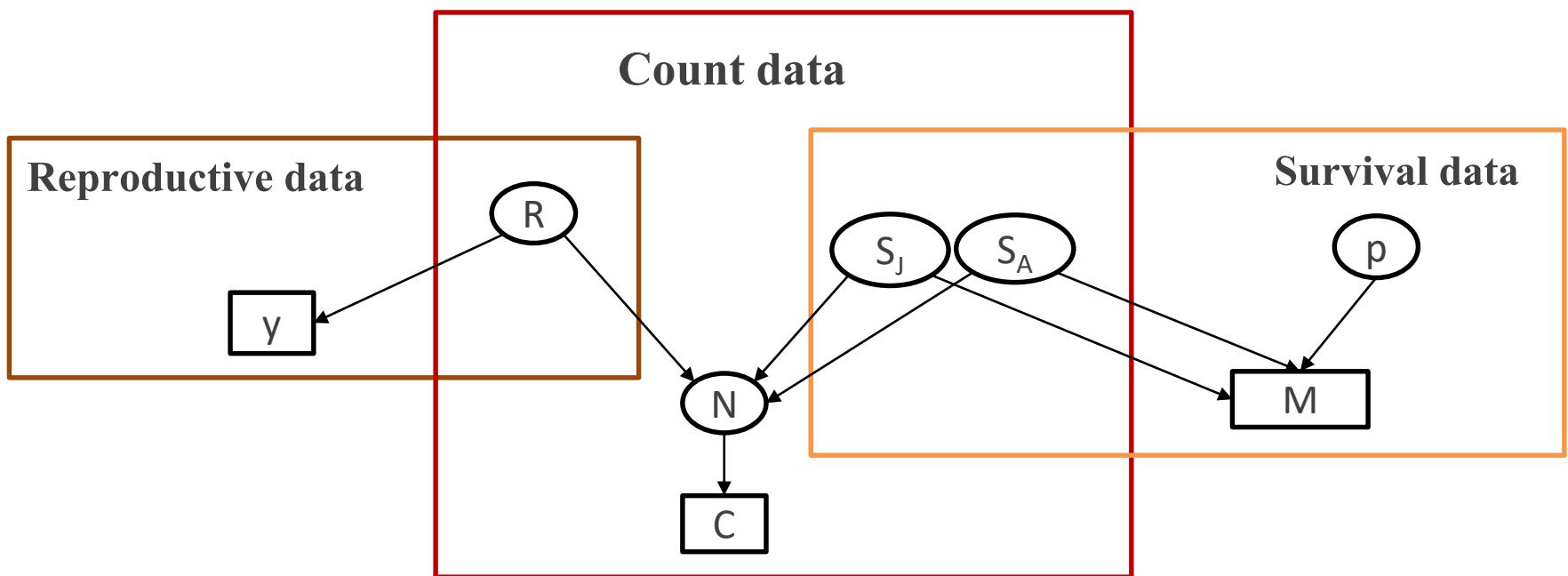
**BUT:   What are the consequences if???**

**BUT: What are the consequences if???**



Count data
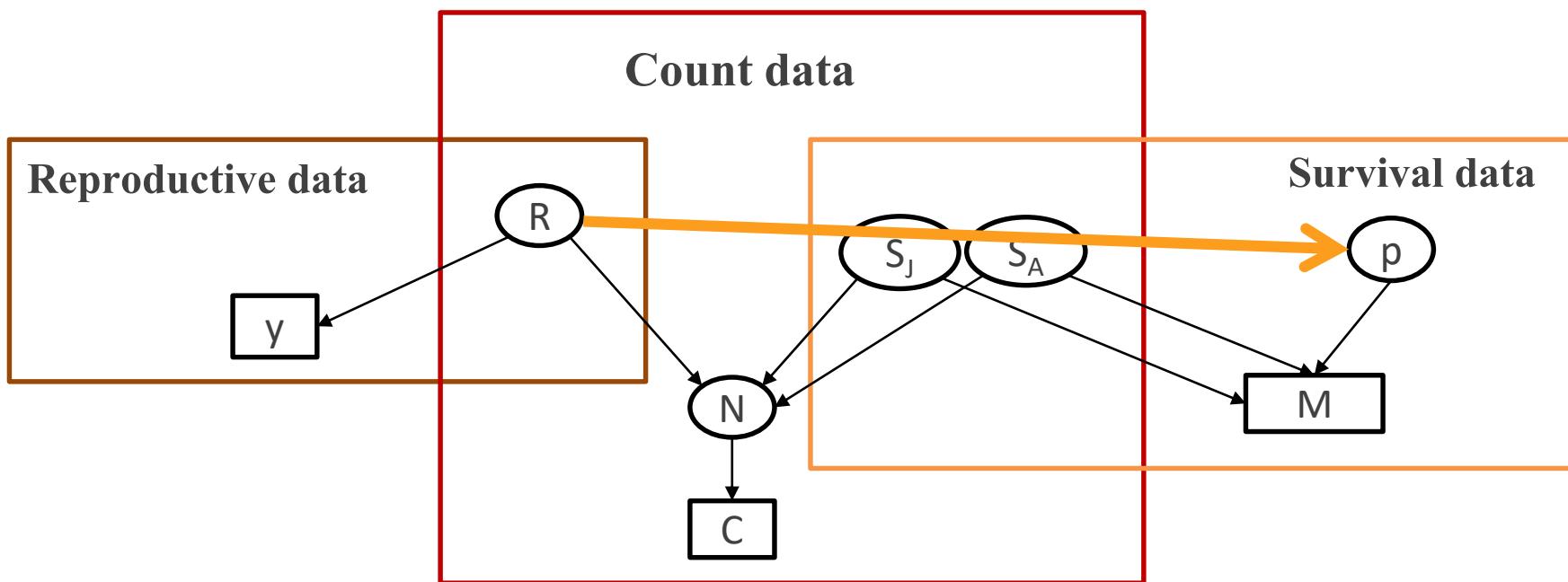
Reproductive data

Survival data

R

y

$S_J$  $S_A$

p

N

M

C

➤ Recapture depends on reproduction?

**BUT: What are the consequences if???**
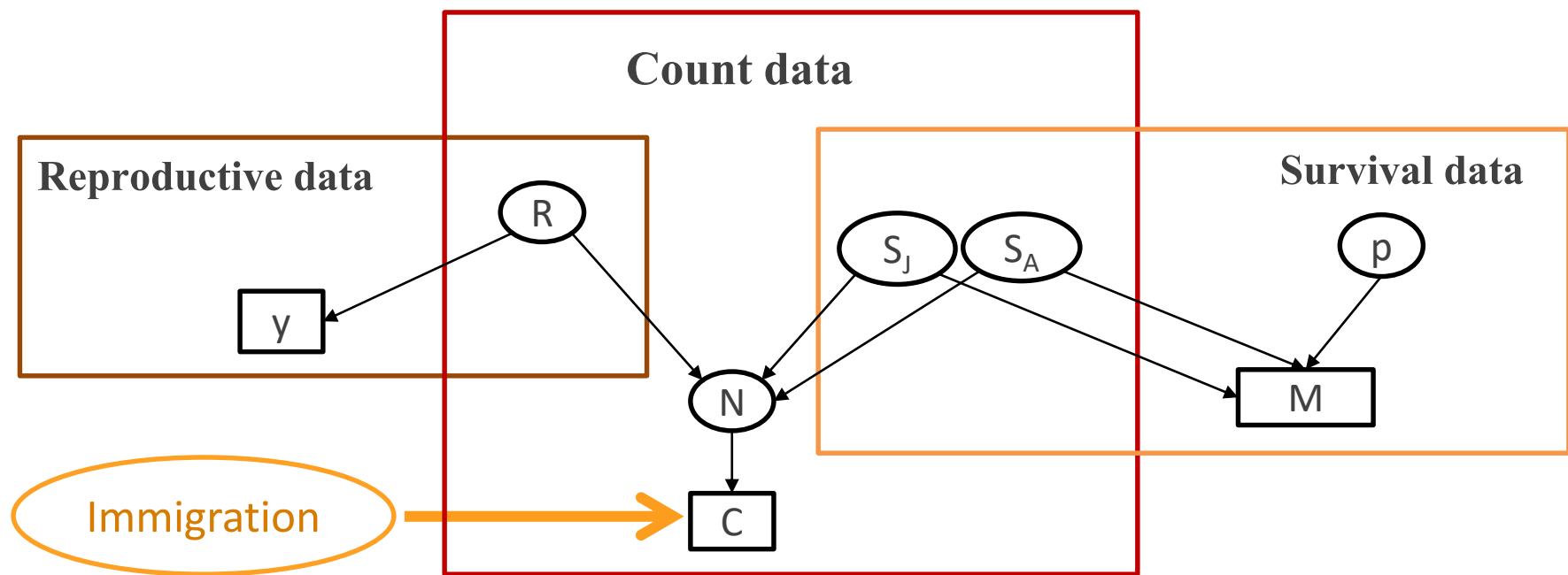


> ➢ Recapture depends on reproduction?
> ➢ Immigration?

# CLASSICAL IPMPOP

## BUT:   What are the consequences if???
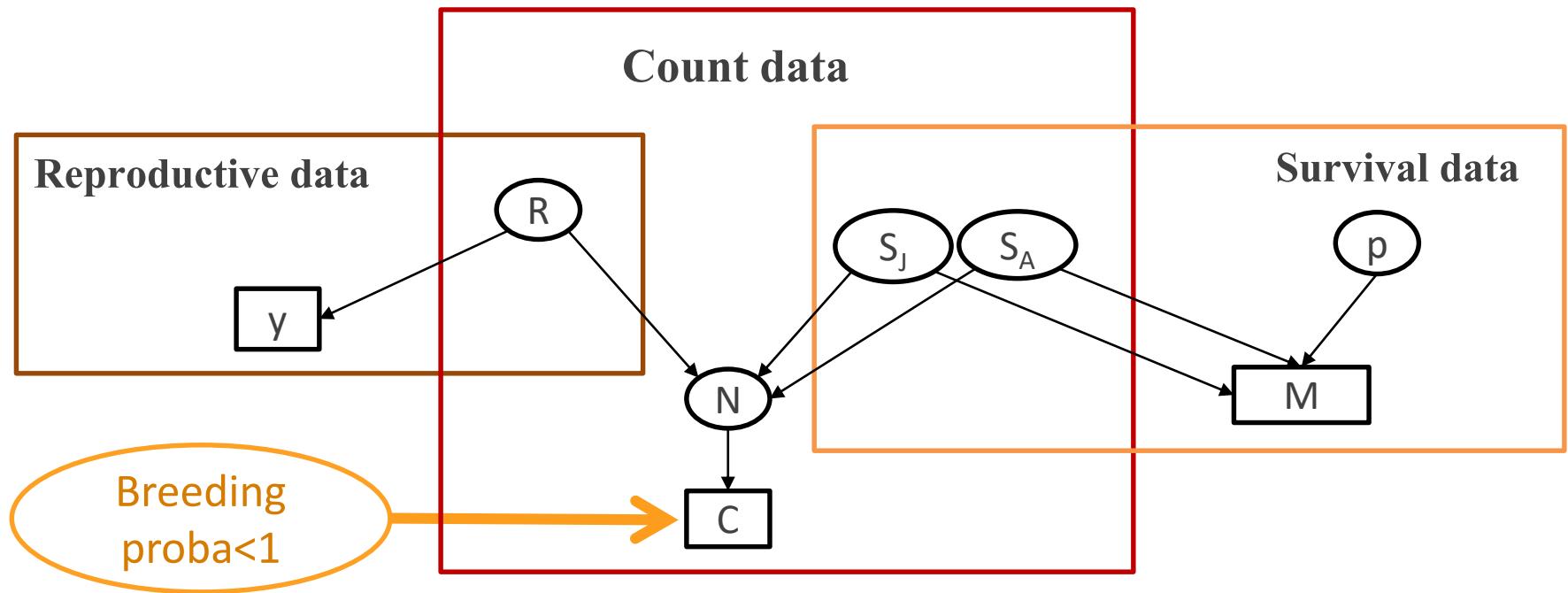


- ➢ Recapture depends on reproduction?
- ➢ Immigration?
- ➢ Presence of non-breeders

# CLASSICAL IPMPOP

BUT:   What are the consequences if???
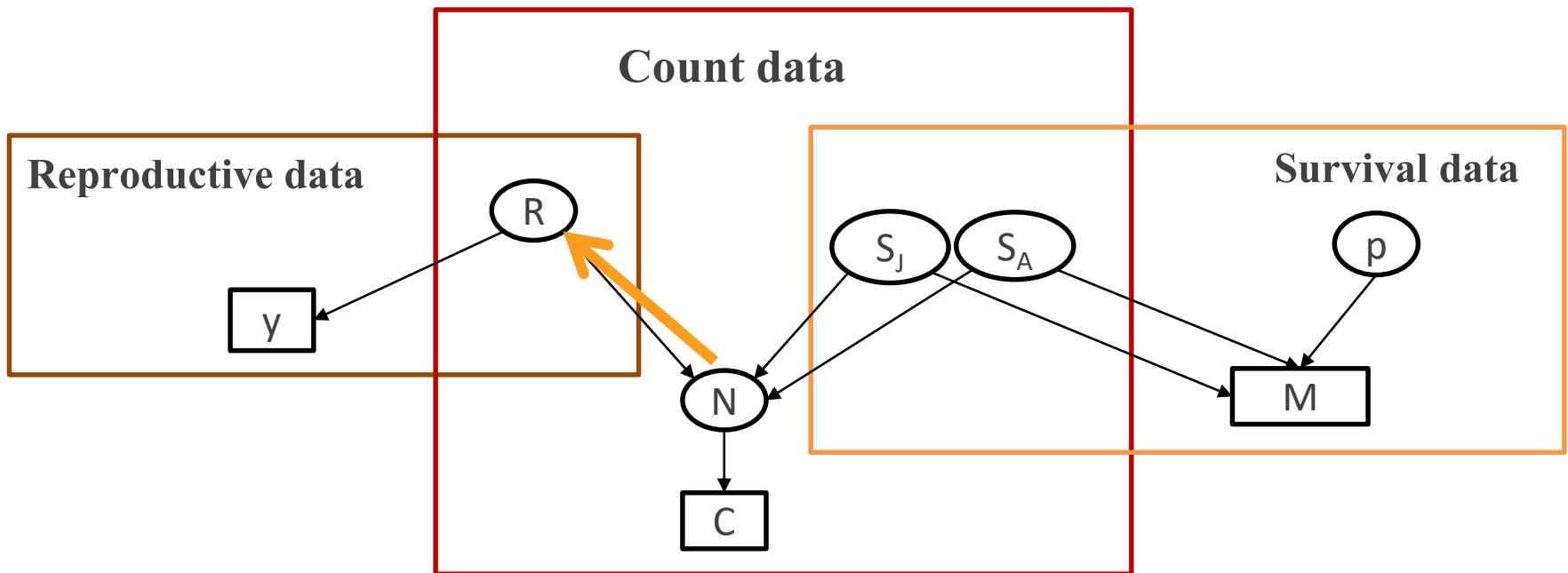


- ➢ Recapture depends on reproduction?
- ➢ Immigration?
- ➢ Presence of non-breeders
- ➢ Density-dependent effect

# 5 DATASETS ANALYZED WITH 3 TYPES OF MODELS

## Simulation of data:

1. Null Model
2. Recapture depends on reproduction
3. Immigration
4. Probability of reproduction <1
5. Density effect

## Analysis of data:



Count data

Reproductive data

Survival data

R

$S_J$    $S_A$    p

y

N

M

Immigration

C

Indpdt models

Classical (biased) IPM

True IPM
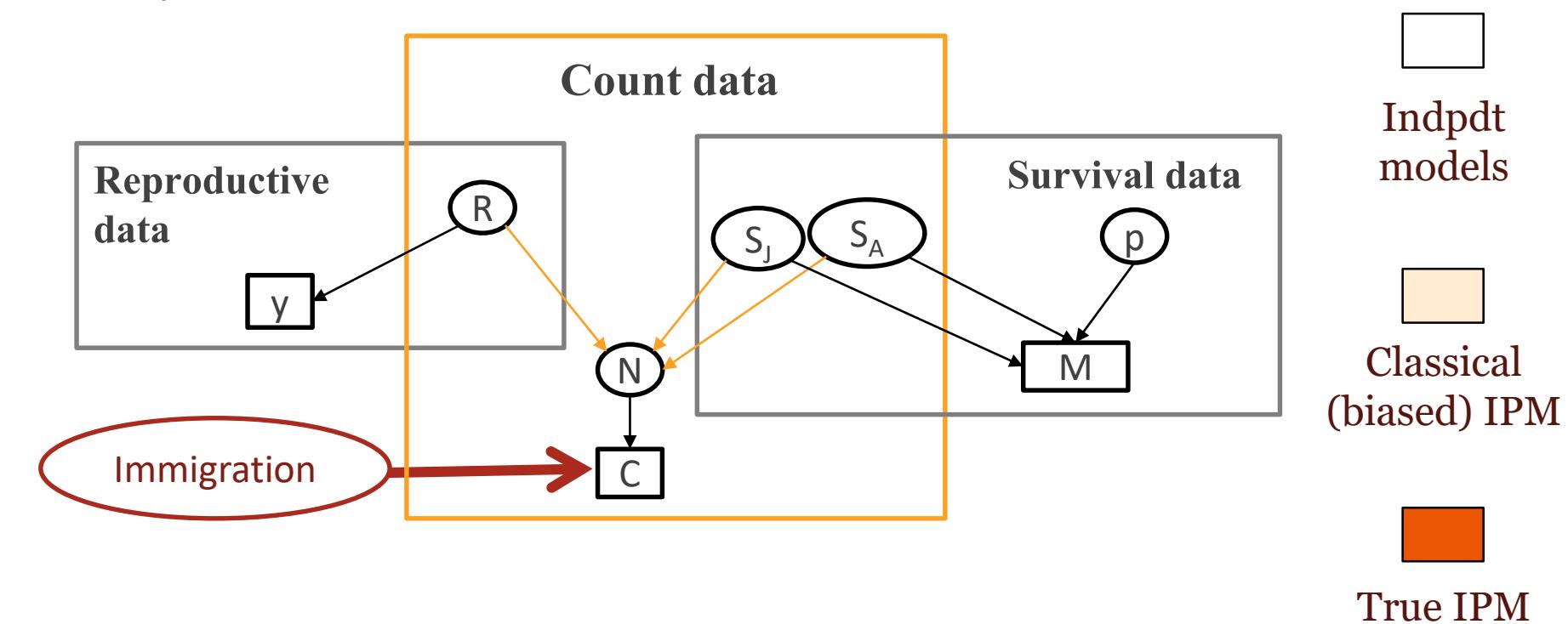
# 5 DATASETS ANALYZED WITH 3 TYPES OF MODELS
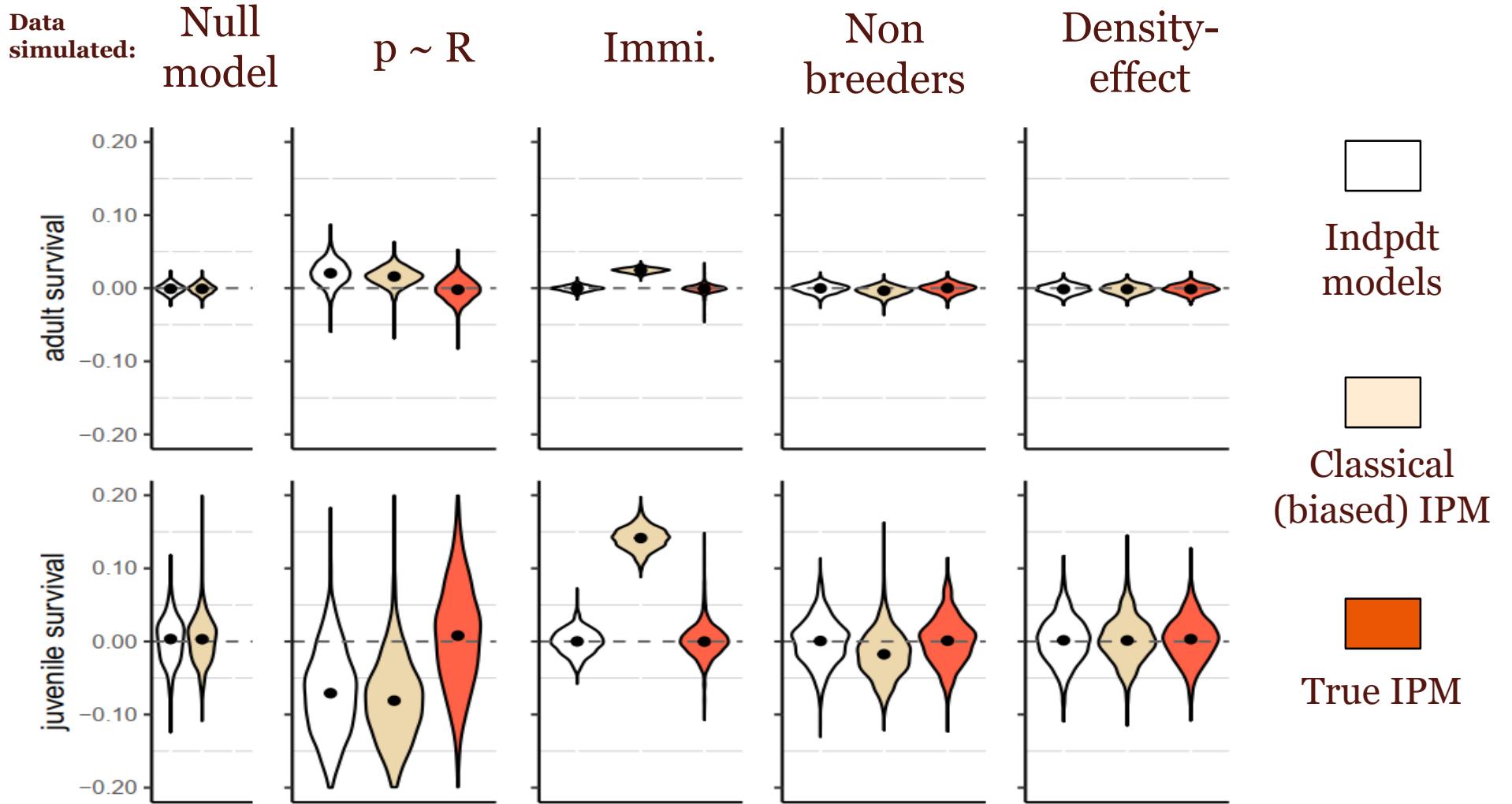


Long-lived species:
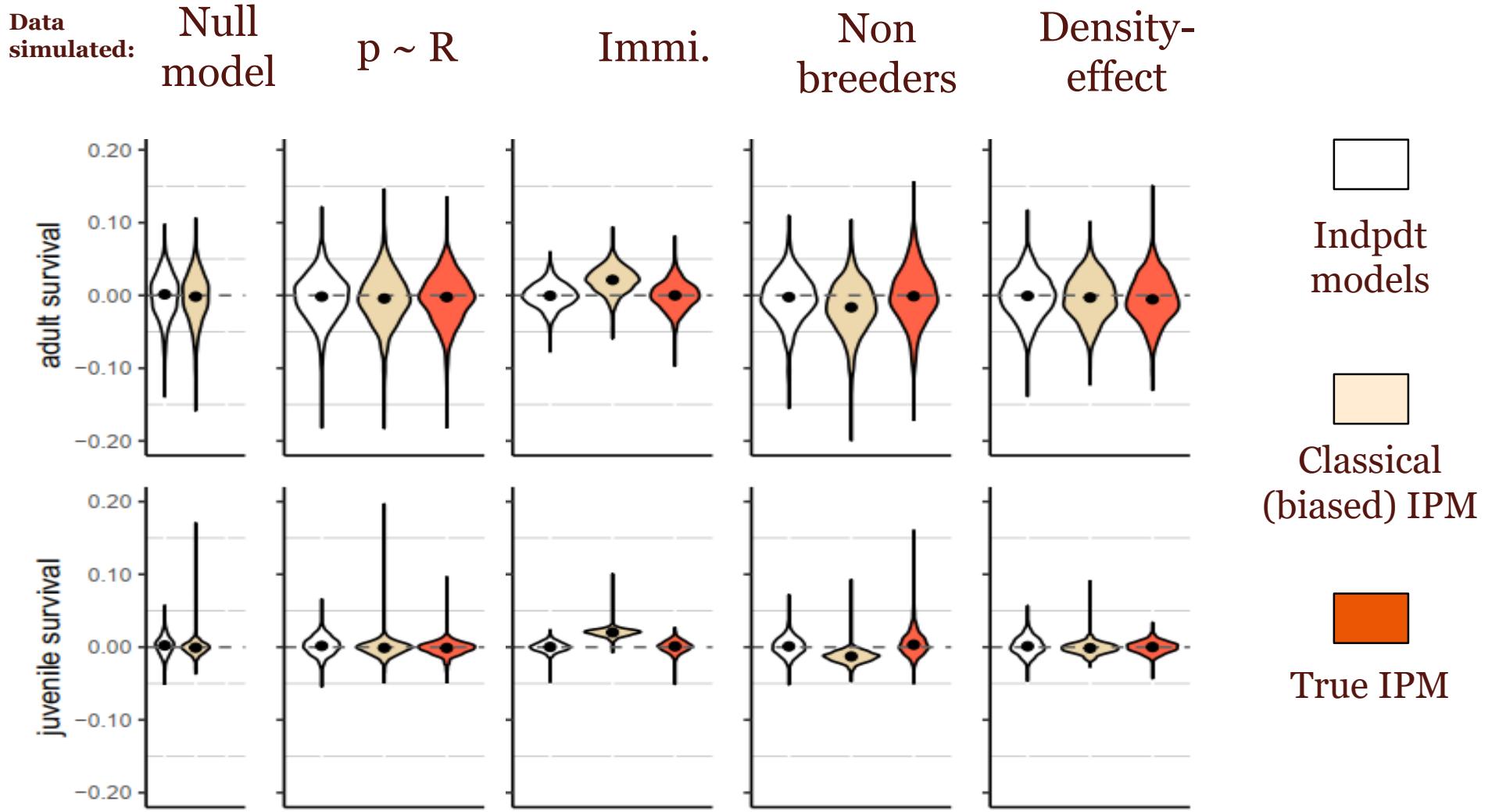
Short-lived species:

**How do I know when my model is wrong?**

| | | GOF: survival | GOF: Reproduction | GOF: count | Comparison: CMR model | Residuals | LL Profile |
|---|---|---|---|---|---|---|---|
| **simple IPM** | Null | 4 | 3 | 4 | 2 | 73 | 29 |
| | 1. Recapture breeders | 20 | 3 | 4 | 2 | 78 | 25 |
| | 2. Immigration | 100 | 100 | 100 | 100 | 100 | 88 |
| | 3. Non-breeders | 5 | 3 | 5 | 5 | 67 | 29 |
| | 4. Density effect | 4 | 5 | 6 | 2 | 69 | 24 |

# Conclusion

1.  For most assumptions, the bias is relatively small. Do simple models whenever possible

2.  Parameter with the highest uncertainty will be the one that will be biased → You cannot not know which assumption is violated

3.  Diagnostic tests are not sensitive to small bias

Solutions:
1.  Compare the results to independent models

2.  Do again your model with fewer data! If your model is correct, mean parameters should be similar…

vogelwarte.ch

**Michael SCHAUB**
**Daniel Turek**

**Thank you for your attention**
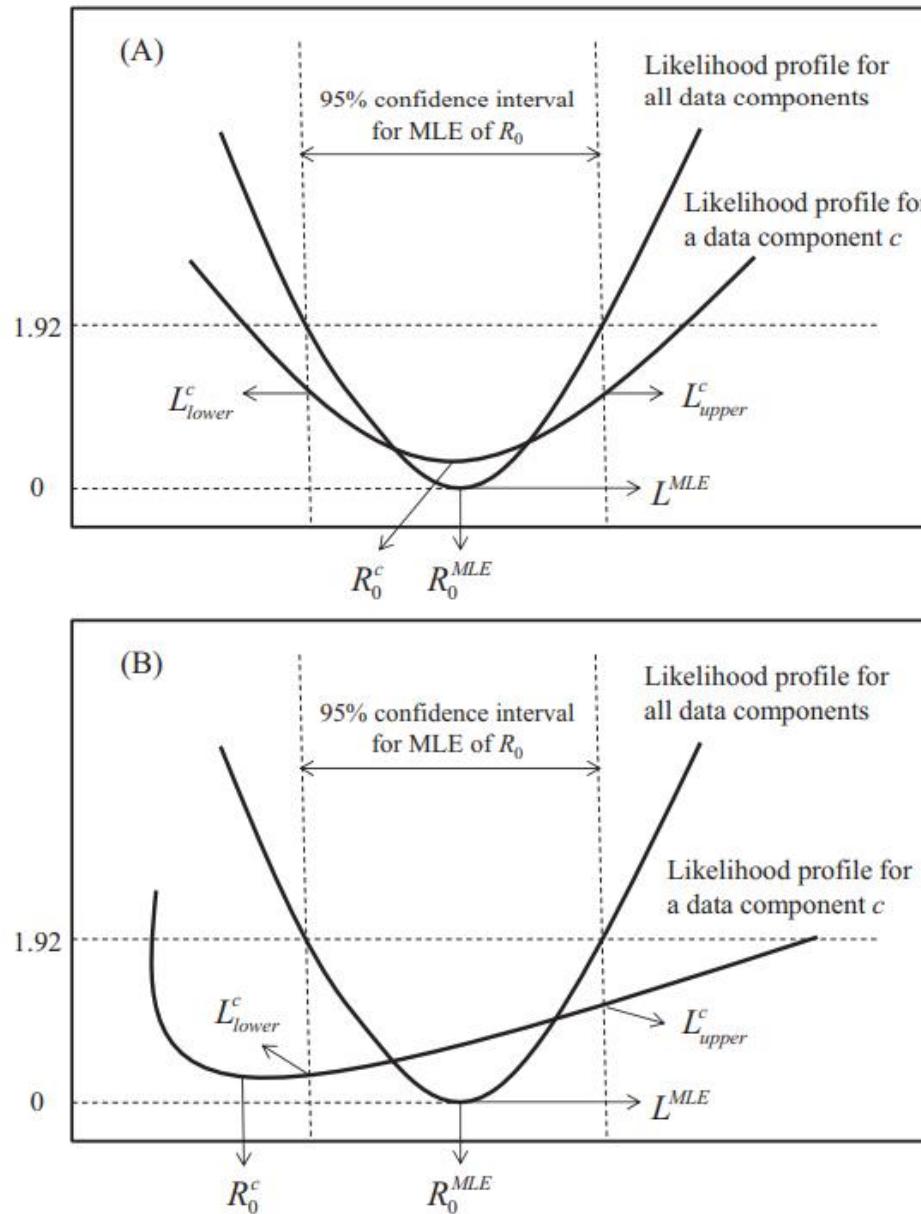
$$\varphi = \begin{cases} \max[(L^c_{\text{lower}} - L^{\text{MLE}}), \ (L^c_{\text{upper}} - L^{\text{MLE}})], & \text{if } R^c_0 \text{ is located within the 95\% confidence interval for } R^{\text{MLE}}_0 \\ \left| L^c_{\text{lower}} - L^c_{\text{upper}} \right|, & \text{otherwise} \end{cases}$$