Integrating toxicology and ecology in population-level risk assessment for wildlife: what data does your modeler really need?

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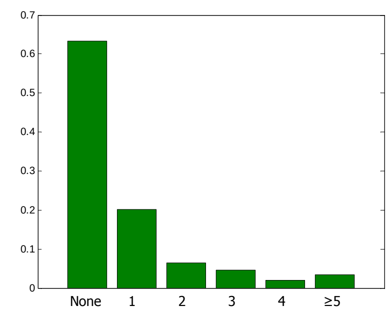

$$\begin{bmatrix} 1 & 0 & 0 & 0 \\ q_s & 0 & 1-q_s & 0 \\ 0 & (1-e)S & 0 & 1-(1-e)S \\ q_f & 0 & 1-q_f & 0 \end{bmatrix}$$

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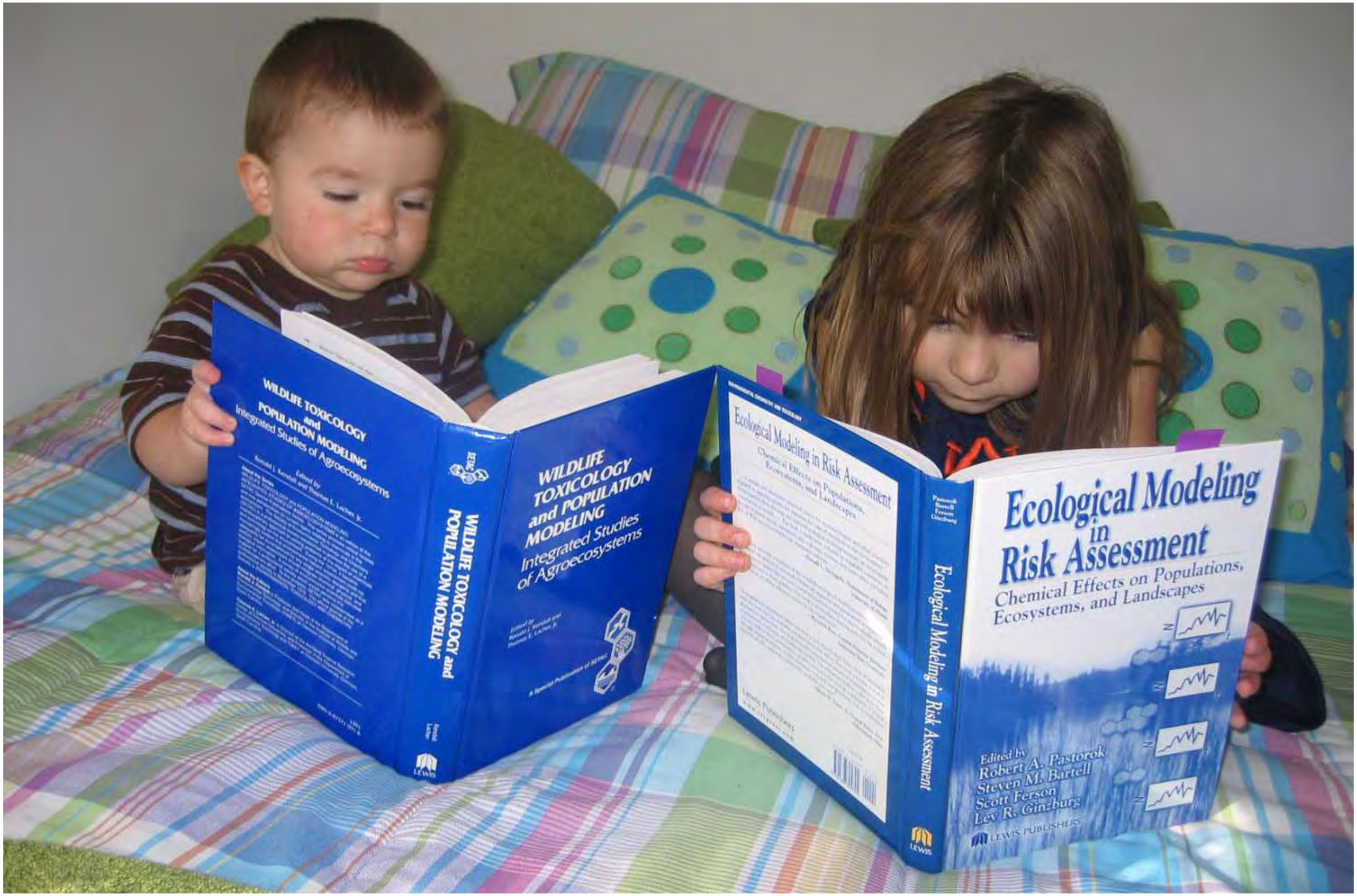
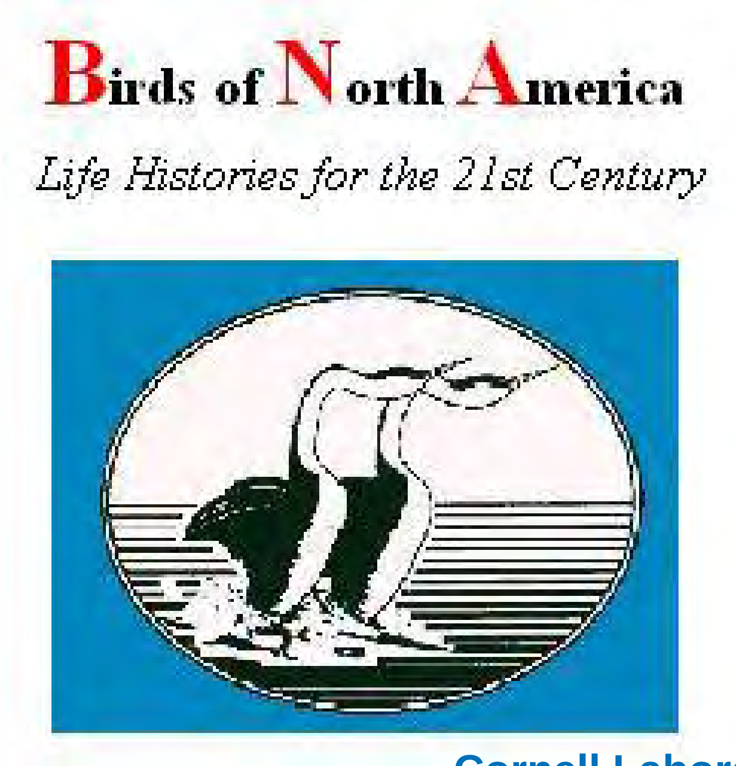


What data does a population modeler really need?

1. Estimated vital rates (survival, fecundity) in the absence of the stressor

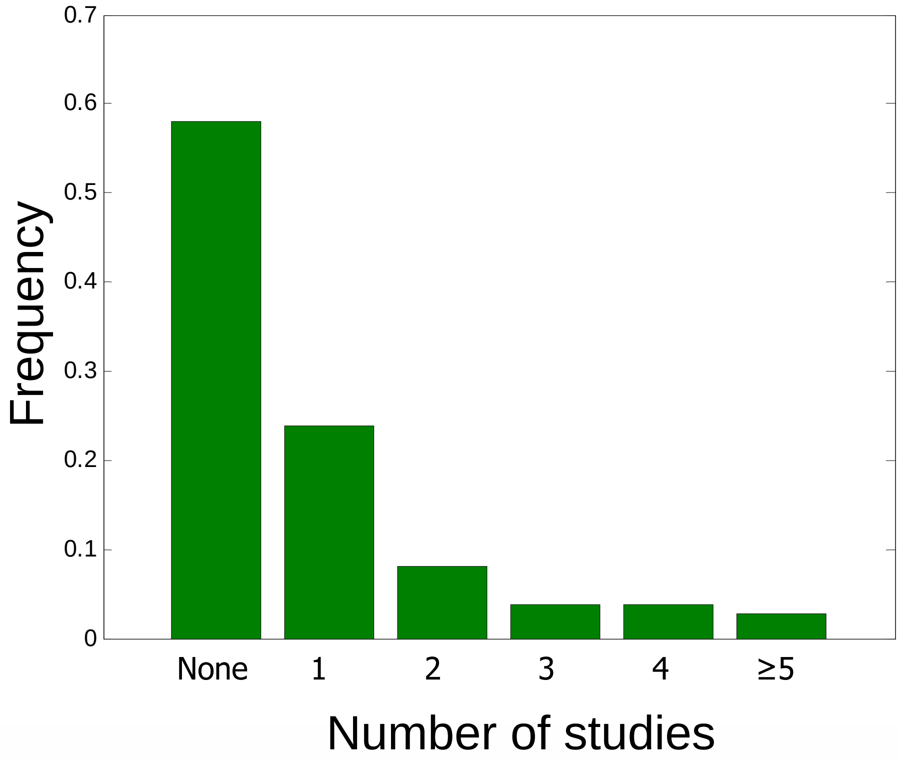
2. Estimated effects of the chemical stressor on vital rates

How much data are there?

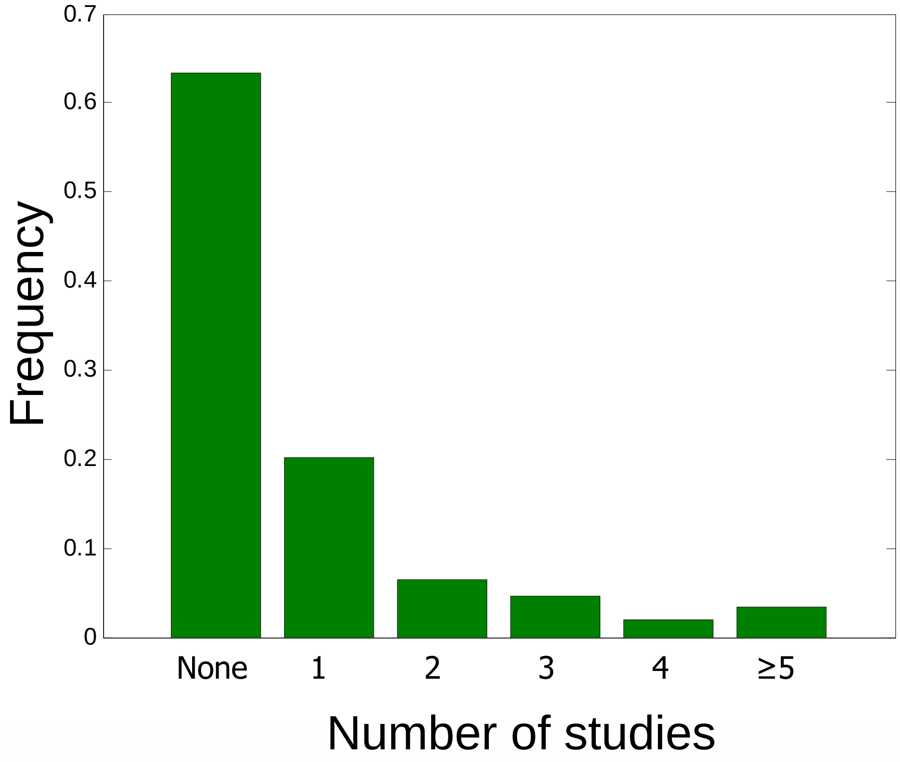


Cornell Laboratory of Ornithology
American Ornithologists' Union

Annual reproductive success



Annual survival



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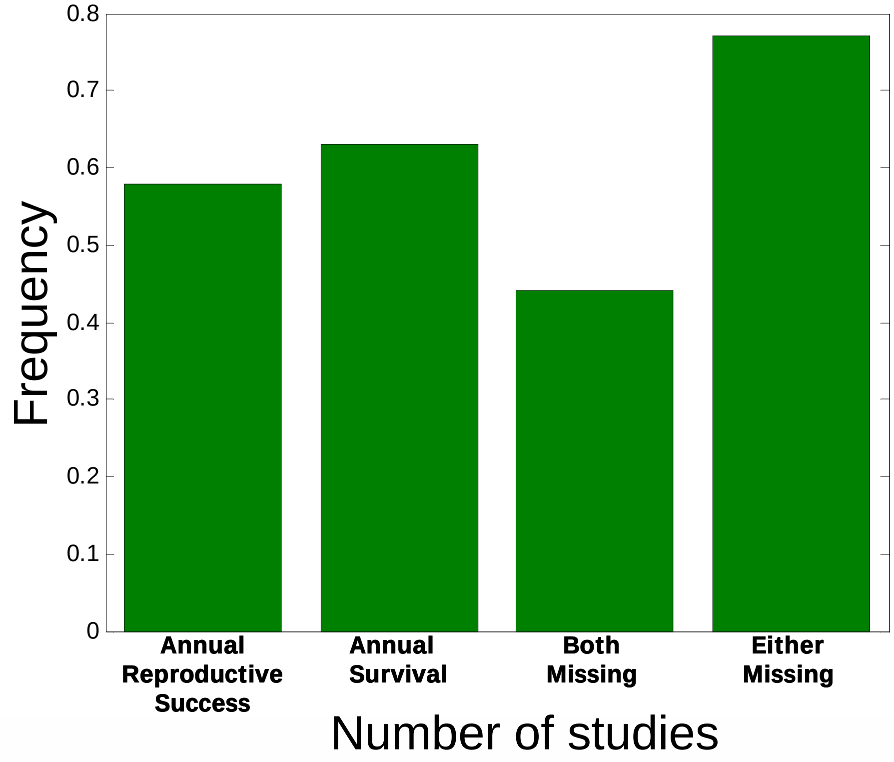
Frequency of “no data”



A fundamental conundrum

- Estimating wildlife demographic data is costly

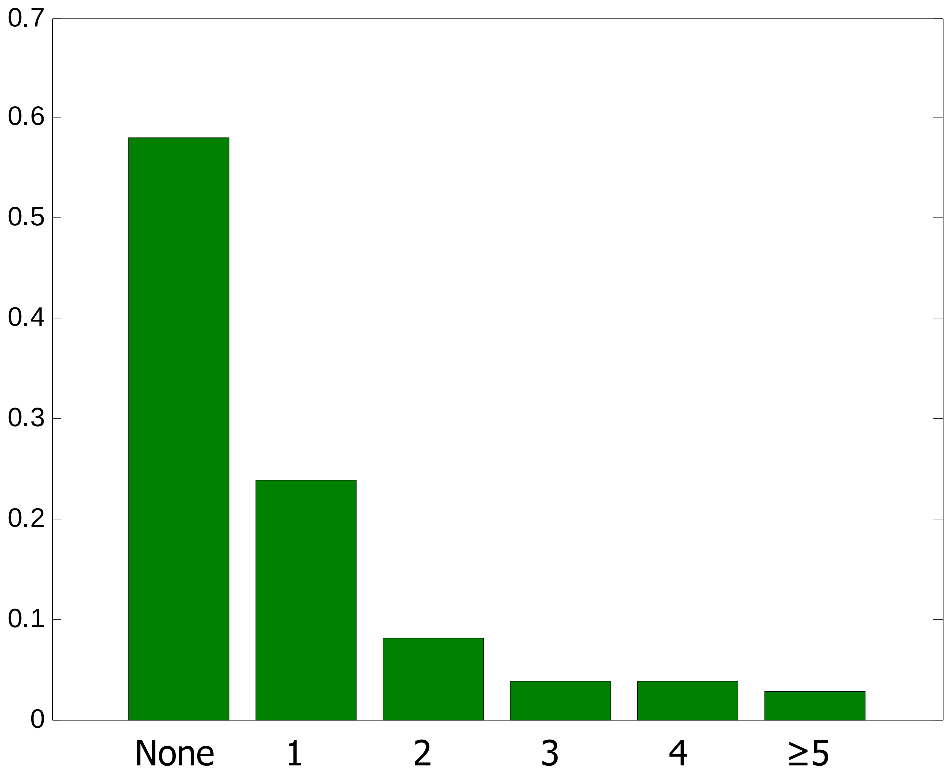
- Extrapolating demographic data is ~~dangerous~~ ~~totally bogus~~ ~~ill-advised~~ ~~somewhat questionable~~ a bit tricky.

Even if data exist, they may not be good enough…

Etterson & Bennett 2006 Human and Ecological Risk Assessment 12:1074-1093

Eastern Meadowlark, a well-studied species?

Reference	Estimate
Kershner et al. 2004	f
Granfors et. al 1996	f
Granfors et. al 1996	f
Lanyon 1957	f
Michel et al. 2005	φ



Sources of error in demographic data

- Sampling error & error propagation
- Currency
- Study design ("best habitat bias")
- Assumptions underlying estimators
- Explanatory variables

Etterson & Bennett 2006 Human and Ecological Risk Assessment 12:1074-1093

What can we learn from population-level risk assessment using these data?

- Predict future population size (forecasting)
- Project future population size (projection)
- Minimize conservative bias

Example: avian reproduction test

- Designed experiment using Mallards (*Anas platyrhynchos*) or Bobwhite (*Colinus virginianus*) that vary in dietary concentration of pesticide.
- Analysis of Variance used to determine highest dietary concentration at which no adverse effects are observed (NOAEC).
- Specific endpoints include:
  - adult body weight
  - egg production and fertility
  - eggshell thickness
  - embryonic development and hatchability
  - survival and weight of young to 14 days.
- NOAECs compared to estimated exposure (risk quotients)
- Core requirement for pesticide registration nationally and internationally

For more background on the avian reproduction test see Bennett & Etterson 2006 Human and Ecological Risk Assessment 12:762-781, and citations therein

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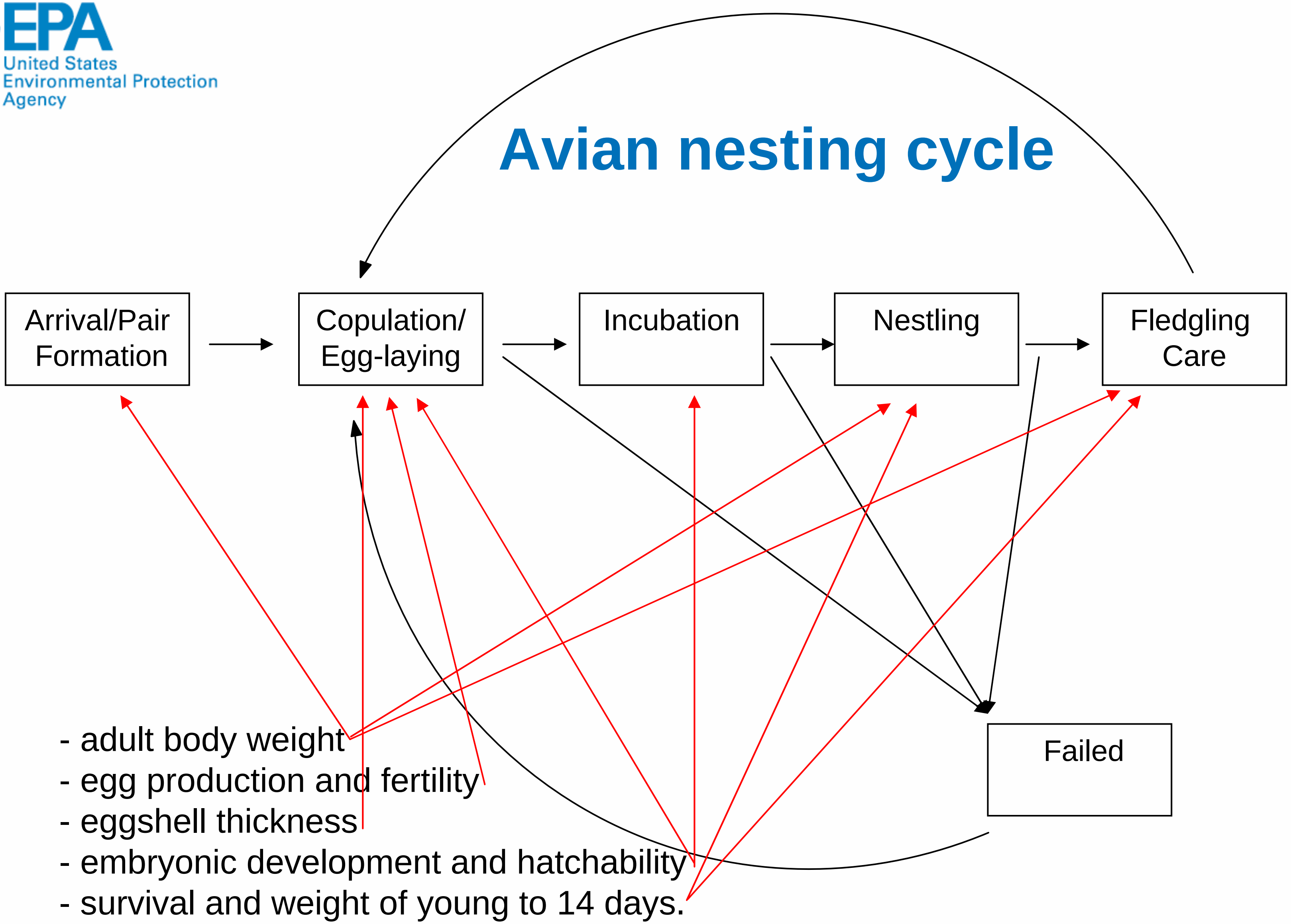
Problems with avian reproduction test

- Test endpoints do not provide direct information on reduced annual reproductive success.
- Birds can renest after failure and/or success
- Avian reproduction test does not provide dose-response information

Avian nesting cycle



- adult body weight
- egg production and fertility
- eggshell thickness
- embryonic development and hatchability
- survival and weight of young to 14 days.

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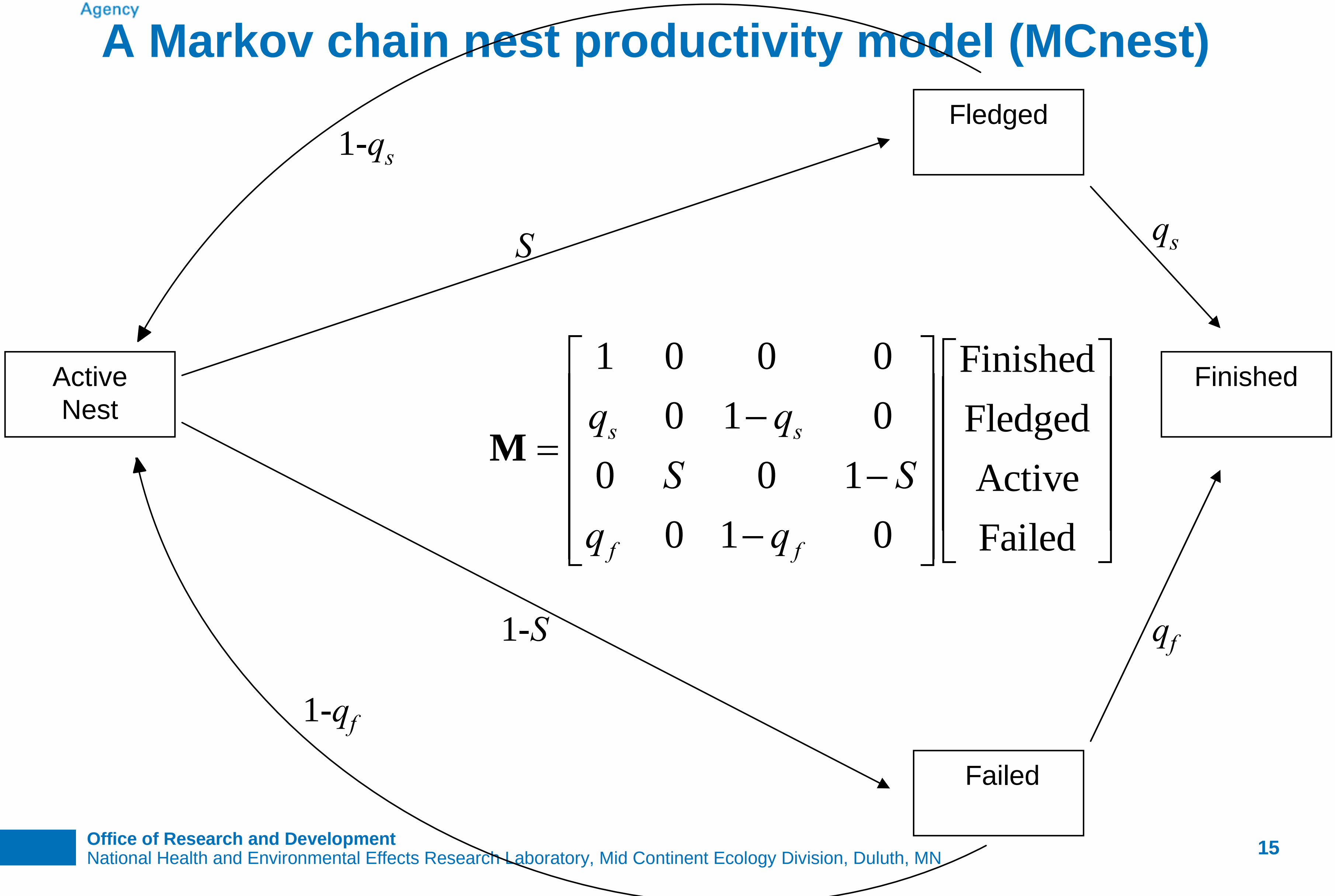
A Markov chain nest productivity model (MCnest)



$$\mathbf{M} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ q_s & 0 & 1-q_s & 0 \\ 0 & S & 0 & 1-S \\ q_f & 0 & 1-q_f & 0 \end{bmatrix} \begin{bmatrix} \text{Finished} \\ \text{Fledged} \\ \text{Active} \\ \text{Failed} \end{bmatrix}$$

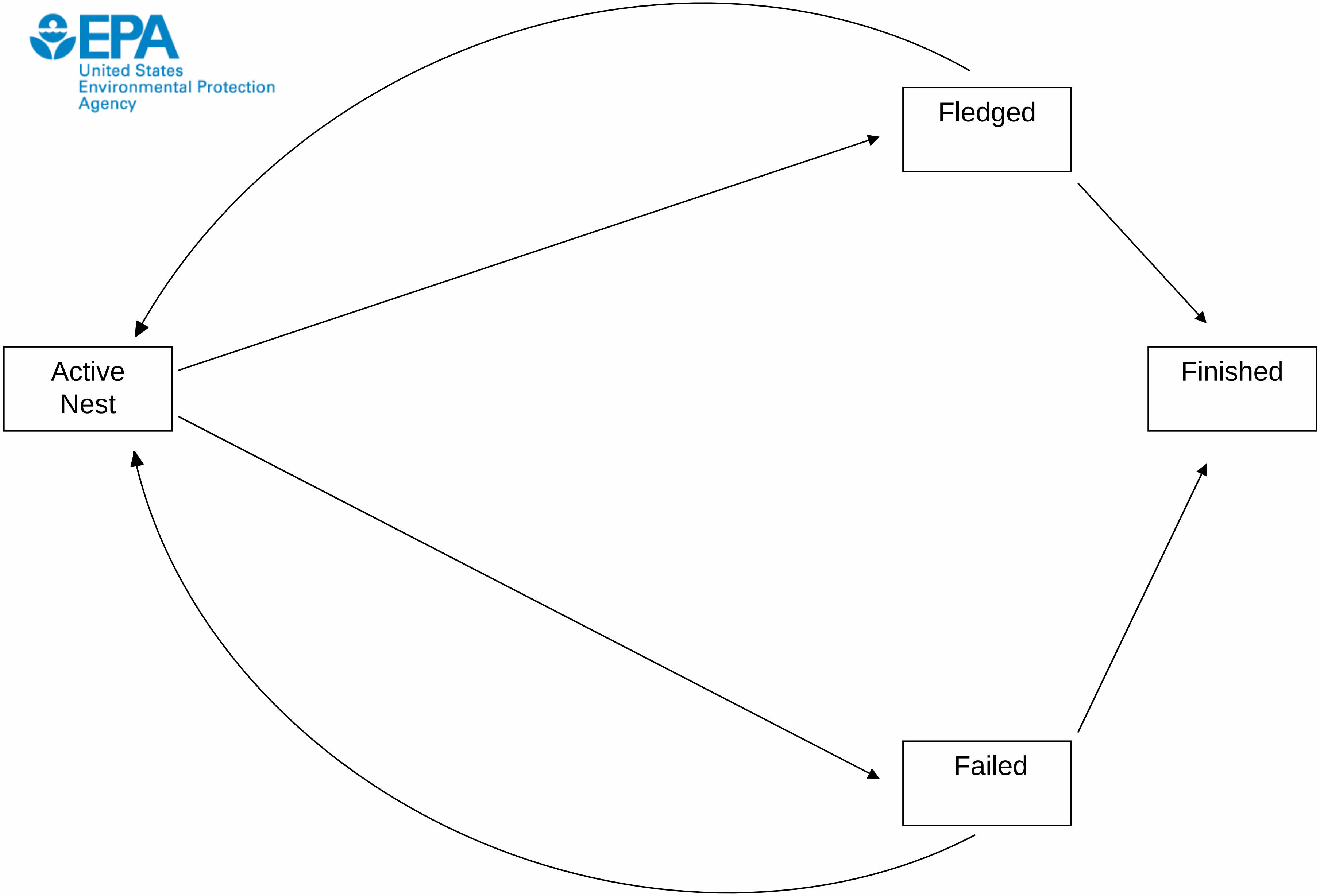
Validation of the MC approach

- Is it really conservative to assume that an exceeded NOAEC results in total nest loss?

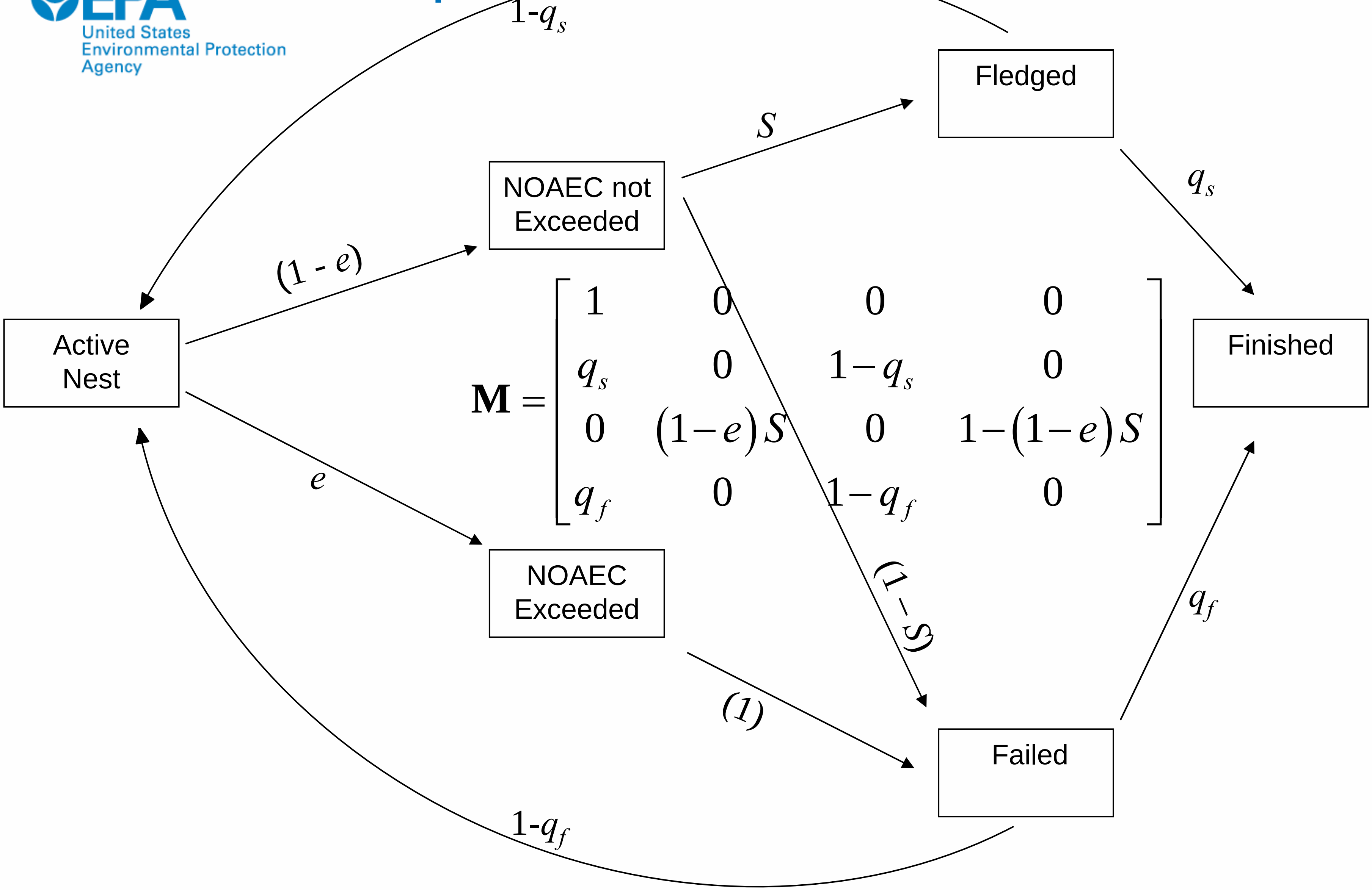
- When estimating effects on reproductive success can we ignore potential effects on survival?

For more background on the Markov chain models see:

Etterson and Bennett. 2005 Ecology
Etterson and Bennett. 2006. Ecological Modelling
Etterson et al. 2007 Studies in Avian Biology
Etterson et al. 2007 Auk.

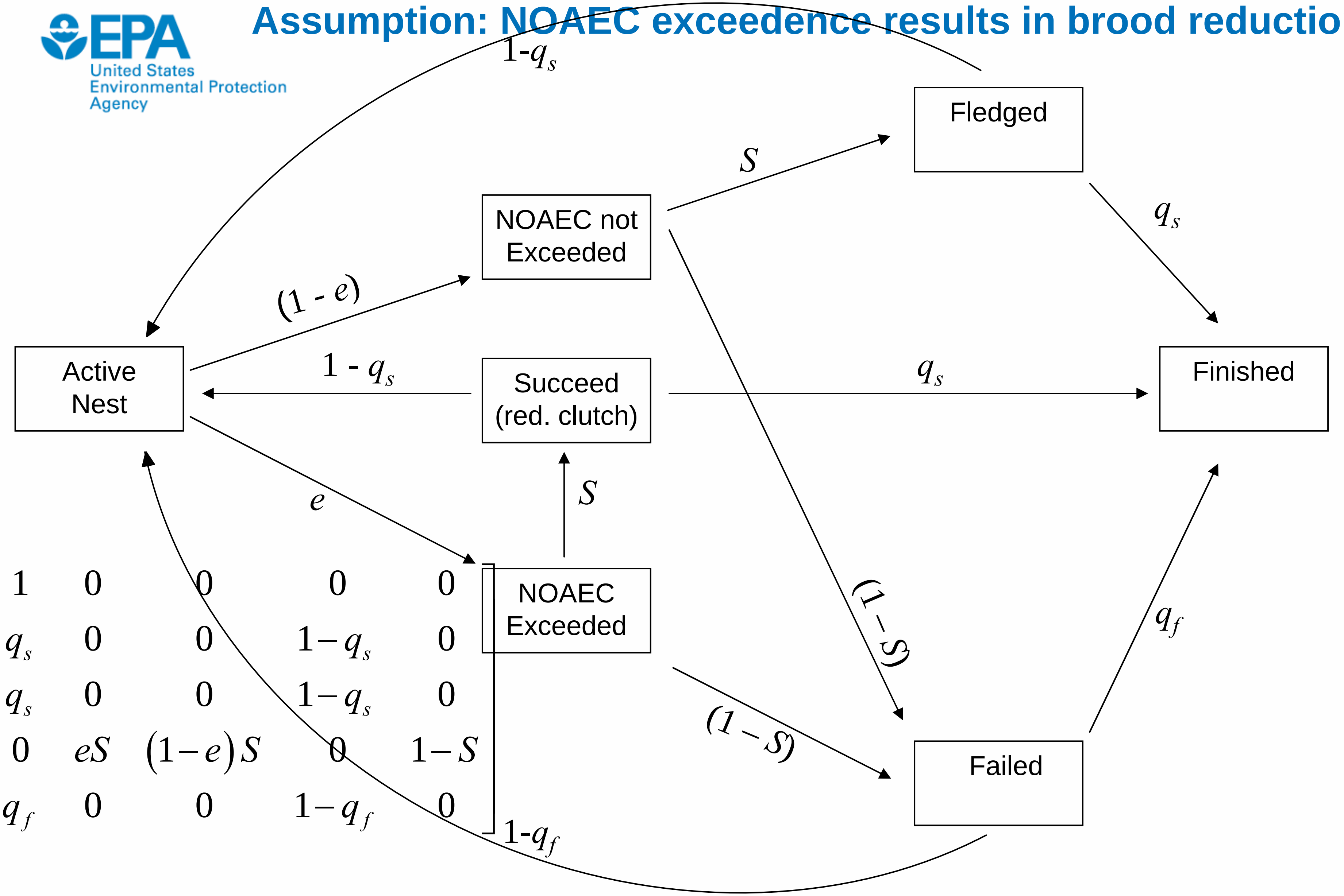

Fledged
Active
Nest
Finished
Failed

Assumption: NOAEC exceedence results in total failure.



$$\mathbf{M} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ q_s & 0 & 1-q_s & 0 \\ 0 & (1-e)S & 0 & 1-(1-e)S \\ q_f & 0 & 1-q_f & 0 \end{bmatrix}$$

Assumption: NOAEC exceedence results in brood reduction



$$\begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ q_s & 0 & 0 & 1-q_s & 0 \\ q_s & 0 & 0 & 1-q_s & 0 \\ 0 & eS & (1-e)S & 0 & 1-S \\ q_f & 0 & 0 & 1-q_f & 0 \end{bmatrix}$$

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The total failure model is protective when: $S > \frac{p}{(1-p)} \frac{1}{(1-e)} \frac{q_f}{(q_s - q_f)}$

What we can learn from this inequality?

1. We are more likely to be protective when:

- proportional brood reduction (1 − p) is large,
- exposure exceeding the NOAEC is *less* likely,
- q_f is small,
- the difference between q_s and q_f is large and positive.

2. We can use it to classify life histories:

- $q_s >\approx q_f \rightarrow$ assuming total failure is never protective
- $q_s < q_f \rightarrow$ assuming total failure is always protective
- $q_s > q_f \rightarrow$ assuming total failure might be protective
- $q_s >> q_f \rightarrow$ assuming total failure is probably protective

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Validation of the MC approach

- Is it really conservative to assume that an exceeded NOAEC results in total nest loss?

  -In most cases, yes, but it depends on life-history characteristics of the nest cycle

- When estimating effects on reproductive success can we ignore potential effects on survival?

  -**No!** similar analyses suggest we cannot ignore survival effects, even when we only wish to estimate reproductive effects.

Summary and conclusions

- Our ability to integrate effects estimates from molecular, cellular, and even individual levels to effects on populations is hampered by a chronic paucity of demographic data on most species of birds (wildlife in general?).
- Even when data exist, they are likely to be imprecisely estimated (and probably biased too).
- And even if you overcome the first two hurdles, data collected in lab or pen are likely to be expressed in a currency that disagrees with what is needed to parameterize a population model.
- Nevertheless, it is possible to make meaningful inference about chemical effects on populations using standard population modeling tools.
- Discussion about life-history traits and reconciliation of data across hierarchical scales is a critical component of model design for wildlife population level risk assessment.
- We believe the approach we have described may be useful for similar problems with other taxa for which laboratory-collected data must be used to make population-level inference