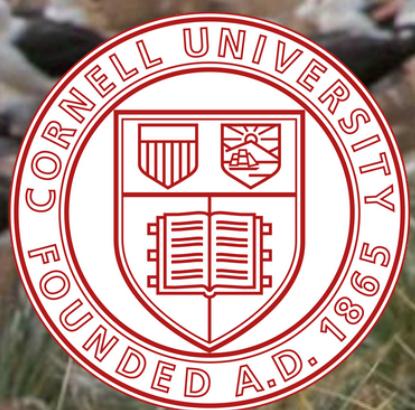


TESTING OF INDUCED DISPERSAL AS AN HPAI MITIGATION MEASURE IN COLONIAL SEABIRDS

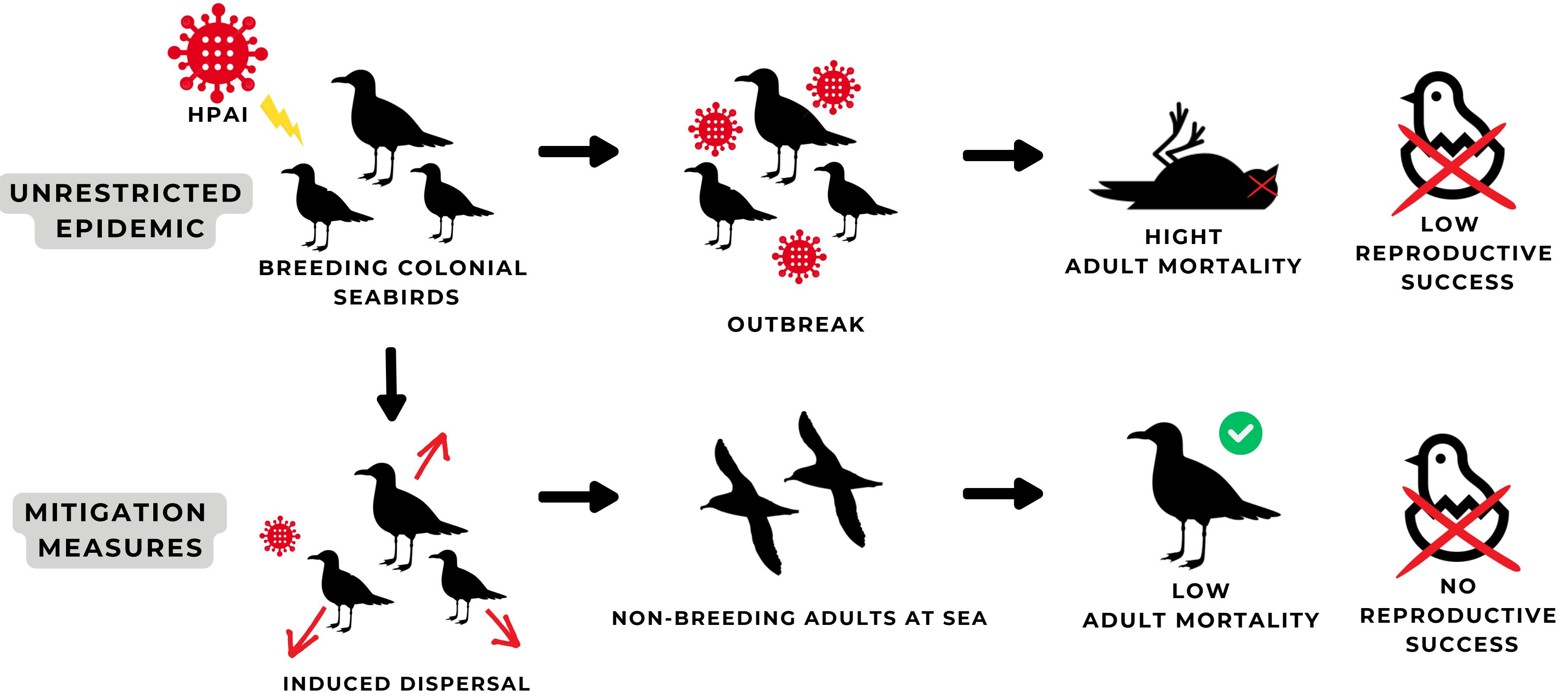
ODIN RUMIANOWSKI

WITH THE SUPERVISION OF
AMANDINE GAMBLE AND AUGUSTIN CLESSIN



09/01/2024

CONTEXT



CONTEXT

Induced dispersal to “dodge” HPAI outbreaks:

- Beneficial?
 - At population, metapopulation scale?
 - Considering varying additional risk of virus spread ?
 - Considering the cost of a failed breeding attempt
- When to proceed to limit these costs?
- The best adapted species?
 - Model sensitivity analysis
 - Known parameters for this species?



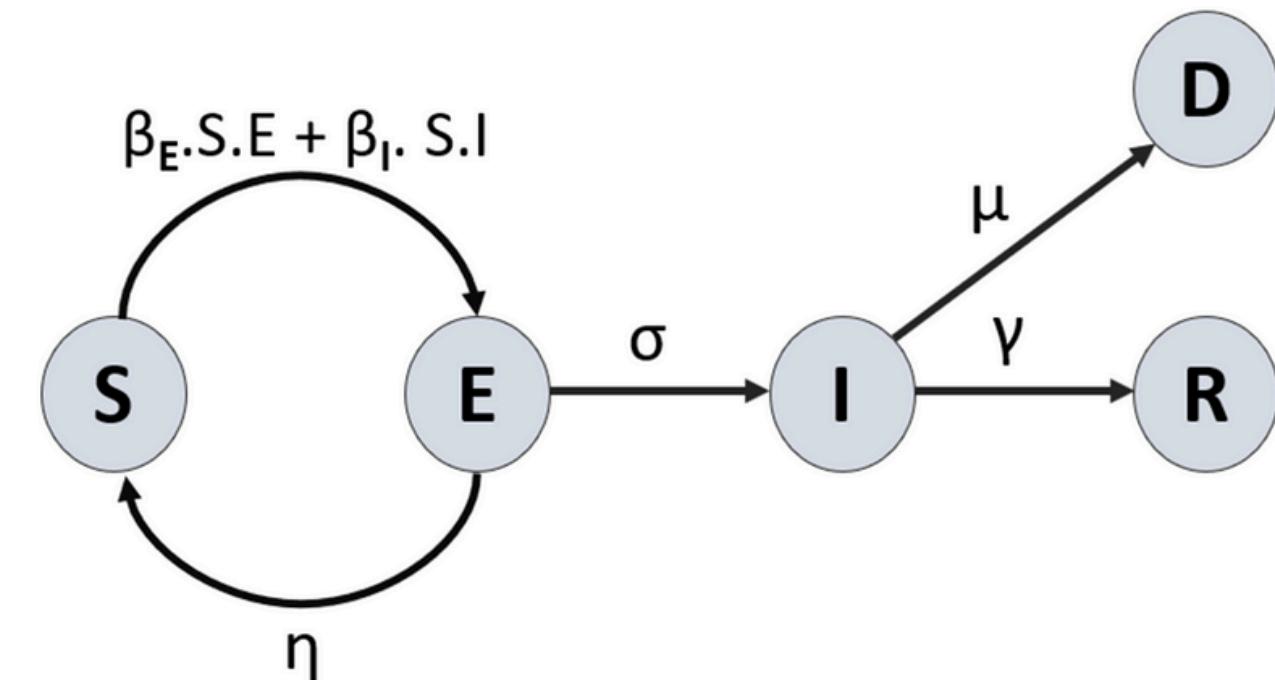
OBJECTIVES

- Building a stochastic model (Continuous time Markov chain) :
Giving epidemiological, demographical and mobility parameters, the model provides the number of survived adults and nestling (response variables)
- Sensitivity analysis:
Hierarchize parameters according to their contribution to measurement performance
- Bibliographic research to identify potential species
- Adapt the model to these species

MODELING

- Epidemiological status:
 - Susceptible (S)
 - Exposed (E)
 - Infectious (I)
 - Recovered (R)
 - Dead (D)
- Reproductive status:
 - Breeder (B) = attached to a colony
 - Nestling (N) = immobile
 - Non-Breeder (NB) = prospector
- Localisation:
 - Colony A
 - Colony B
 - Colony C

Conceptual diagram of the epidemiological model



MODELING

EPIDEMIOLOGY

- β_E : Transmission rate from exposed individuals
- β_I : Transmission rate from infectious individuals
- η : Rate of progression from exposed to susceptible
- σ : Rate of progression from exposed to infectious
- γ : Recovery rate
- μ : Disease-related mortality rate

MOBILITY

- ζ : Movement between colony and sea for breeders
- Ψ : Transition from breeder to non-breeder (reproductive failure)
- ρ : Movement between colony and sea for non-breeders
- Ω : Transition from one colony to another (prospecting)

DEMOGRAPHY

- F : Fecundity, number of nestling per pair
- K : Probability of reproductive accession, that a nestling become a breeder

MODELING

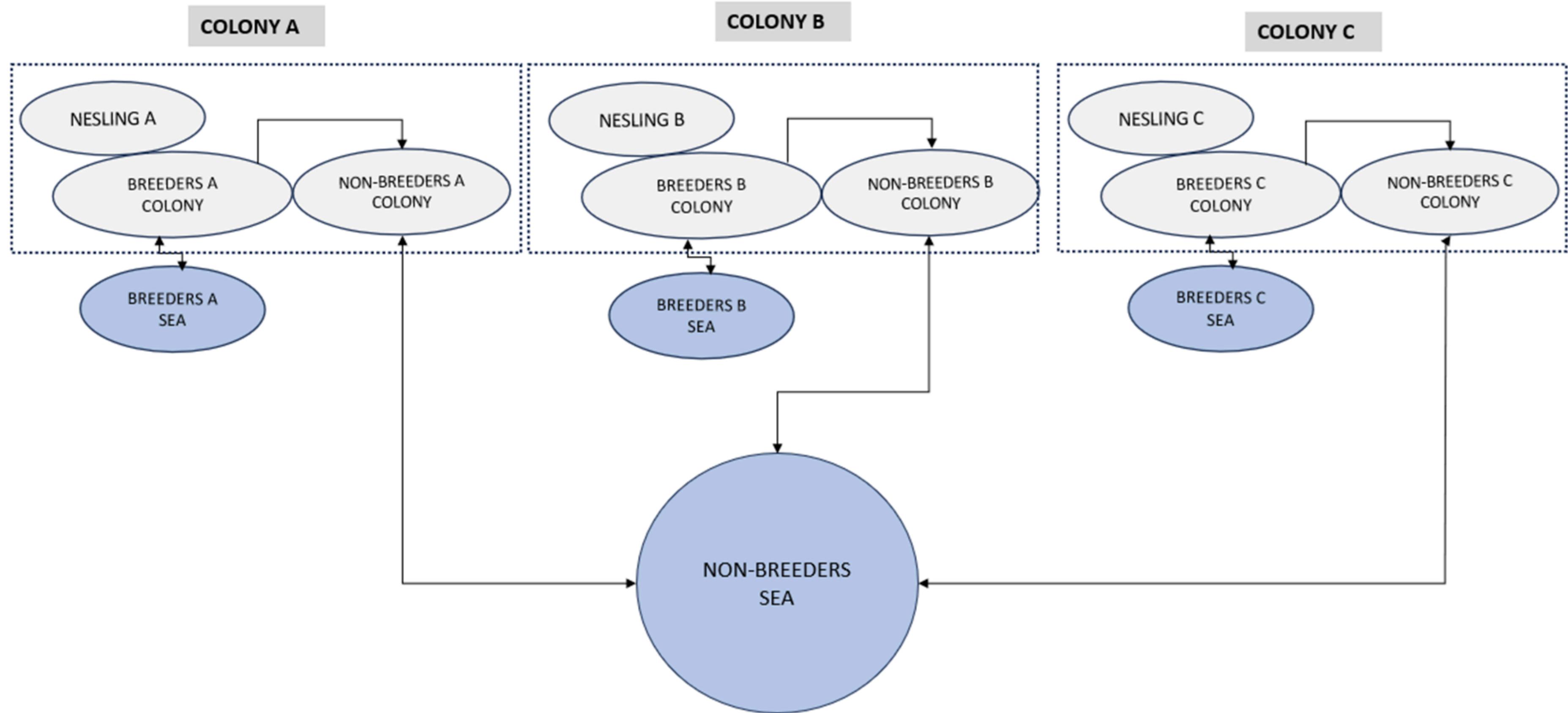
Rate of infection:

- Infection rate of an individual in colonie A :

$$\beta_E \cdot S_{\text{Colony A},X} \cdot (E_{\text{Colony A,Breeder}} + E_{\text{Colony A,Nestling}} + E_{\text{Colony A,Non-Breeder}}) + \\ \beta_I \cdot S_{\text{Colony A},X} \cdot (I_{\text{Colony A,Breeder}} + I_{\text{Colony A,Nestling}} + I_{\text{Colony A,Non-Breeder}})$$

MODELING

Overview of the spatial transmission process



MODELING

Special events:

- Induced Dispersal:

- Two days after the first death, all breeders in colony A become non-breeders.

- The emergence of Nestlings:

- At a fixed date, a number of nestlings equal to the number of breeders alive /2 appear for each colony.

Combined event:

- Death of a nestling => two breeders become non-breeders

- Death of an adult => one breeder becomes non-breeder and one chick dies (+ correction to account for the fact that some death might affect partners)

MODELING

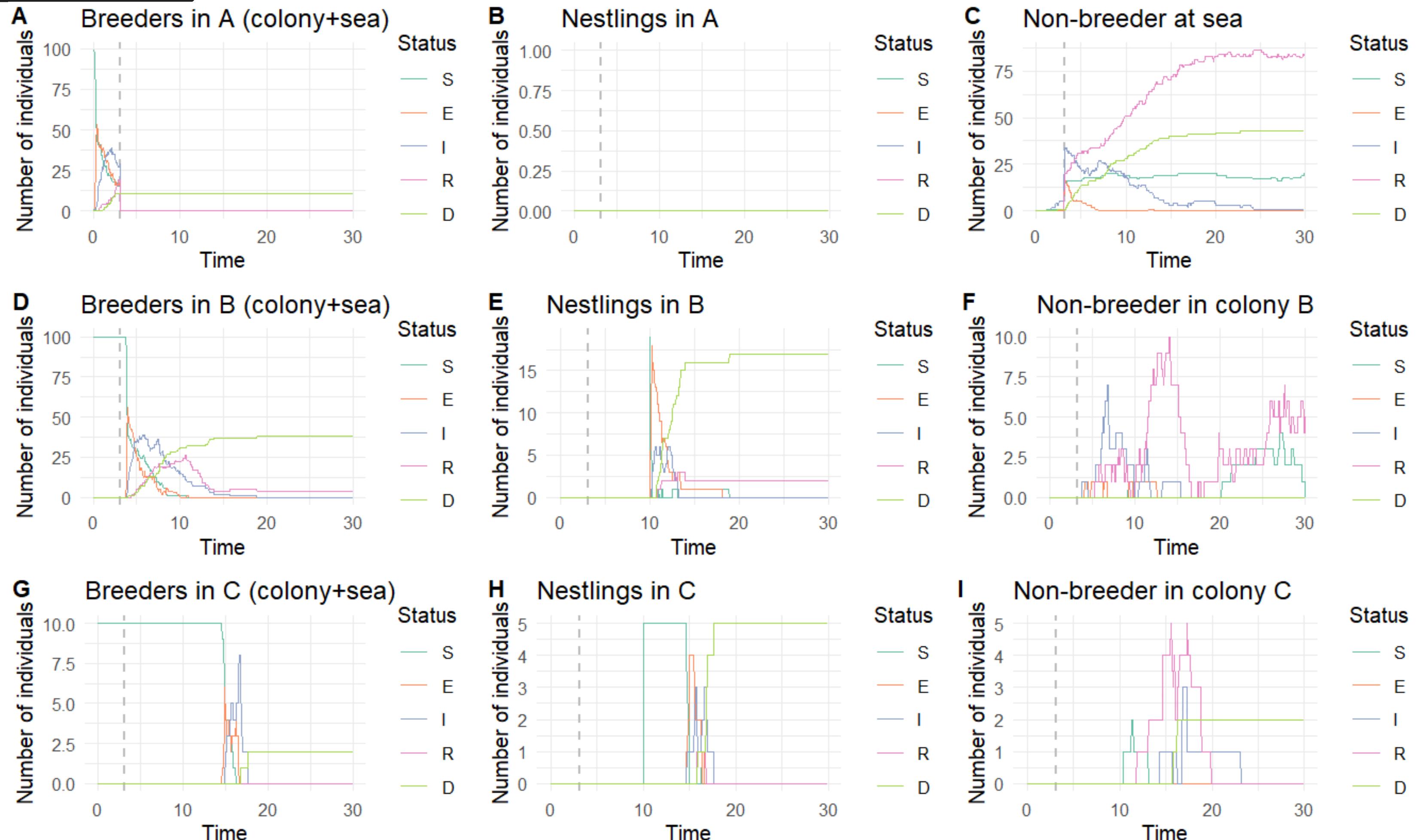
- Scenario:

- 0 : No initial infected breeder and no induced dispersal (baseline on a healthy site)
- 1 : **One initial infected breeder** and no induced dispersal (baseline on an outbreak site)
- 2 : **One initial infected breeder** and **induced dispersal** (reactive measure)
- 2.5 : Initial infected breeder not detected (E but not I) and **induced dispersal** (“too-late” proactive measure, e.g., outbreak detected in a neighboring species, not in the model)
- 3 : No initial infected breeder and **induced dispersal** (proactive measure, e.g., outbreak detected in a neighboring species, not in the model)

- Model output:

- Number of surviving adults
- Number of surviving nestlings
- Equivalent number of adults : Adults + P(access reproduction) x Nestling
- Number of affected colonies

FOR NOW



FOR NOW

