CONTRIBUTION OF CMR METHODS IN UNDERSTANDING THE VIRUS LOCAL EPIDEMIOLOGICAL DYNAMICS IN A POPULATION OF WILD BIRDS

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AGRICULTURAL RESEARCH
FOR DEVELOPMENT

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AVIAN INFLUENZA VIRUSES IN WILD BIRDS

- Wildbirds, particularly Anatideae (ducks, geese and swans)
  - HPAI viruses sometimes detected and important mortality waves
  - Main natural reservoir of LPAI viruses

- Transmission of AIV from wild to domestic birds known to occur, particularly in openly grazed rice fields in parts of Southeast Asia and Africa

- Genetic reassortment/recombination of LPAI viruses in a wild/domestic host
  - New, sometimes HPAI, strains

- Anatideae = migratory birds
  - Capacity to disperse AI viruses over long distances

➡ Understanding the mechanisms underlying the dynamics of AI viruses in wild birds is important for global surveillance and control strategies.

HOST ECOLOGY AND ENVIRONMENT INFLUENCE THE DYNAMICS OF AIV IN ANATIDEAE

- Anatideae = asymptomatic carries of LPAIV

- Transmission: faecal-water-oral (contaminated food/water) and airborne
  - Environment: AIV reservoir,
  - Persistence of AIV in environment influenced by climatic conditions.

- Host density → contact rate → AIV transmission
  - Autumn peak prevalence in boreal ducks → seasonal flocking migrating birds

- Susceptibility of juveniles > Susceptibility of adults
  - Immunity

- Decline in prevalence in boreal wildfowl in late autumn
  - Seasonal ↗ population immunity

Epidemiological investigations in wildlife

- Most results arise from experiments on animals held in captivity

- Wild animals are difficult to monitor in their natural environment at the individual level
  - Not easy to catch, even more difficult to recatch

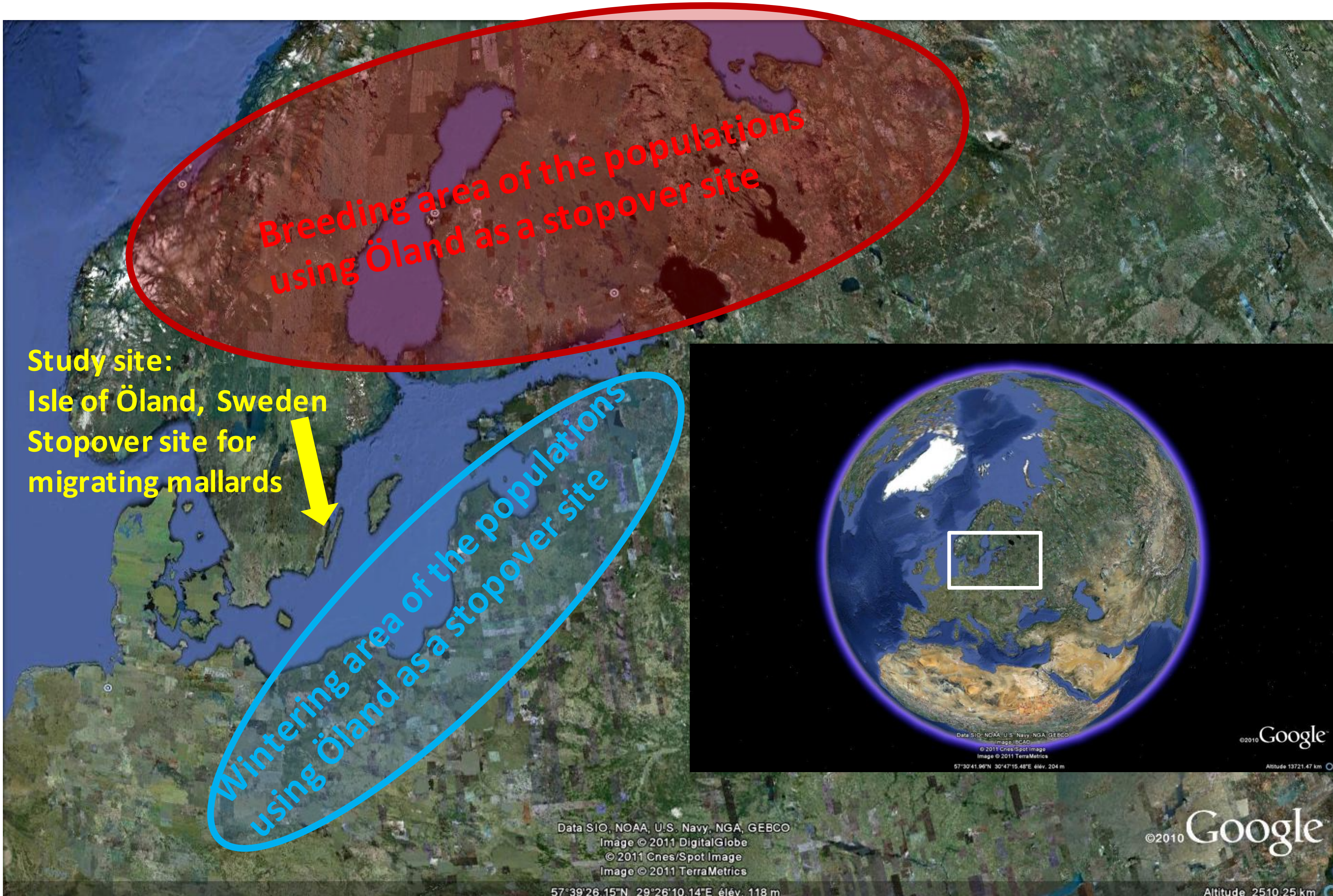
- In situ, only information at the population level can be obtained
  - Prevalences
  - Incidences

- The parameters (force of infection, recovery rate, virulence, R0) that drive the epidemiological dynamics of viruses can usually not be measured directly in wild animal population

A monitoring program for understanding the dynamics of AIV in natural Mallard population

- Migratory populations of Mallards *Anas platyrhynchos* at Ottenby Bird Observatory on the island of Öland in southeastern Sweden

- Populations passing the sampling area in autumn
  - Breeding: Baltic Sea, Russia, Belarus
  - Wintering at the German and Danish Baltic Sea coasts


Breeding area of the populations
using Öland as a stopover site
Study site:
Isle of Öland, Sweden
Stopover site for
migrating mallards
Wintering area of the populations
using Öland as a stopover site
Data SIO, NOAA, U.S. Navy, NGA, GEBCO
Image © 2011 DigitalGlobe
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57°39'26.15"N 29°26'10.14"E élév. 118 m
©2010 Google
Altitude 2510.25 km

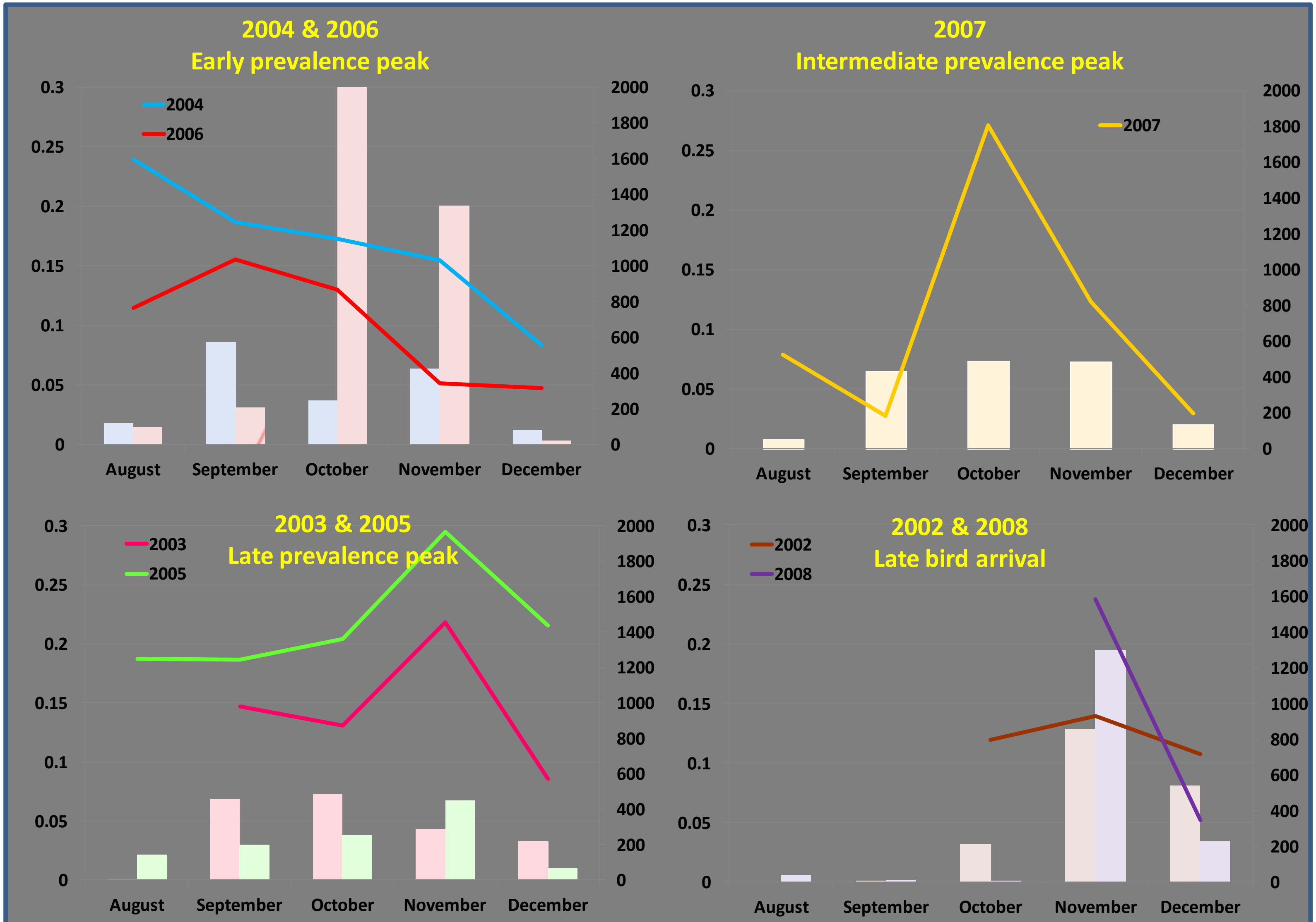
A monitoring program for understanding the dynamics of AIV in natural Mallard population

- ❖ Daily monitoring protocol March to December 2002 – 2009. Daily trapping (baited traps), ringing and sampling

❖More than 5,000 individuals captured at least once
❖A same individual can be captured up to 43 times in a same year
❖Individual monitoring data include large gaps (days when the duck is still on the site but not captured)

❖1,850 Avian Influenza virus detections
❖600 Avian Influenza viruses isolated (most of them are low pathogenic viruses)

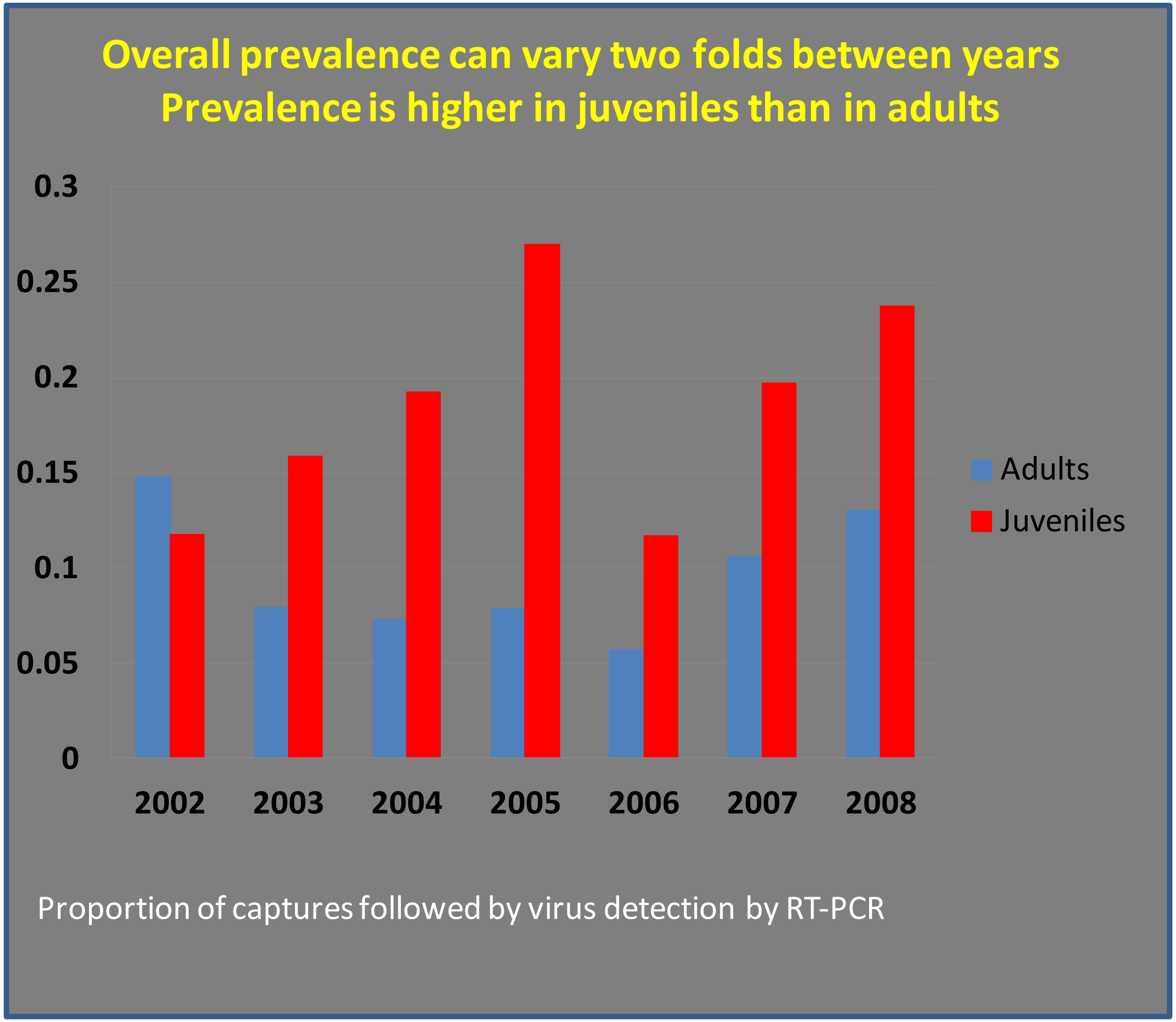
Seasonal Prevalence patterns



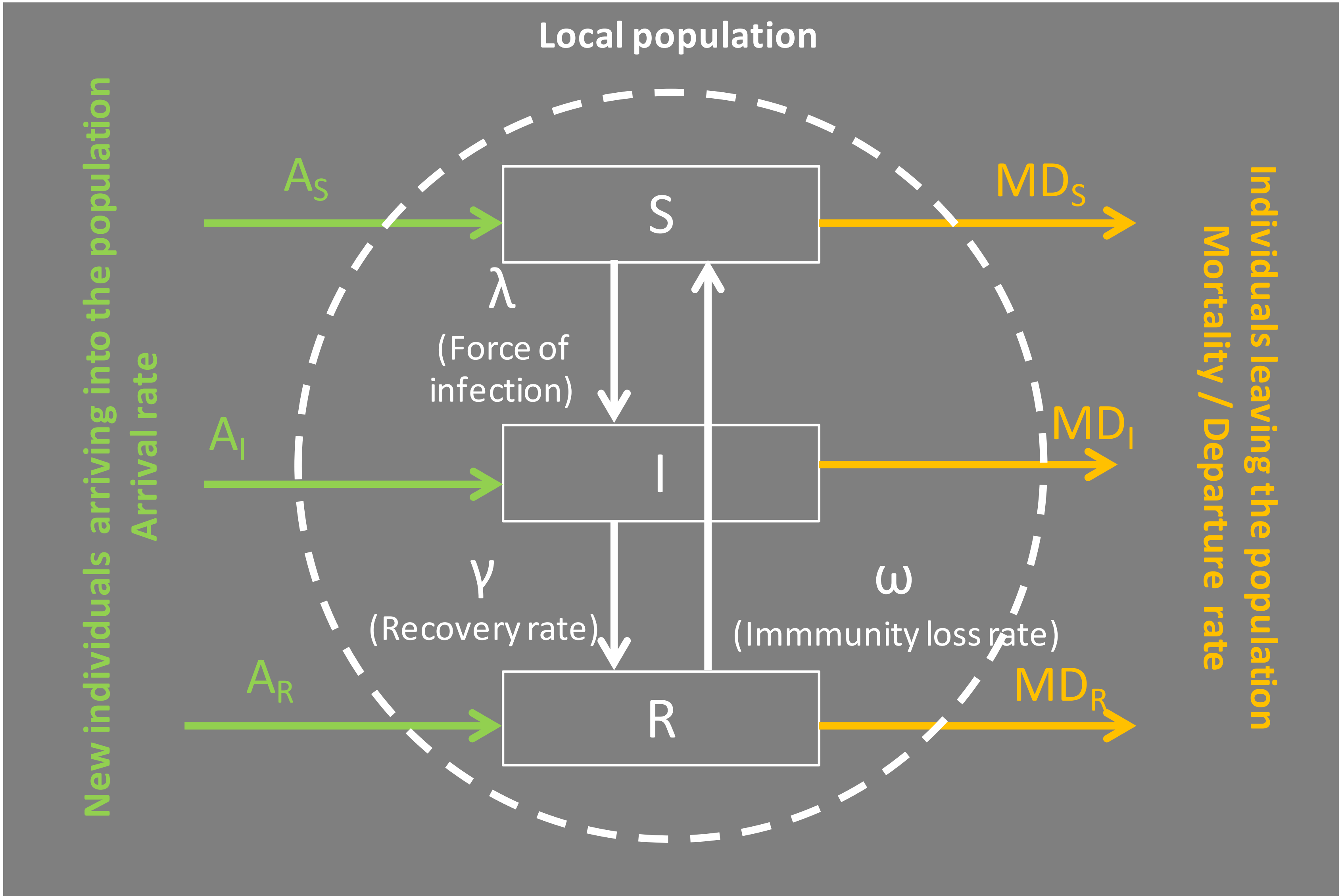
Bars: number of captures

Lines: proportion of captures for which virus has been detected by RT-PCR

AGE AND YEAR PREVALENCE PATTERNS



Structure of a SIR model for the local dynamics of AI viruses in migratory Mallards at a stop-over site on the island of Öland (Sweden)



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CAPTURE HISTORIES

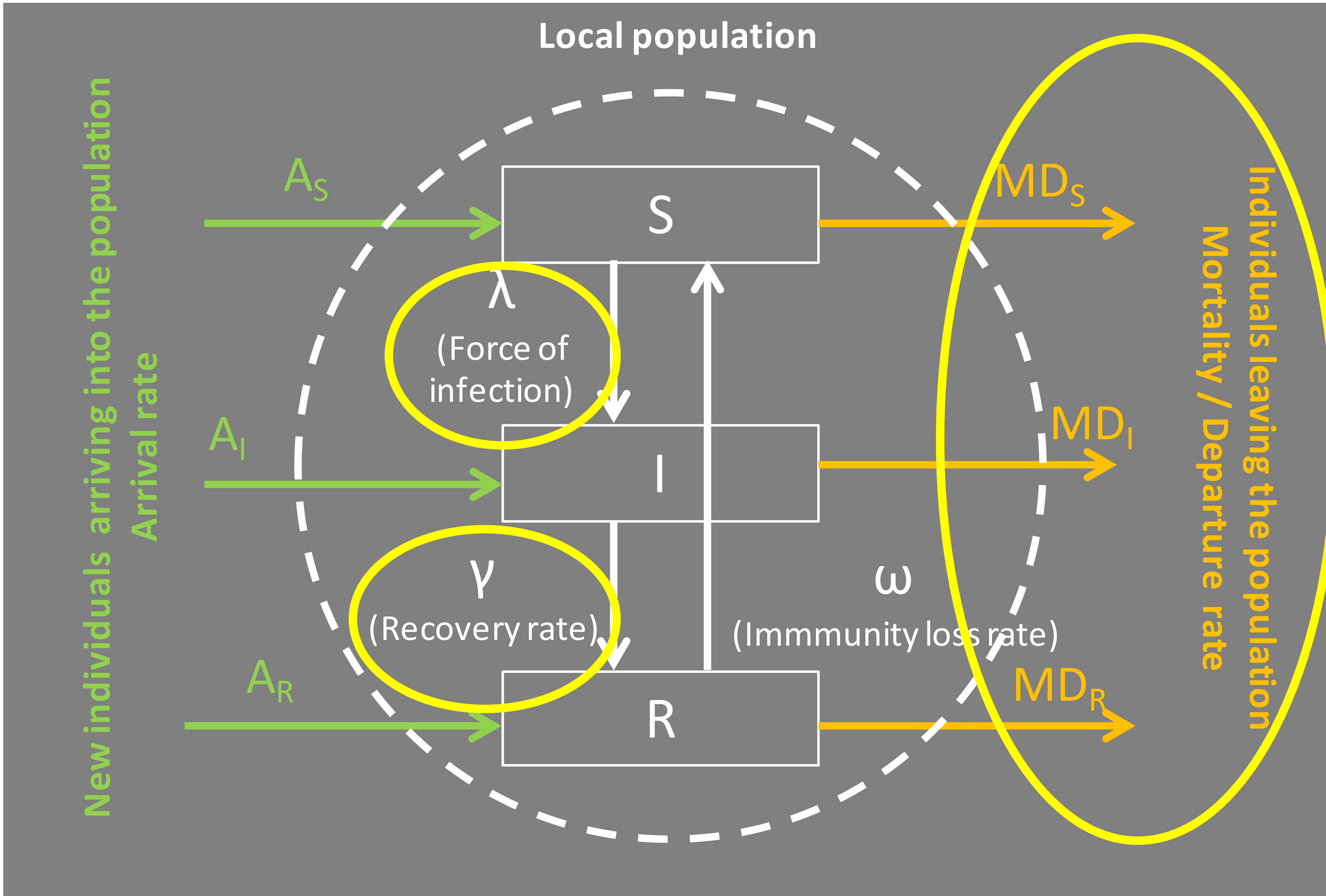
RingNr	Year	Sex	Age																																																																									
90A71348	2006	Male	A	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71349	2006	Male	U	2	0	0	2	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71350	2006	Female	A	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71351	2006	Female	J	1	1	0	1	0	0	1	0	1	2	1	1	1	1	0	0	0	1	1	1	1	1	2	1	2	1	1	1	1	0	1	1	1	1	1	0	0	1	1	1	1	1	1	0	1	0	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71352	2006	Male	J	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71353	2006	Female	A	1	0	1	1	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71354	2006	Male	J	1	0	0	0	0	0	1	0	0	0	1	1	0	1	1	0	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71355	2006	Male	A	1	0	0	1	0	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71356	2006	Male	U	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71357	2006	Male	A	0	1	0	0	2	0	1	0	1	1	0	1	1	0	1	0	2	0	1	0	1	0	1	1	0	1	0	1	1	1	1	0	1	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71358	2006	Male	A	0	1	0	0	0	0	1	0	0	0	1	1	0	0	1	0	1	0	0	1	1	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71359	2006	Female	A	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71360	2006	Female	J	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71361	2006	Male	J	0	0	2	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71362	2006	Female	J	0	0	1	0	1	1	2	1	1	1	1	2	1	0	1	1	0	0	0	0	0	0	1	1	0	1	1	1	1	1	1	2	1	1	1	1	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71363	2006	Male	J	0	0	2	2	0	1	1	2	1	1	0	0	1	0	1	1	1	1	1	0	1	1	1	1	1	1	0	0	1	1	2	0	1	1	0	0	1	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71364	2006	Male	U	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71365	2006	Male	U	0	0	1	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71366	2006	Female	J	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90A71367	2006	Male	J	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2	1	1	0	2	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

90A71367	2006	Male	J	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2	1	1	0	2	1	1	1	1

Analysing the individual multi-viral-status capture histories

- Multistate CMR model
  - States = Virus detected (infected) / No virus detected (uninfected)
- The likelihood of each capture history is a function of the following parameters
  - State dependent local mortalities (=departure probability)
  - State dependent recapture probabilities
  - Transition between states
- Fitting/estimation by Maximum Likelihood methods (Software ESURGE, CEFE-CNRS)

Structure of a SIR model for the local dynamics of AI viruses in migratory Mallards at a stop-over site on the island of Öland (Sweden)



CANDIDATE MODELS

	Prob. of emigration	Prob. of capture	Prob. become infected	Prob. recovering from infection
Age	Juveniles and adults ≠ phenology		Young birds less likely to have acquired immunity	
Body condition	Staging for refueling		Poor condition → Infection ↑ Recovery ↓	
Gender				
Infection state	Behavioral effects of infection		Previous infections should provide immunity	
Seasonal trend	Migration = seasonal behavior		Prevalence / Immunity vary with season	
Year	Phenology variation		Circulating strain variation	
Crowding			Crowding ↑ Contact rate ↑	
Weather	Influences migratory behavior	Weather influences behavior	Weather → Body condition → Infection/Recovery	

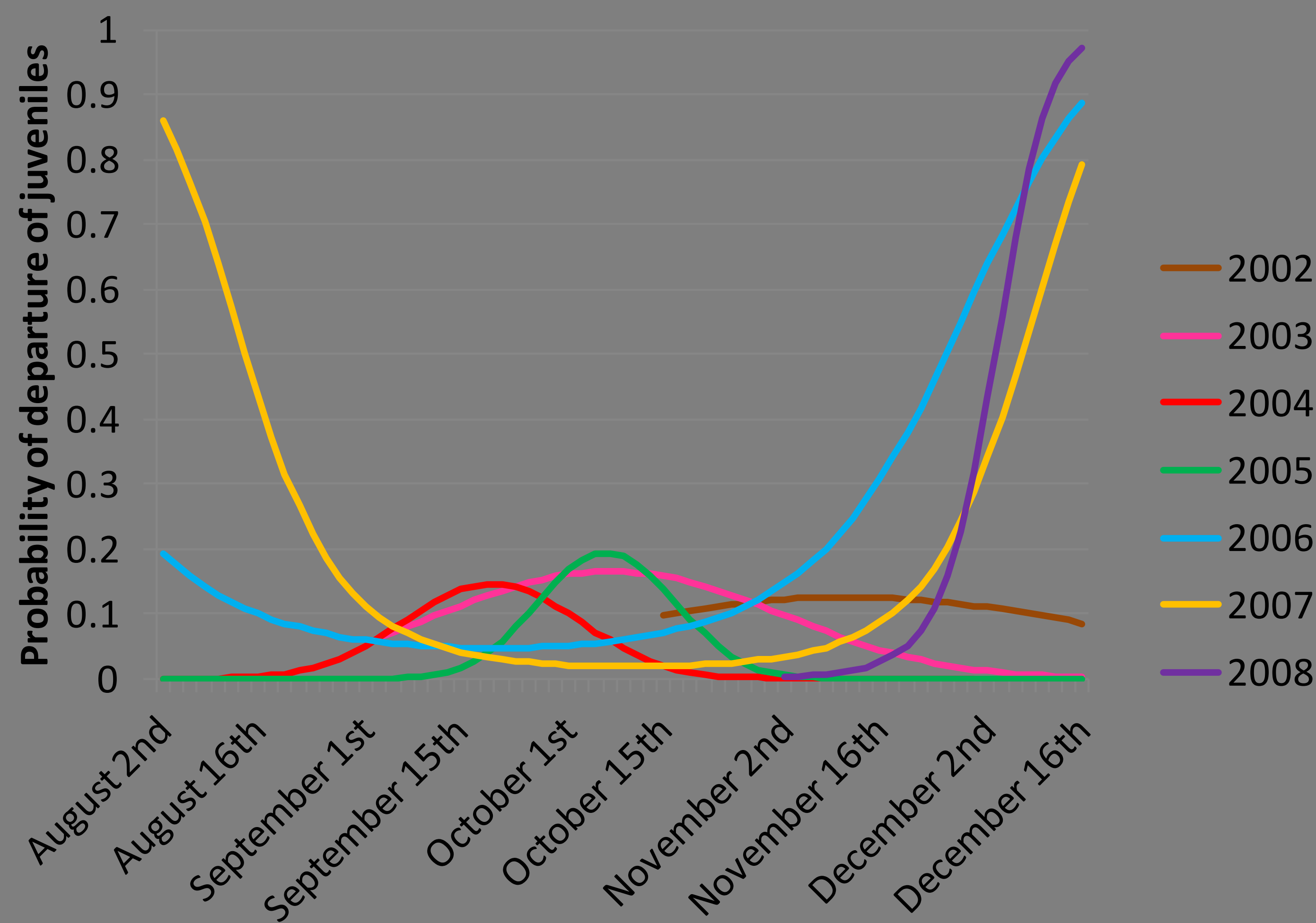
AIC based model selection

THE BEST MODEL SO FAR

	Departure probability	Recapture probability	Infection Probability	Probability of recovering
Age				
Seasonal trend (2nd order polynomial of date)				
Year				
Age * Seasonal trend				
Year * Seasonal trend				

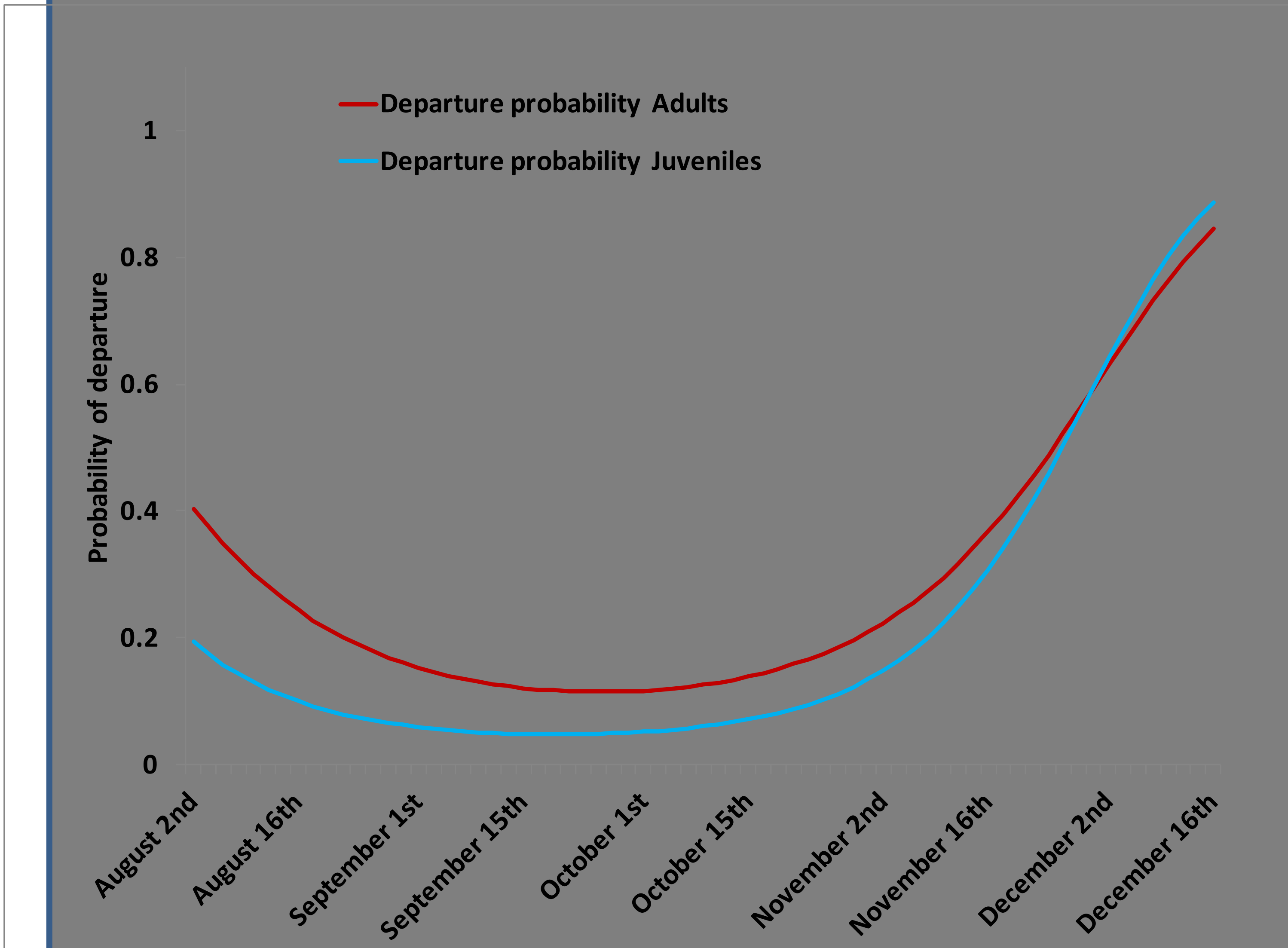
Orange: effects included in the model
Grey: effect not included in the model

PROBABILITY OF DEPARTURE SEASON AND YEAR VARIATION IN JUVENILES



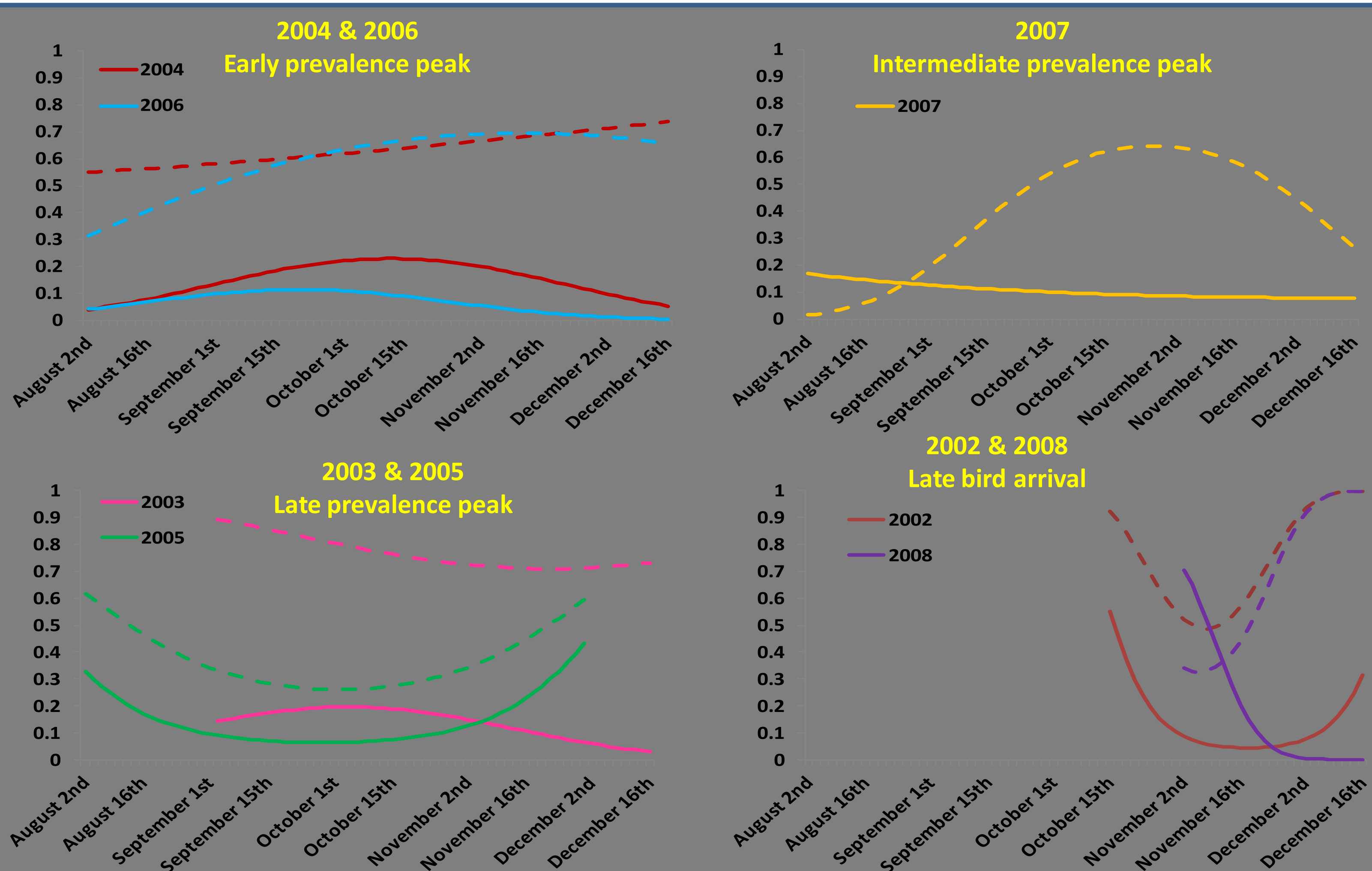
Migration phenology shows important between years variations

PROBABILITY OF DEPARTURE SEASON AGE VARIATION IN 2006



Juveniles stay longer than adults on the stopover site

YEAR & SEASONAL VARIATION IN EPIDEMIOLOGICAL PARAMETERS

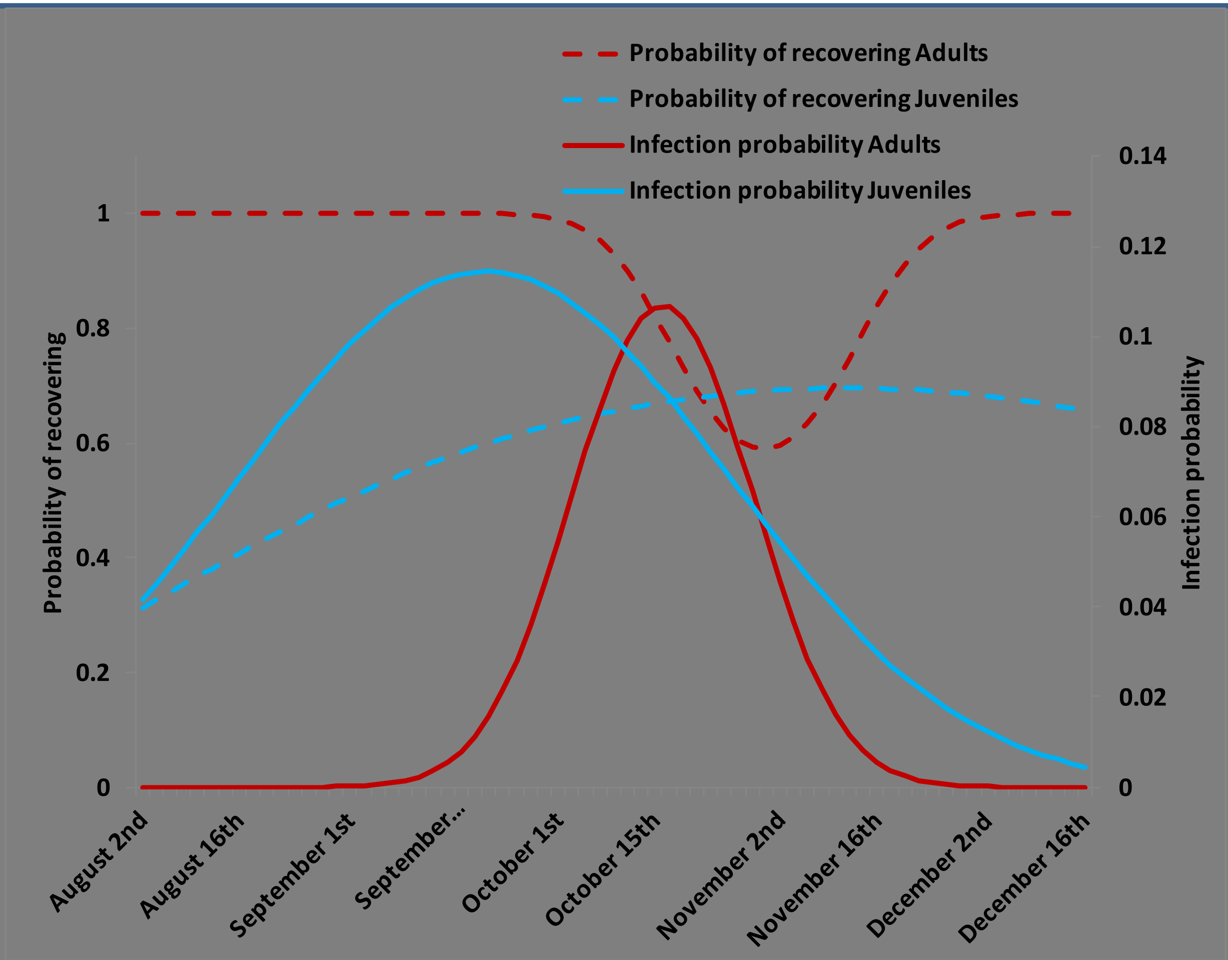


———: probability of infection in juveniles

----------: probability of recovering in juveniles

- ❖ Important inter-annual variation in the seasonal variation pattern
- ❖ Some patterns seem recurrent (2004 & 06; 2002 & 08)
- ❖ In 2004-06: progressive increase of immunity and mid-season prevalence peak
- ❖ In 2002-08: high infection probability late in the season and quick immunity increase
- ❖ A same prevalence pattern can arise from distinct epidemiological parameter patterns (2003-05)

AGE AND SEASONAL VARIATION IN EPIDEMIOLOGICAL PARAMETERS IN 2006

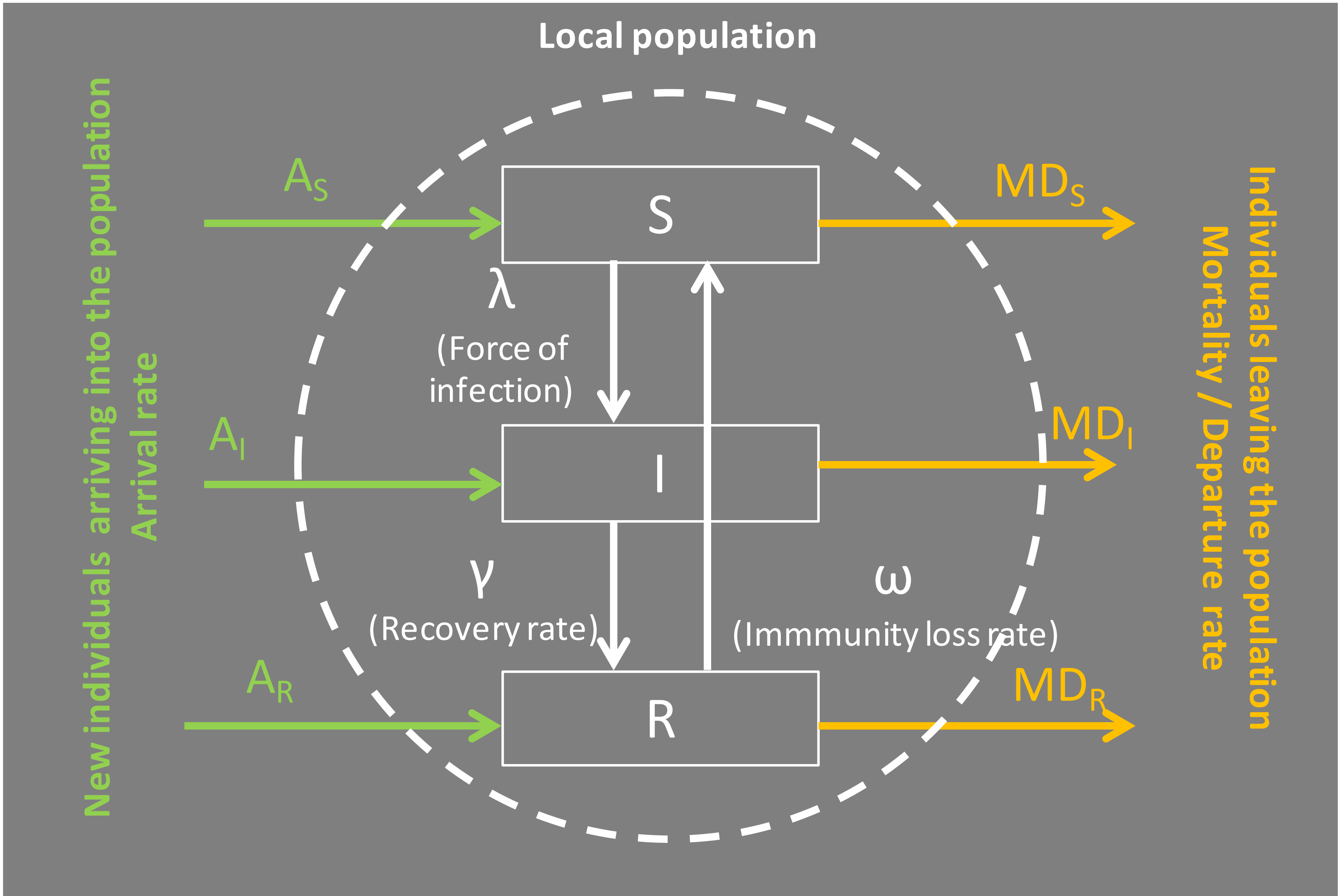


- ➢Infection probability of juveniles is higher than that of adults over most of the season
- ➢Infection probability of juveniles peaks earlier in the season than that of adults
- ➢Probability of recovering of adults is higher than that of juveniles
- ➢Probability of recovering seasonal patterns differs between juveniles and adults

CONCLUSIONS

- A complex epidemiological system (in particular because the host population is extremely open)

Structure of a SIR model for the local dynamics of AI viruses in migratory Mallards at a stop-over site on the island of Öland (Sweden)



Conclusions

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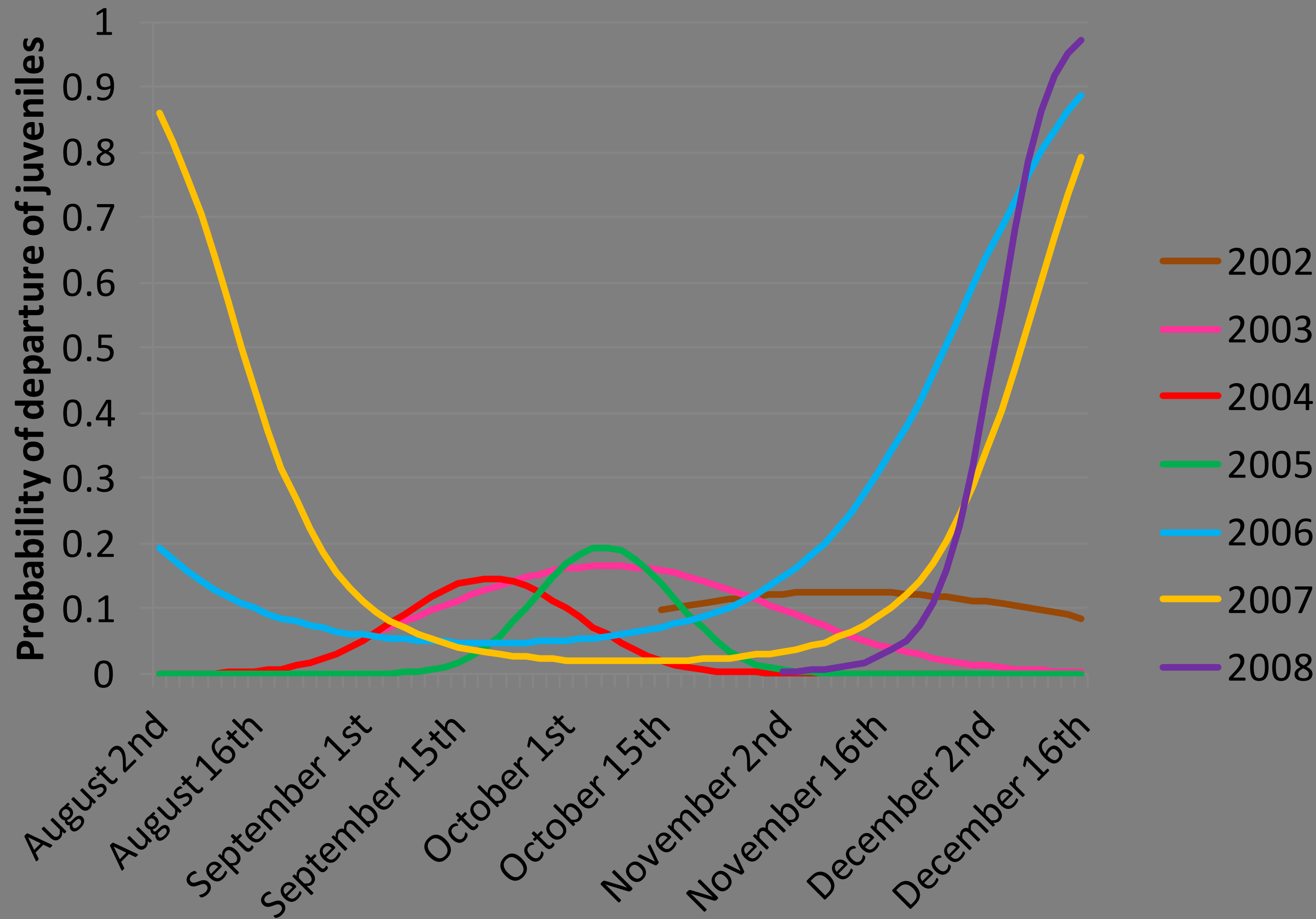
- All parameters show variation between years in their seasonal patterns (difficult to identify typical patterns)

Probability of departure season and year variation in juveniles



Migration phenology shows important between years variations

CONCLUSIONS

- A complex epidemiological system (in particular because the host population is extremely open)
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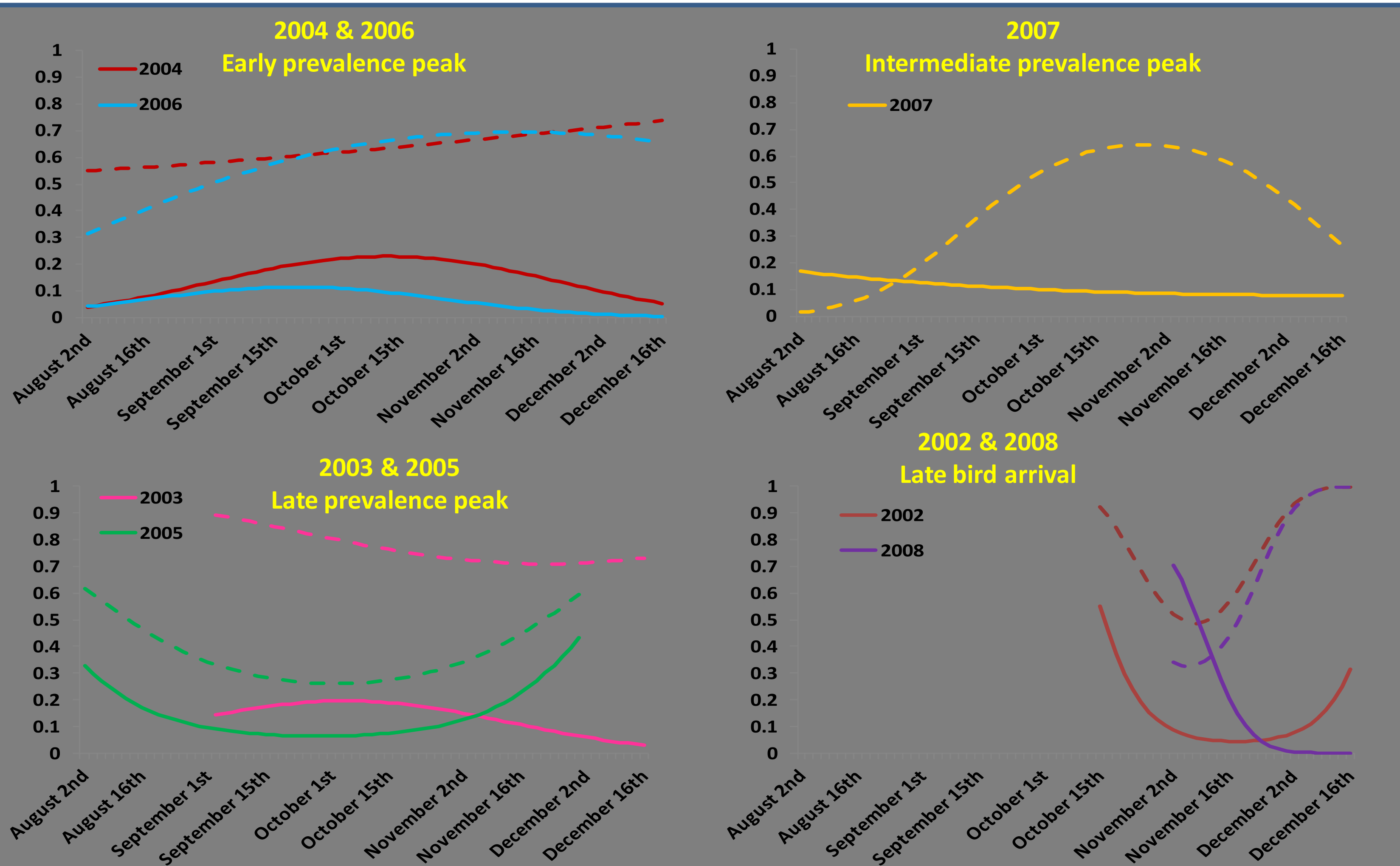
- It seems however that some patterns are recurrent

YEAR & SEASONAL VARIATION IN EPIDEMIOLOGICAL PARAMETERS



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CONCLUSIONS

- A complex epidemiological system (in particular because the host population is extremely open)

- All parameters show variation between years in their seasonal patterns (difficult to identify typical patterns)

- It seems however that some patterns are recurrent

- An important parameter still needs to be described: the rate at which individuals in different epidemiological states arrive at the stopover site

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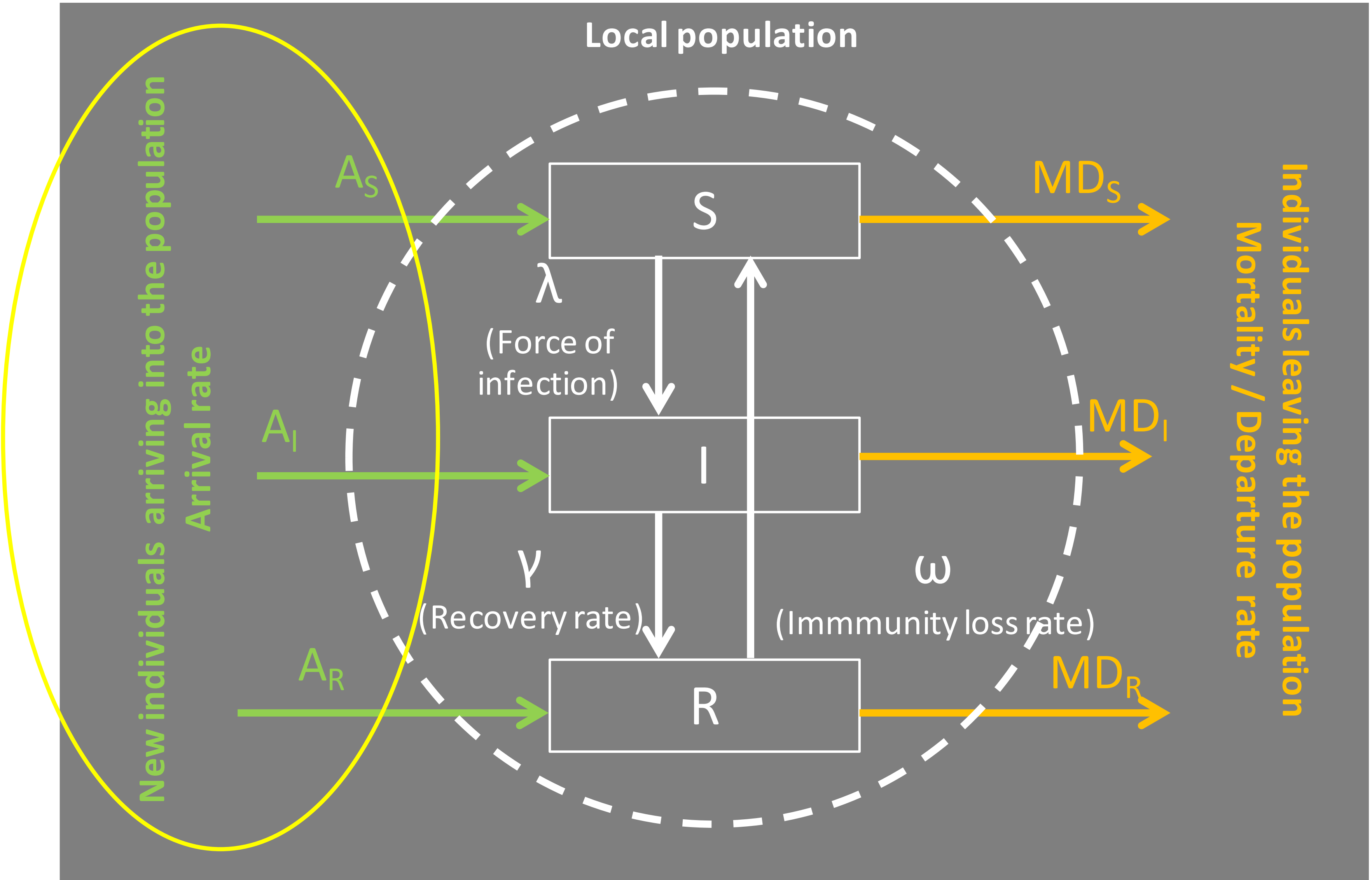

CMR METHODS IN OTHER CONTEXTS

- Not a tool for early detection / warning system / sentinel

- An excellent tool for retrospective analyses:
  - Describing epidemiological dynamics
  - Parameterizing epidemiological models (SIR type models)
  - Inferring epidemiological mechanisms

- Can be applied to:
  - Other wild or domestic hosts
  - Could be used with information on antibody production
  - An ongoing CMR study on backyard chicken and antobidies of Newcastle disease in Zimbabwe

- Many other CMR models to tackle imperfect detection issues:
  - Multi-event models that account for state uncertainty
  - Multi-list or Uni-list CR models to estimate the size of infected population
  - Patch occupancy models to estimate prevalences and incidences