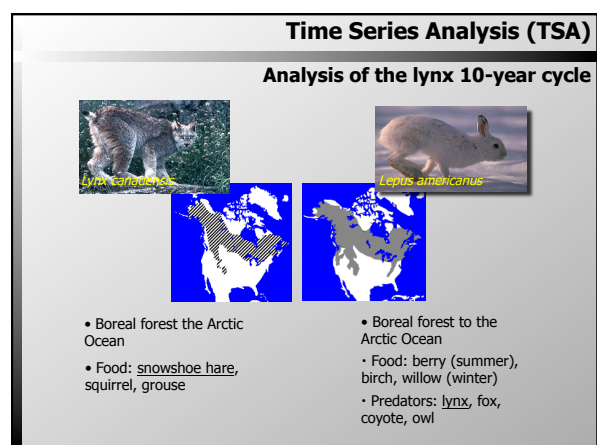
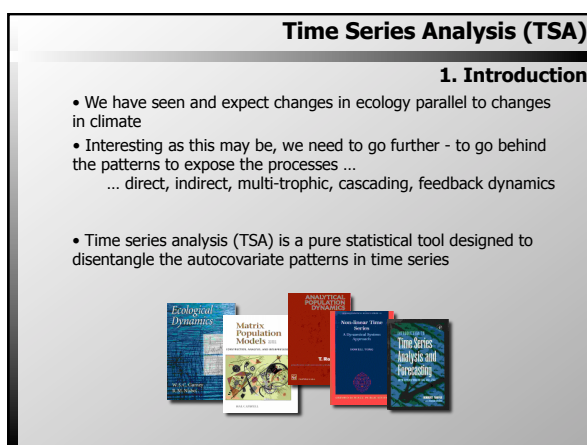
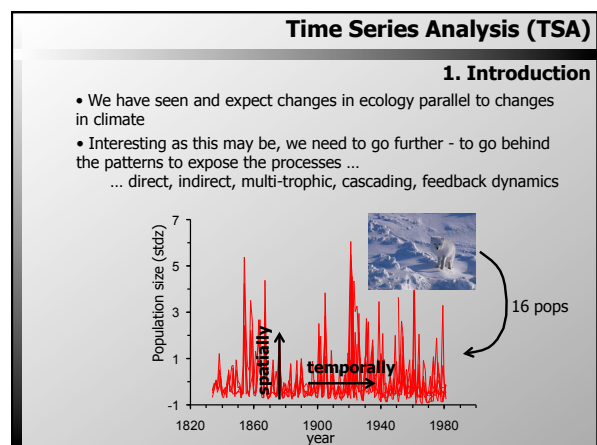
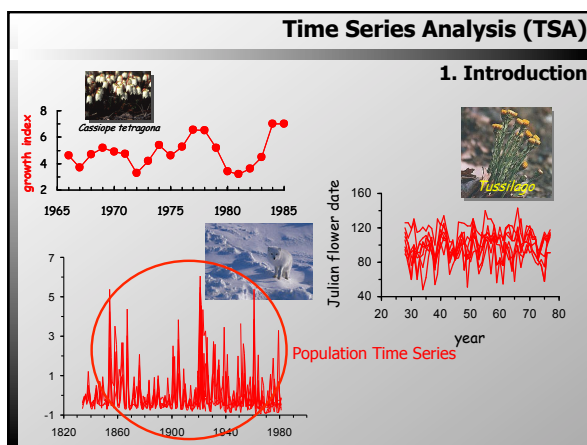
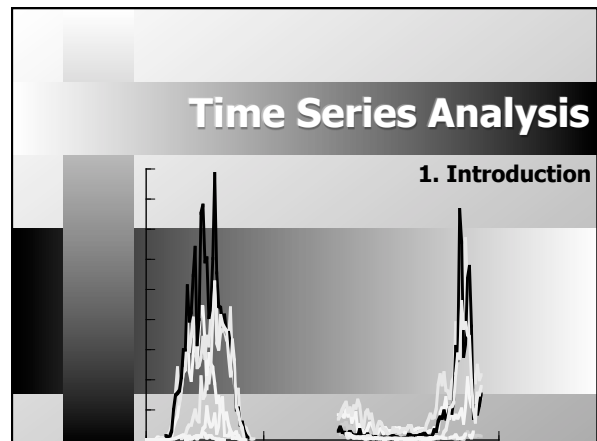
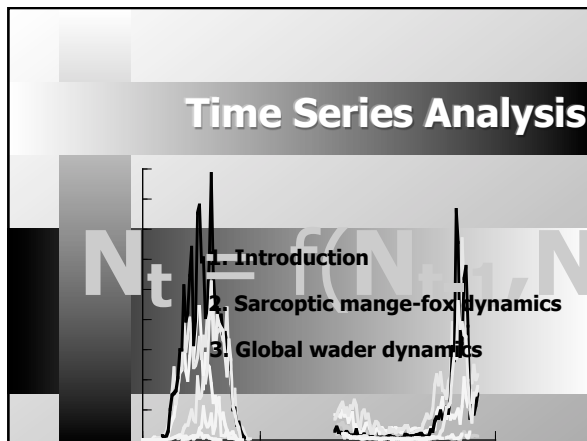




Time Series Analysis (TSA)

An example: the lynx 10-year cycle

Distinct 10-year cycle (harvest data)

Processor?: obscure!

EXTRINSIC (DID): Lunar cycles (moonlight quality), Weather, Forest-fire (plant)
 INTRINSIC (DD): Hare population, Plant-Hare, Lynx-Hare

Sun spots

Time Series Analysis (TSA)

An example: the lynx 10-year cycle

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Time Series Analysis (TSA)

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Processor?: obscure!

EXTRINSIC (DID): Lunar cycles (moonlight quality), Weather, Forest-fire (plant)
 INTRINSIC (DD): Hare population, Plant-Hare, Lynx-Hare

Sun spots

Hmm!

Pure correlation analyses not good!

Time Series Analysis (TSA)

An example: the lynx 10-year cycle

What to do?

Time Series Analysis (TSA)

An example: the lynx 10-year cycle

Kluane indicates that hare-predator interactions are central.

$N_t = f(N_{t-1}, N_{t-2}, \dots, N_{t-11})!$
 ... dynamics non-linear!

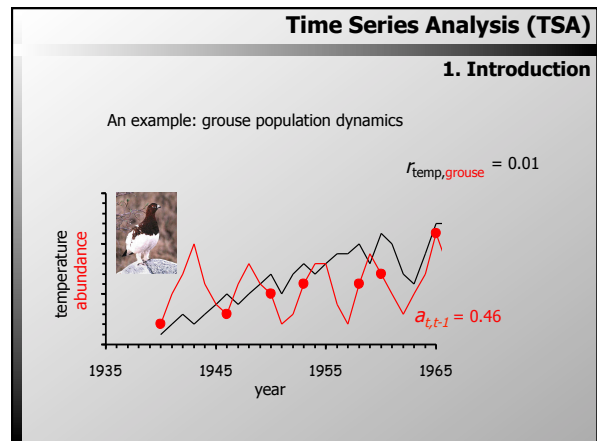
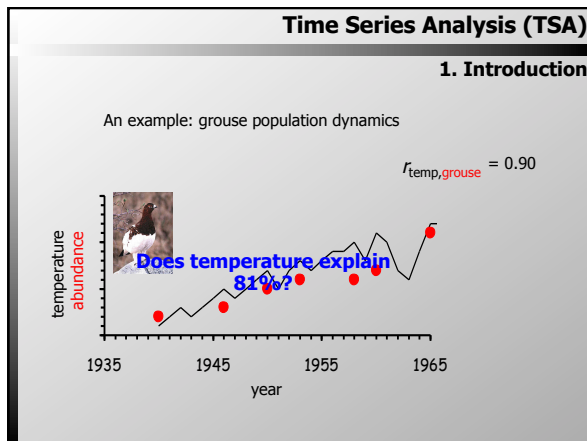
High dependence (80%) on hare density ...

$N_t = \begin{cases} f(N_{t-1}, N_{t-2}) & \text{increase} \\ f(N_{t-1}, N_{t-2}) & \text{decrease} \end{cases}$

Time Series Analysis (TSA)

1. Introduction

An example: grouse population dynamics



Time Series Analysis (TSA)

1. Introduction

(i) Scale is important: data must reflect biology
(ii) Data often have an "internal dependence" (populations and phenology)

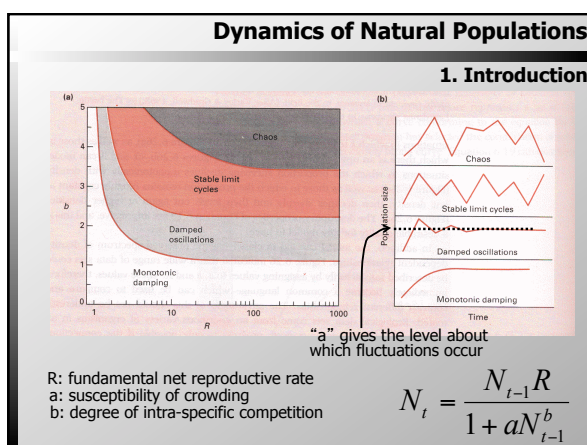
John Maynard Smith
... "mathematics without ecology are sterile" ...

- TSA makes no sense without an ecological framework

Time Series Analysis (TSA)

1. Introduction

Maynard Smith – Slatkin population model

$$N_t = \frac{N_{t-1}R}{1 + aN_{t-1}^b}$$


Time Series Analysis (TSA)

1. Introduction

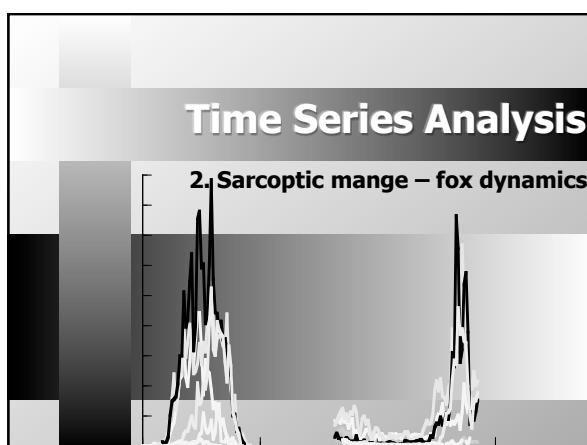
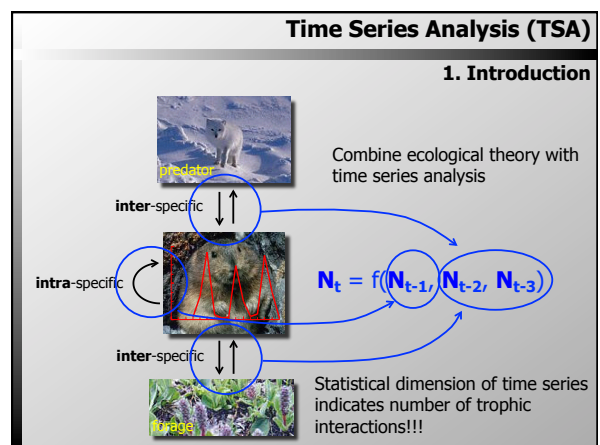
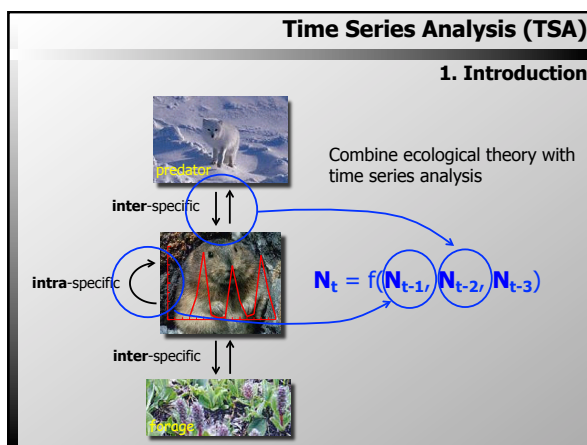
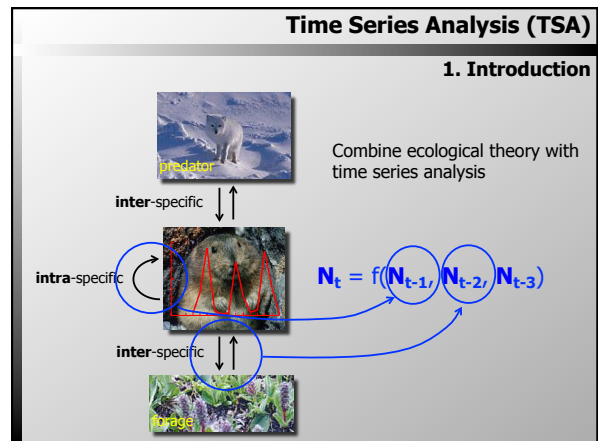
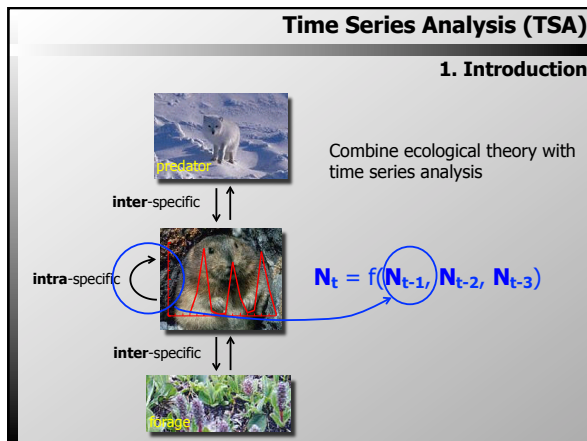
Maynard Smith – Slatkin population model

$$N_t = \frac{N_{t-1}R}{1 + aN_{t-1}^b}$$

$$X_t = X_{t-1} + r - \log_e(1 + aN_{t-1}^b)$$

$$X_t = (r - b \log_e(a)) + (1 - b)X_{t-1}$$

Autoregressive model (AR)



Time Series Analysis (TSA)

2. Sarcoptic mange – fox dynamics

- The disease sarcoptic mange is caused by the skin-dwelling mite (*Sarcoptes scabiei* var. *vulpes*) and has been reported in red fox populations in Europe, North America and Russia.
- Approximately one month after exposure, infected foxes commonly develop skin lesions characteristic of hyperkeratosis. Severe loss of hair and progressive deterioration of body condition then follows and, in the majority of observed cases, infected foxes eventually die from starvation.

Time Series Analysis (TSA)

2. Sarcoptic mange – fox dynamics

The figure displays a map of Sweden with 14 locations marked by arrows pointing to time series plots of fox dynamics ($X(t)$) from 1950 to 1990. The locations are: Norrtälje, Århus, Norrtälje, Västervik, Ringebu, Rättvik, Västervik, Söderköping, Kårehamn, Söderköping, Bornholm, Söderköping, Fyn, and Skåne. Each plot shows the fox dynamics over time, with arrows indicating the location of the data source.

Time Series Analysis (TSA)

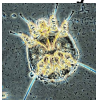
2. Sarcoptic mange – fox dynamics

X-level



$M_t = M_{t-1} \exp [f(X_{t-1}, Y_{t-1})]$

Y-level



$N_t = N_{t-1} \exp [g(X_{t-1}, Y_{t-1})]$

$\alpha_{XY} = \partial f / \partial X$


$\alpha_{YX} = \partial g / \partial X$


$\alpha_{YX} = \partial g / \partial Y$


$$X_t = \beta_0 + \beta_1 X_{t-1} + \beta_2 X_{t-1}$$

Density
dependence

Effect of
mange

Time Series Analysis (TSA)

2. Sarcocytic mange – fox dynamics

Density dependence Effect of mange

$$X_t = \beta_0 + \beta_1 X_{t-1} + \beta_2 X_{t-1}$$

 **AR(1)** **<1** **0**

 **AR(2)** **1** **<0**

Time Series Analysis (TSA)

2. Sarcoptic mange – fox dynamics

The graph illustrates the relationship between β_1 (x-axis) and β_2 (y-axis) for fox dynamics. The x-axis ranges from -2 to 2, and the y-axis ranges from -1 to 1. A triangular region is defined by the lines $\beta_1 = -2$, $\beta_1 = 2$, and $\beta_2 = 1$. A curve is plotted within this region, separating the area into two parts: "not exposed to sarcoptic mange" (above the curve) and "exposed to sarcoptic mange" (below the curve). An inset scatter plot shows various locations (NYJ, ARH, VIB, BOR, RIN, VEJ, RIB, SJY) with arrows indicating transitions between them.

Time Series Analysis (TSA)

2. Prey dynamics with climate

Diagram illustrating a predator-prey model with climate influence:

- Predator (fox):** $Y_t = \ln(P_t)$. Influenced by $a_1(t-1)$ (self-loop) and $a_2(t)$ (from prey).
- Prey (deer):** $X_t = \ln(N_t)$. Influenced by $b_1(t-1)$ (self-loop) and $b_2(t)$ (from climate).
- Climate:** U_t (represented by a cloud).

Mathematical models for the time series:

$$P_t = P_{t-1} \exp(a_0 + a_1 Y_{t-1} + a_2 X_{t-2} + a_3 U_t)$$

$$N_t = N_{t-1} \exp(b_0 + b_1 X_{t-1} + b_2 Y_t + b_3 U_t)$$

State transition equations (highlighted in red in the original image):

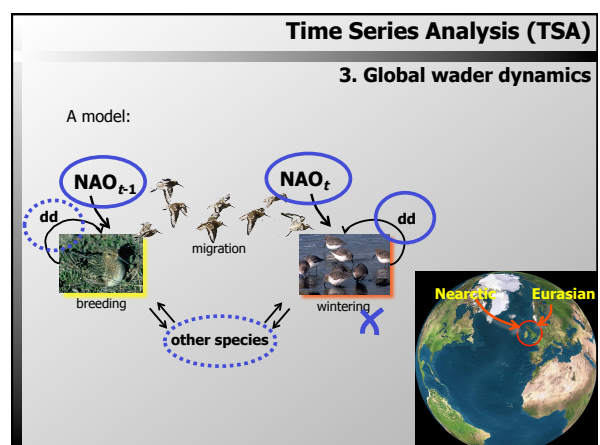
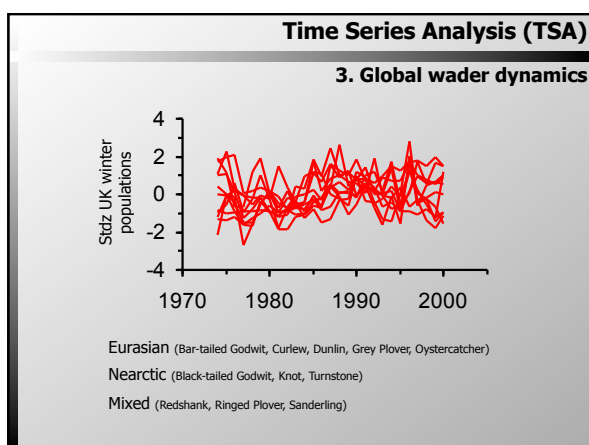
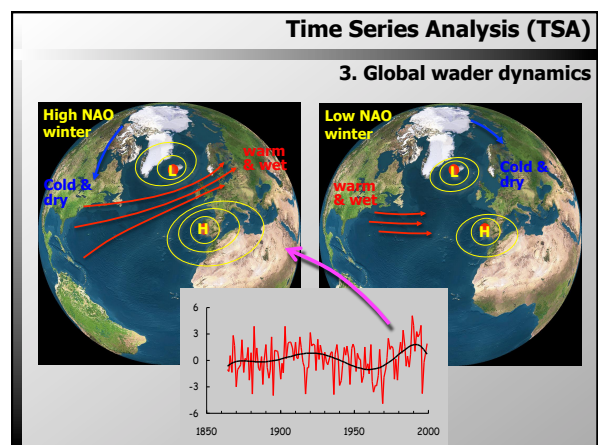
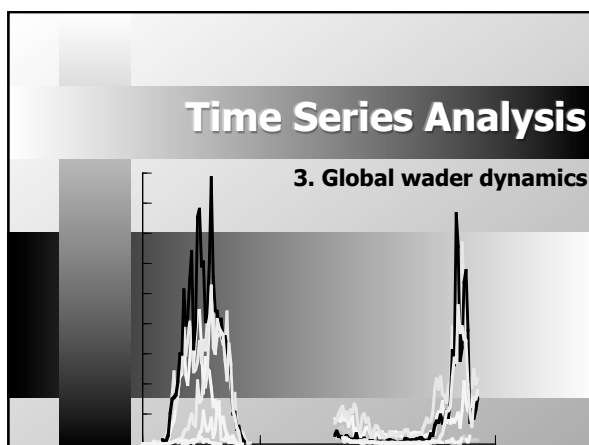
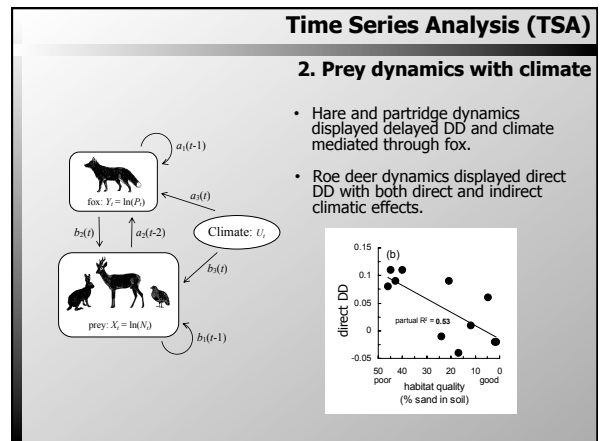
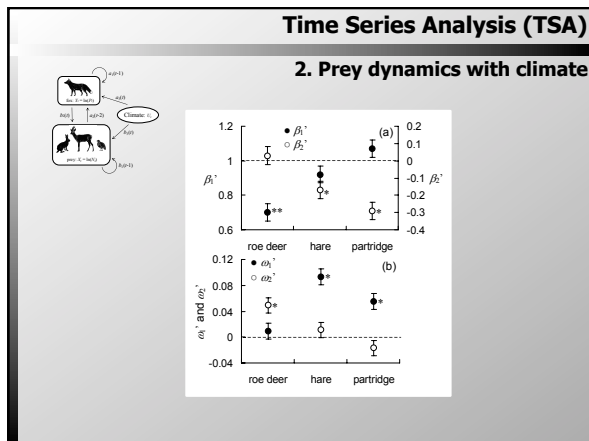
$$X_t = (b_0 a_0 - a_1 b_0) + (2 + a_1 + b_1) X_{t-1} + (b_2 a_2 - b_1 - a_1 - a_1 b_1 - 1) X_{t-2} + (b_3 + b_2 a_3) U_t + (-b_3 a_1 - b_2) U_{t-1}$$

ARMA (2,2): $X_t = \beta_0 + \beta_1 X_{t-1} + \beta_2 X_{t-2} + \omega_1 U_t + \omega_2 U_{t-1}$

Time Series Analysis (TSA)

2. Prey dynamics with climate

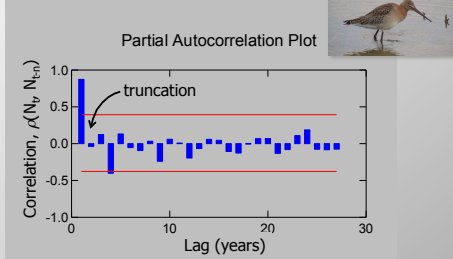
Statistical coefficients	Ecological coefficients	Ecological interpretation
β_1	$2+a_1+b_1$	direct density dependence: function of intra-trophic interactions $\{a_1, b_1\}$ only.
β_2	$b_2 a_2 - b_1 - a_1 b_1 - 1$	delayed density dependence: function of intra-trophic interactions $\{a_2, b_2\}$ and a complex function of intra-trophic interactions $\{a_1, b_1\}$.
ω_1	$b_3 + b_2 a_3$	additive effect of direct $\{b_3\}$ and indirect climatic influence through predator dynamics $\{a_3, b_2\}$.
ω_2	$-b_3 a_1 - b_3$	direct climatic influence $\{b_3\}$ relative to its interaction with fox density dependence $\{a_1\}$.



Time Series Analysis (TSA)

3. Global wader dynamics

Autocovariate structure: lagged influence of N on N

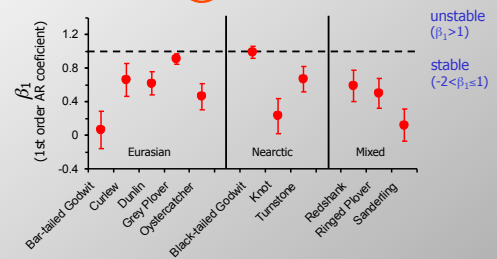


AR(1) process!: $N_t = f(N_{t-1}, \text{NAO}_t, \text{NAO}_{t-1})$

Time Series Analysis (TSA)

3. Global wader dynamics

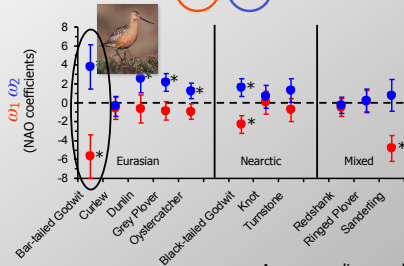
Autocovariate structure: $N_t = f(N_{t-1}, \text{NAO}_t, \text{NAO}_{t-1})$



Time Series Analysis (TSA)

3. Global wader dynamics

Covariate structure: $N_t = f(N_{t-1}, \text{NAO}_t, \text{NAO}_{t-1})$

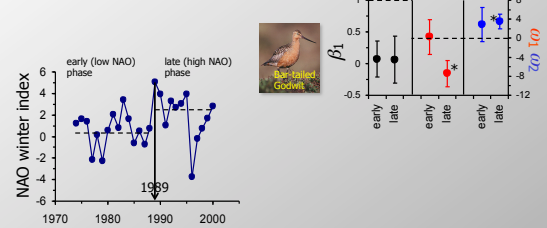


Assumes a linear relationship between NAO and N!

Time Series Analysis (TSA)

3. Global wader dynamics

Non-linear effects of the NAO: a TAR model

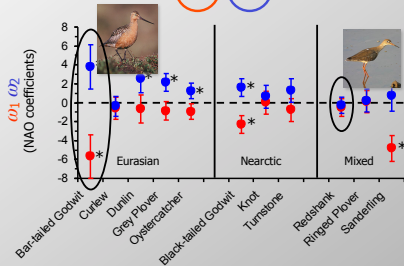


Tree-regression analysis (reduce deviance by splitting)

Time Series Analysis (TSA)

3. Global wader dynamics

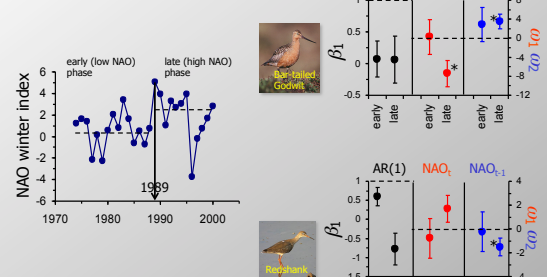
Covariate structure: $N_t = f(N_{t-1}, \text{NAO}_t, \text{NAO}_{t-1})$



Time Series Analysis (TSA)

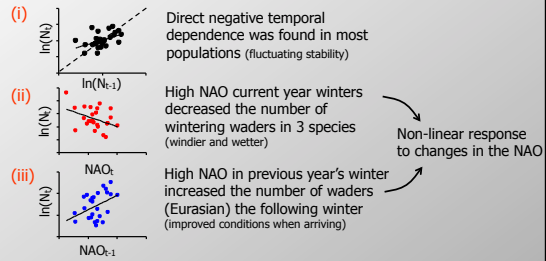
3. Global wader dynamics

Non-linear effects of the NAO: a TAR model



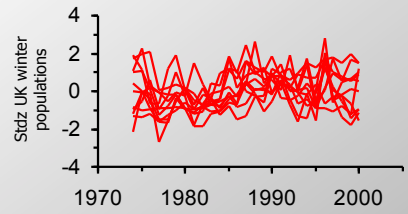
Time Series Analysis (TSA)

3. Global wader dynamics



Time Series Analysis (TSA)

3. Global wader dynamics



Eurasian (Bar-tailed Godwit, Curlew, Dunlin, Grey Plover, Oystercatcher)

Nearctic (Black-tailed Godwit, Knot, Turnstone)

Mixed (Redshank, Ringed Plover, Sanderling)



Mads C. Forchhammer
Aarhus University
Department of Bioscience
Arctic Research Centre (ARC)
CIRCE
email: mcf@dmu.dk