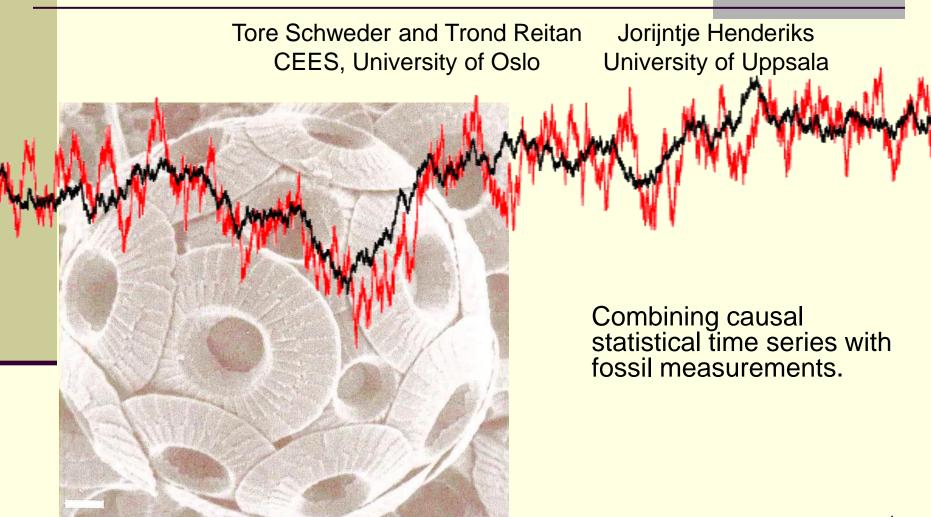
## Layered continuous time processes in biology



#### Overview

- 1. Introduction Motivating example:
  - Coccolith data (microfossils)
  - Phenotypic evolution: irregular time series related by (possibly common) latent processes
- 2. Causality in continuous time processes
- 3. Stochastic differential equation vector processes
  - Ito representation and diagonalization
  - Tracking processes and hidden layers
  - Kalman filtering
  - Model variants
- 4. Inference and results
  - Bayesian inference on model properties, models, process parameters and process states
  - Results for the coccolith data.
- 5. Second application: Phenotypic evolution on a phylogenetic tree
  - Primates preliminary results
- 6. Conclusion

# Irregular time series related by latent processes: evolution of body size in *Coccolithus*

Henderiks - Schweder - Reitan

The size of a single cell algae (*Coccolithus*) is measured by the diameter of its fossilized coccoliths (calcite platelets). Want to model the evolution of a lineage found at six sites.

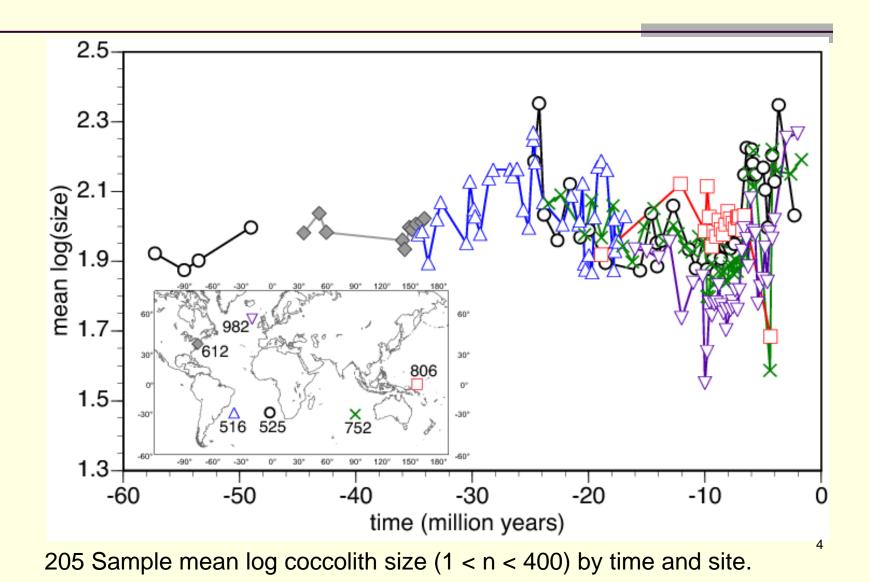
Phenotype (size) is a process in continuous time

and changes continuously.

19,899 coccolith measurements, 205 sediment samples (1< n < 400) of body size by site and time (0 to -60 my).



## Our data - Coccolith size measurements



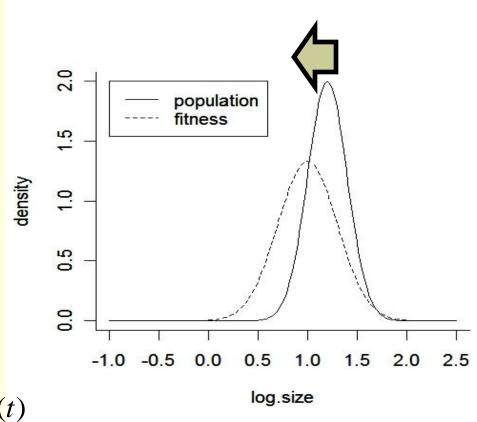
## Evolution of size distribution

Fitness = expected number of reproducing offspring.

The population tracks the fitness curve (natural selection)
The fitness curve moves about, the population follow.

With a known fitness,  $\mu$ , the mean phenotype should be an Ornstein-Uhlenbeck process (Lande 1976).

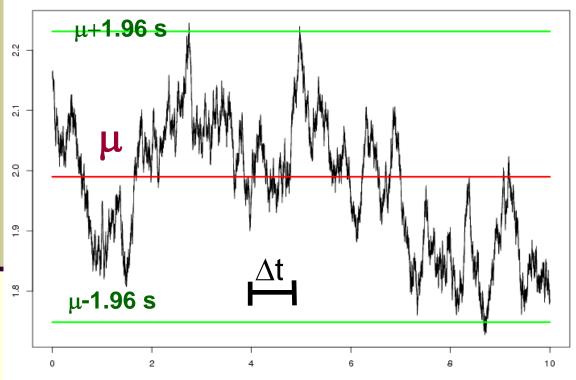
$$dX(t) = -\alpha \mathbf{V}(t) - \mu dt + \sigma dW(t)$$



With fitness as a process,  $\mu(t)$ , we can make a tracking model:  $dX(t) = -\alpha (X(t) - \mu(t)) dt + \sigma dW(t)$ <sub>5</sub>

## The Ornstein-Uhlenbeck process

$$dX(t) = -\alpha \langle X(t) - \mu \rangle dt + \sigma dW(t)$$



#### Attributes:

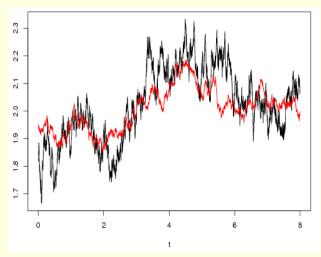
- Stationary
  - Normally distributed
  - $\triangleright$  long-term level:  $\mu$
  - > Standard deviation:  $s=\sigma/\sqrt{2}\alpha$
- Markovian
  - > α: pull
  - $\triangleright$  corr(x(0),x(t))=e<sup>- $\alpha$ t</sup>
  - Time for the correlation to drop to 1/e:  $\Delta t = 1/\alpha$

The parameters  $(\mu, \Delta t, s)$  can be estimated from the data. In this case:  $\mu \approx 1.99$ ,  $\Delta t = 1/\alpha \approx 0.80$ Myr,  $s \approx 0.12$ .

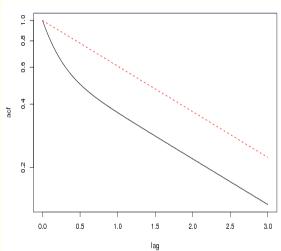
## One layer tracking another

$$dX_{1}(t) = -\alpha_{1} X_{1}(t) - X_{2}(t) dt + \sigma_{1} dW_{1}(t)$$

$$dX_{2}(t) = -\alpha_{2} X_{2}(t) - \mu dt + \sigma_{2} dW_{2}(t)$$



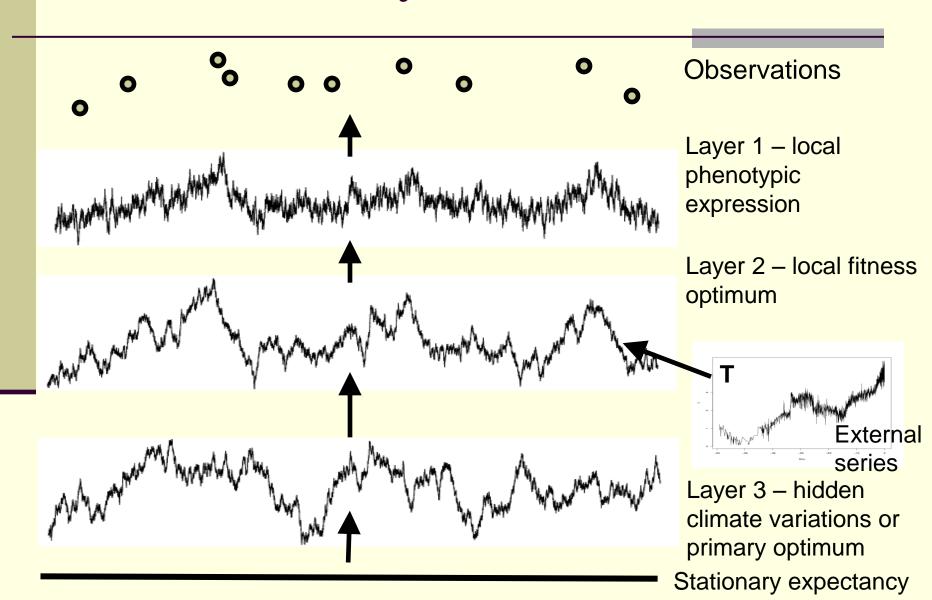
Black process ( $\Delta t_1 = 1/\alpha_1 = 0.2$ ,  $s_1 = 2$ ) tracking red process ( $\Delta t_2 = 1/\alpha_2 = 2$ ,  $s_2 = 1$ )



Auto-correlation of the upper (black) process, compared to a one-layered SDE model.

A slow-tracking-fast can always be re-scaled to a fast-tracking slow process. Impose identifying restriction:  $\alpha_1 \ge \alpha_2$ 

# Process layers - illustration



# Causality in SDE processes

We want to express in process terms the fact that climate affects the phenotypic optimum which again affects the actual phenotype.

Local independence (Schweder 1970):

- Context: Composable continuous time processes.
- Component A is locally independent of B iff transition prob. of A does not depend on B.
- If B is locally dependent on A but not vice versa, we write A→B.

Local dependence can form a notion of causality in cont. time processes the same way Granger causality does for discrete time processes.

# Stochastic differential equation (SDE) vector processes

X(t): p - dimensiona 1 vector state process

W(t):q - dimensiona 1 vector Wi ener process (Brownian motion)

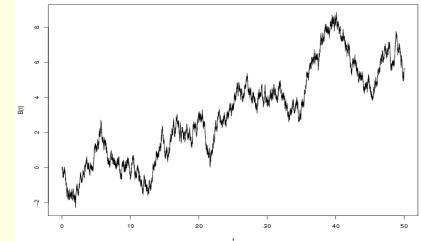
 $\mu(t) = \beta u(t)$ : p-dimensiona l level process,  $\beta$  a  $p \times r$  regression matrix

 $A: p \times p$  dimensiona 1 pull matrix

 $\sum p \times q$  dimensiona 1 diffusion matrix

$$dX(t) = (AX(t) + \mu(t))dt + \Sigma dW(t)$$

Ito solution:



$$X(t) = B(t)^{-1} \left\{ X(0) + \int_{0}^{t} B(u)\mu(u)du + \int_{0}^{t} B(u)\Sigma dW(u) \right\}$$

$$B(t) = e^{-At} = \sum_{n=0}^{\infty} A^n (-t)^n / n! = V^{-1} e^{-\Lambda t} V$$
 (when existing)

 $\Lambda$  is a diagonal eigenvalue matrix of A, V is the left eigenvector matrix.

## Stochastic differential equation (SDE) vector processes

#### Causal structure in linear SDEs:

If we want to have the causal structure  $X_L \to X_{L-1} \to \cdots \to X_2 \to X_1$ we would express this as a system of OU - like tracking processes

$$dX_{L} = -\alpha_{L}(X_{L} - \mu)dt + \sigma_{L}dB_{L}(t)$$

$$dX_{L-1} = -\alpha_{L-1}(X_{L-1} - X_{L})dt + \sigma_{L-1}dB_{L-1}(t)$$

$$\vdots$$

$$dX_{1} = -\alpha_{1}(X_{1} - X_{2})dt + \sigma_{1}dB_{1}(t)$$

Expressed in vectori al form, this will yield a pull matrix looking like this:

$$\mathbf{A} = \begin{pmatrix} -\alpha_1 & \alpha_1 & 0 & \cdots & 0 & 0 \\ 0 & -\alpha_2 & \alpha_2 & \cdots & 0 & 0 \\ \ddots & \ddots & \ddots & \ddots & \ddots & \ddots \\ 0 & 0 & 0 & \cdots & -\alpha_{L-1} & \alpha_{L-1} \\ 0 & 0 & 0 & \cdots & 0 & -\alpha_L \end{pmatrix}$$
 The zeros in this matrix defined by the local independencies.

The zeros in this matrix determines

## Model variants for Coccolith evolution

#### Model variations:

- 1, 2 or 3 layers (possibly more)
- Inclusion of external time series or extra internal time series in connection to the one we are modelling
- In a single layer:
  - Local or global parameters
  - Correlation between sites (inter-regional correlation)
  - Deterministic response to the lower layer
  - Random walk (no tracking)

## Likelihood: Kalman filter

Need a linear, normal Markov chain with independent normal observations:

The Ito solution

$$X(t) = B(t)^{-1} \left\{ X(0) + \int_{0}^{t} B(u)\mu(u)du + \int_{0}^{t} B(u)\Sigma dW(u) \right\}$$

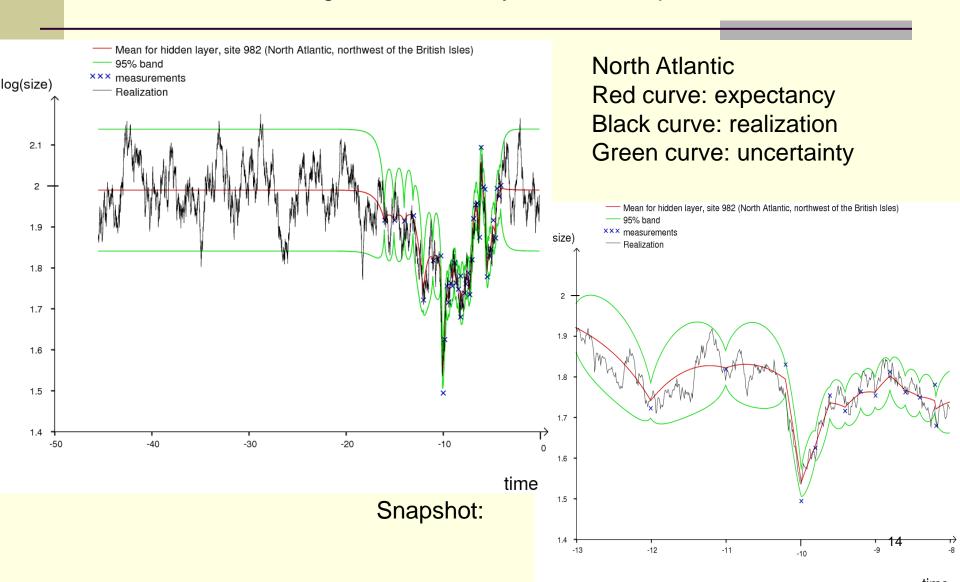
gives, together with measurement variances, what is needed to calculate the likelihood using the Kalman filter:

$$E(z_i | z_1, ..., z_{i-1}) \equiv m_i \text{ and } Var(z_i | z_1, ..., z_{i-1}) \equiv v_i$$

$$f(\underline{z} \mid \theta) = \prod_{i=1}^{n} f_{N}(z_{i} \mid m_{i}, v_{i}, \theta)$$

## Kalman smoothing (state inference)

A tracking model with 3 layers and fixed parameters

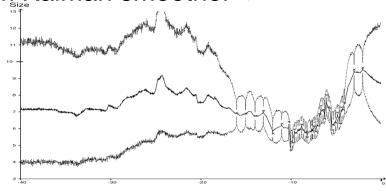


## Parameter and model inference

- Wide but informative prior distributions respecting identifying restrictions
- MCMC for parameter inference on individual models:

MCMC samples+state samples from Kalman smoother ->

Possible to do inference on the process state conditioned only on the data.



- Model likelihood (using an importance sampler) for model comparison (posterior model probabilities).
- Posterior weight of a property C from model likelihoods:

$$W(C) = \frac{\frac{1}{n_C} \sum_{M \in C} f(data \mid M)}{\sum_{C'} \frac{1}{n_{C'}} \sum_{M \in C'} f(data \mid M)}$$
15

## Bayesian inference on the 723 models

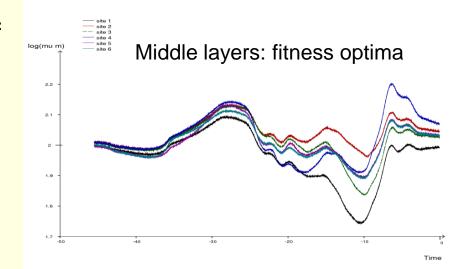
Table 2. Posterior weights for different properties. Number of models in parenthesis.

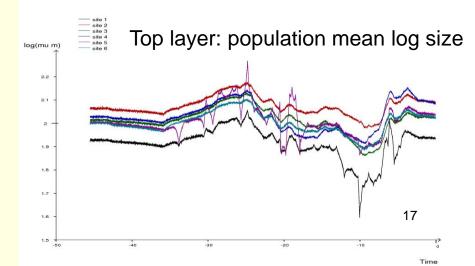
Property	Options			
Number of Layers:	1	2	3	
	4.3% (19)	45.8% (112)	49.9% (592)	
Regionality in:	none or $\mu_0$	pull	diffusion	
	0.15% (252)	79.5% (300)	20.4% (171)	
Regional parameters in:	no layer	upper layer	middle layer	lower layer
	0.09% (252)	20.7% (144)	23.1% (180)	56.1% (147)
Inter-regional	none	intermediate (6D)	perfect (1D)	
correlations:	19.0% (39)	62.3% (169)	18.7% (515)	
Random walk in	no	yes		
lowest layer	90.4% (393)	9.6% (330)		

$$W(C) = \frac{\frac{1}{n_{C}} \sum_{M \in C} f(data \mid M)}{\sum_{C'} \frac{1}{n_{C'}} \sum_{M \in C'} f(data \mid M)}$$

#### Results

- Best 5 models in good agreement. (together, 19.7% of summed integrated likelihood):
  - Three layers.
  - Common expectancy in bottom layer.
  - No impact of exogenous temperature series.
  - Lowest layer: Inter-regional correlations,  $\rho \approx 0.5$ . Sitespecific pull.
  - Middle layer: Intermediate tracking.
  - Upper layer: Very fast tracking.





# Phenotypic evolution on a phylogenetic tree: Body size of primates

Measuremen ts  $i \in \{1,...,209\}$  92 extant measuremen ts, 117 fossils)

 $X_{i,1}(t)$  = mean phenotype (log mass)

 $X_{i,2}(t)$  = fitness optimum

 $X_{i,3}(t)$  = underlying environment, primary optimum

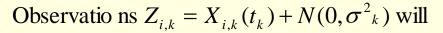
 $X_{i,3} \to X_{i,2} \to X_{i,1}$  same tracking model as for coccoliths

#### Phylogenet ic tree:

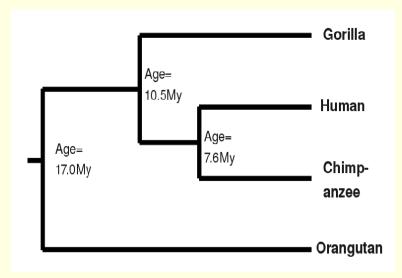
 $T_{i,j}$  = Time when *i* split from *j*.

$$X_{i,l}(t) = X_{j,l}(t)$$
 when  $t \le T_{i,j}$ .

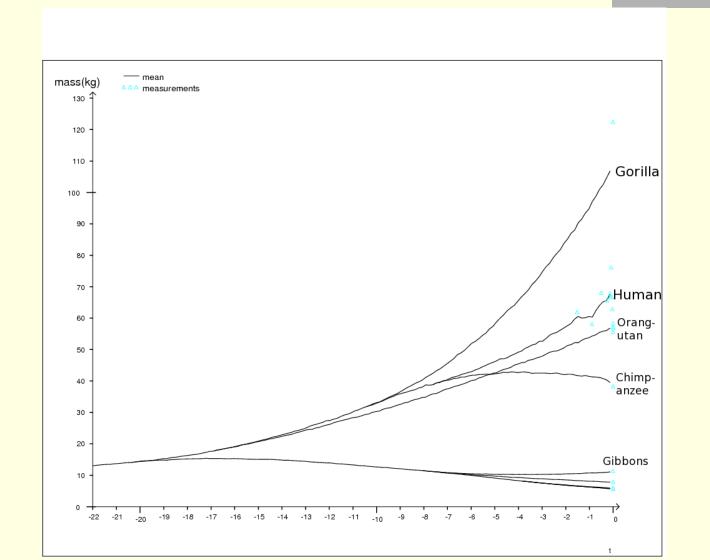
Condition on these equalities for the given tree.



be multi - normally distribute d with mean vector and covariance matrix as parametric expression s from the SDE model.



## First results for some primates



#### Why linear SDE processes?

- Parsimonious: Simplest way of having a stochastic continuous time process that can track something else.
- Tractable: The likelihood,  $L(\theta) \equiv f(Data \mid \theta)$ , can be analytically calculated by the Kalman filter or directly by the parameterized multinormal model for the observations. ( $\theta = model$  parameter set)
- Can code for causal structure (local dependence/independence).
- Some justification in biology, see Lande (1976), Estes and Arnold (2007), Hansen (1997), Hansen et. al (2008).
- Great flexibility, widely applicable...
- Thinking and modelling might then be more natural in continuous time.
- Allows for varying observation frequency, missing data and observations arbitrary spaced in time.
- Extensions:
  - Non-linear SDE models...
  - Non-Gaussian instantaneous stochasticity (jump processes).

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Source codes, examples files and supplementary information can be found at http://folk.uio.no/trondr/layered/.