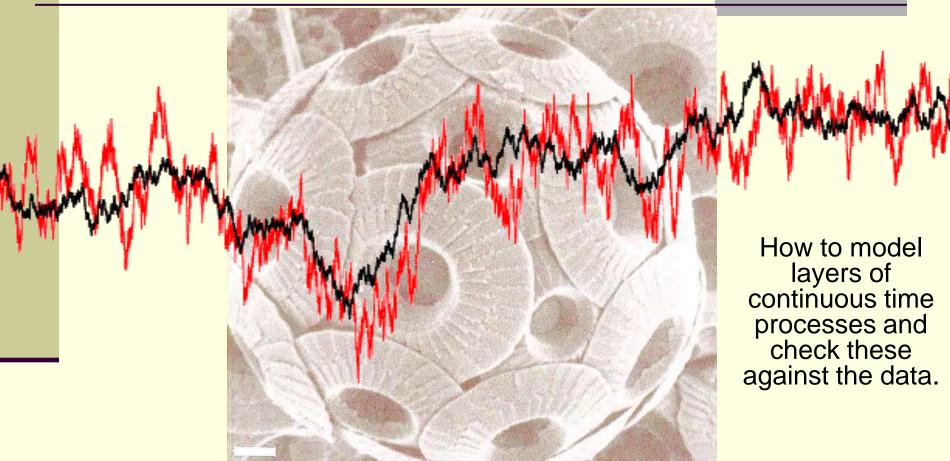
Modelling phenotypic evolution using layered stochastic differential equations (with applications for Coccolith data)



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Our data - Coccoliths

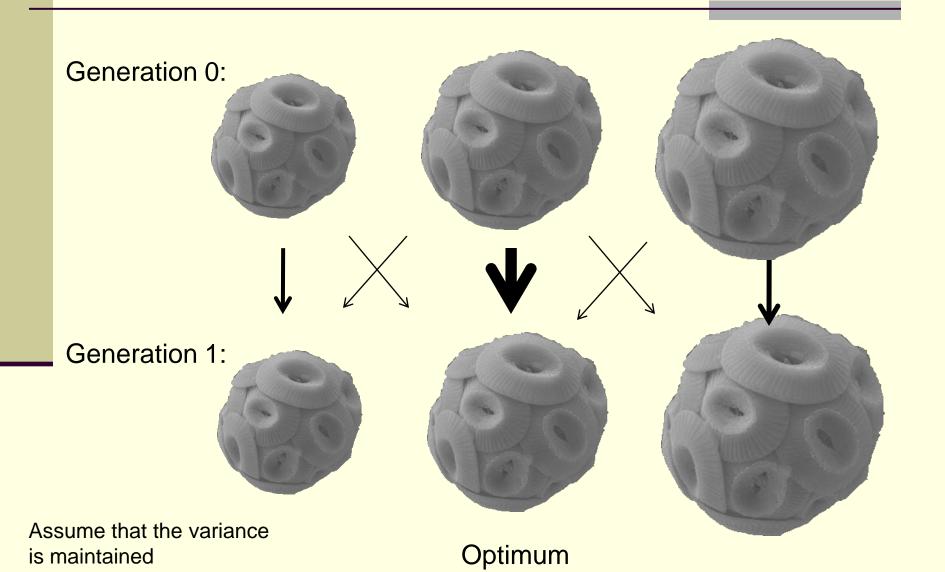
Measurements are on the diameter of Coccoliths from marine, calcifying single cell algae (Haptophyceae).

These are covered by calcite platelets ('coccoliths' forming a 'coccosphere')

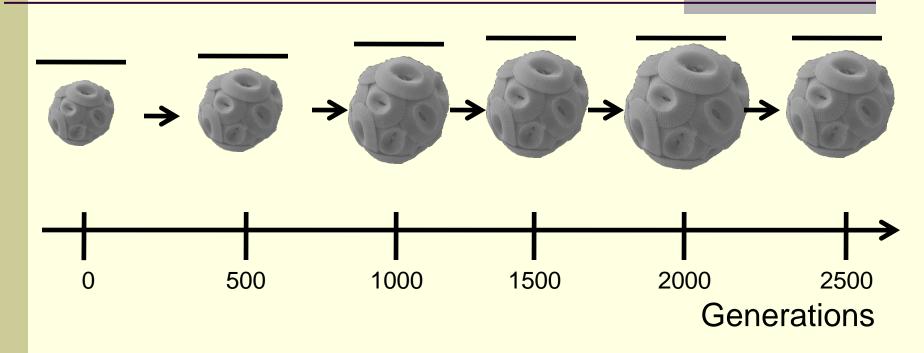


SEM image: J. Henderiks, Stockholm University

Size (phenotype) variation



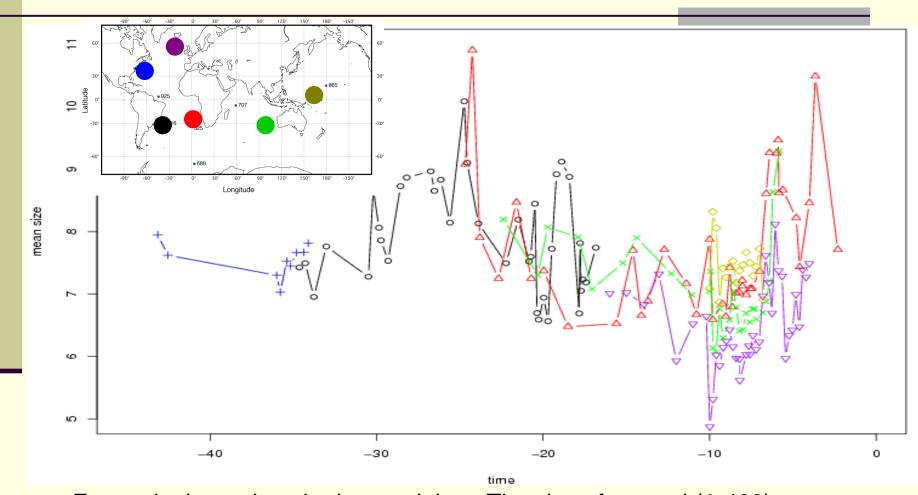
Change of the average in time



Mean changes. Pulled towards the optimum, but always with some fluctuations. => Stochastic process Lande, 1976: This is an Ornstein-Uhlenbeck process

But: The optimum may also change!

Our data – Coccolith size measurements



For each site and each observed time: The size of several (1-400) Coccoliths was measured. Mean size shown. (For analysis, the data was log-transformed. After data massage: n=178 different mean sizes.)

Concepts

- Data: Several size measurements for different ages and sites. => average and variance
- Should express something about an underlying set of processes, optima-layers, belonging to the lineage.
- Non-equidistant time series: Continuous in time
- Stochastic
- Can we use the data to say something about the processes?

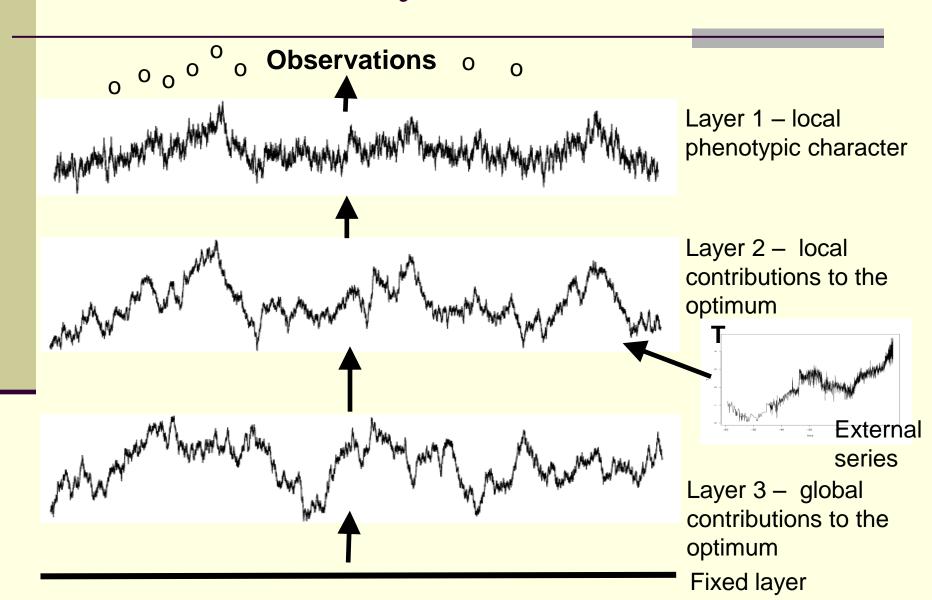
Background

- Data:Jorijntje Henderiks.
- Tore Schweder: Idea and mathematical foundation.
- Me: Inference, programming and control calculations.

Multiple layers of hidden processes – why?

- Measured mean size is a noisy indicator of overall mean size at a given moment.
- Even with perfect measurements, what happens between needs inference.
- A phenotype character will track an evolutionary optimum (natural selection).
- The optimum changes also. Can be further divided into layers describing global and local contributions.
- Each layer is responding to what happens in a lower layer.

Process layers - illustration

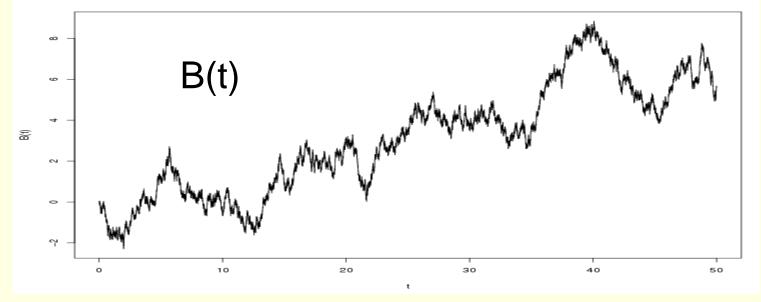


Variants

- Can have different number of layers.
- In a single layer, one has the choice of:
 - Local or global parameters
 - The stochastic contribution can be global or local (site-specific)
 - Correlation between sites (inter-regional correlation)
 - Deterministic response to the lower layer
 - Random walk (not responding to anything else, no tracking)
- In total: 750 models examined

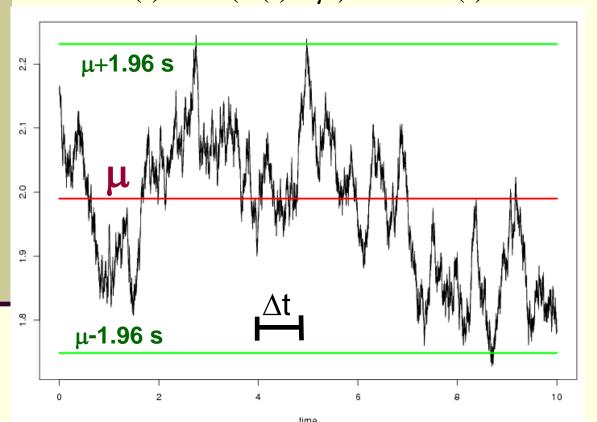
The toolbox – stochastic differential equations, the Wiener process

- Need something that is continuous in time, has a direction and a stochastic element.
- Stochastic differential equations (SDEs): Combines differential equations with the Wiener process.
- Wiener process: continuous time random walk



The Ornstein-Uhlenbeck (mean-reverting) process

$$dY(t) = -a(Y(t) - \mu)dt + \sigma dB(t)$$



Attributes:

- Normally distributed
- Markovian
- Expectancy: μ
- Standard deviation:

s=σ/√2a

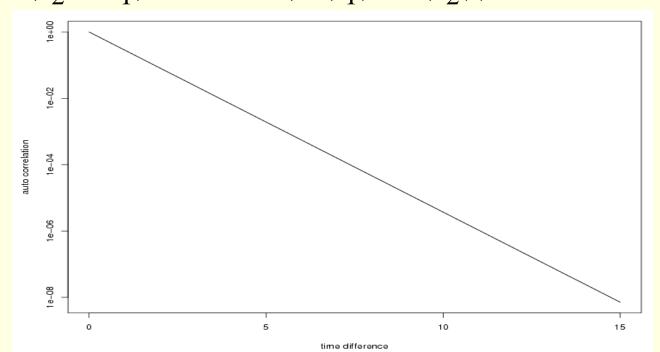
- •a: pull
- Time for the correlation to drop to 1/e: Λt =1/a

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

Autocorrelation

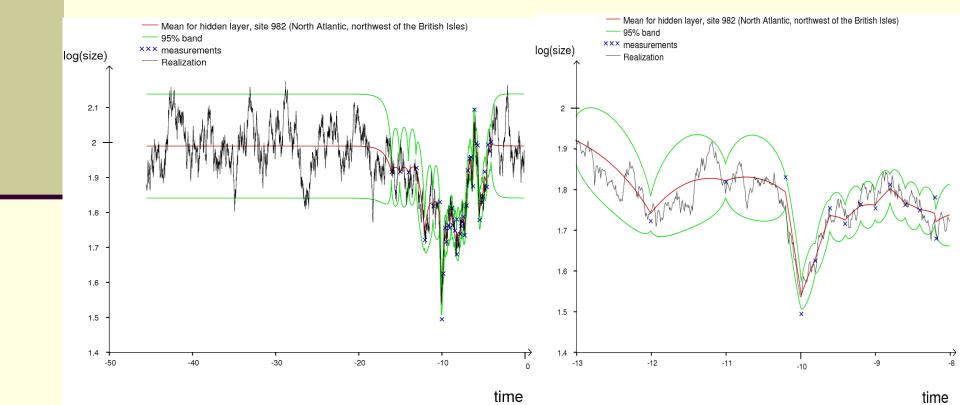
- The autocorrelation function is the correlation between the process state at one time, t_1 , and the process state a later time, t_2 .
- A function of the time difference, t₂-t₁.
- For a single layer OU process,

$$c(t_2 - t_1) \equiv corr(x(t_1), x(t_2)) = e^{-(t_2 - t_1)/\Delta t}$$



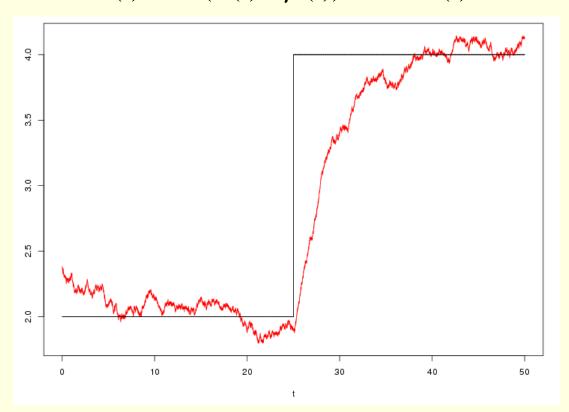
Curiosity: OU process conditioned on data

It's possible to realize an OU process conditioned on the data, also (using the Kalman framework, which will be described later).



OU process tracking another process

$$dY(t) = -a(Y(t) - \mu(t))dt + \sigma dB(t)$$



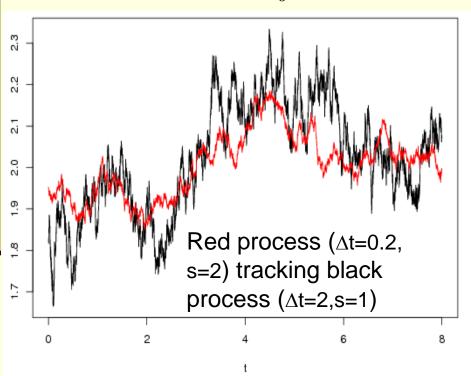
Tracks the underlying function/process, $\mu(t)$, with response time equal to the characteristic time, Δt =1/a

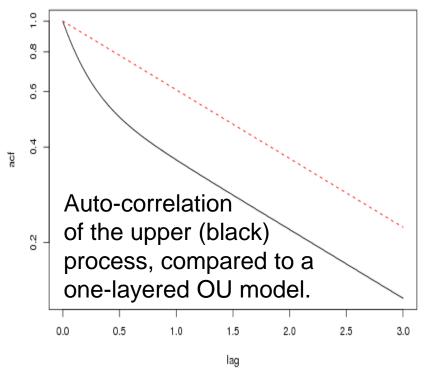
Idea: Let the underlying process be expressed the same way.

OU-like process tracking another OU process

$$dY(t) = -a(Y(t) - \mu(t))dt + \sigma dB(t)$$

$$d\mu(t) = -b(\mu(t) - \mu_0)dt + \omega dW(t)$$





Vectorial linear stochastic differential equation

The two coupled SDEs on the previous slide can be written as:

$$\underline{A}\underline{X}(t) = \left[\underline{A}\underline{X}(t) + \underline{m}(t) \right] dt + \Sigma d\underline{W}(t) \quad \text{when}$$

$$\underline{X}(t) = \begin{pmatrix} y(t) \\ \mu(t) \end{pmatrix} A = \begin{pmatrix} -a & a \\ 0 & -b \end{pmatrix} \quad \underline{m}(t) = \begin{pmatrix} 0 \\ b\mu_0 \end{pmatrix} \Sigma^2 = \begin{pmatrix} \sigma^2 & 0 \\ 0 & \omega^2 \end{pmatrix}$$

Generalization to 3 layers and several sites per layer:

$$\underline{X}(t) = \begin{pmatrix} \underline{X}_{1}(t) \\ \underline{X}_{2}(t) \\ \underline{X}_{3}(t) \end{pmatrix} A = \begin{pmatrix} -A_{1} & A_{1} & 0 \\ 0 & -A_{2} & A_{2} \\ 0 & 0 & A_{3} \end{pmatrix} \underline{m}(t) = \begin{pmatrix} 0 \\ 0 \\ A_{3}\underline{\mu}_{0} \end{pmatrix} \Sigma^{2} = \begin{pmatrix} \Sigma^{2}_{1} & 0 & 0 \\ 0 & \Sigma^{2}_{2} & 0 \\ 0 & 0 & \Sigma^{2}_{3} \end{pmatrix}$$

Solving vectorial linear SDEs

Solve by eigen-representation: $VA = \Lambda V$

Eigenvectors: V

Eigenvalues, $\Lambda = \text{diag}(\underline{\lambda})$

Formal solution:

$$\underline{X}(t) = V^{-1}e^{\Lambda t}VX(0) + V^{-1}\int_{0}^{t}e^{\Lambda(t-u)}V\underline{m}(u)du + V^{-1}\int_{0}^{t}e^{\Lambda(t-u)}V\Sigma d\underline{B}(u)$$

Gaussian process, only expectation and covariance needed!

$$E\underline{X}(t) = V^{-1}e^{\Lambda t}V\underline{X}(0) + V^{-1}\int_{0}^{t}e^{\Lambda(v-u)}V\underline{m}(u)du$$

$$\operatorname{cov}(\underline{X}(v),\underline{X}(t)) = V^{-1} \left[\int_{0}^{v} e^{\Lambda(v-u)} V \Sigma^{2} V' e^{\Lambda(t-u)} du \right] (V^{-1})'$$

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. ($\theta = model parameter set$)
- Some justification from biology, see Lande (1976), Estes and Arnold (2007), Hansen (1997), Hansen et. al (2008).
- Great flexibility...

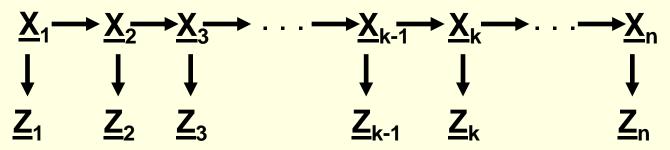
Inference

- Don't know the details of the model or the model parameters, θ. Need to do inference.
- Classic: Search for $\hat{\theta} = \underset{\theta}{\operatorname{arg max}} f(Data \mid \theta)$
 - Use BIC for model comparison.
- Bayesian: $f(\theta | Data) = \frac{f(Data | \theta)f(\theta)}{\int f(Data | \theta)f(\theta)d\theta}$
 - > Need a prior distribution, $f(\theta)$, on the model parameters.
 - Use f(Data|M) for model comparison.
- Technical: Numeric methods for both kinds of analysis.
 - ML: Multiple hill-climbing
 - Bayesian: MCMC + Importance sampling

Calculating the likelihood - Kalman filtering

Basis:

- Hidden linear <u>normal</u> Markov process,
- Observations centered normally around the hidden process,



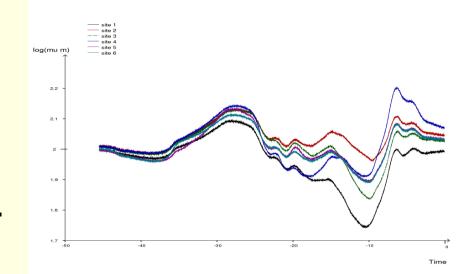
- We can find the transition and covariance matrices for the processes.
- Analytical results for doing inference on a given state and observation given the previous observations.
- Can also do inference on the state given all the observations (Kalman smoothing)

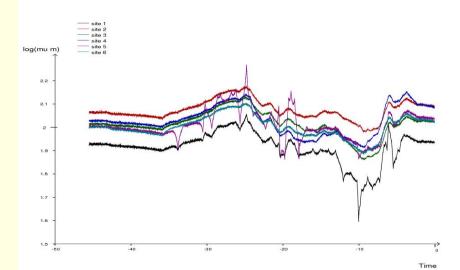
Do we have enough data for full model selection?

- Assume the data has been produced by a given model in this framework.
 - > Can we detect it with the given amount of data?
 - How much data is needed in order to reliably detect this by classic and Bayesian means?
- Check artificial data against the original model plus 25 likely suspects.
- So far: Slight tendency to find the correct number of layers with the Bayesian approach. BIC seems generally too stingy on the number of layers.

Bayesian model comparison result

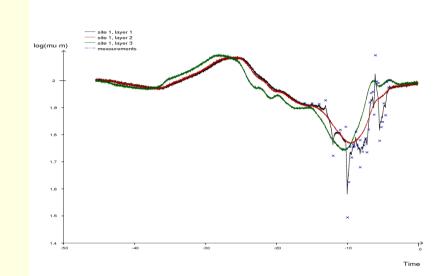
- Best: 3 layer model (Pr(M|D)=9.9%)
 - Lowest layer: Interregional correlations,
 ρ=0.63. Δt≈6.1 Myr.
 - Middle layer: Deterministic, ∆t≈1.4 Myr.
 - Upper layer: Wide credibility band for the pull, which is local, ∆t∈(1yr,1Myr)

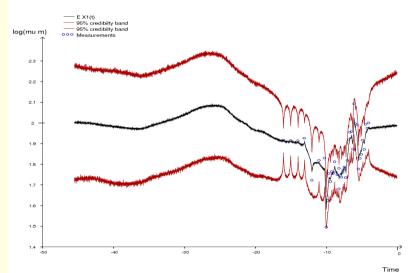




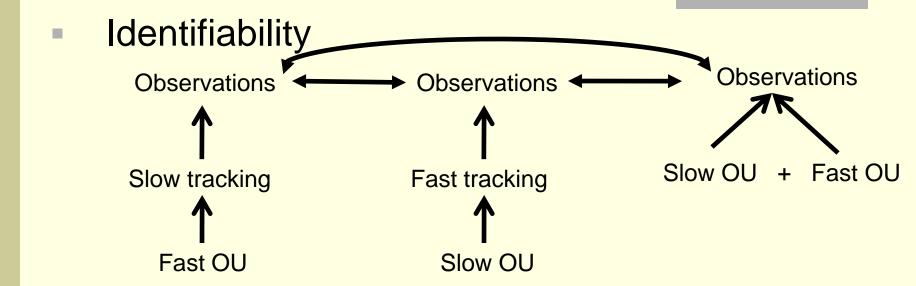
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Problems / Future developments



- Multimodal observations speciation
- Handling several lineages and several phenotypes of each lineage: phylogeny, hierarchical models

Conclusions

- Possible to do inference on a model with multiple layers.
- There are methods for doing model comparison.
- Not enough data to get conclusive results regarding the model choice.
- Possible to find sites that "don't follow the norm".
- Productive framework which may be used in other settings also.
- Gives biological insight into processes in spite of sparse data.
- Bayesian priors wanted!

Links and bibliography

Presentation:

http://folk.uio.no/trondr/stoch_layers7.ppt http://folk.uio.no/trondr/stoch_layers7.pdf

Bibliography:

- Lande R (1976), Natural Selection and Random Genetic Drift in Phenotypic Evolution, *Evolution* 30, 314-334
- Hansen TF (1997), Stabilizing Selection and the Comparative Analysis of Adaptation, *Evolution*, 51-5, 1341-1351
- Estes S, Arnold SJ (2007), Resolving the Paradox of Stasis: Models with Stabilizing Selection Explain Evolutionary Divergence on All Timescales, *The American Naturalist*, 169-2, 227-244
- Hansen TF, Pienaar J, Orzack SH (2008), A Comparative Method for Studying Adaptation to a Randomly Evolving Environment, *Evolution* 62-8, 1965-1977