

Structural Break Detection in Time Series Models

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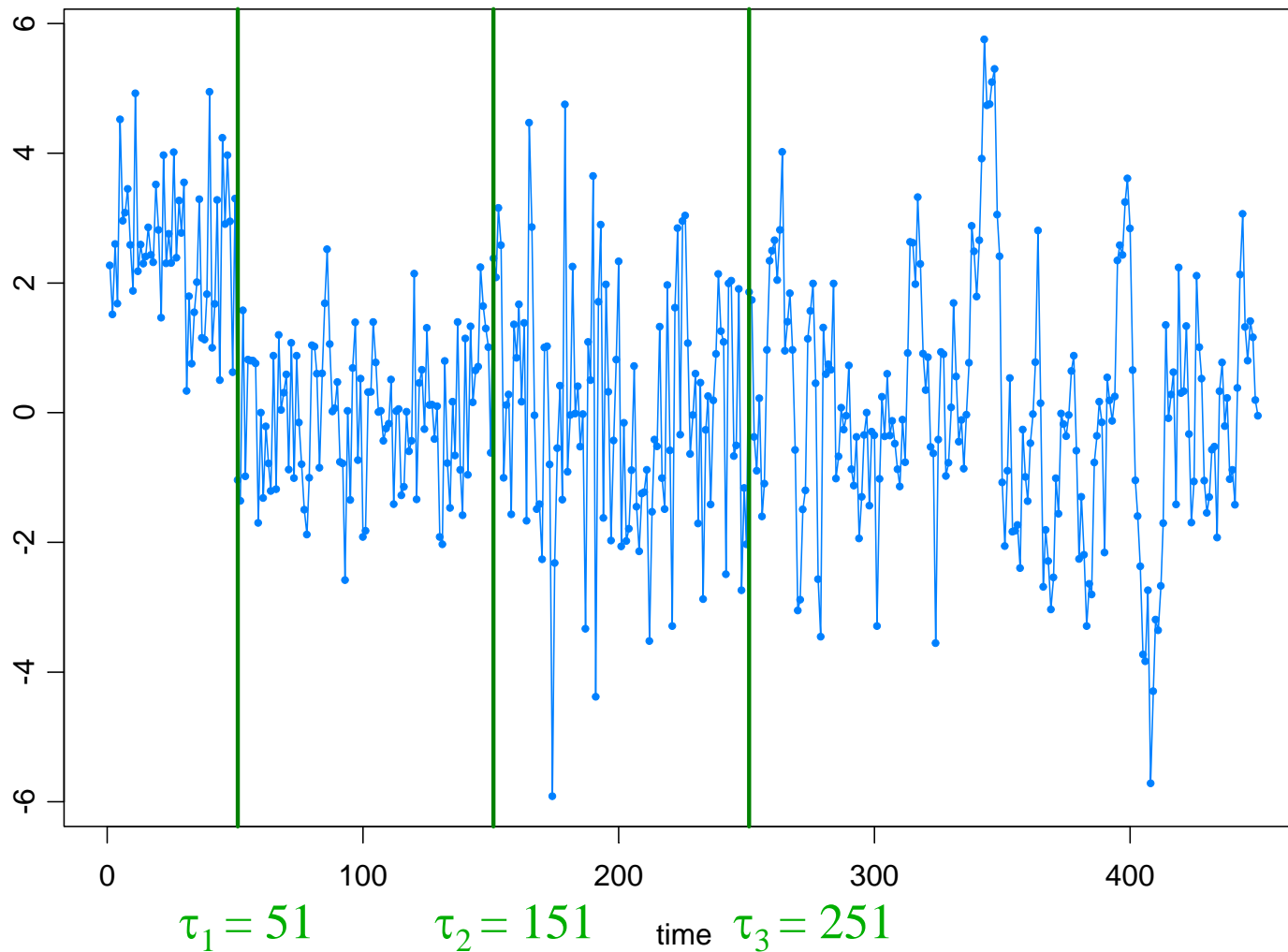
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(<http://www.stat.colostate.edu/~rdavis/lectures>)

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Illustrative Example

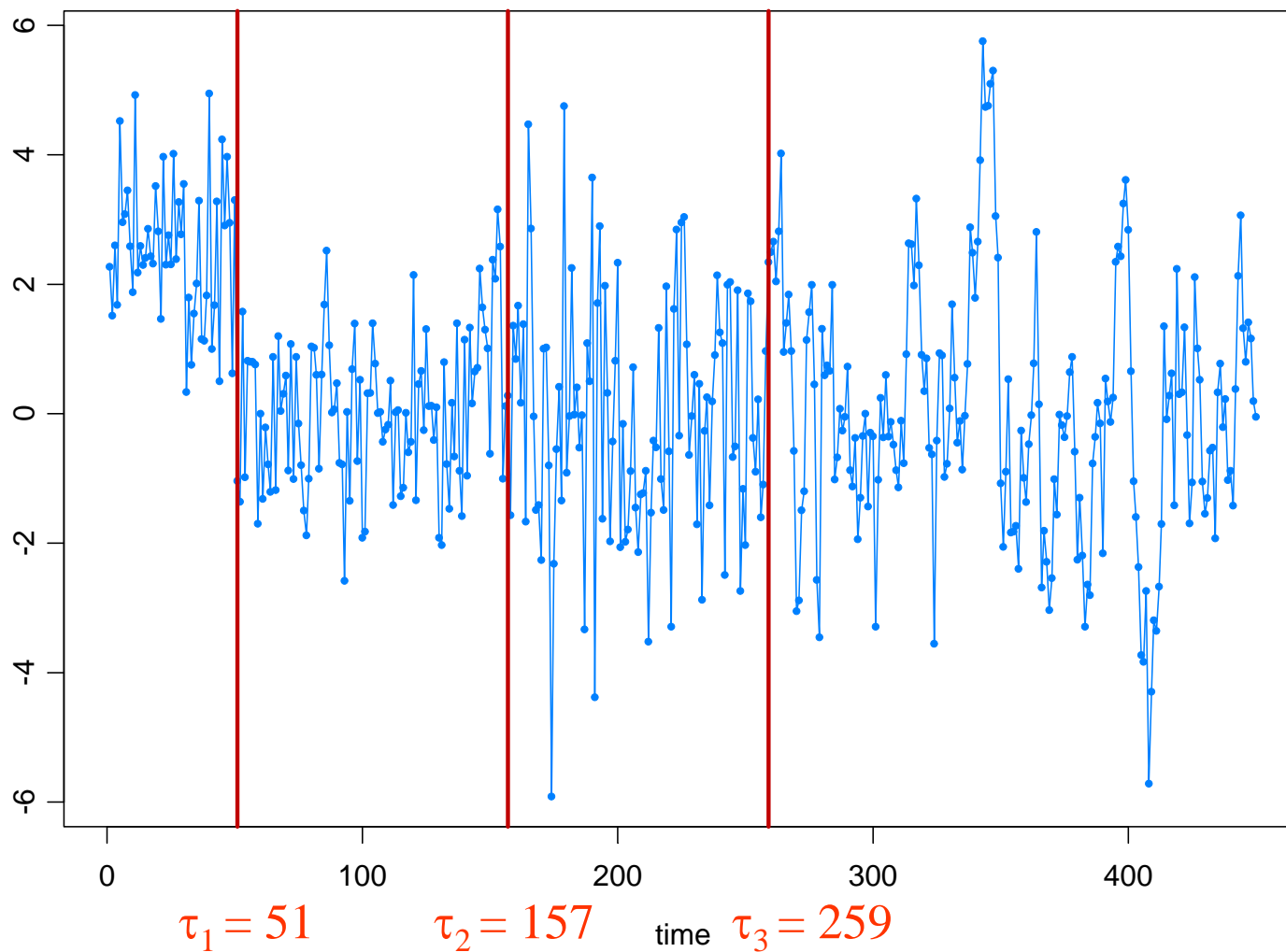
How many segments do you see?



Illustrative Example

Auto-PARM=Auto-Piecewise AutoRegressive Modeling

4 pieces, 2.58 seconds.



- Introduction
 - Examples
 - AR
 - GARCH
 - Stochastic volatility
 - State space models
- Model selection using Minimum Description Length (MDL)
 - General principles
 - Application to AR models with breaks
- Optimization using a Genetic Algorithm
 - Basics
 - Implementation for structural break estimation
- Simulation results
- Applications
- Simulation results for GARCH and SV models

Examples

1. Piecewise AR model:

$$Y_t = \gamma_j + \phi_{j1}Y_{t-1} + \dots + \phi_{jp_j}Y_{t-p_j} + \sigma_j\varepsilon_t, \quad \text{if } \tau_{j-1} \leq t < \tau_j,$$

where $\tau_0 = 1 < \tau_1 < \dots < \tau_{m-1} < \tau_m = n + 1$, and $\{\varepsilon_t\}$ is IID(0,1).

Goal: Estimate

m = number of segments

τ_j = location of j^{th} break point

γ_j = level in j^{th} epoch

p_j = order of AR process in j^{th} epoch

$(\phi_{j1}, \dots, \phi_{jp_j})$ = AR coefficients in j^{th} epoch

σ_j = scale in j^{th} epoch

Piecewise AR models (cont)

Structural breaks:

Kitagawa and Akaike (1978)

- fitting locally stationary autoregressive models using AIC
- computations facilitated by the use of the Householder transformation

Davis, Huang, and Yao (1995)

- likelihood ratio test for testing a change in the parameters and/or order of an AR process.

Kitagawa, Takanami, and Matsumoto (2001)

- signal extraction in seismology-estimate the arrival time of a seismic signal.

Ombao, Raz, von Sachs, and Malow (2001)

- orthogonal complex-valued transforms that are localized in time and frequency- smooth localized complex exponential (SLEX) transform.
- applications to EEG time series and speech data.

Motivation for using piecewise AR models:

Piecewise AR is a special case of a *piecewise stationary process* (see Adak 1998),

$$\tilde{Y}_{t,n} = \sum_{j=1}^m Y_t^j I_{[\tau_{j-1}, \tau_j)}(t/n),$$

where $\{Y_t^j\}$, $j = 1, \dots, m$ is a sequence of stationary processes. It is argued in Ombao et al. (2001), that if $\{Y_{t,n}\}$ is a locally stationary process (in the sense of Dahlhaus), then there exists a piecewise stationary process $\{\tilde{Y}_{t,n}\}$ with

$$m_n \rightarrow \infty \quad \text{with } m_n/n \rightarrow 0, \text{ as } n \rightarrow \infty,$$

that approximates $\{Y_{t,n}\}$ (in average mean square).

Roughly speaking: $\{Y_{t,n}\}$ is a locally stationary process if it has a time-varying spectrum that is approximately $|A(t/n, \omega)|^2$, where $A(u, \omega)$ is a continuous function in u .

Examples (cont)

2. Segmented GARCH model:

$$Y_t = \sigma_t \varepsilon_t,$$
$$\sigma_t^2 = \omega_j + \alpha_{j1} Y_{t-1}^2 + \dots + \alpha_{jp_j} Y_{t-p_j}^2 + \beta_{j1} \sigma_{t-1}^2 + \dots + \beta_{jq_j} \sigma_{t-q_j}^2, \quad \text{if } \tau_{j-1} \leq t < \tau_j,$$

where $\tau_0 = 1 < \tau_1 < \dots < \tau_{m-1} < \tau_m = n + 1$, and $\{\varepsilon_t\}$ is IID(0,1).

3. Segmented stochastic volatility model:

$$Y_t = \sigma_t \varepsilon_t,$$
$$\log \sigma_t^2 = \gamma_j + \phi_{j1} \log \sigma_{t-1}^2 + \dots + \phi_{jp_j} \log \sigma_{t-p_j}^2 + v_j \eta_t, \quad \text{if } \tau_{j-1} \leq t < \tau_j.$$

4. Segmented state-space model (SVM a special case):

$$p(y_t | \alpha_t, \dots, \alpha_1, y_{t-1}, \dots, y_1) = p(y_t | \alpha_t) \text{ is specified}$$
$$\alpha_t = \gamma_j + \phi_{j1} \alpha_{t-1} + \dots + \phi_{jp_j} \alpha_{t-p_j} + \sigma_j \eta_t, \quad \text{if } \tau_{j-1} \leq t < \tau_j.$$

Model Selection Using Minimum Description Length

Basics of MDL:

Choose the model which *maximizes the compression* of the data or, equivalently, select the model that *minimizes the code length* of the data (i.e., amount of memory required to encode the data).

M = class of operating models for $y = (y_1, \dots, y_n)$

$L_F(y)$ = code length of y relative to $F \in M$

Typically, this term can be decomposed into two pieces (*two-part code*),

$$L_F(y) = L(\hat{F}/y) + L(\hat{e} | \hat{F}),$$

where

$L(\hat{F}/y)$ = code length of the fitted model for F

$L(\hat{e} | \hat{F})$ = code length of the residuals based on the fitted model

Illustration Using a Simple Regression Model (see T. Lee '01)

Encoding the data: $(x_1, y_1), \dots, (x_n, y_n)$

1. “Naïve” case

$$\begin{aligned}L(\text{"naive"}) &= L(x_1, \dots, x_n) + L(y_1, \dots, y_n) \\ &= L(x_1) + \dots + L(x_n) + L(y_1) + \dots + L(y_n)\end{aligned}$$

2. Linear model; suppose $y_i = a_0 + a_1 x_i, i = 1, \dots, n$. Then

$$\begin{aligned}L(\text{"p=1"}) &= L(x_1, \dots, x_n) + L(a_0, a_1) \\ &= L(x_1) + \dots + L(x_n) + L(a_0) + L(a_1)\end{aligned}$$

3. Linear model with noise; suppose $y_i = a_0 + a_1 x_i + \varepsilon_i, i = 1, \dots, n$, where $\{\varepsilon_i\} \sim \text{IID } N(0, \sigma^2)$. Then

$$L(\text{"p=1"}) = L(x_1) + \dots + L(x_n) + \underbrace{L(\hat{a}_0) + L(\hat{a}_1) + L(\hat{\sigma}^2) + L(\hat{\varepsilon}_1, \dots, \hat{\varepsilon}_n | \hat{a}_0, \hat{a}_1, \hat{\sigma}^2)}_A$$

If $A < L(y_1) + \dots + L(y_n)$, then “p=1” encoding scheme dominates the “naïve” scheme.

Model Selection Using Minimum Description Length (cont)

Applied to the segmented AR model:

$$Y_t = \gamma_j + \phi_{j1}Y_{t-1} + \dots + \phi_{jp_j}Y_{t-p_j} + \sigma_j \varepsilon_t, \quad \text{if } \tau_{j-1} \leq t < \tau_j,$$

First term $L(\hat{\mathbf{F}}/y)$:

$$\begin{aligned} L(\hat{\mathbf{F}}/y) &= L(m) + L(\tau_1, \dots, \tau_m) + L(p_1, \dots, p_m) + L(\hat{\psi}_1 | y) + \dots + L(\hat{\psi}_m | y) \\ &= \log_2 m + m \log_2 n + \sum_{j=1}^m \log_2 p_j + \sum_{j=1}^m \frac{p_j + 2}{2} \log_2 n_j \end{aligned}$$

Encoding:

integer l : $\log_2 l$ bits (if l unbounded)

$\log_2 l_U$ bits (if l bounded by l_U)

MLE $\hat{\theta}$: $\frac{1}{2} \log_2 N$ bits (where N = number of observations used to compute $\hat{\theta}$; Rissanen (1989))

Second term $L(\hat{e} | \hat{\mathbf{F}})$: Using Shannon's classical results on information theory, Rissanen demonstrates that the code length of can be approximated by the **negative of the log-likelihood** of the fitted model, i.e., by

$$L(\hat{e} | \hat{\mathbf{F}}) \approx -\sum_{j=1}^m \log_2 L(\hat{\psi}_j | y)$$

For fixed values of $m, (\tau_1, \rho_1), \dots, (\tau_m, \rho_m)$, we define the MDL as

$$\begin{aligned} MDL(m, (\tau_1, \rho_1), \dots, (\tau_m, \rho_m)) \\ = \log_2 m + m \log_2 n + \sum_{j=1}^m \log_2 p_j + \sum_{j=1}^m \frac{p_j + 2}{2} \log_2 n_j - \sum_{j=1}^m \log_2 L(\hat{\psi}_j | y) \end{aligned}$$

The strategy is to find the best segmentation that minimizes $MDL(m, \tau_1, \rho_1, \dots, \tau_m, \rho_m)$. To speed things up for AR processes, we use **Y-W estimates** of AR parameters and we replace

$$-\log_2 L(\hat{\psi}_j | y) \text{ with } \log_2(2\pi\hat{\sigma}_j^2) + n_j$$

Optimization Using Genetic Algorithms

Basics of GA:

Class of optimization algorithms that mimic natural evolution.

- Start with an initial set of *chromosomes*, or population, of possible solutions to the optimization problem.
- Parent chromosomes are randomly selected (proportional to the rank of their objective function values), and produce offspring using *crossover* or *mutation* operations.
- After a sufficient number of offspring are produced to form a second generation, the process then *restarts to produce a third generation*.
- Based on Darwin's *theory of natural selection*, the process should produce future generations that give a *smaller (or larger)* objective function.

Application to Structural Breaks—(cont)

Genetic Algorithm: Chromosome consists of n genes, each taking the value of -1 (no break) or p (order of AR process). Use natural selection to find a *near* optimal solution.

Map the break points with a chromosome c via

$$(m, (\tau_1, p_1), \dots, (\tau_m, p_m)) \longleftrightarrow c = (\delta_1, \dots, \delta_n),$$

where

$$\delta_t = \begin{cases} -1, & \text{if no break point at } t, \\ p_j, & \text{if break point at time } t = \tau_{j-1} \text{ and AR order is } p_j. \end{cases}$$

For example,

$$c = (2, -1, -1, -1, -1, 0, -1, -1, -1, -1, 0, -1, -1, -1, 3, -1, -1, -1, -1, -1)$$

t: 1	6	11	15
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would correspond to a process as follows:

$$\text{AR}(2), t=1:5; \text{AR}(0), t=6:10; \text{AR}(0), t=11:14; \text{AR}(3), t=15:20$$

Implementation of Genetic Algorithm—(cont)

Generation 0: Start with L (200) randomly generated chromosomes, c_1, \dots, c_L with associated MDL values, $MDL(c_1), \dots, MDL(c_L)$.

Generation 1: A new child in the next generation is formed from the chromosomes c_1, \dots, c_L of the previous generation as follows:

- with probability π_c , *crossover* occurs.
 - two parent chromosomes c_i and c_j are selected at random with probabilities proportional to the ranks of $MDL(c_i)$.
 - k^{th} gene of child is $\delta_k = \delta_{i,k}$ w.p. $\frac{1}{2}$ and $\delta_{j,k}$ w.p. $\frac{1}{2}$
- with probability $1 - \pi_c$, *mutation* occurs.
 - a parent chromosome c_i is selected
 - k^{th} gene of child is $\delta_k = \delta_{i,k}$ w.p. π_1 ; -1 w.p. π_2 ; and p w.p. $1 - \pi_1 - \pi_2$.

Implementation of Genetic Algorithm—(cont)

Execution of GA: Run GA until *convergence* or until a *maximum number of generations* has been reached. .

Various Strategies:

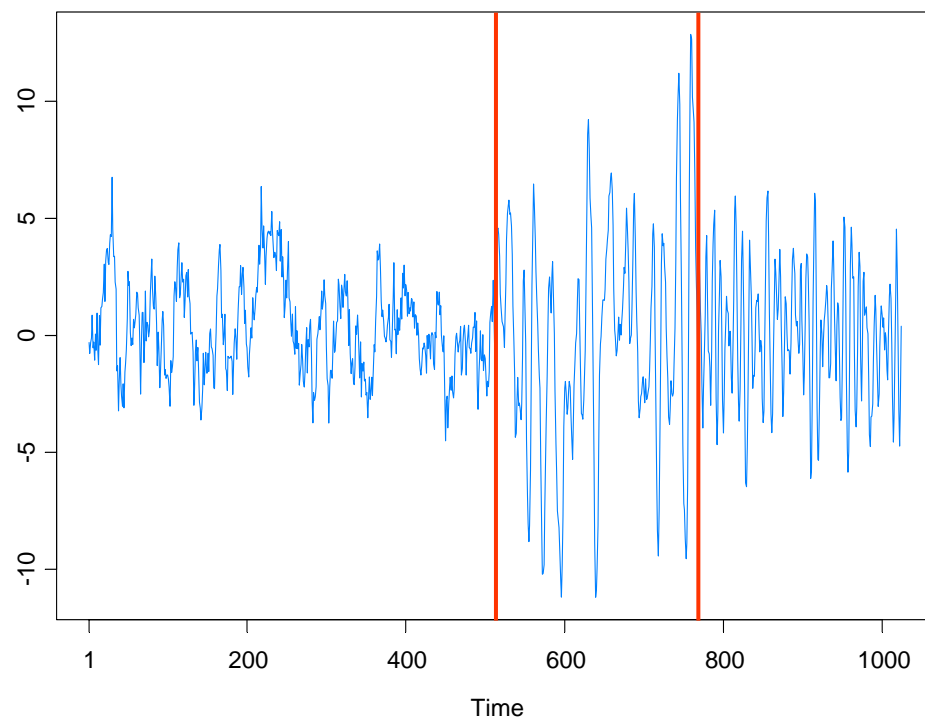
- include the *top ten* chromosomes from last generation in next generation.
- use multiple *islands*, in which populations run independently, and then allow *migration* after a fixed number of generations. This implementation is amenable to *parallel computing*.

Simulation Examples-based on Ombao et al. (2001) test cases

1. Piecewise stationary with dyadic structure: Consider a time series following the model,

$$Y_t = \begin{cases} .9Y_{t-1} + \varepsilon_t, & \text{if } 1 \leq t < 513, \\ 1.69Y_{t-1} - .81Y_{t-2} + \varepsilon_t, & \text{if } 513 \leq t < 769, \\ 1.32Y_{t-1} - .81Y_{t-2} + \varepsilon_t, & \text{if } 769 \leq t \leq 1024, \end{cases}$$

where $\{\varepsilon_t\} \sim \text{IID } N(0,1)$.

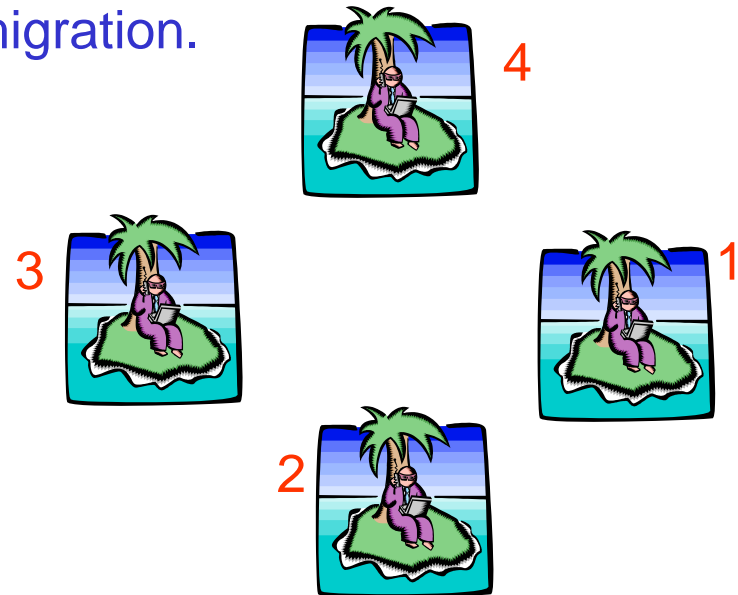


1. Piecewise stat (cont)

Implementation: Start with $NI = 50$ islands, each with population size $L = 200$.

After every $Mi = 5$ generations, allow migration.

Replace worst 2 in Island 2 with best 2 from Island 4.



Stopping rule: Stop when the max MDL does not change for 10 consecutive migrations or after 100 migrations.

Span configuration for model selection: Max AR order $K = 10$,

p	0	1	2	3	4	5	6	7-10	11-20
m_p	10	10	12	14	16	18	20	25	50
π_p	1/21	1/21	1/21	1/21	1/21	1/21	1/21	1/21	1/21

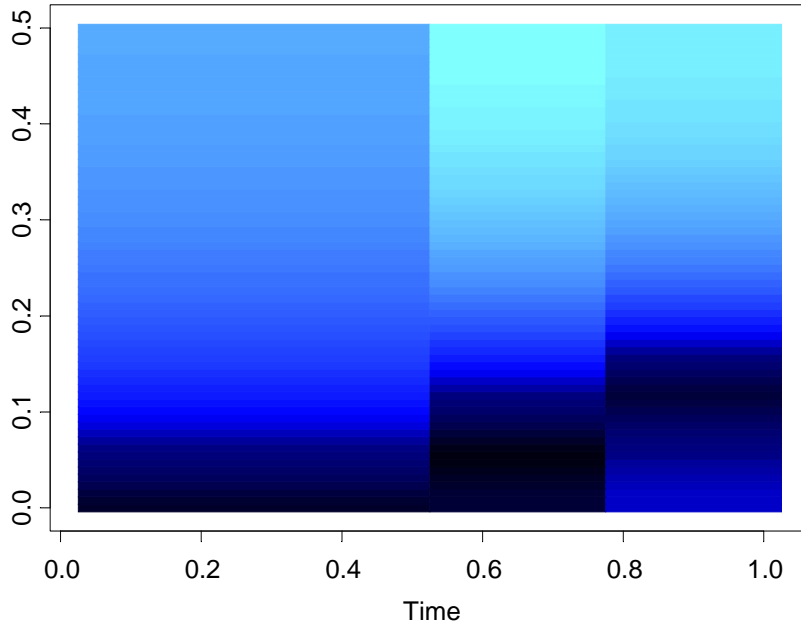
1. Piecewise stat (cont)

GA results: 3 pieces breaks at $\tau_1=513$; $\tau_2=769$. Total run time 16.31 secs

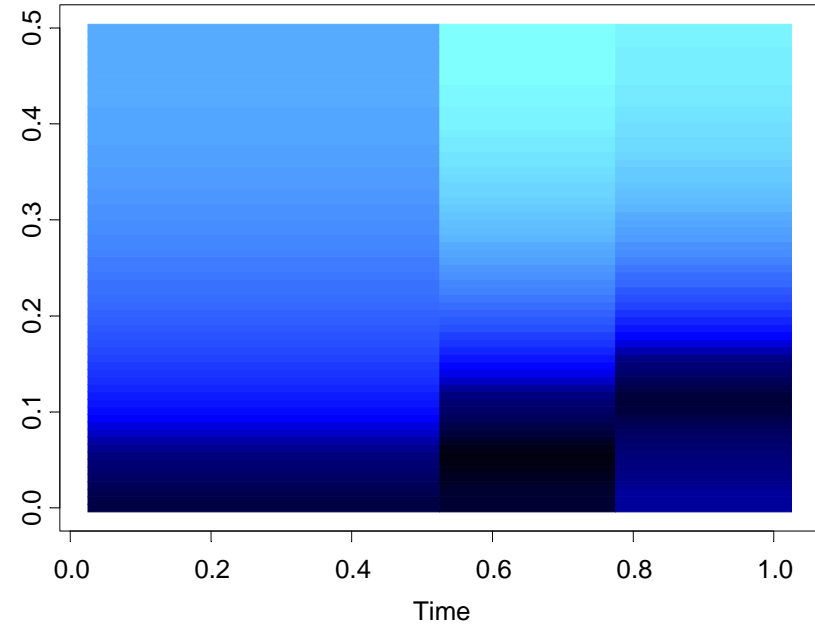
Fitted model:

	ϕ_1	ϕ_2	σ^2
1- 512:	.857		.9945
513- 768:	1.68	-0.801	1.1134
769-1024:	1.36	-0.801	1.1300

True Model



Fitted Model

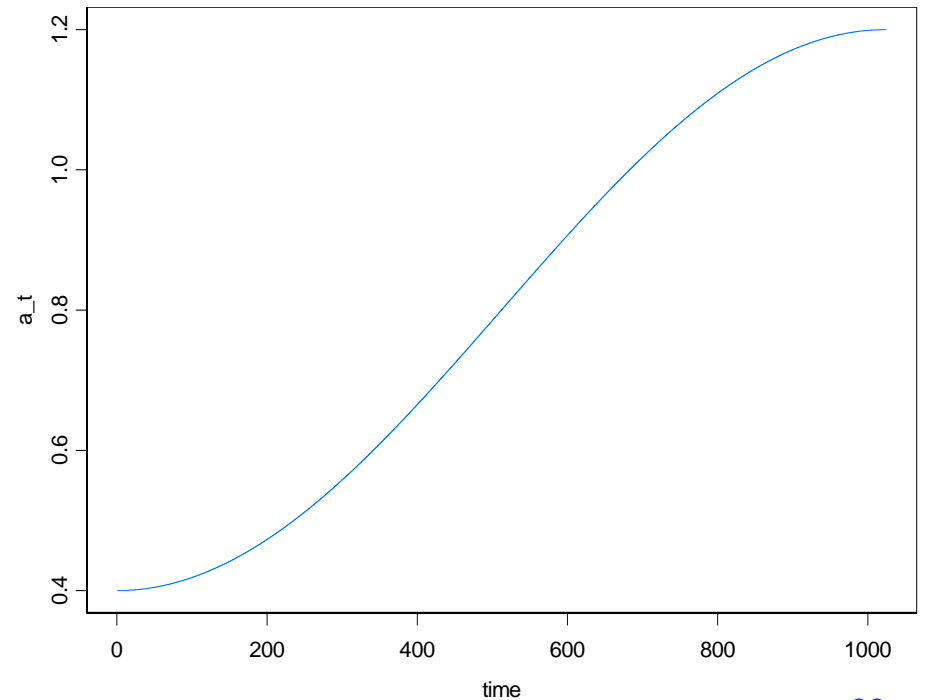
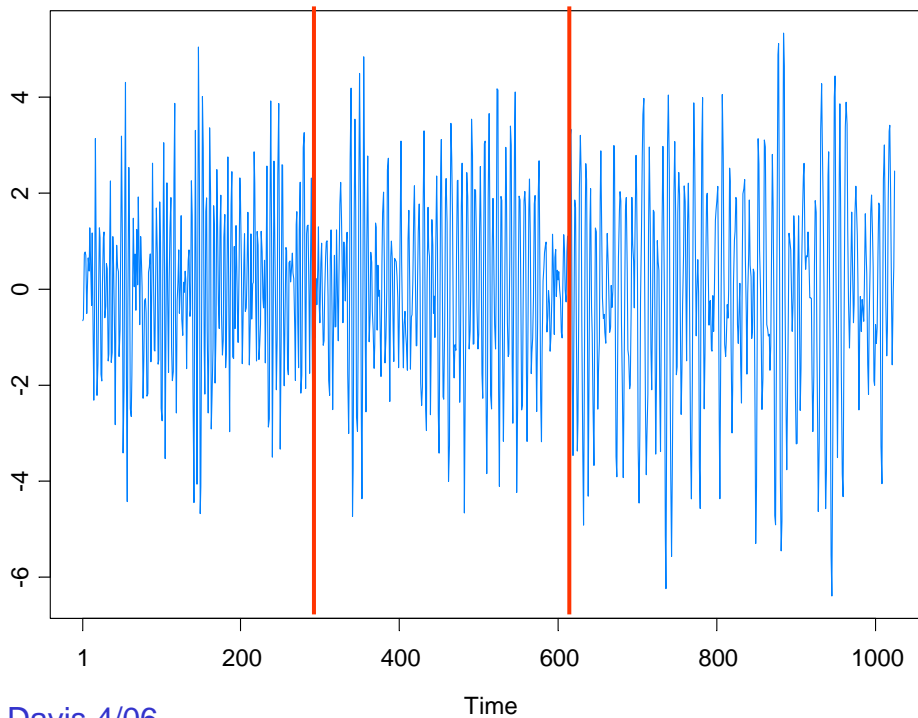


Simulation Examples (cont)

2. Slowly varying AR(2) model:

$$Y_t = a_t Y_{t-1} - .81 Y_{t-2} + \varepsilon_t \quad \text{if } 1 \leq t \leq 1024$$

where $a_t = .8[1 - 0.5 \cos(\pi t / 1024)]$, and $\{\varepsilon_t\} \sim \text{IID } N(0,1)$.



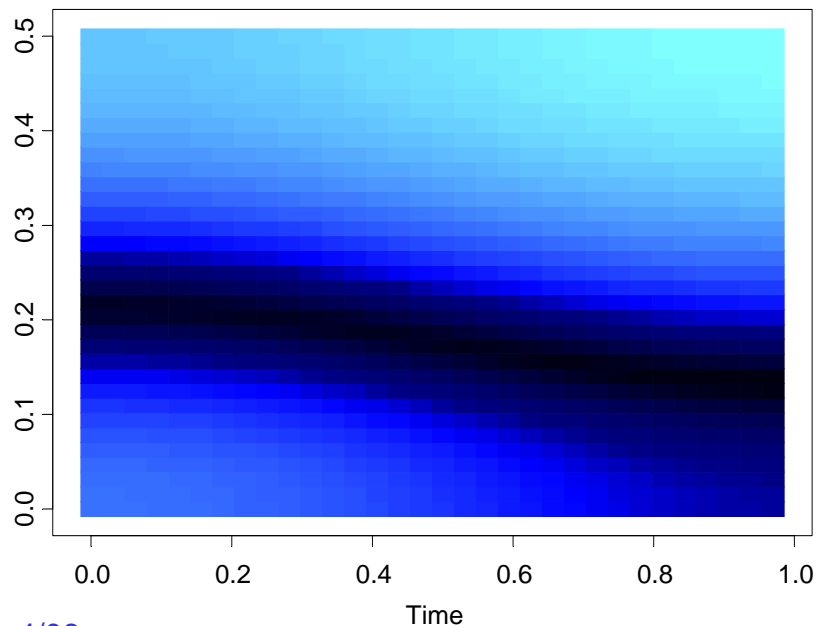
2. Slowly varying AR(2) (cont)

GA results: 3 pieces, breaks at $\tau_1=293$, $\tau_2=615$. Total run time 27.45 secs

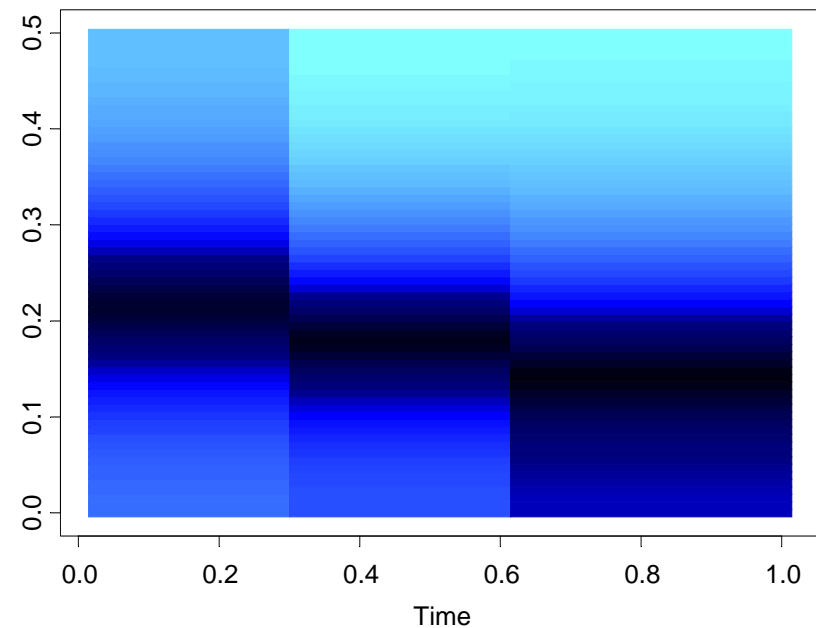
Fitted model:

	ϕ_1	ϕ_2	σ^2
1- 292:	.365	-0.753	1.149
293- 614:	.821	-0.790	1.176
615-1024:	1.084	-0.760	0.960

True Model



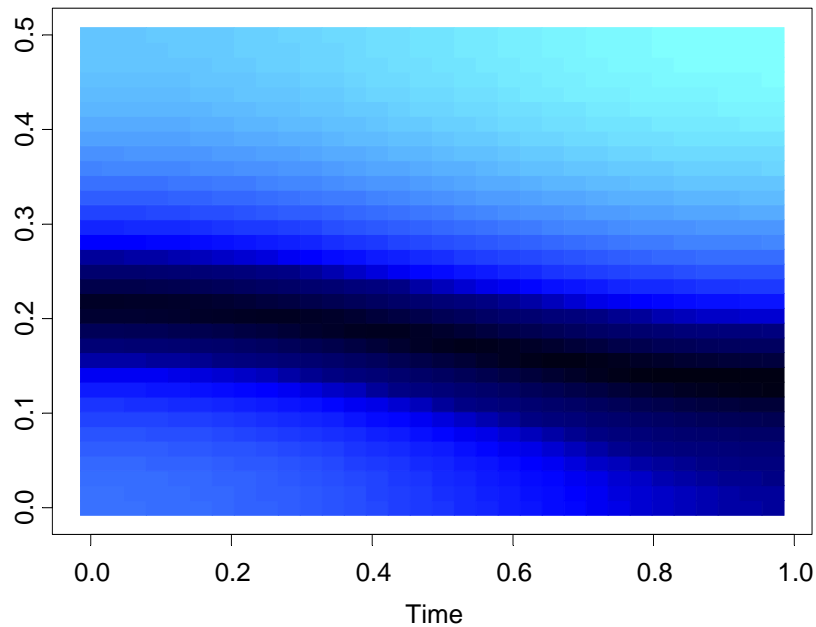
Fitted Model



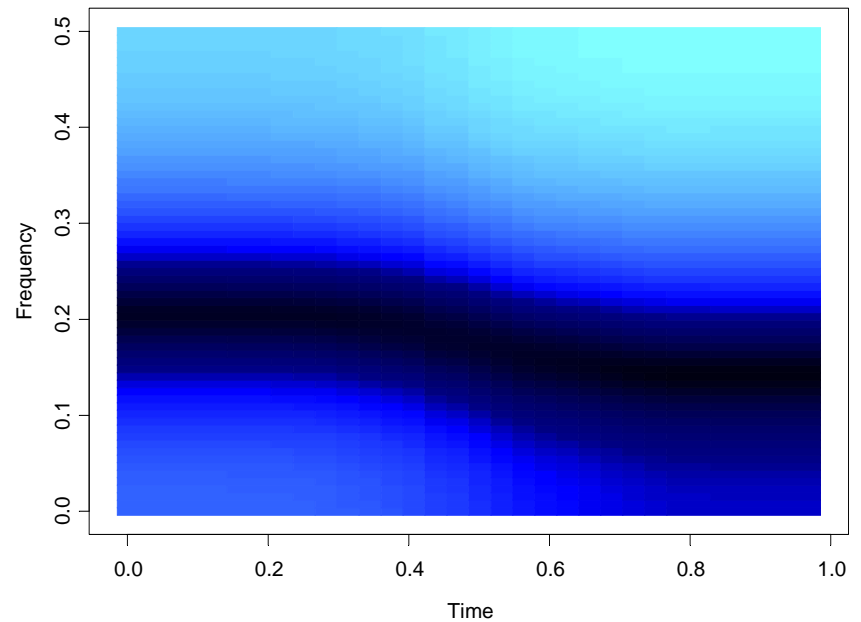
2. Slowly varying AR(2) (cont)

In the graph below right, we average the spectrogram over the *GA fitted models* generated from each of the 200 simulated realizations.

True Model



Average Model

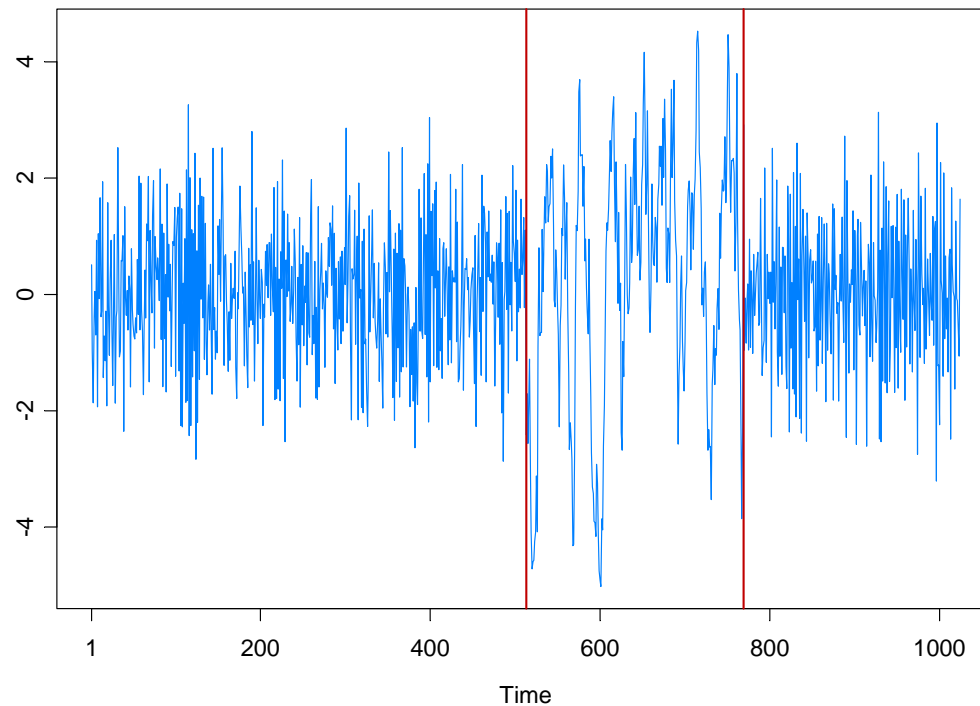


Simulation Examples (cont)

3. Piecewise ARMA:

$$Y_t = \begin{cases} -.9Y_{t-1} + \varepsilon_t + .7\varepsilon_{t-1}, & \text{if } 1 \leq t < 513, \\ .9Y_{t-1} + \varepsilon_t, & \text{if } 513 \leq t < 769, \\ \varepsilon_t - .7\varepsilon_{t-1}, & \text{if } 769 \leq t \leq 1024. \end{cases}$$

where $\{\varepsilon_t\} \sim \text{IID } N(0,1)$.

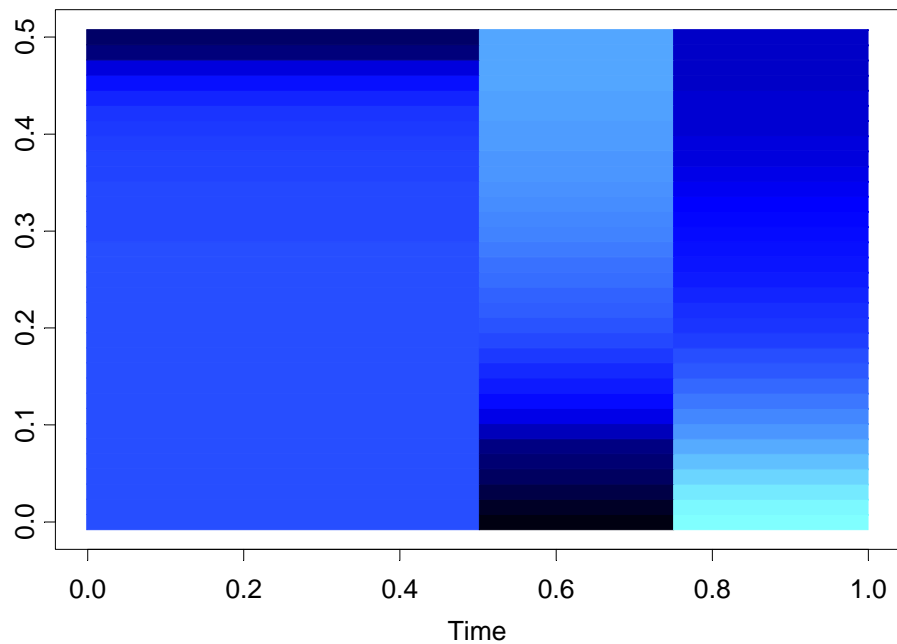


3. Piecewise ARMA (cont)

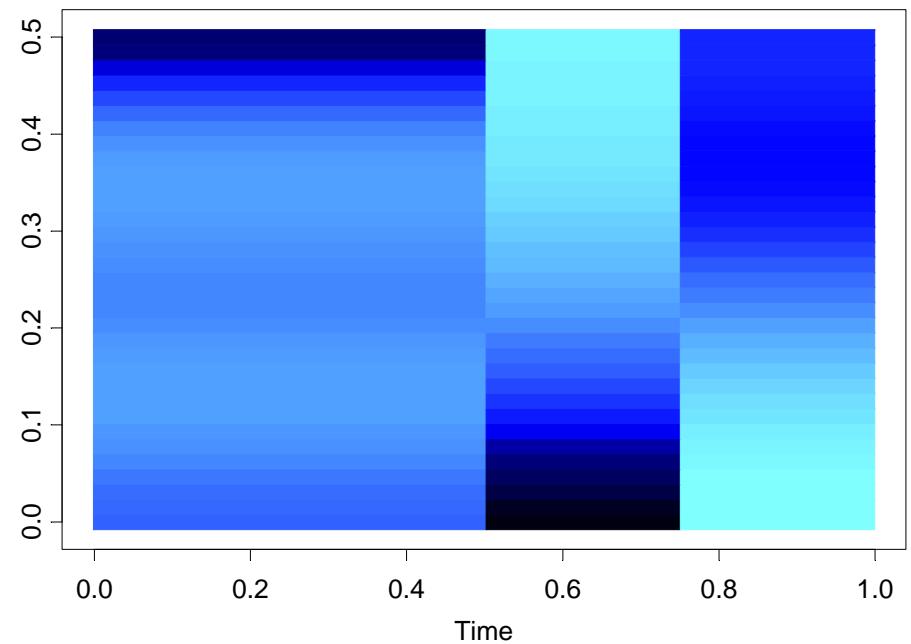
GA results: 3 pieces, breaks at $\tau_1=513$, $\tau_2=769$. Total run time 1.53 secs

Fitted model: AR orders 4, 1, 2

True Model



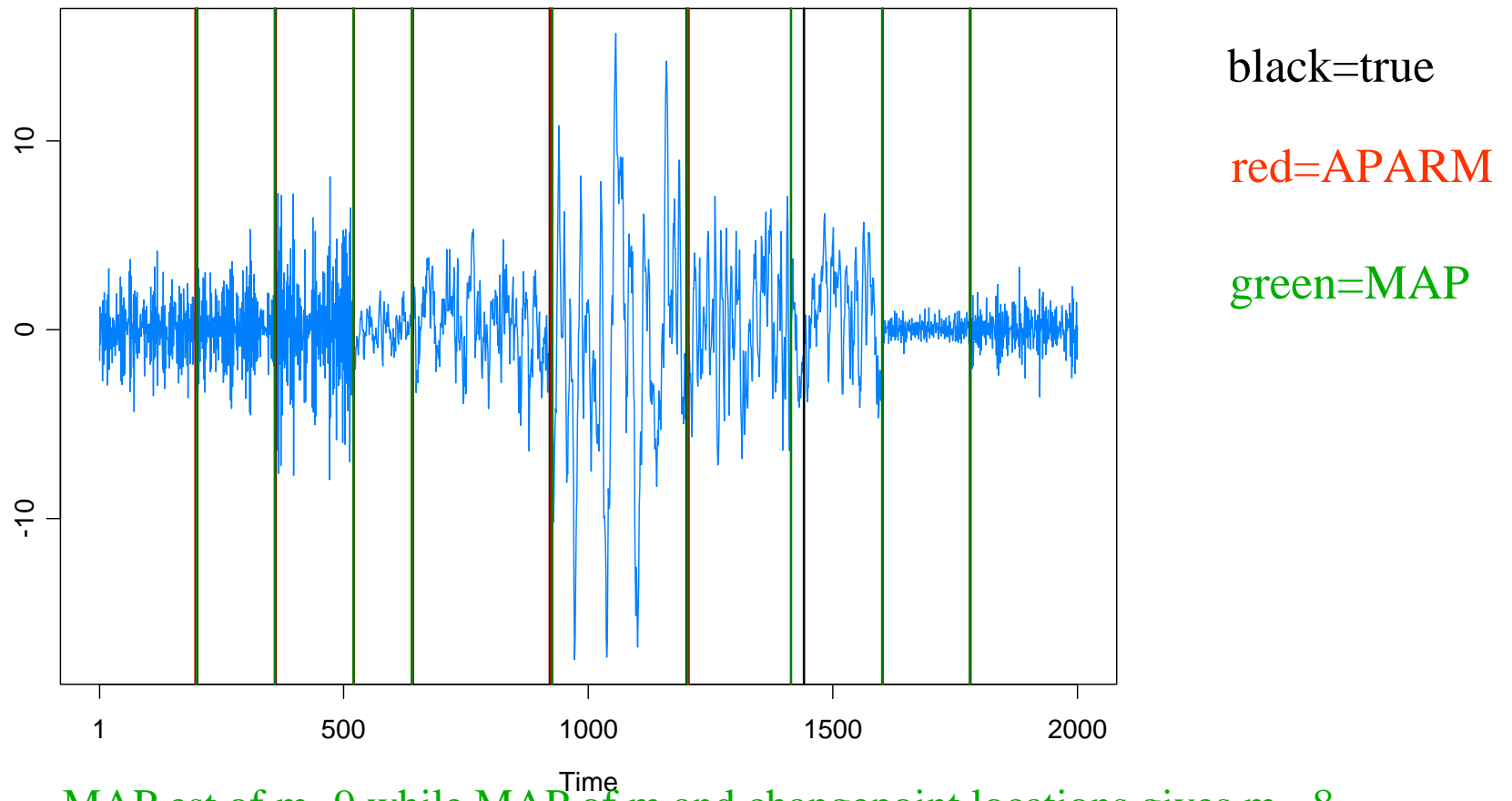
Fitted Model



Simulation Examples (cont)

4. Simulated data from Fearnhead (2005):

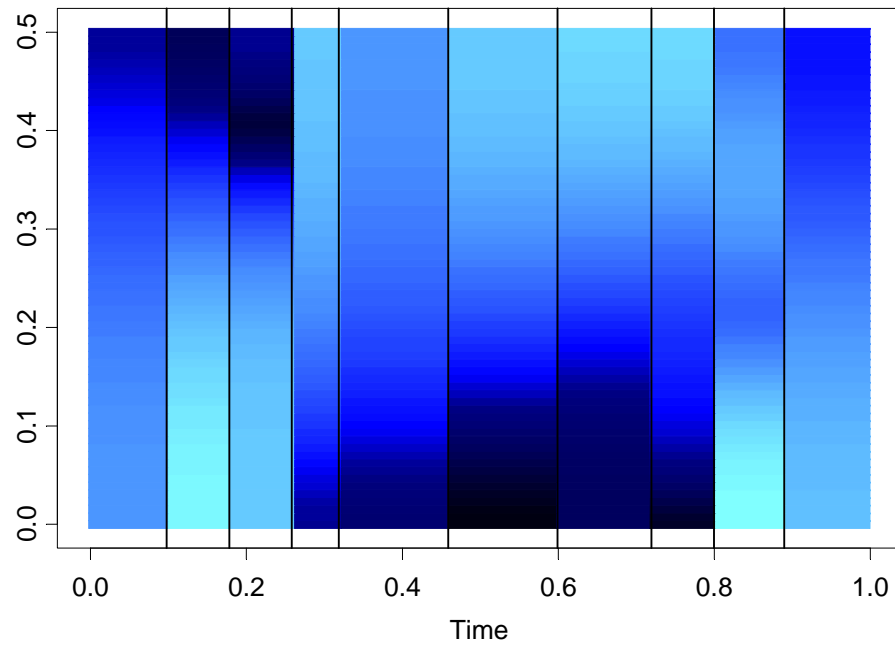
True model has 9 changepoints



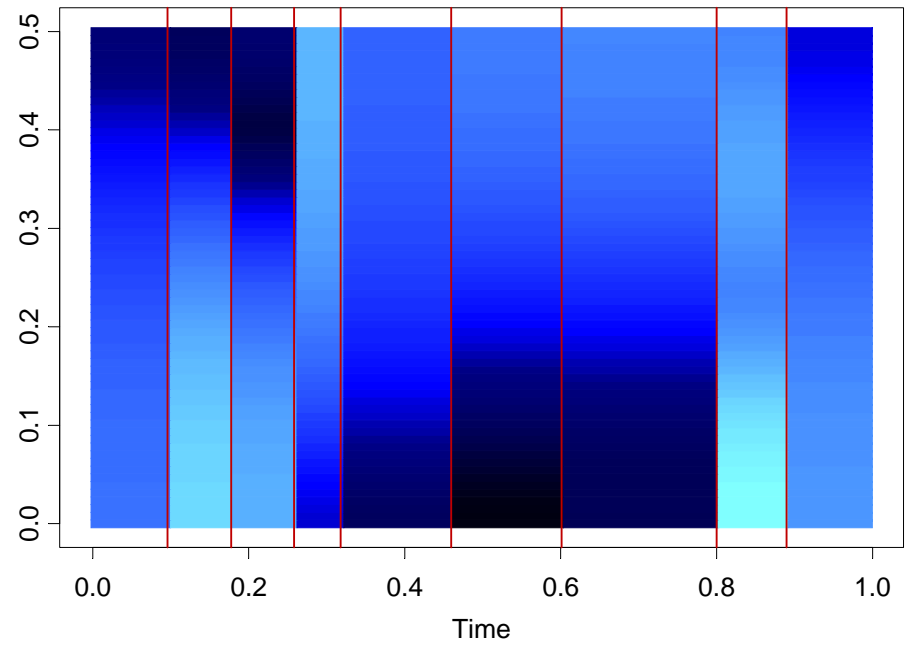
MAP est of $m=9$ while MAP of m and changepoint locations gives $m=8$ changepts. Plot is conditional on 9 changepoints.

4. Fearnhead example

True Model



Fitted APARM Model



Theory

Consistency.

Suppose the number of change points m is known and let

$$\lambda_1 = \tau_1/n, \dots, \lambda_m = \tau_m/n$$

be the relative (true) changepoints. Then

$$\hat{\lambda}_j \rightarrow \lambda_j \text{ a.s.}$$

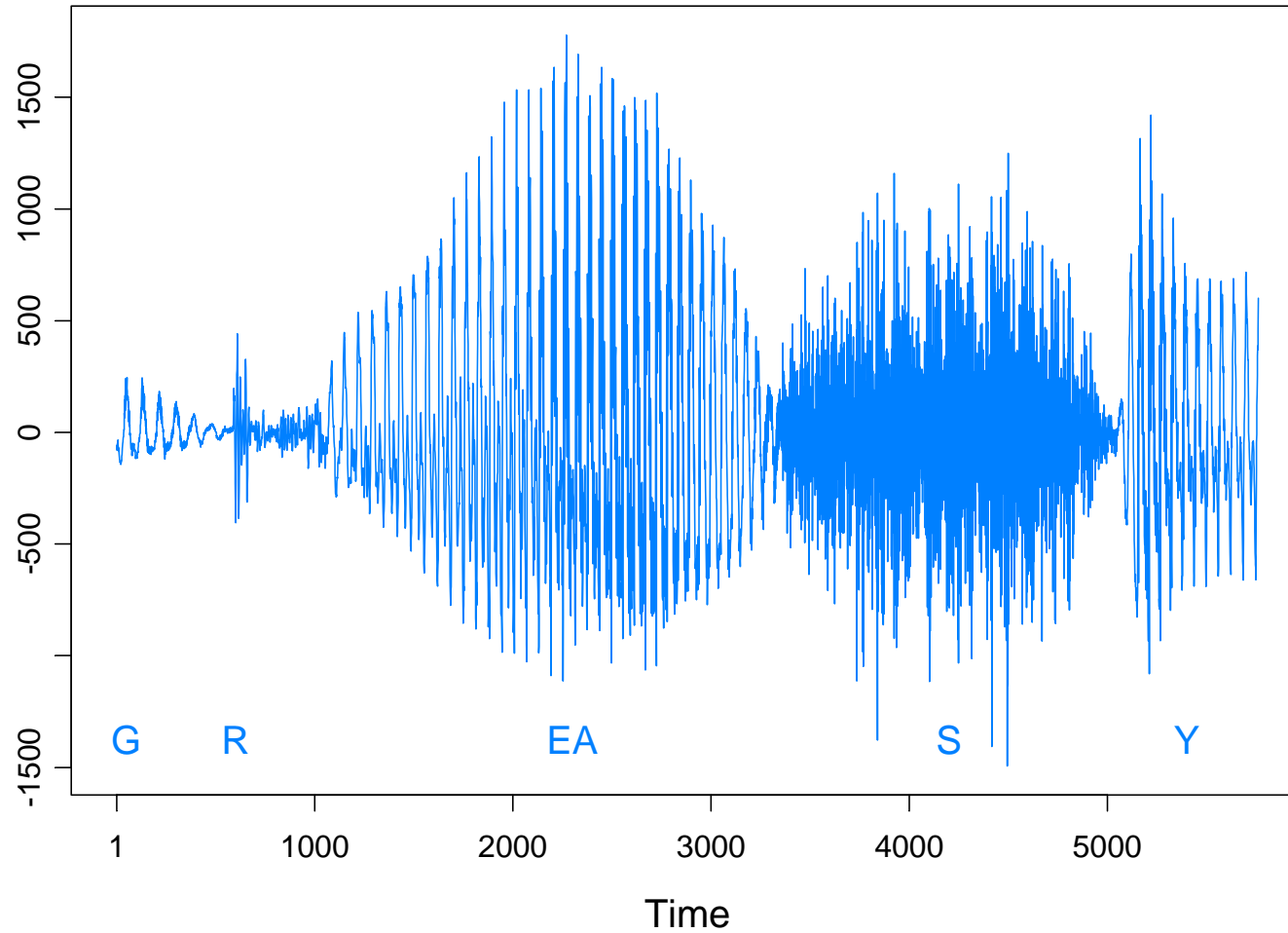
where $\hat{\lambda}_j = \hat{\tau}_j/n$ and $\hat{\tau}_j = \text{Auto-PARM estimate of } \tau_j$.

Consistency of the estimate of m ?

- For n large, Auto-PARM estimate is $\geq m$.
- Have not proved equality.

Examples

Speech signal: GREASY

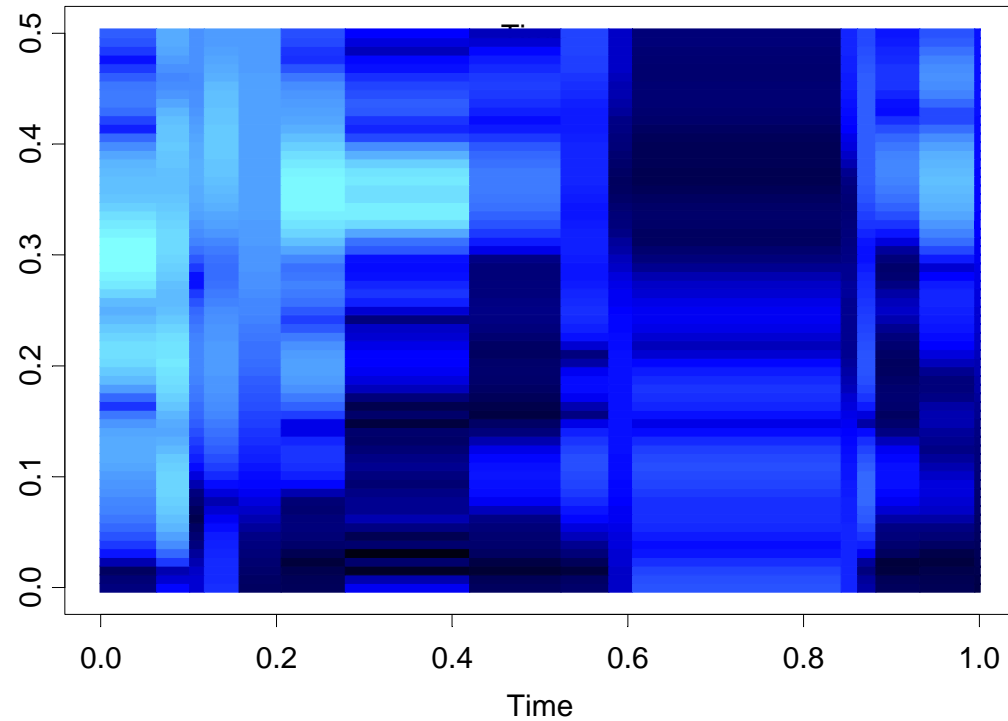
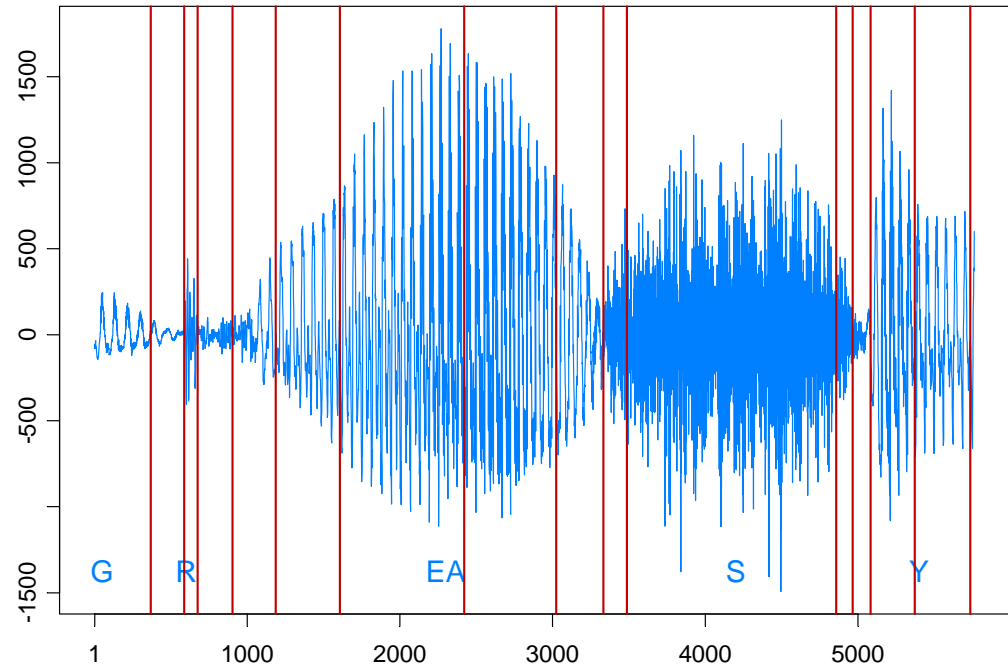


Speech signal: GREASY

$n = 5762$ observations

$m = 15$ break points

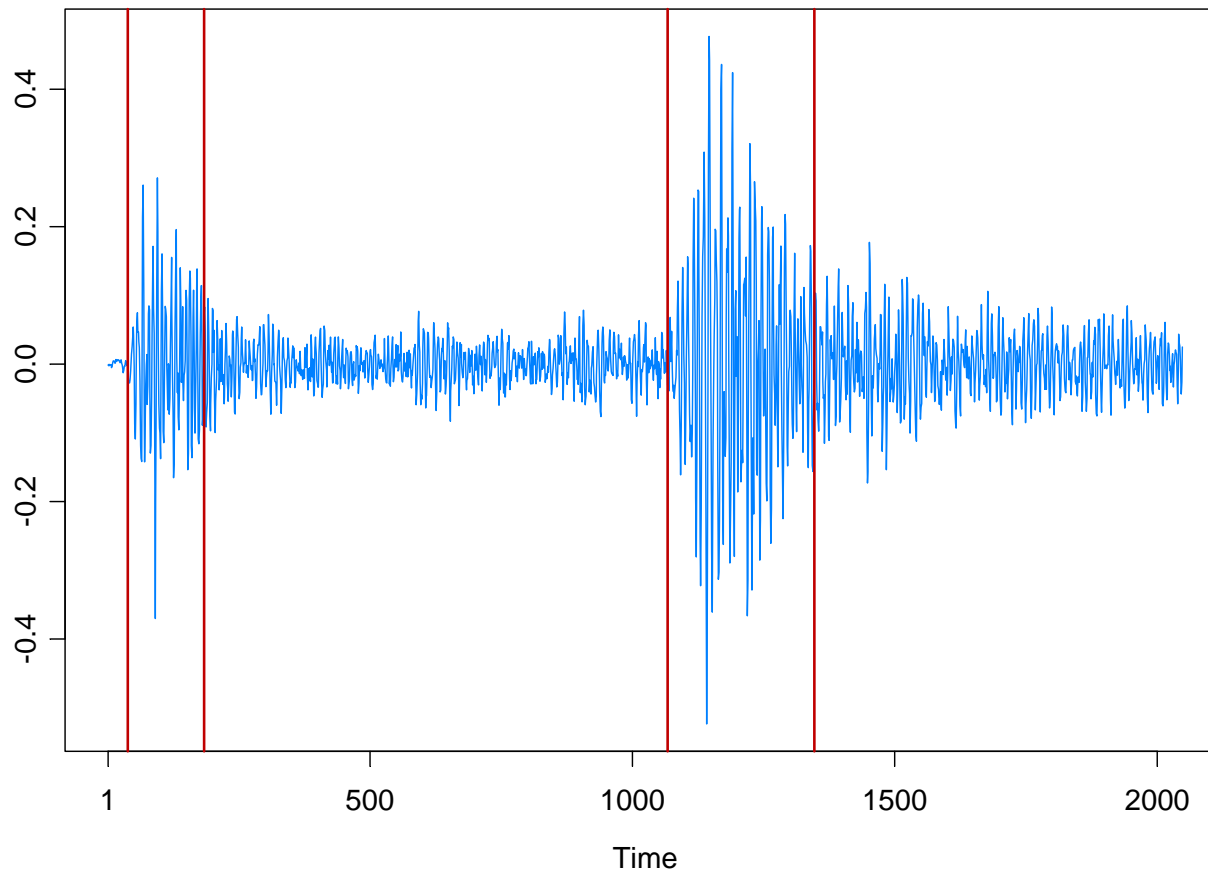
Run time = 18.02 secs



Examples

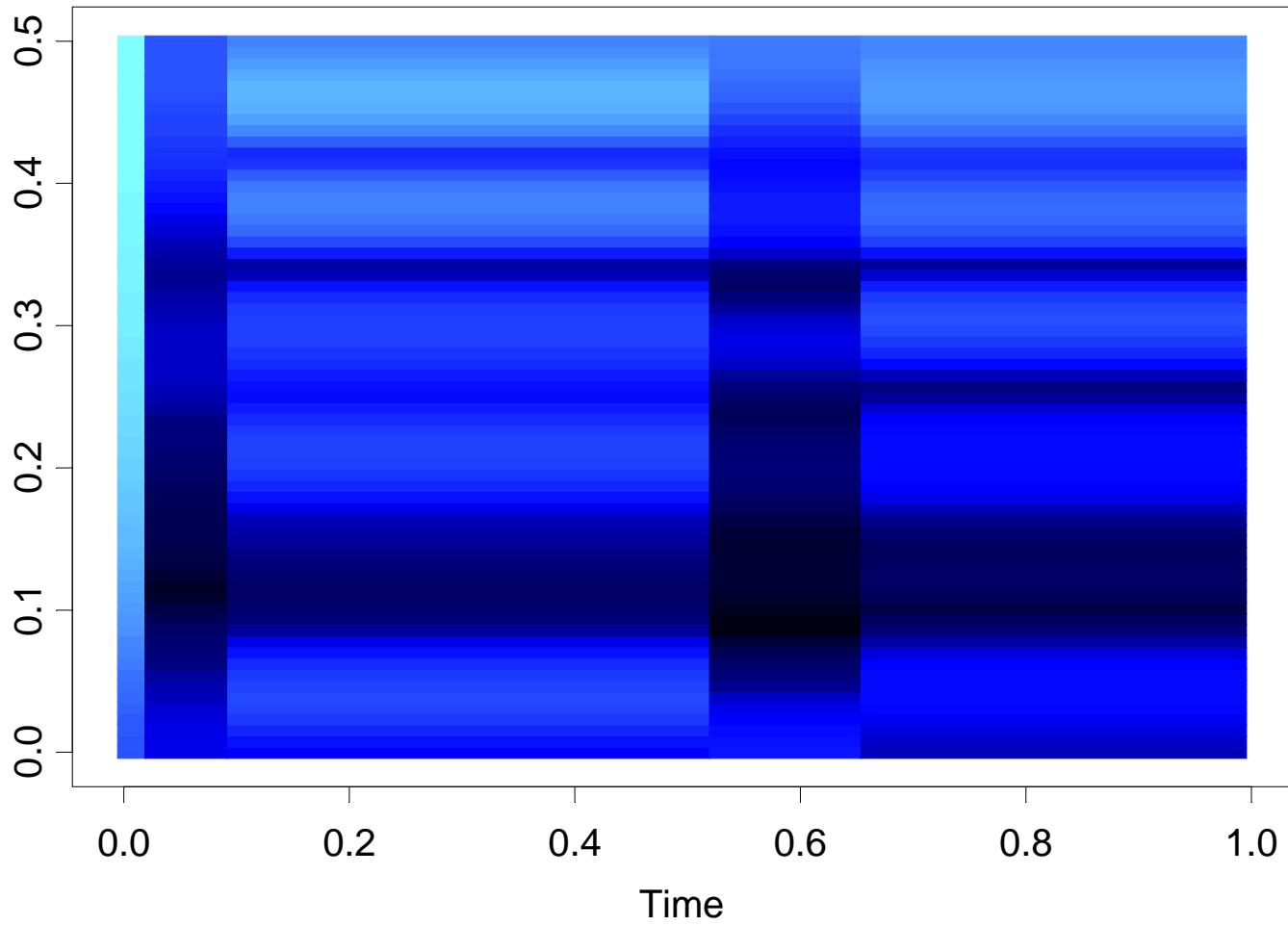
Mine explosion seismic trace in Scandinavia: (Shumway and Stoffer 2000, Stoffer et al. 2005)

Two waves: P (primary) compression wave and S (shear) wave



Examples

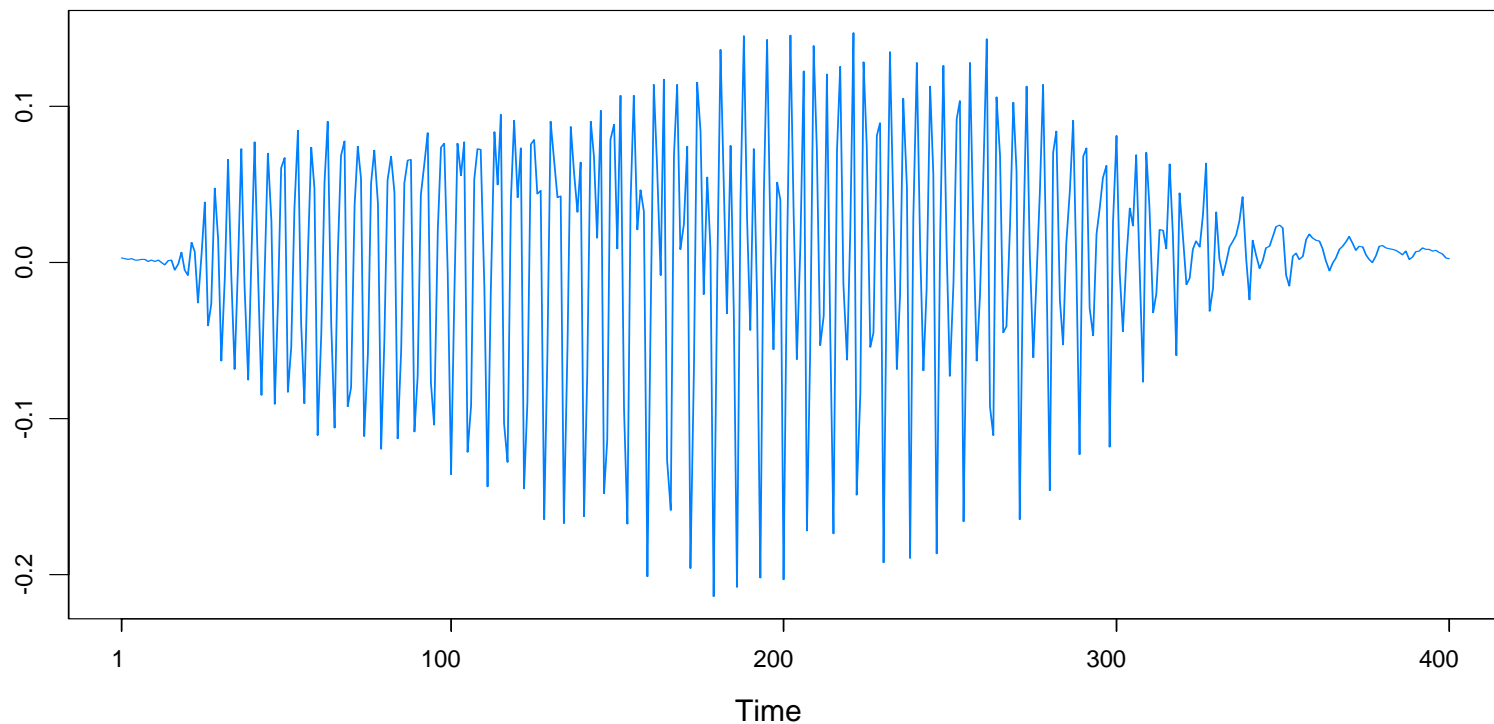
AR orders: 1 7 17 13 15



Examples

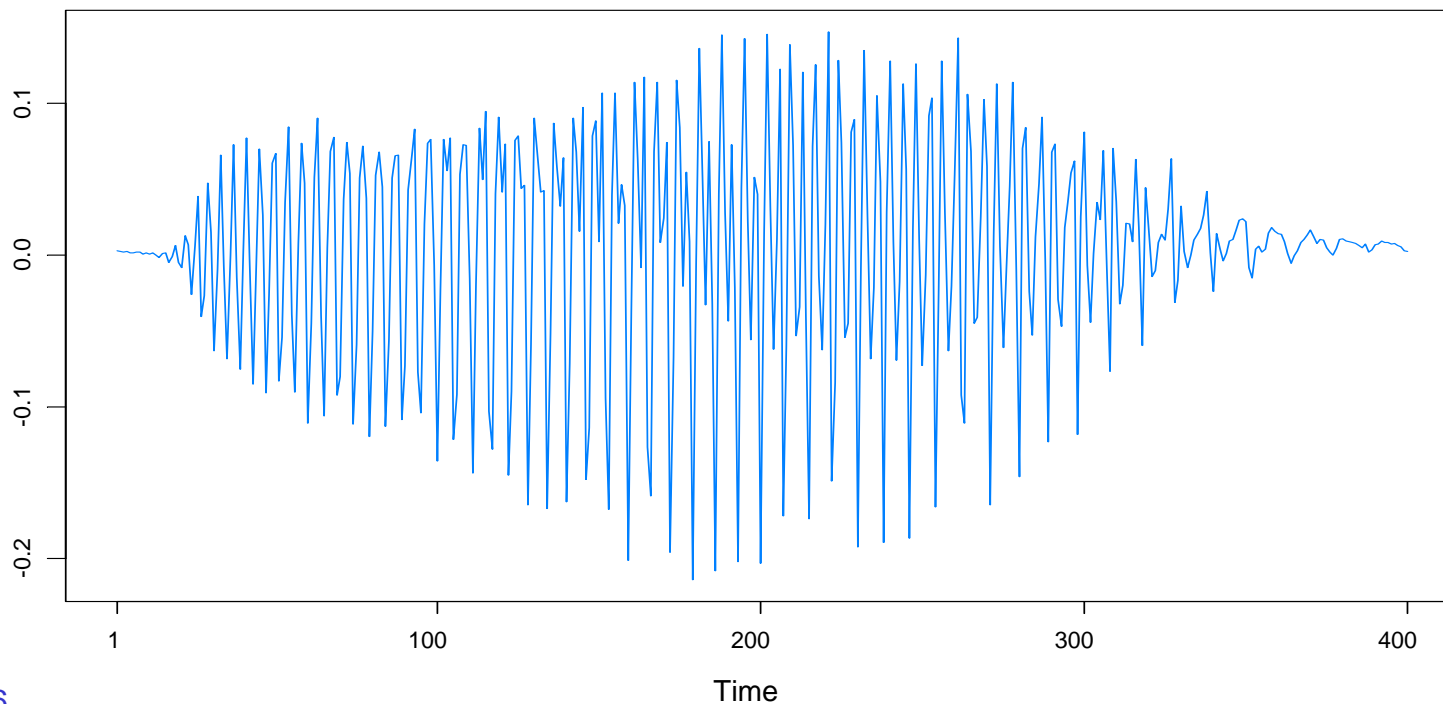
Large brown bat echolocation: 400 data points taken at 7microsecond intervals (total duration of .0028 seconds). Data and ideas about M-stationarity described here are from Buddy Gray, Wayne Woodward, and their group at SMU. <http://faculty.smu.edu/hgray/research.htm>

bat echolocation



Features of data:

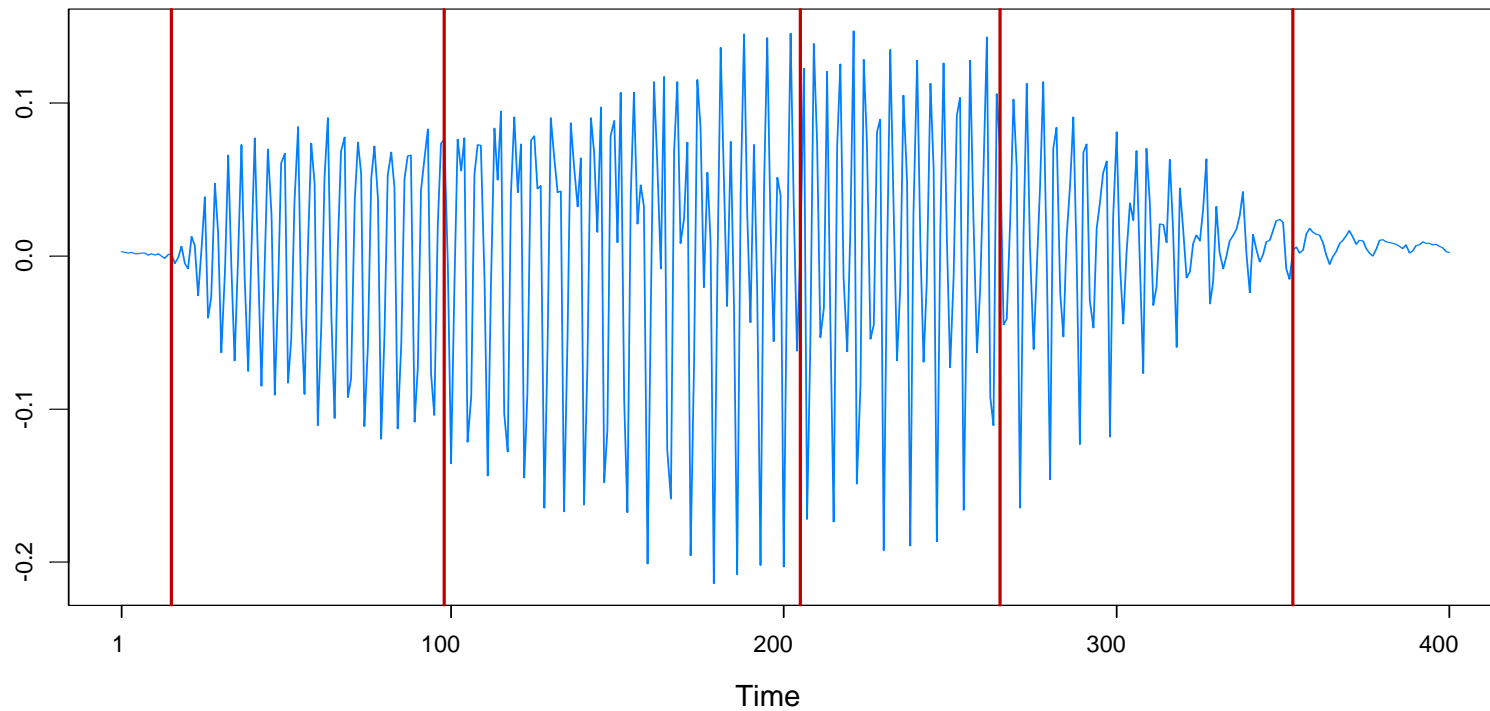
- *time varying frequency*, examples of which are *chirps* and *doppler signals* found in *radar*, *sonar*, and *communication theory*.
- data appears to be made up of *two signals*.
- each signal has a *frequency* that is changing linearly in time. i.e., that is the *cycle* is *lengthening* in time.
- an AR(20) model is the *best fitting* AR model. Residuals are *uncorrelated* but *not independent*.



Examples (bat data cont)

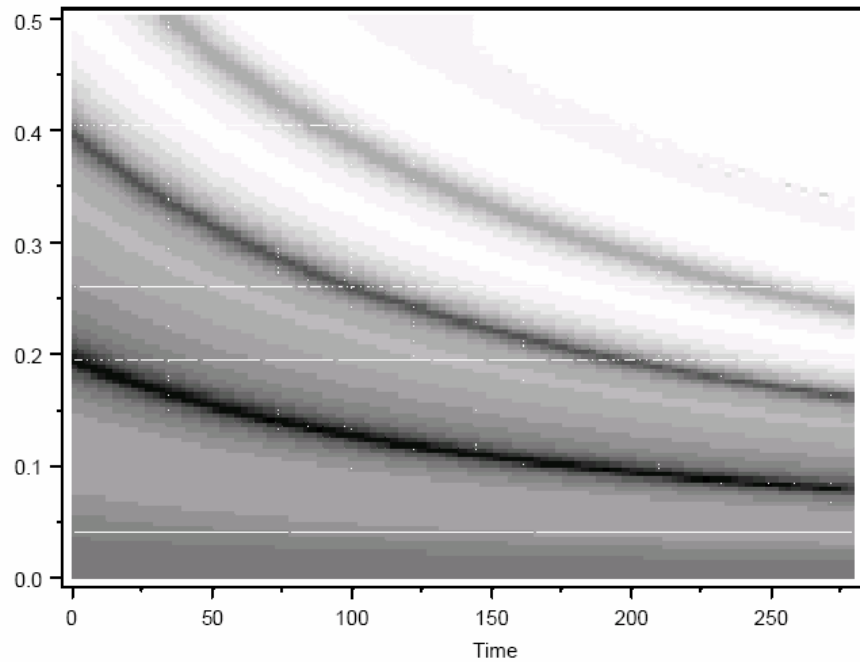
GA results: 6 pieces, breaks at $\tau_1=16$, $\tau_2=98$, $\tau_3=205$, $\tau_4=265$, $\tau_5=353$.

Fitted model: AR orders 1, 6, 13, 7, 13, 5; Total run time 4.7 secs

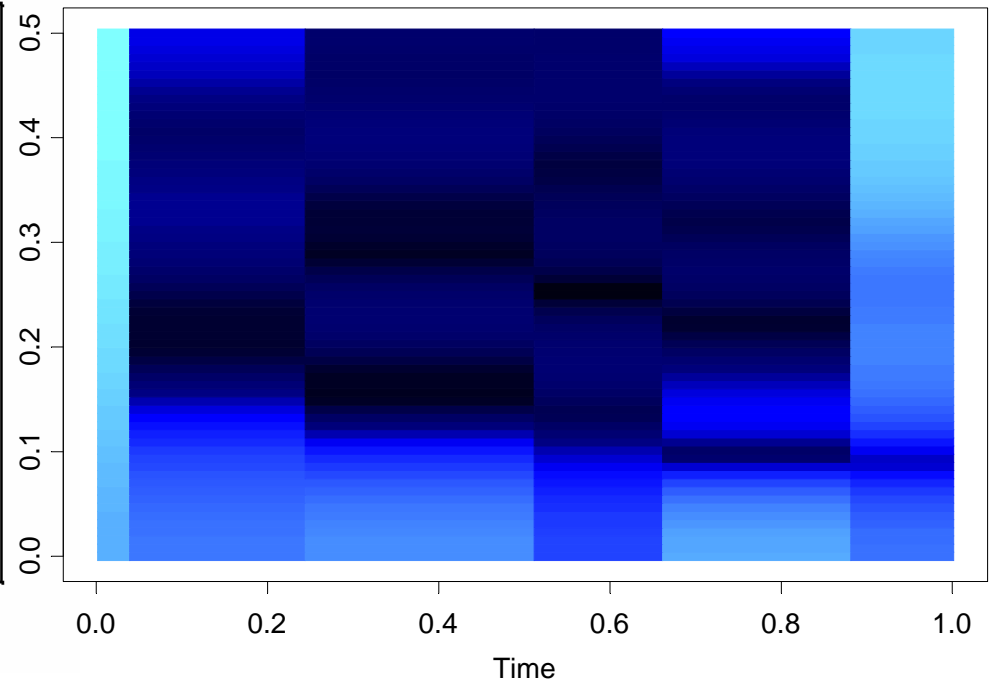


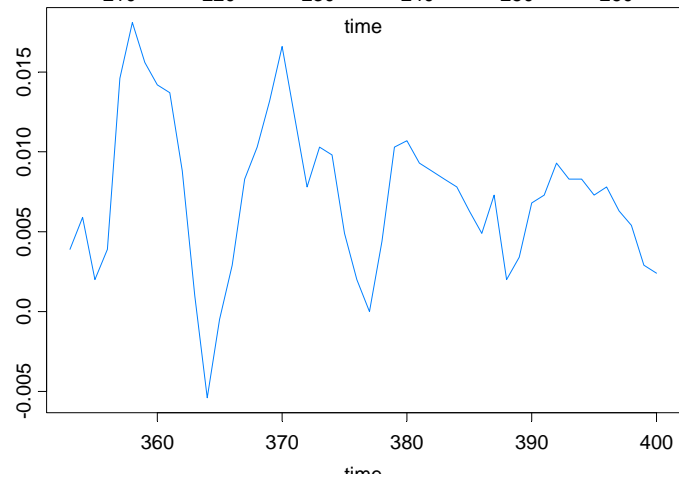
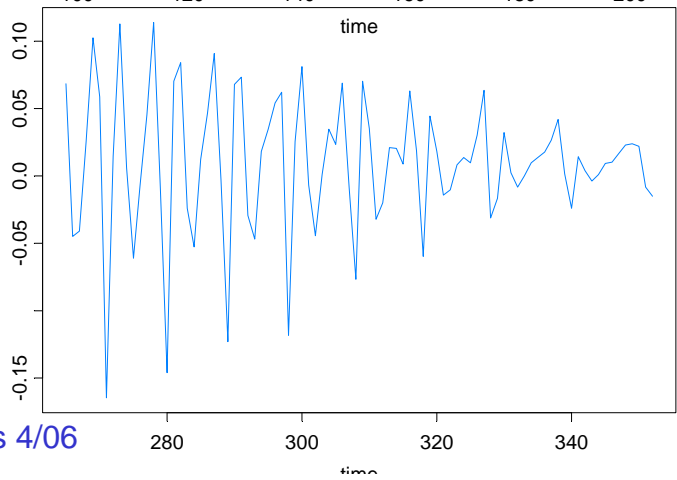
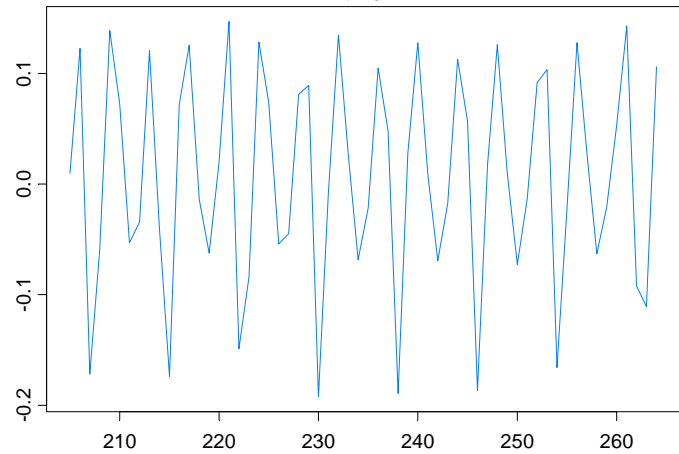
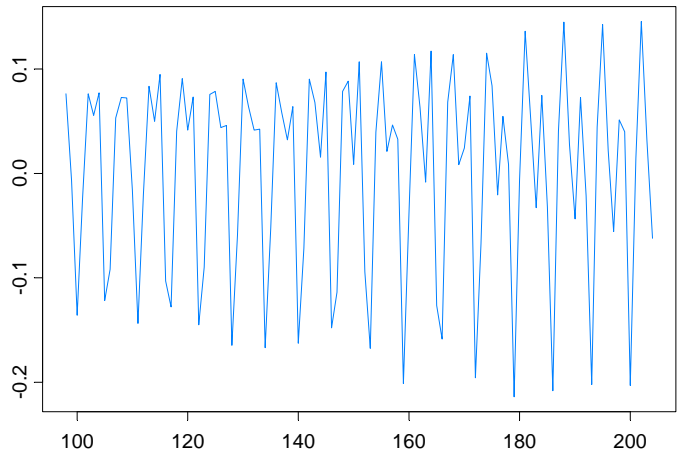
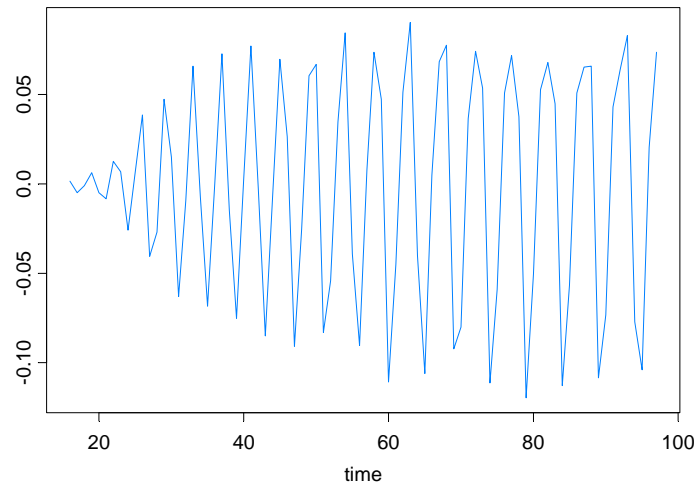
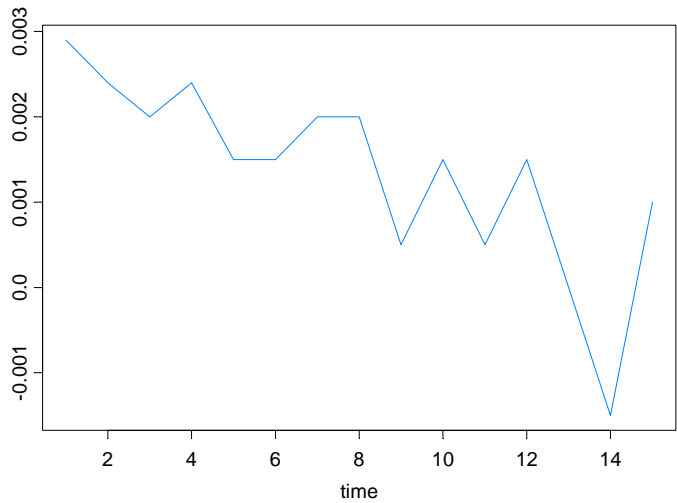
Examples (bat data spectrograms)

Euler(12), Gray et al



Auto-PARM





Application to Multivariate Time Series

Multivariate time series (d-dimensional): $\mathbf{y}_1, \dots, \mathbf{y}_n$

Piecewise AR model:

$$\mathbf{Y}_t = \boldsymbol{\gamma}_j + \Phi_{j1} \mathbf{Y}_{t-1} + \dots + \Phi_{jp_j} \mathbf{Y}_{t-p_j} + \Sigma_j^{1/2} \mathbf{Z}_t, \quad \text{if } \tau_{j-1} \leq t < \tau_j,$$

where $\tau_0 = 1 < \tau_1 < \dots < \tau_{m-1} < \tau_m = n + 1$, and $\{\mathbf{Z}_t\}$ is IID($\mathbf{0}$, I_d).

In this case,

$$\begin{aligned} MDL(m, (\tau_1, p_1), \dots, (\tau_m, p_m)) &= \log m + m \log n + \sum_{j=1}^m \log p_j \\ &+ \sum_{j=1}^m \frac{p_j d^2 + d + d(d+1)/2}{2} \log n_j + \sum_{j=1}^m \frac{1}{2} \sum_{t=\tau_{j-1}}^{\tau_j-1} \left(\log(|\hat{V}_t|) + (\mathbf{Y}_t - \hat{\mathbf{Y}}_t)^T \hat{V}_t^{-1} (\mathbf{Y}_t - \hat{\mathbf{Y}}_t) \right), \end{aligned}$$

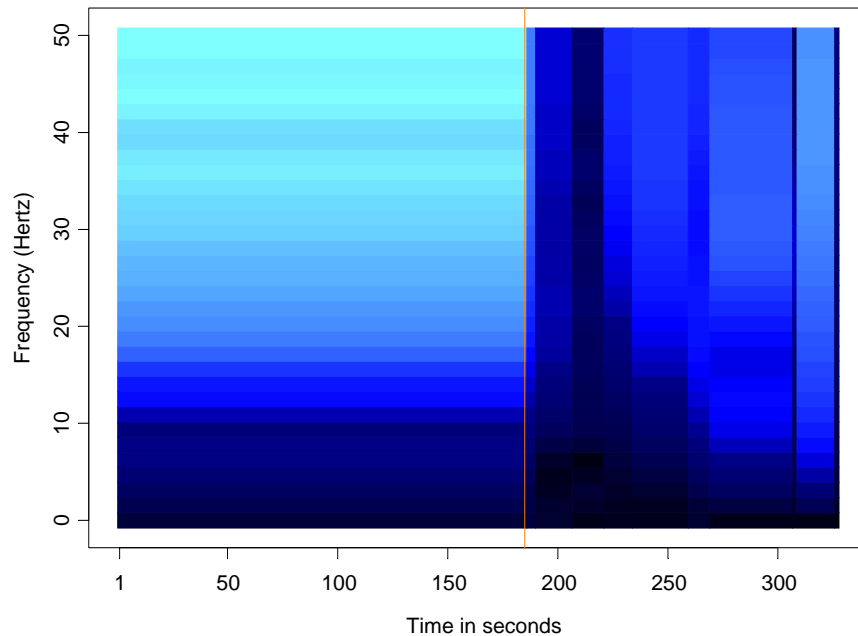
where $\hat{\mathbf{Y}}_t = E(\mathbf{Y}_t | \mathbf{Y}_1, \dots, \mathbf{Y}_t)$ and $\hat{V}_t = E(\mathbf{Y}_t - \hat{\mathbf{Y}}_t)^2$ and the AR parameters are estimated by the multivariate Y-W equations based on Whittle's generalization of the Durbin-Levinson algorithm.

Example: EEG Time series (cont)

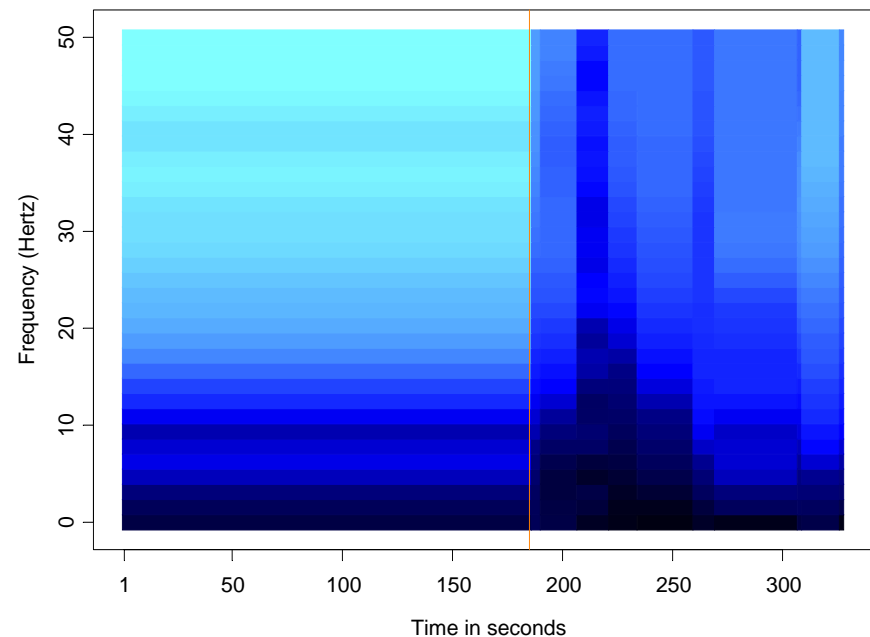
Remarks:

- the general conclusions of this analysis are similar to those reached in Ombao et al.
- prior to seizure, power concentrated at lower frequencies and then spread to high frequencies.
- power returned to the lower frequencies at conclusion of seizure.

T3 Channel



P3 Channel

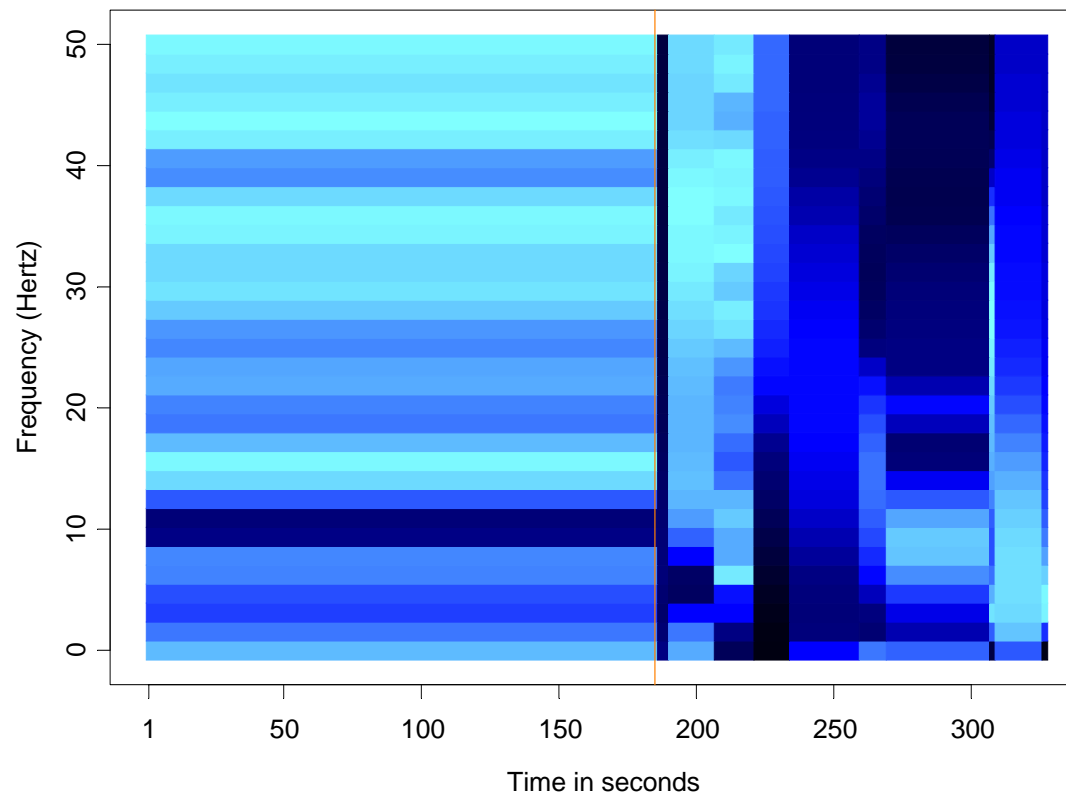


Example: EEG Time series (cont)

Remarks (cont):

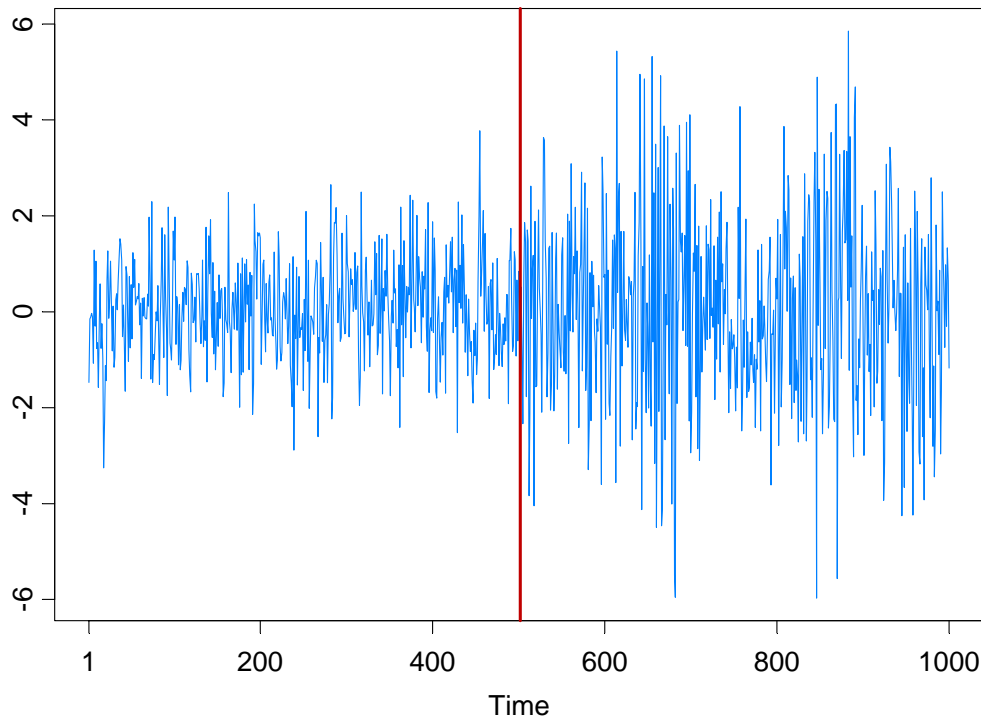
- T3 and P3 strongly coherent at 9-12 Hz prior to seizure.
- strong coherence at low frequencies just after onset of seizure.
- strong coherence shifted to high frequencies during the seizure.

T3/P3 Coherency



Application to GARCH (cont)

Garch(1,1) model: $Y_t = \sigma_t \varepsilon_t, \quad \{\varepsilon_t\} \sim \text{IID}(0,1)$
 $\sigma_t^2 = \omega_j + \alpha_j Y_{t-1}^2 + \beta_j \sigma_{t-1}^2, \quad \text{if } \tau_{j-1} \leq t < \tau_j.$



$$\sigma_t^2 = \begin{cases} .4 + .1Y_{t-1}^2 + .5\sigma_{t-1}^2, & \text{if } 1 \leq t < 501 \\ .4 + .1Y_{t-1}^2 + .8\sigma_{t-1}^2, & \text{if } 501 \leq t < 1000 \end{cases}$$

# of CPs	GA %	AG %
0	0.0	0.0
1	96.4	95.0
≥ 2	3.6	0.5

CP estimate = 502

AG = Andreou and Ghysels (2002)

Application to GARCH (cont)

More simulation results for Garch(1,1) : $Y_t = \sigma_t \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID}(0,1)$

$$\sigma_t^2 = \begin{cases} .05 + .4Y_{t-1}^2 + .3\sigma_{t-1}^2, & \text{if } 1 \leq t < \tau_1, \\ 1.00 + .3Y_{t-1}^2 + .2\sigma_{t-1}^2, & \text{if } \tau_1 \leq t < 1000 \end{cases}$$

τ_1		Mean	SE	Med	Freq
50	GA	52.62	11.70	50	.98
	Berkes	71.40	12.40	71	
250	GA	251.18	4.50	250	.99
	Berkes	272.30	18.10	271	
500	GA	501.22	4.76	502	.98
	Berkes	516.40	54.70	538	

Berkes = Berkes, Gombay, Horvath, and Kokoszka (2004).

Application to Parameter-Driven SS Models

State Space Model Setup:

Observation equation:

$$p(y_t | \alpha_t) = \exp\{\alpha_t y_t - b(\alpha_t) + c(y_t)\}.$$

State equation: $\{\alpha_t\}$ follows the piecewise AR(1) model given by

$$\alpha_t = \gamma_k + \phi_k \alpha_{t-1} + \sigma_k \varepsilon_t, \quad \text{if } \tau_{k-1} \leq t < \tau_k,$$

where $1 = \tau_0 < \tau_1 < \dots < \tau_m < n$, and $\{\varepsilon_t\} \sim \text{IID } N(0,1)$.

Parameters:

m = number of break points

τ_k = location of break points

γ_k = level in k^{th} epoch

ϕ_k = AR coefficients k^{th} epoch

σ_k = scale in k^{th} epoch

Application to Structural Breaks—(cont)

Estimation: For $(m, \tau_1, \dots, \tau_m)$ fixed, calculate the approximate likelihood evaluated at the “MLE”, i.e.,

$$L_a(\hat{\psi}; y_n) = \frac{|G_n|^{1/2}}{(K + G_n)^{1/2}} \exp\{y_n^T \alpha^* - 1^T \{b(\alpha^*) - c(y_n)\} - (\alpha^* - \mu)^T G_n (\alpha^* - \mu) / 2\},$$

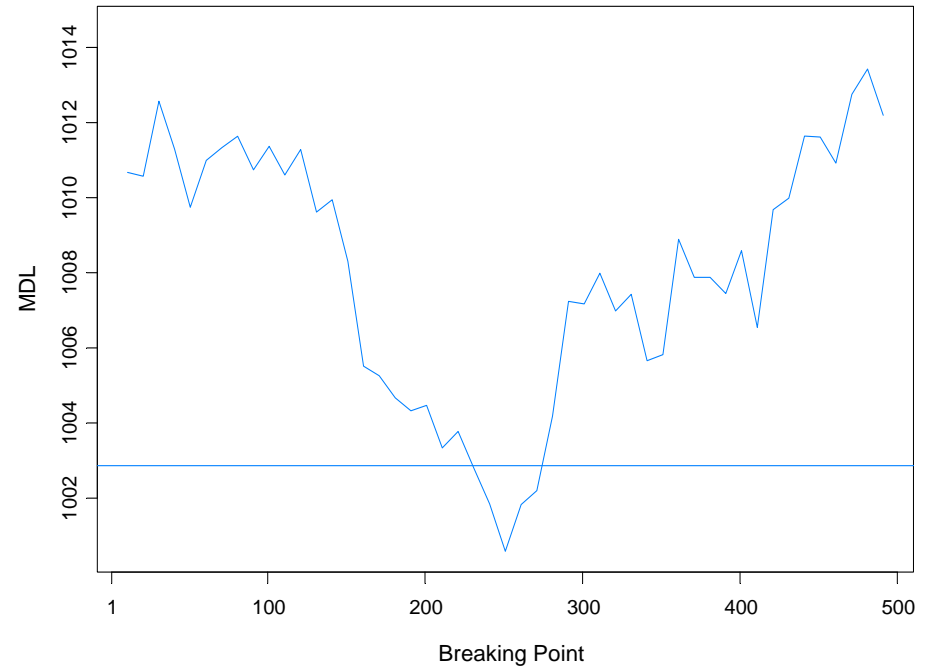
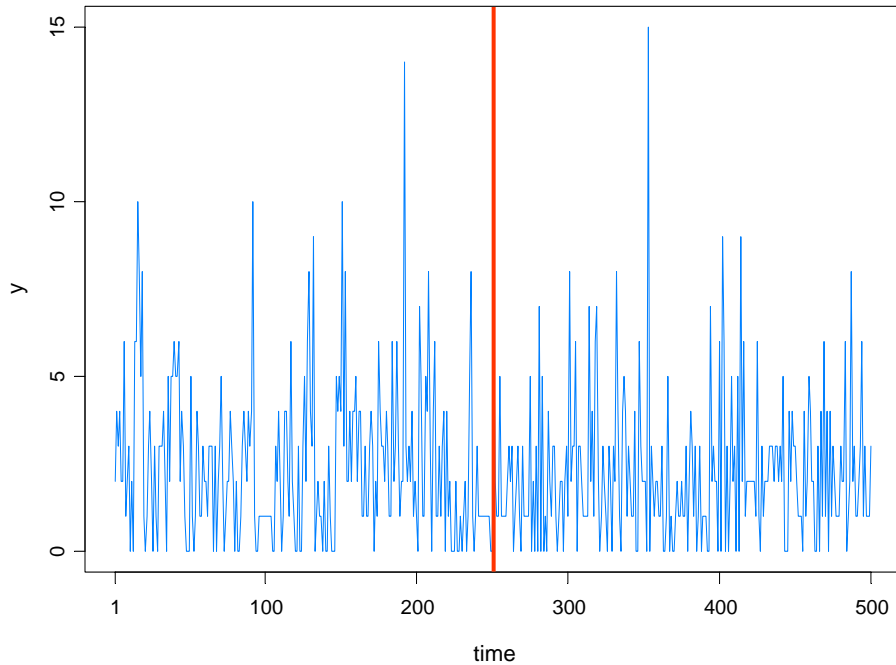
where $\hat{\psi} = (\hat{\gamma}_1, \dots, \hat{\gamma}_m, \hat{\phi}_1, \dots, \hat{\phi}_m, \hat{\sigma}_1^2, \dots, \hat{\sigma}_m^2)$ is the MLE.

Goal: Optimize an *objective function* over $(m, \tau_1, \dots, \tau_m)$.

- use minimum description length (MDL) as an objective function
- use genetic algorithm for optimization

Count Data Example

Model: $Y_t | \alpha_t \sim \text{Pois}(\exp\{\beta + \alpha_t\})$, $\alpha_t = \phi\alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, \sigma^2)$

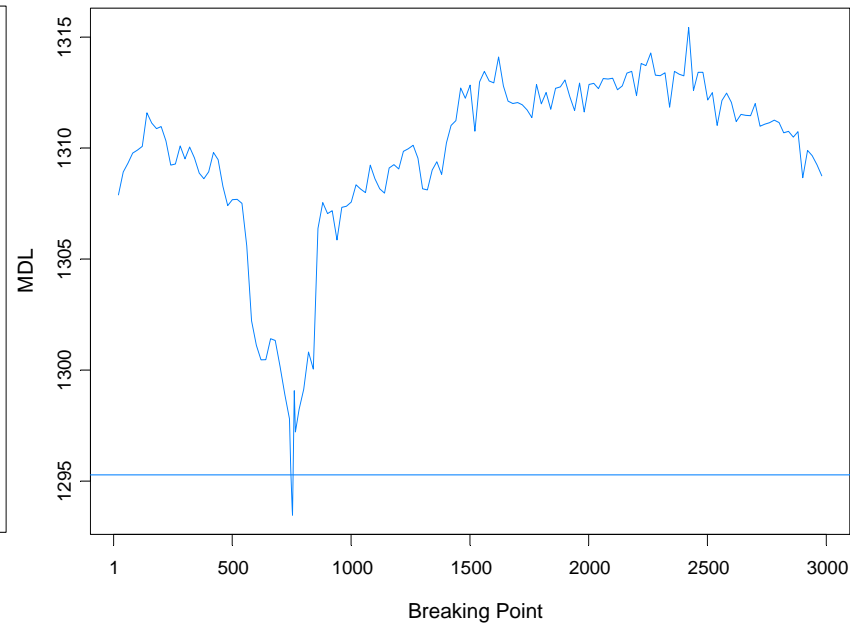
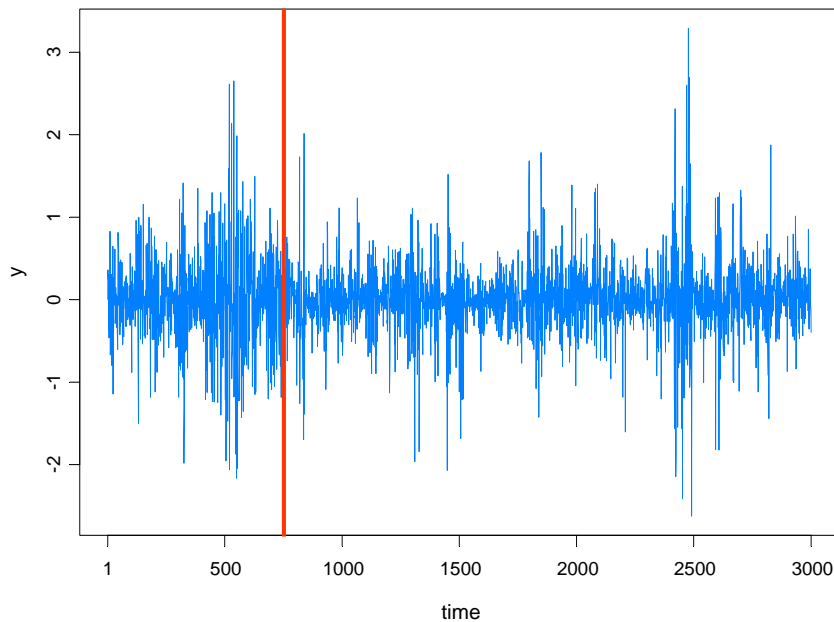


True model:

- $Y_t | \alpha_t \sim \text{Pois}(\exp\{.7 + \alpha_t\})$, $\alpha_t = .5\alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, .3)$, $t < 250$
- $Y_t | \alpha_t \sim \text{Pois}(\exp\{.7 + \alpha_t\})$, $\alpha_t = -.5\alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, .3)$, $t > 250$.
- GA estimate 251, time 267secs

SV Process Example

Model: $Y_t | \alpha_t \sim N(0, \exp\{\alpha_t\})$, $\alpha_t = \gamma + \phi \alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, \sigma^2)$

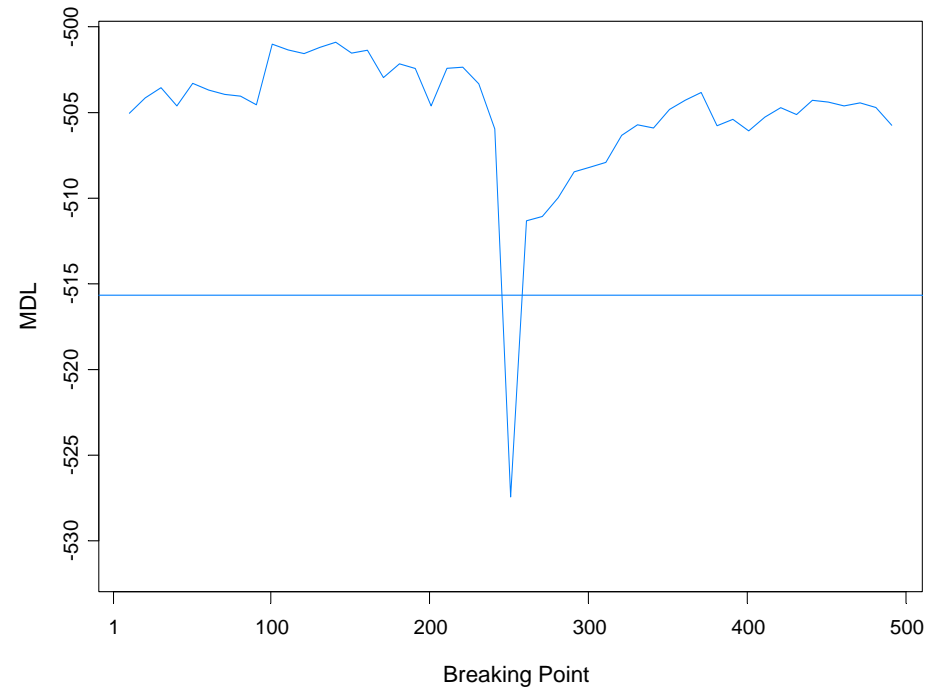
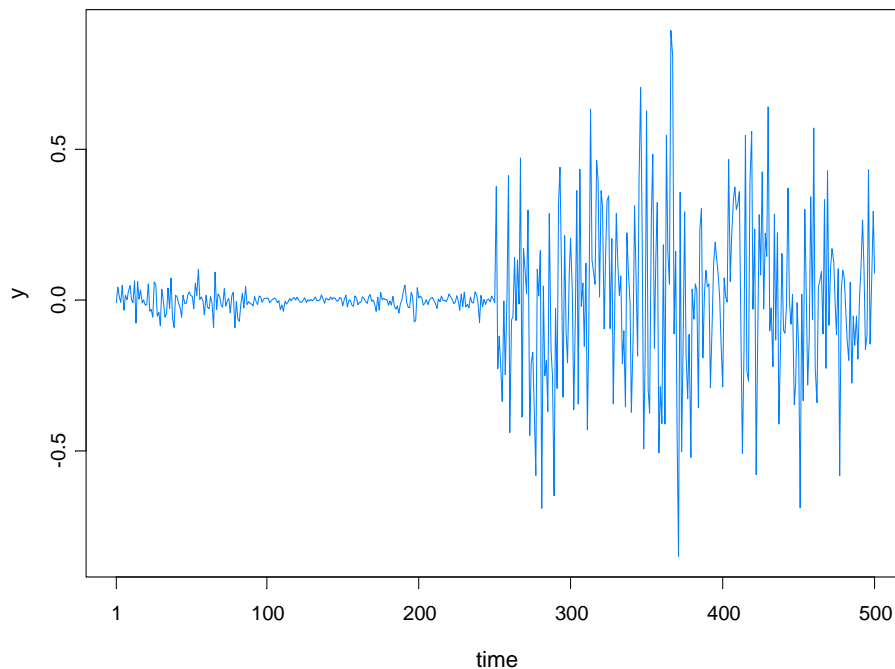


True model:

- $Y_t | \alpha_t \sim N(0, \exp\{\alpha_t\})$, $\alpha_t = -.05 + .975\alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, .05)$, $t \leq 750$
- $Y_t | \alpha_t \sim N(0, \exp\{\alpha_t\})$, $\alpha_t = -.25 + .900\alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, .25)$, $t > 750$.
- GA estimate 754, time 1053 secs

SV Process Example

Model: $Y_t | \alpha_t \sim N(0, \exp\{\alpha_t\})$, $\alpha_t = \gamma + \phi \alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, \sigma^2)$



True model:

- $Y_t | \alpha_t \sim N(0, \exp\{\alpha_t\})$, $\alpha_t = -.175 + .977\alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, .1810)$, $t \leq 250$
- $Y_t | \alpha_t \sim N(0, \exp\{\alpha_t\})$, $\alpha_t = -.010 + .996\alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, .0089)$, $t > 250$.
- GA estimate 251, time 269s

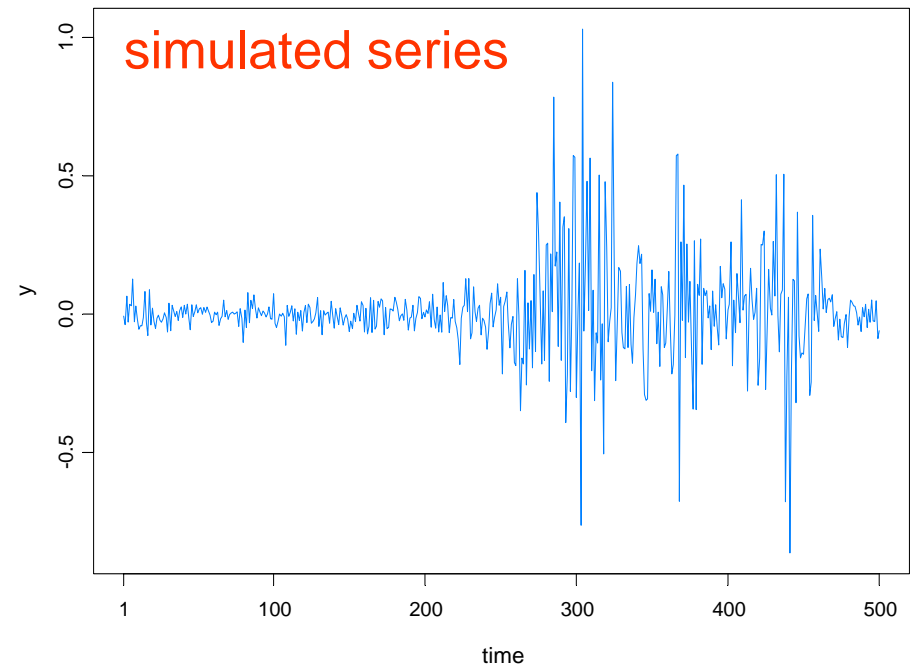
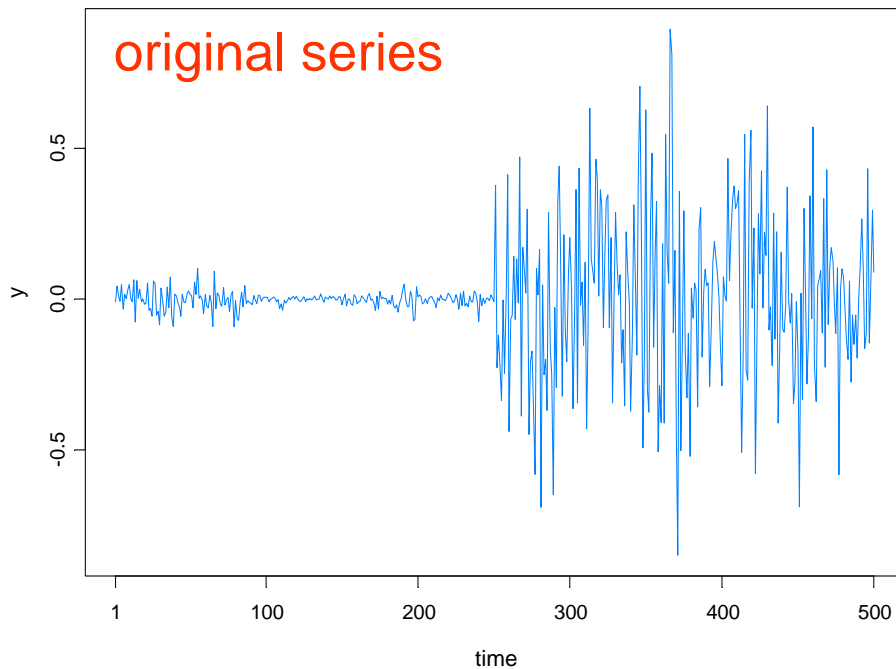
SV Process Example-(cont)

True model:

- $Y_t | \alpha_t \sim N(0, \exp\{a_t\})$, $\alpha_t = -.175 + .977\alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, .1810)$, $t \leq 250$
- $Y_t | \alpha_t \sim N(0, \exp\{\alpha_t\})$, $\alpha_t = -.010 + .996\alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, .0089)$, $t > 250$.

Fitted model based on no structural break:

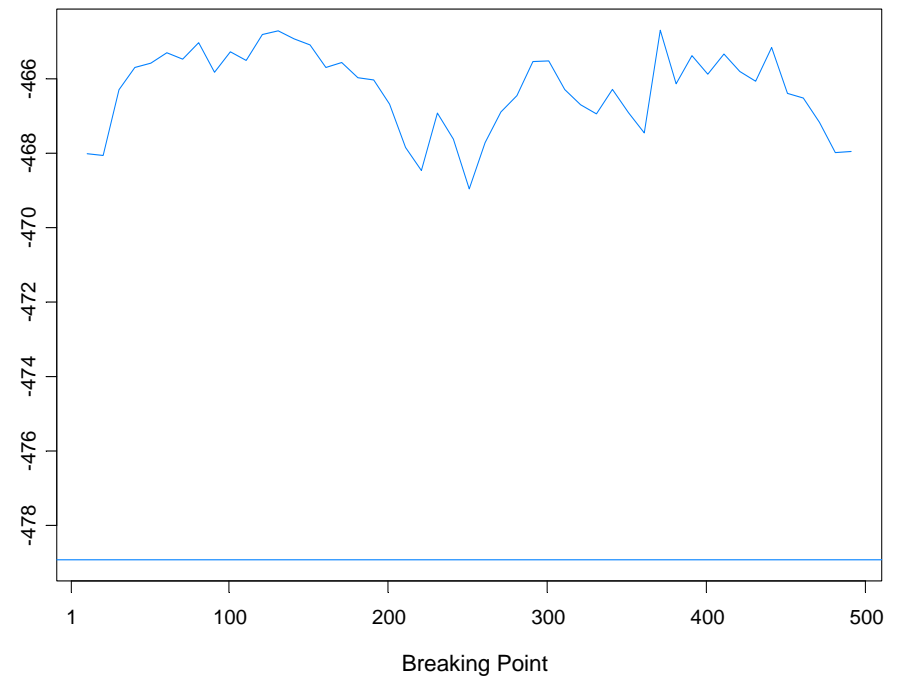
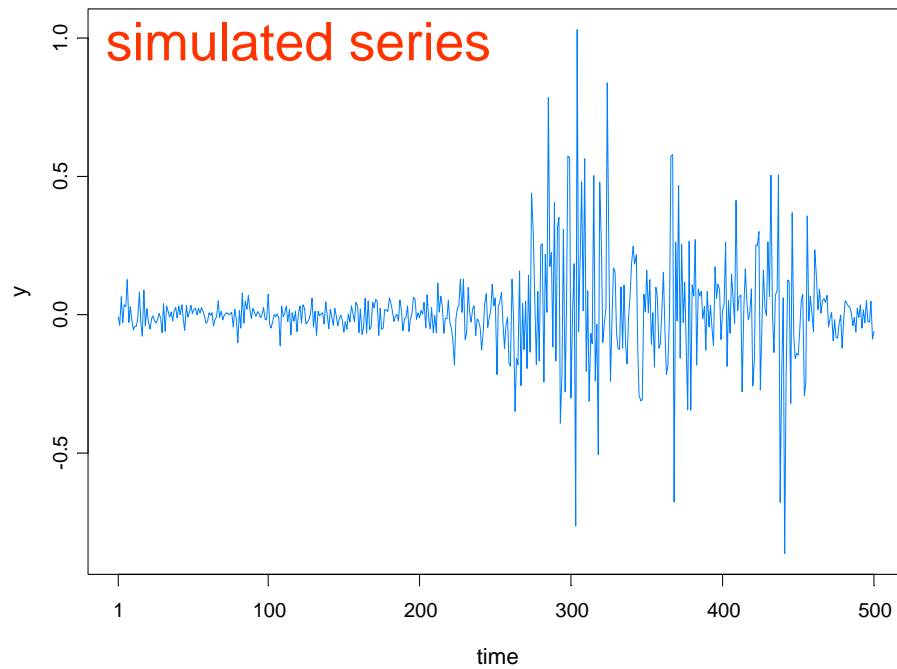
- $Y_t | \alpha_t \sim N(0, \exp\{\alpha_t\})$, $\alpha_t = -.0645 + .9889\alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, .0935)$



SV Process Example-(cont)

Fitted model based on no structural break:

- $Y_t | \alpha_t \sim N(0, \exp\{\alpha_t\})$, $\alpha_t = -.0645 + .9889\alpha_{t-1} + \varepsilon_t$, $\{\varepsilon_t\} \sim \text{IID } N(0, .0935)$



Summary Remarks

1. *MDL* appears to be a good criterion for detecting structural breaks.
2. Optimization using a *genetic algorithm* is well suited to find a near optimal value of MDL.
3. This procedure extends easily to *multivariate* problems.
4. While estimating structural breaks for nonlinear time series models is *more challenging*, this paradigm of using *MDL together GA* holds promise for break detection in *parameter-driven* models and other nonlinear models.