Structural Break Detection in Time Series Models

Richard A. Davis

Thomas Lee

Gabriel Rodriguez-Yam

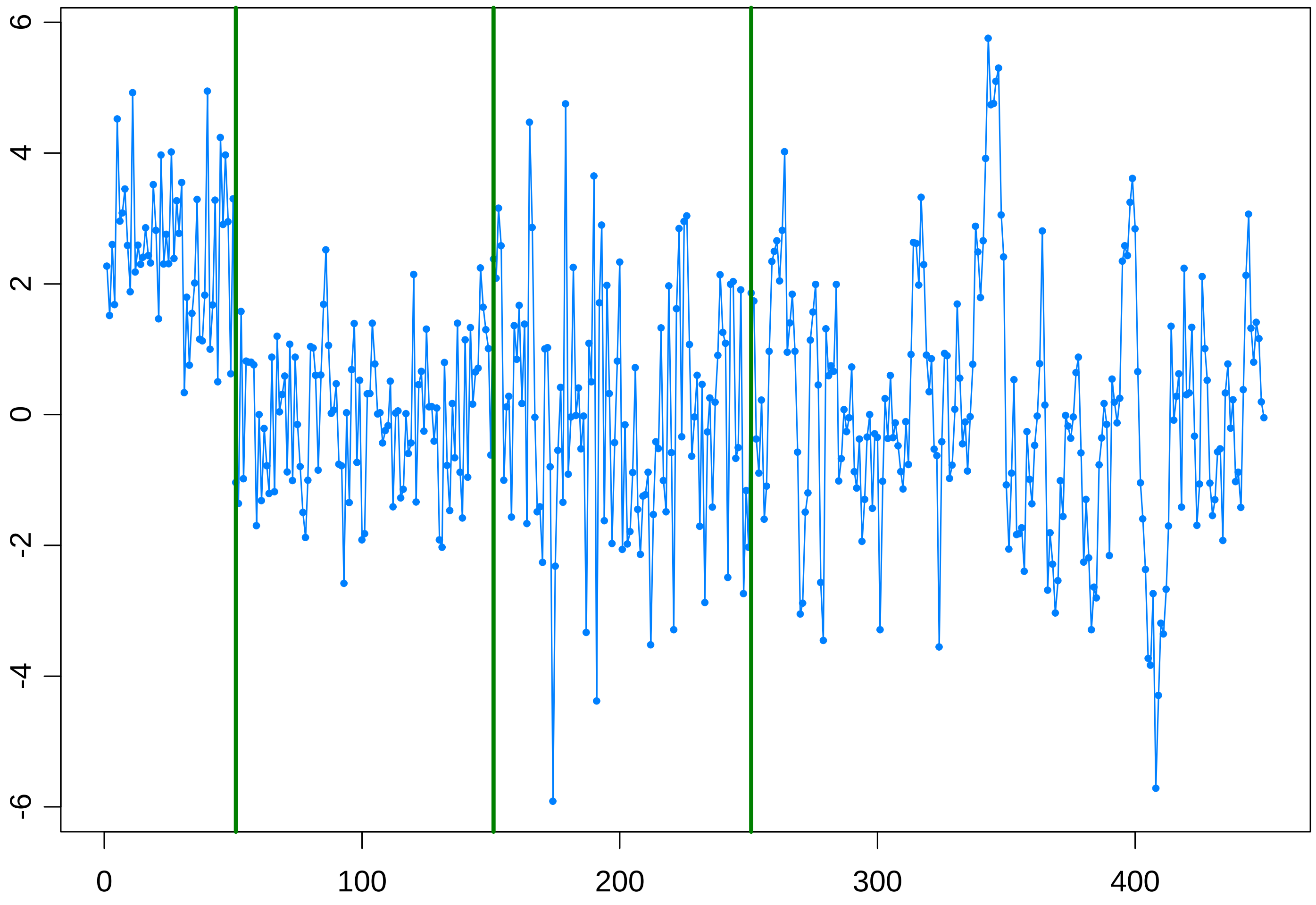
Colorado State University

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

This research supported in part by an IBM faculty award.

Illustrative Example

How many segments do you see?

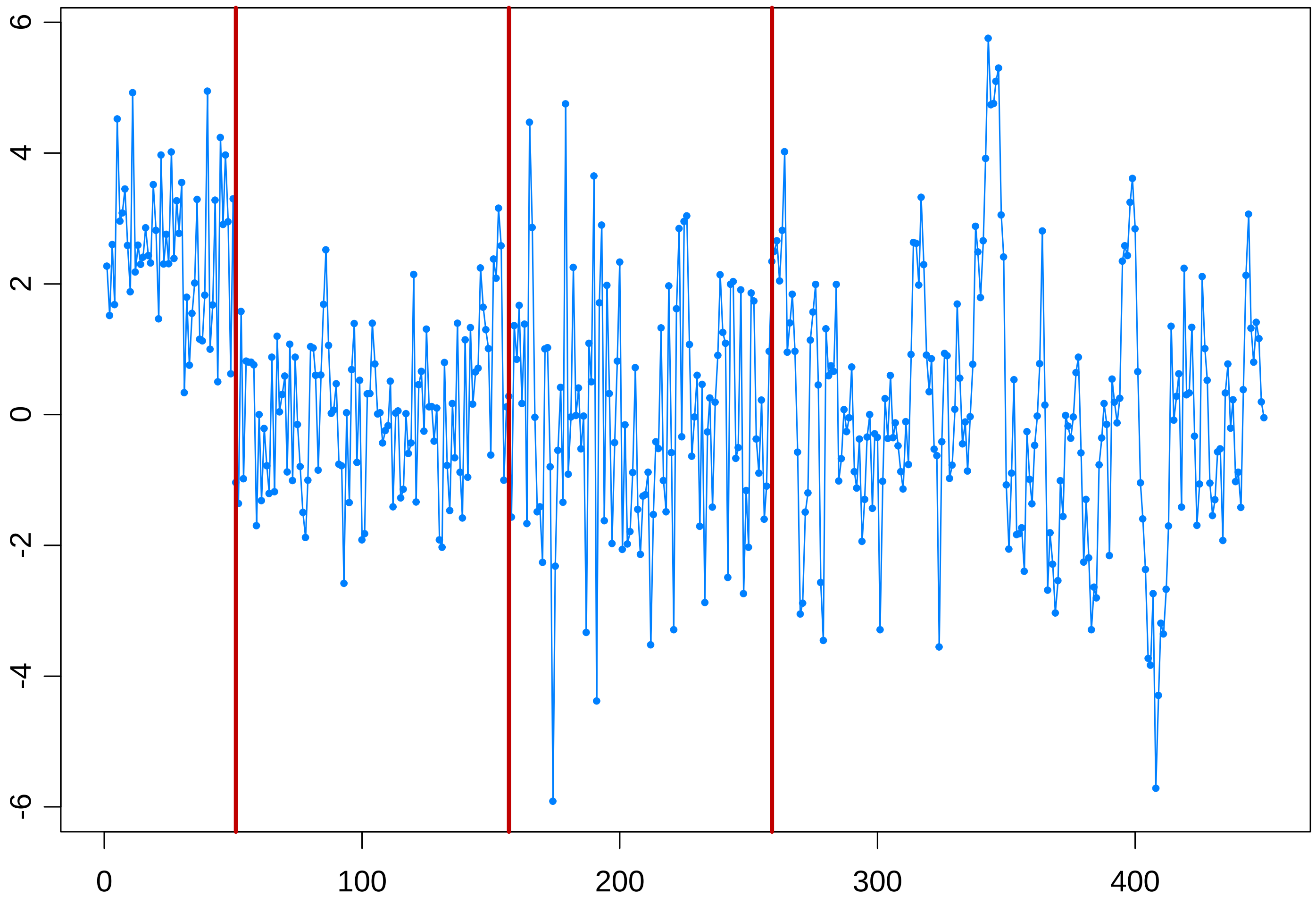


$\tau_1 = 51$ $\tau_2 = 151$ $\tau_3 = 251$

Illustrative Example

Auto-PARM=Auto-Piecewise AutoRegressive Modeling

4 pieces, 2.58 seconds.



$\tau_1 = 51$ $\tau_2 = 157$ $\tau_3 = 259$

- 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:

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

where $\tau_0 = 1 < \tau_1 < \ldots < \tau_{m-1} < \tau_m = n + 1$, 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

$(\phi_{j1}, \ldots, \phi_{jp_j})$ = 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 $\{Y_t^j\}$, $j = 1, \ldots, m$ 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

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

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:

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

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

3. Segmented stochastic volatility model:

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

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

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

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).

$\boldsymbol{M}$ = class of operating models for $y = (y_1, \ldots, y_n)$

$L_{\boldsymbol{F}}(y)$ = code length of y relative to $\boldsymbol{F} \in \boldsymbol{M}$

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

$$L_{\boldsymbol{F}}(y) = L(\hat{\boldsymbol{F}}|y) + L(\hat{e}\,|\,\hat{\boldsymbol{F}}),$$

where

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

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

Model Selection Using Minimum Description Length (cont)

Applied to the segmented AR model:

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

First term $L(\hat{\mathcal{F}}|y)$:

$$L(\hat{\mathcal{F}}|y) = L(m) + L(\tau_1, \ldots, \tau_m) + L(p_1, \ldots, p_m) + L(\hat{\psi}_1 \mid y) + \cdots + L(\hat{\psi}_m \mid y)$$

$$= \log_2 m + m \log_2 n + \sum_{j=1}^{m} \log_2 p_j + \sum_{j=1}^{m} \frac{p_j + 2}{2} \log_2 n_j$$

Encoding:

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

$\log_2 I_U$ bits (if I bounded by I_U)

MLE $\hat{\theta}$: ½ $\log_2 N$ bits (where N = number of observations used to compute $\hat{\theta}$; Rissanen (1989))

Second term $L(\hat{e}\,|\,\hat{F})$: 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

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

For fixed values of m, $(\tau_1, p_1), \ldots, (\tau_m, p_m)$, we define the MDL as

$$MDL(m, (\tau_1, p_1), \ldots, (\tau_m, p_m))$$

$$= \log_2 m + m \log_2 n + \sum_{j=1}^{m} \log_2 p_j + \sum_{j=1}^{m} \frac{p_j + 2}{2} \log_2 n_j - \sum_{j=1}^{m} \log_2 L(\hat{\psi}_j \,|\, y)$$

The strategy is to find the best segmentation that minimizes $MDL(m, \tau_1, p_1, \ldots, \tau_m, p_m)$. To speed things up for AR processes, we use Y-W estimates of AR parameters and we replace

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

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

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

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

would correspond to a process as follows:

AR(2), t=1:5; AR(0), t=6:10; AR(0), t=11:14; AR(3), t=15:20

Implementation of Genetic Algorithm—(cont)

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

Generation 1: A new child in the next generation is formed from the chromosomes $c_1, \ldots, c_L$ 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. ½ and $\delta_{j,k}$ w.p. ½
- 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:

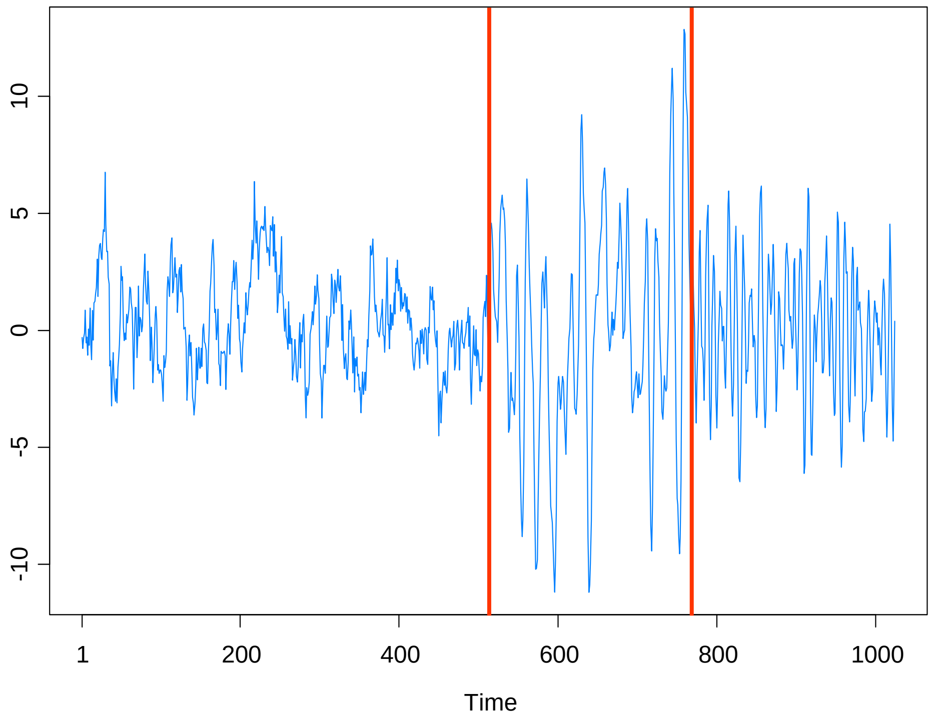
- include the *top ten* chromosomes from last generation in next generation.
- use multiple *islands*, in which populations run independently, and then allow *migration* after a fixed number of generations. This implementation is amenable to *parallel computing*.

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

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

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

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

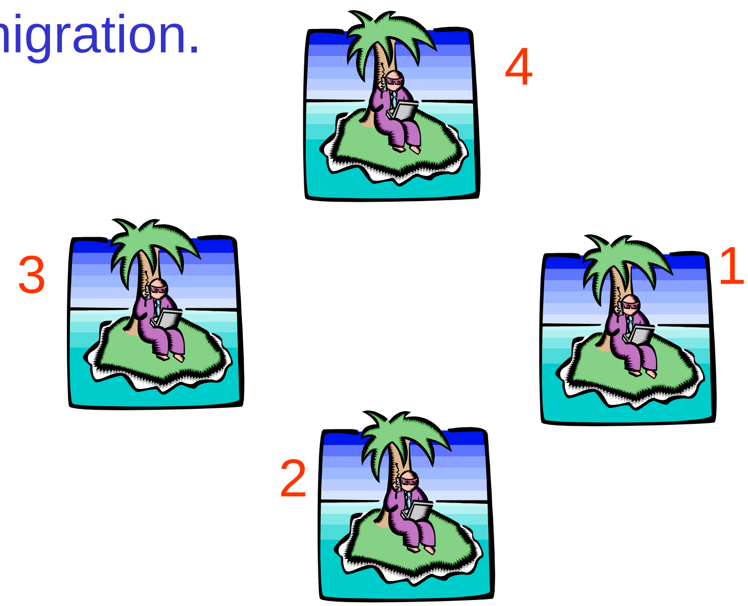


1. Piecewise stat (cont)

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 1.



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

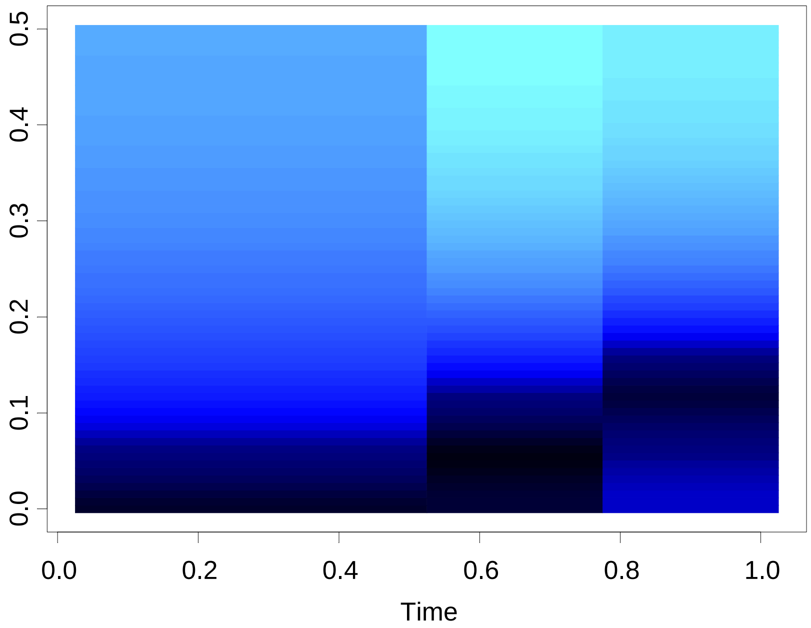
1. Piecewise stat (cont)

GA results: 3 pieces breaks at τ_1=513; τ_2=769. Total run time 16.31 secs

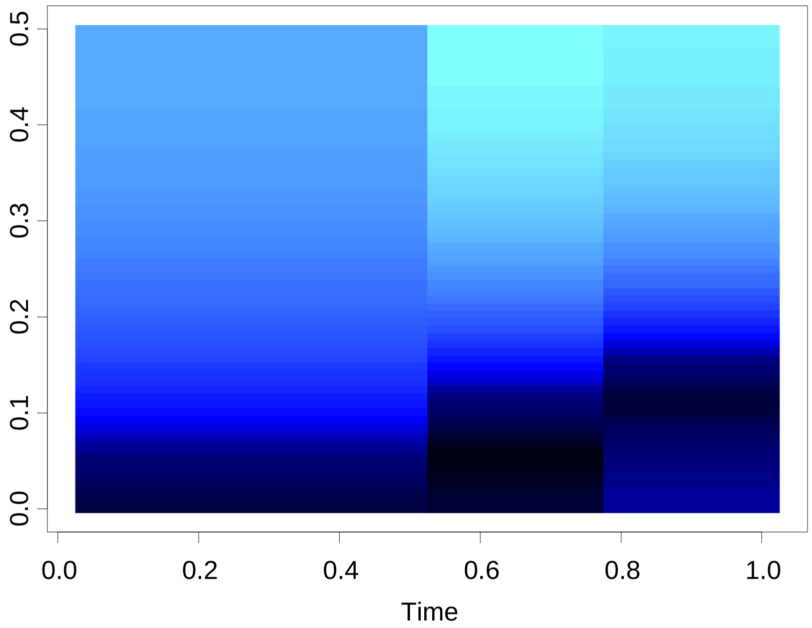
Fitted model:

	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

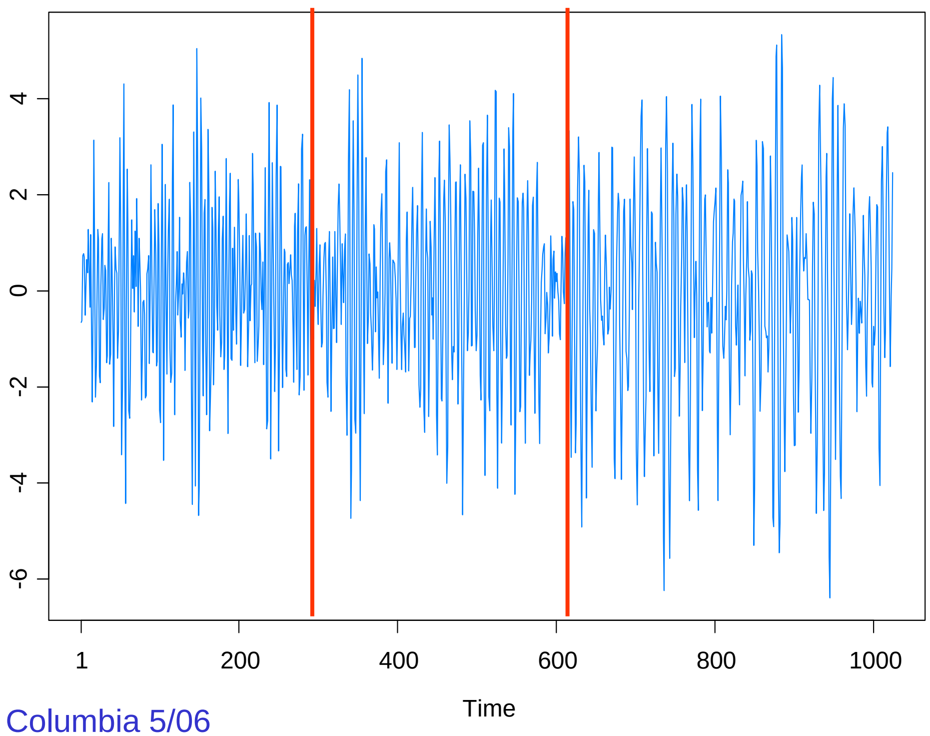


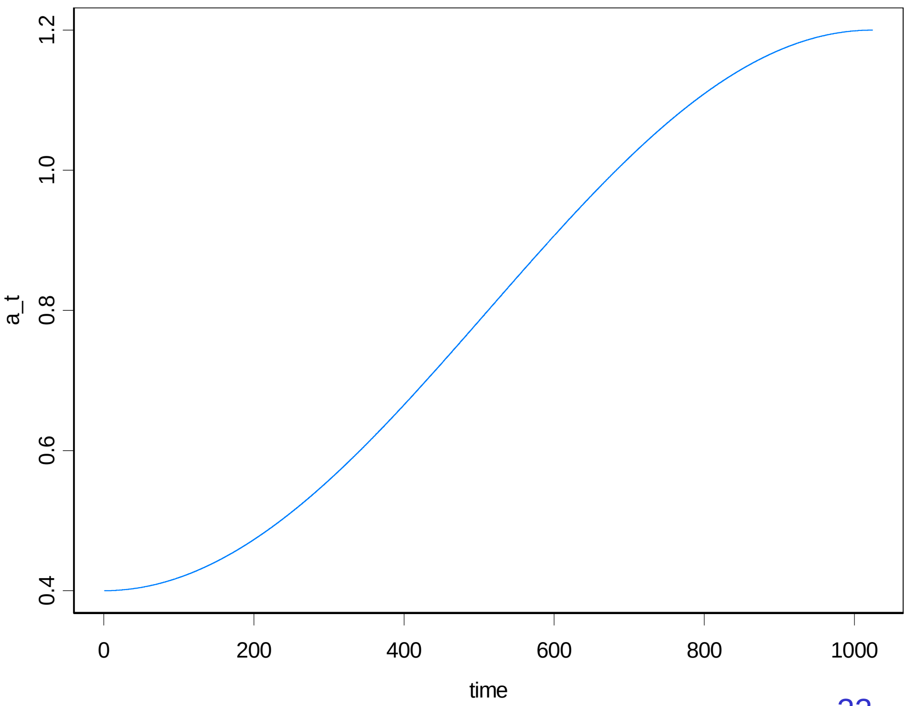
Simulation Examples (cont)

2. Slowly varying AR(2) model:

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

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





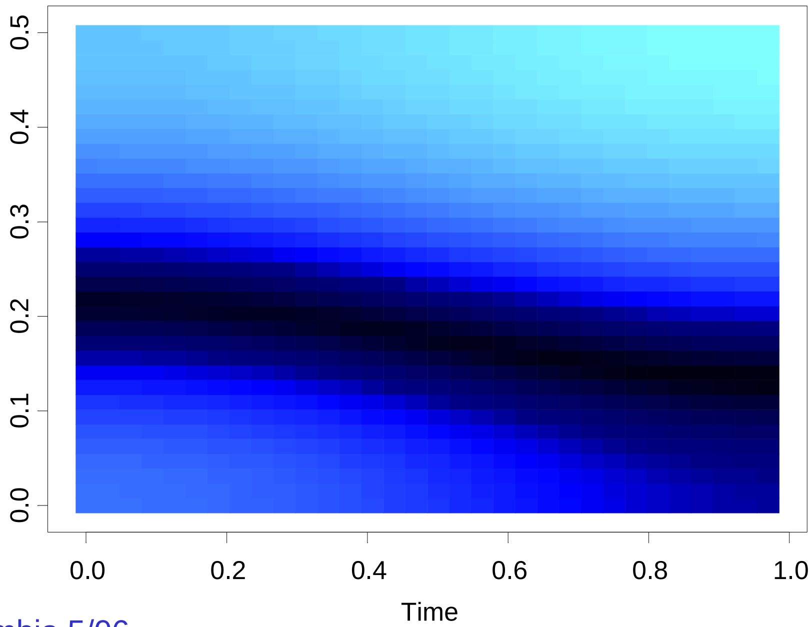
2. Slowly varying AR(2) (cont)

GA results: 3 pieces, breaks at τ_1=293, τ_2=615. Total run time 27.45 secs

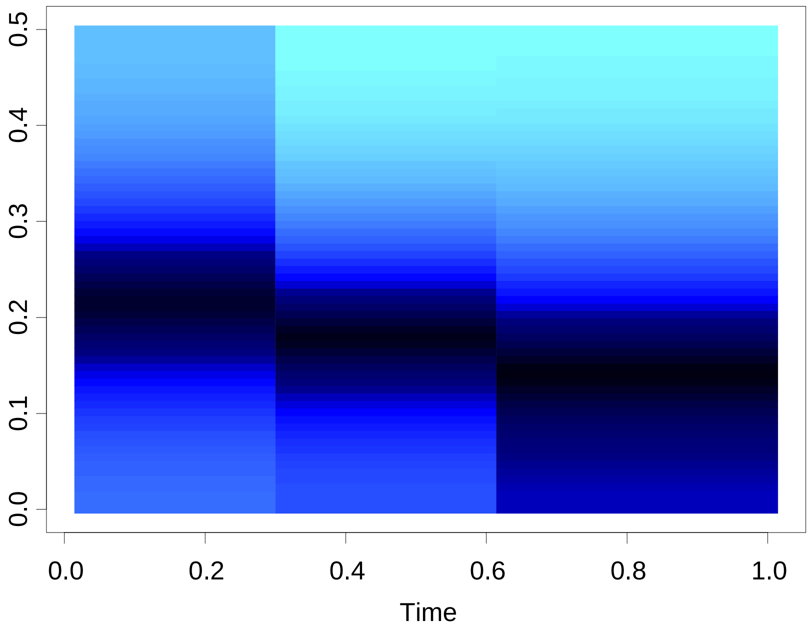
Fitted model:

	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



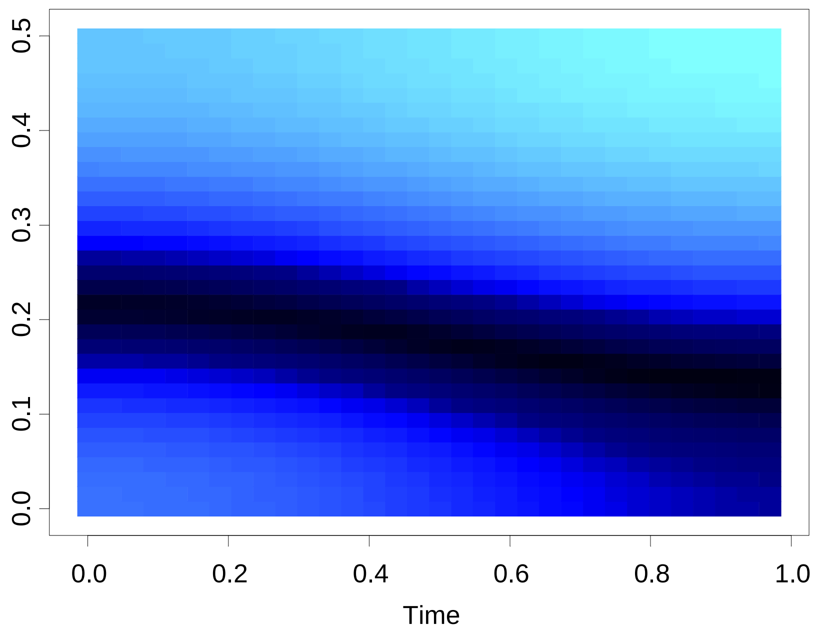
Fitted Model



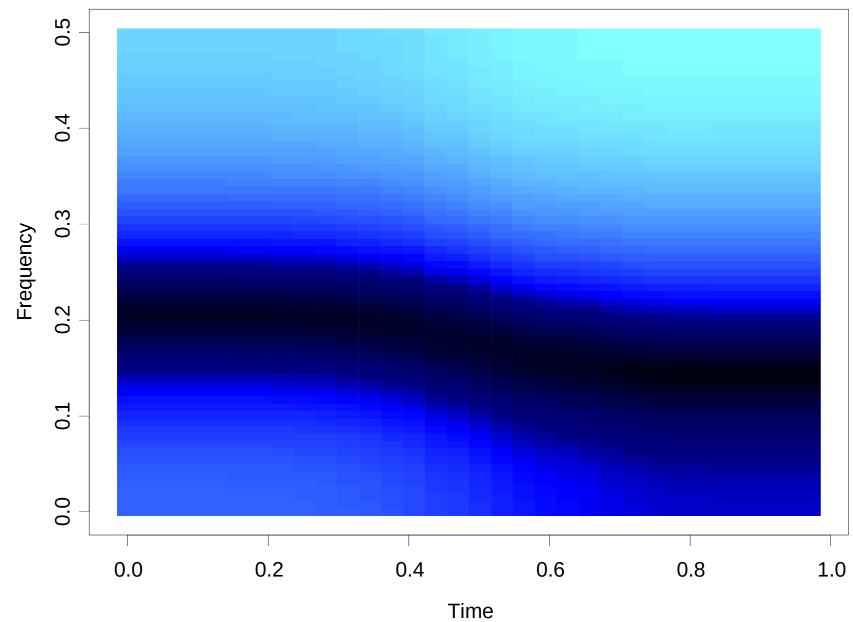
2. Slowly varying AR(2) (cont)

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

True Model



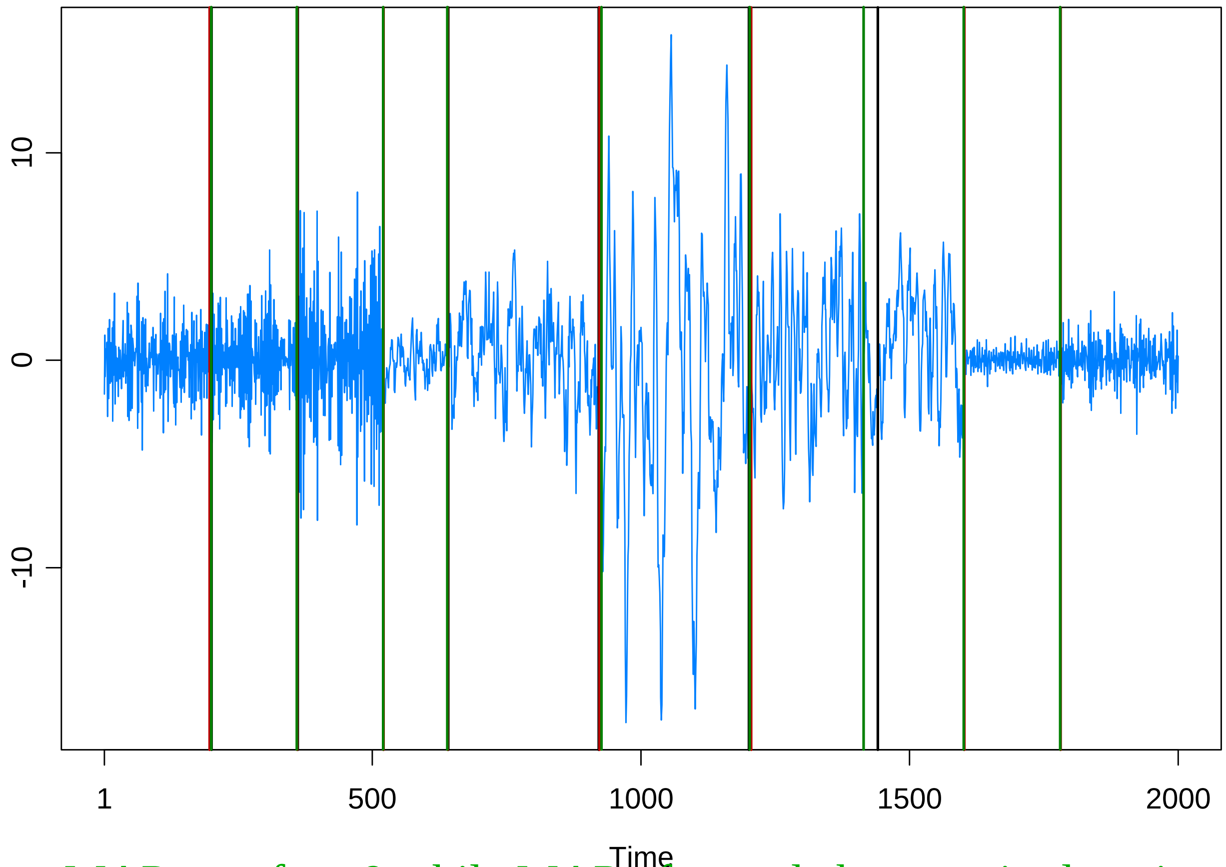
Average Model



Simulation Examples (cont)

4. Simulated data from Fearnhead (2005):

True model has 9 changepoints



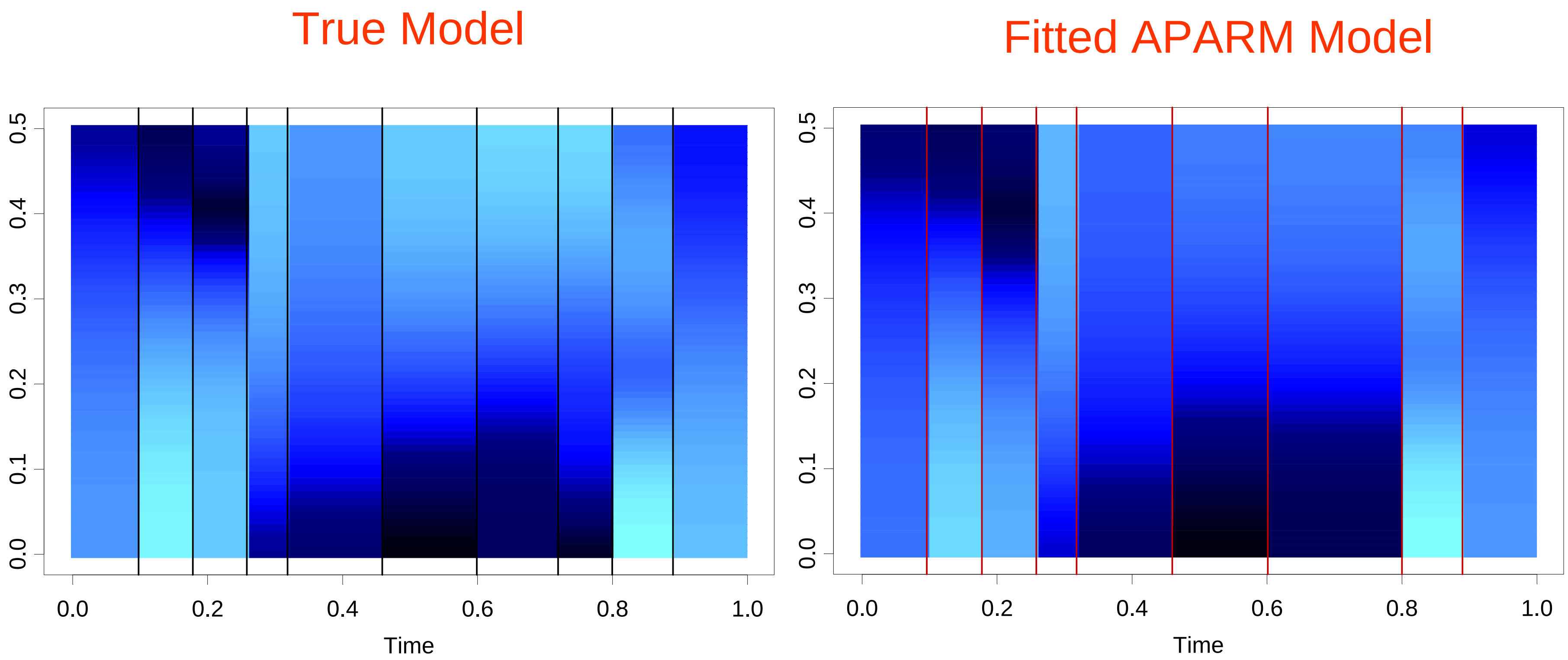
black=true

red=APARM

green=MAP

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



Theory

Consistency.

Suppose the number of change points m is known and let

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

be the relative (true) changepoints. Then

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

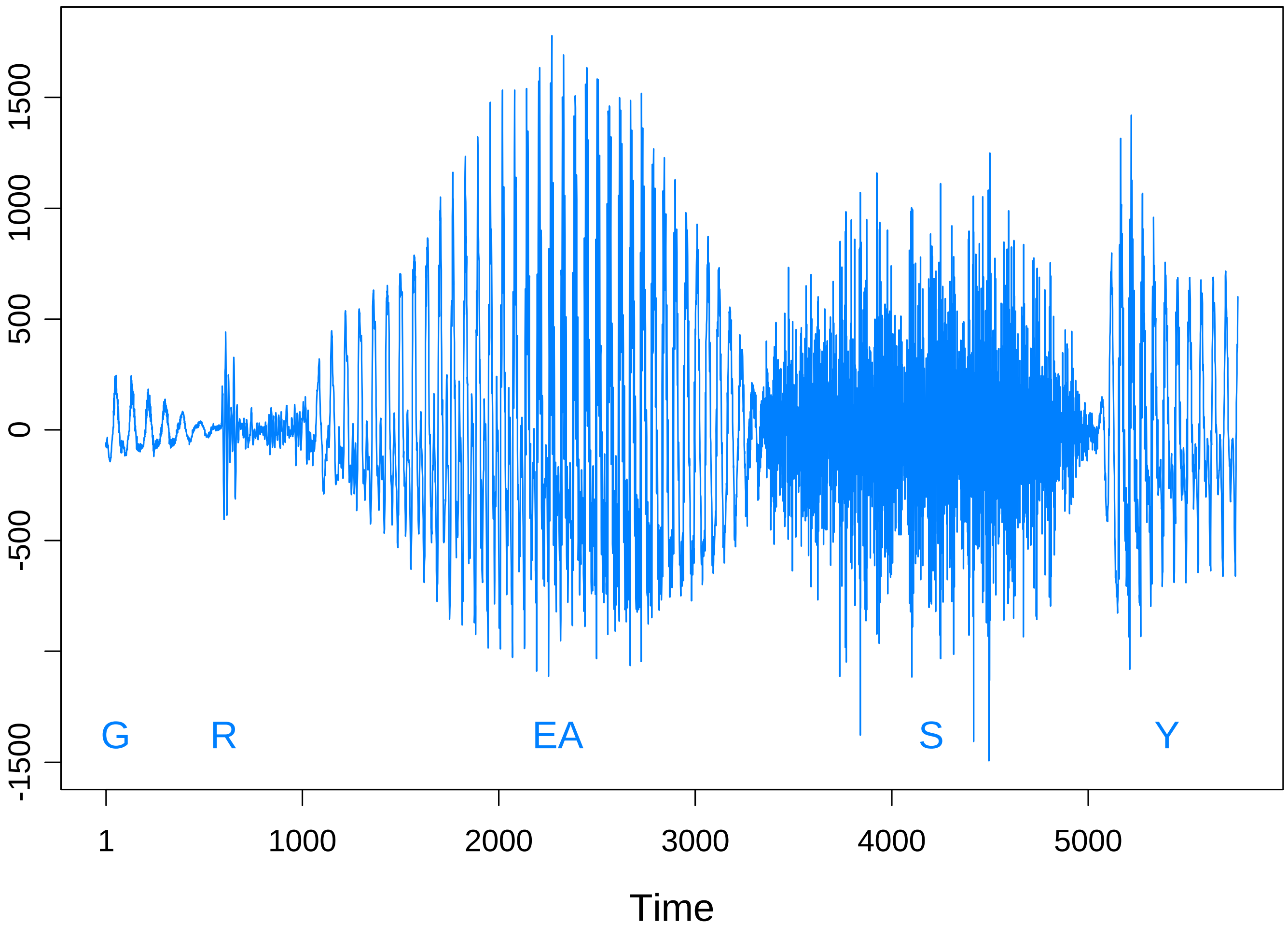
where $\hat{\lambda}_j = \hat{\tau}_j/n$ and $\hat{\tau}_j$ = Auto-PARM estimate of τ_j.

Consistency of the estimate of *m*?

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

Examples

Speech signal: GREASY

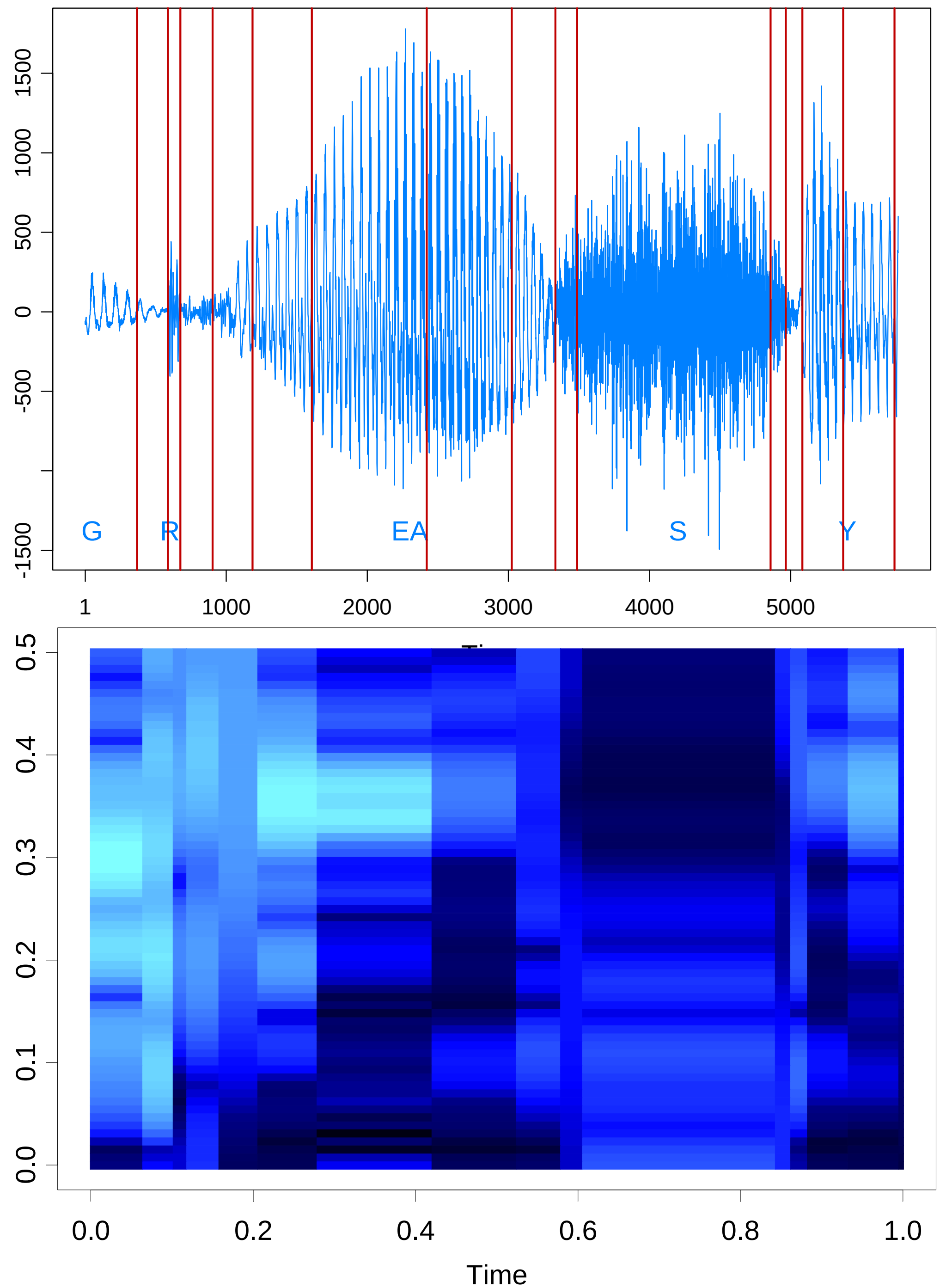


Speech signal: GREASY

n = 5762 observations

m = 15 break points

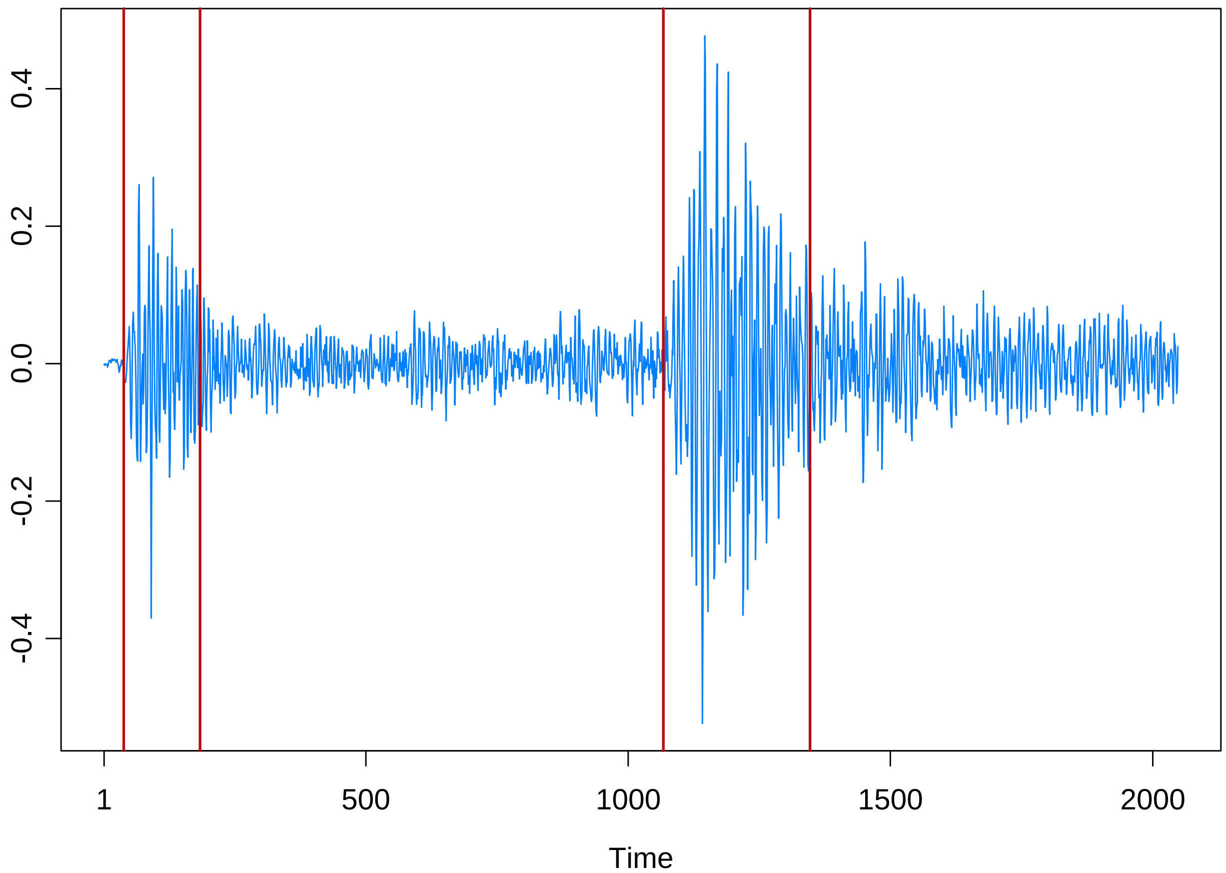
Run time = 18.02 secs



Examples

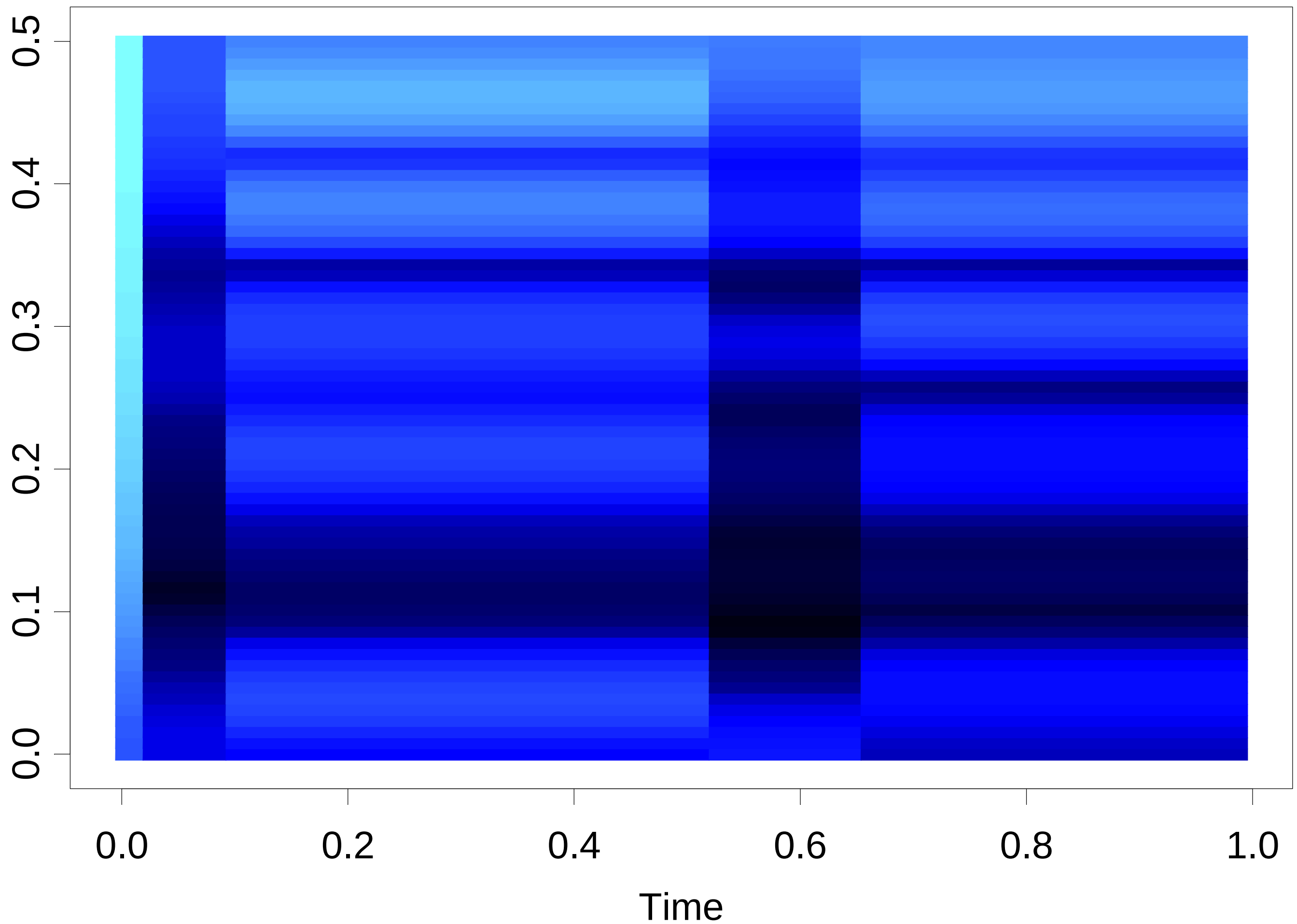
Mine explosion seismic trace in Scandinavia: (Shumway and Stoffer 2000, Stoffer et al. 2005)

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



Examples

AR orders: 1 7 17 13 15

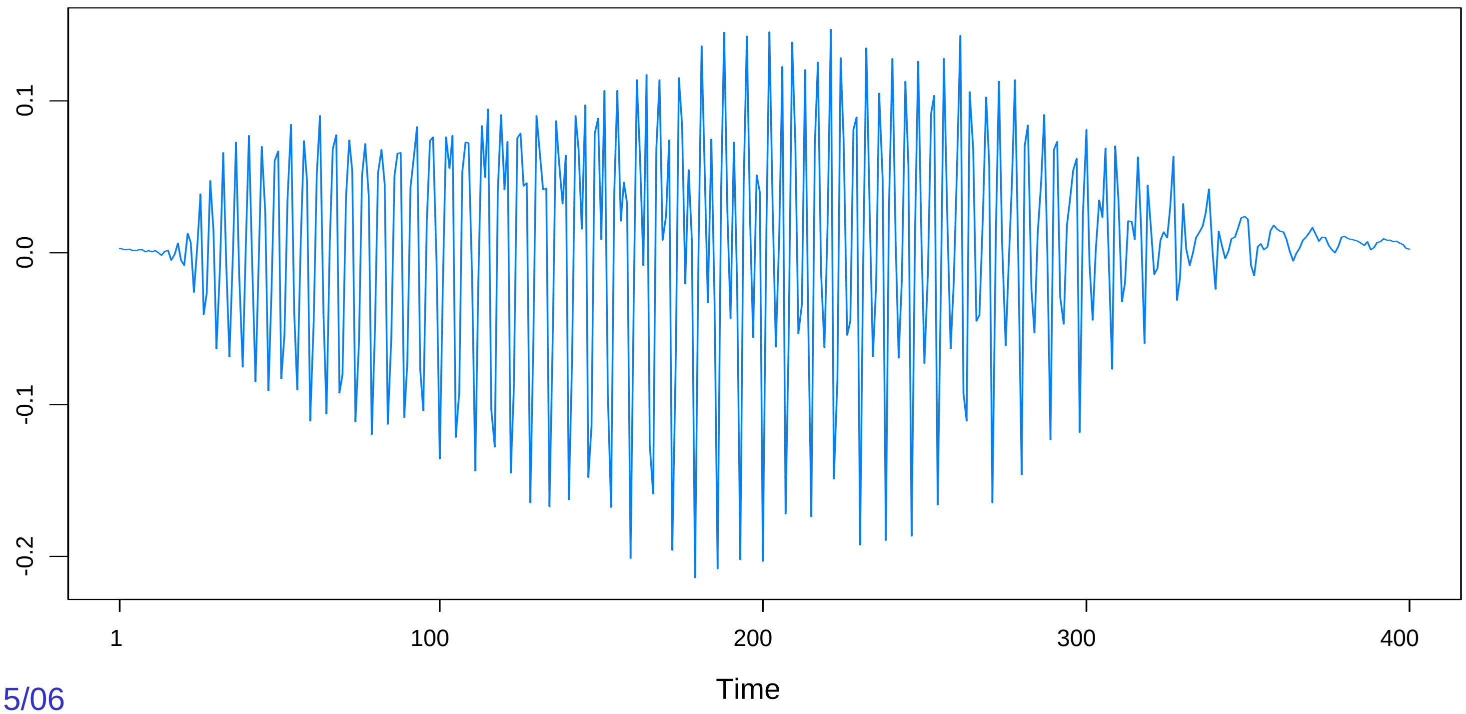


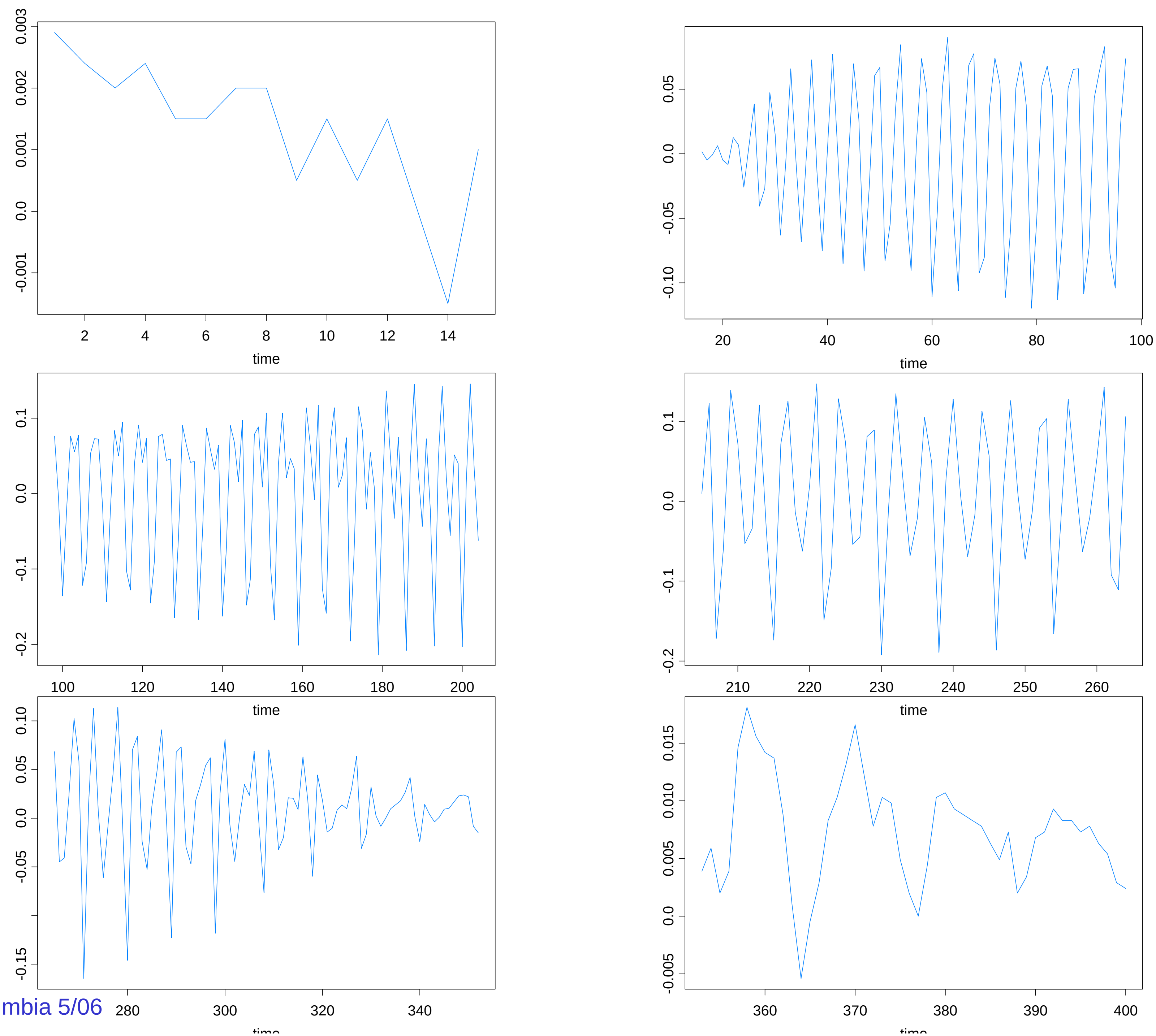
Examples (bat data cont)

M-Stationarity (Gray et al): $\text{Cov}(Y(t), Y(t\tau)) = \text{R}(\tau)$.

- This notion corresponds to a *time-deformation* (logarithmic in this case) to make the transformed process stationary in the ordinary sense.

- The *Euler* process (Gray and Zhang `98) is an example of an M-stationary process.

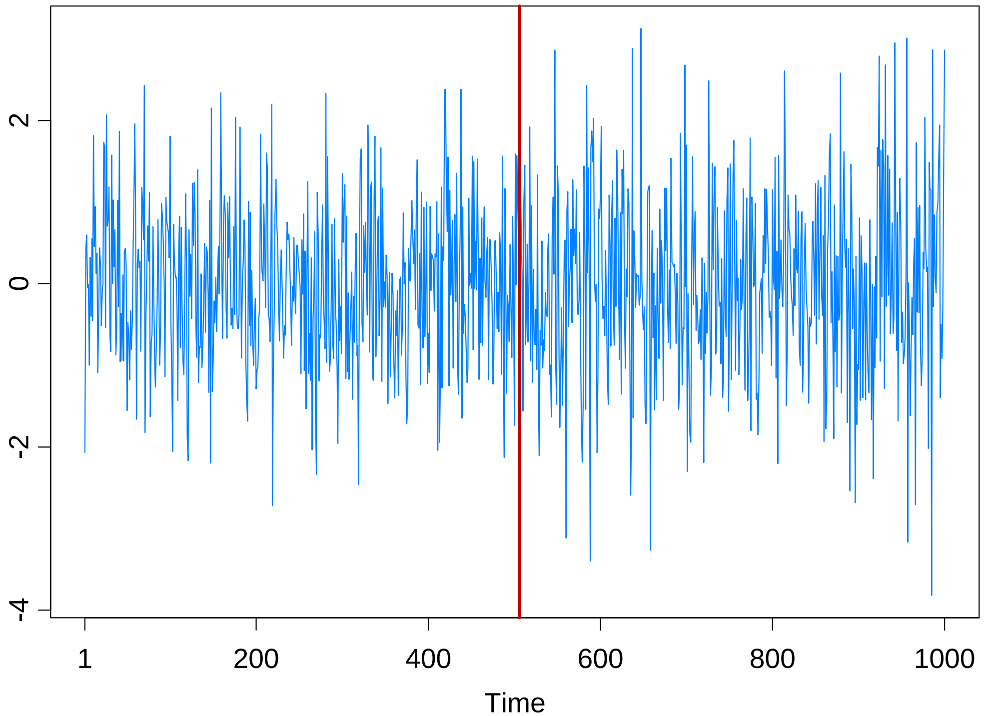



0.003
0.002
0.001
0.0
-0.001
2 4 6 8 10 12 14
time
0.05
0.0
-0.05
-0.10
20 40 60 80 100
time
0.1
0.0
-0.1
-0.2
100 120 140 160 180 200
time
0.1
0.0
-0.1
-0.2
210 220 230 240 250 260
time
0.10
0.05
0.0
-0.05
-0.15
280 300 320 340
0.015
0.010
0.005
0.0
-0.005
360 370 380 390 400

Application to GARCH (cont)

Garch(1,1) model: $Y_t = \sigma_t \varepsilon_t, \qquad \{\varepsilon_t\} \sim \text{IID}(0,1)$

$$\sigma_t^2 = \omega_j + \alpha_j Y_{t-1}^2 + \beta_j \sigma_{t-1}^2, \qquad \text{if } \tau_{j\text{-}1} \le t < \tau_j.$$



$$\sigma_t^2 = \begin{cases} .4 + .1Y_{t-1}^2 + .5\sigma_{t-1}^2, & \text{if } 1 \le t < 501, \\ .4 + .1Y_{t-1}^2 + .6\sigma_{t-1}^2, & \text{if } 501 \le t < 1000 \end{cases}$$

# of CPs	GA %	AG %
0	80.4	72.0
1	19.2	24.0
≥ 2	0.4	0.4

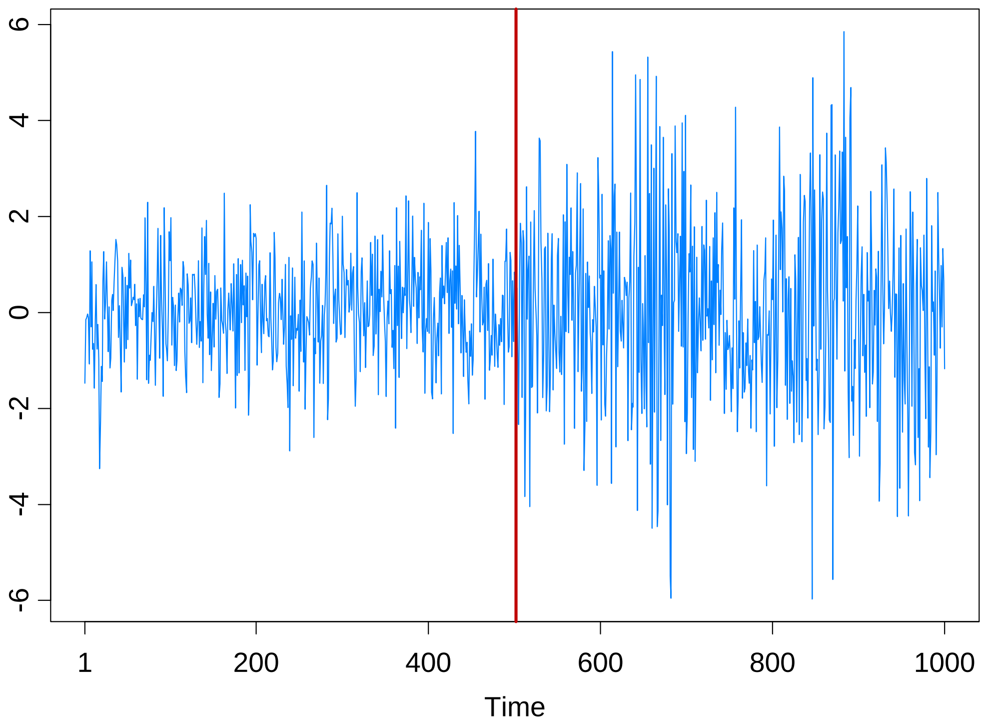
CP estimate = 506

AG = Andreou and Ghysels (2002)

Application to GARCH (cont)

Garch(1,1) model: $Y_t = \sigma_t \varepsilon_t, \quad \{\varepsilon_t\} \sim \text{IID}(0,1)$

$$\sigma_t^2 = \omega_j + \alpha_j Y_{t-1}^2 + \beta_j \sigma_{t-1}^2, \quad \text{if } \tau_{j\text{-}1} \le t < \tau_j.$$



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

# 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) : $Y_t = \sigma_t \varepsilon_t, \qquad \{\varepsilon_t\} \sim \text{IID}(0,1)$

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

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:

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

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

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

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

Parameters:

m = number of break points

τ_k = location of break points

γ_k = level in kth epoch

ϕ_k = AR coefficients kth epoch

σ_k = scale in kth epoch

Application to Structural Breaks—(cont)

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

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

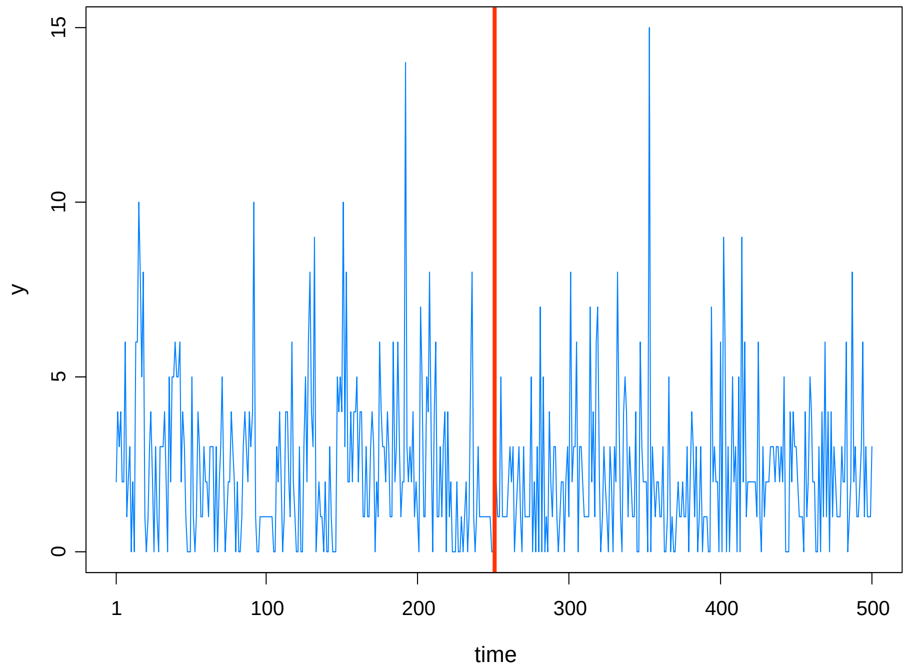
where $\hat{\psi} = (\hat{\gamma}_1, \ldots, \hat{\gamma}_m, \hat{\phi}_1, \ldots, \hat{\phi}_m, \hat{\sigma}_1^2, \ldots, \hat{\sigma}_m^2)$ is the MLE.

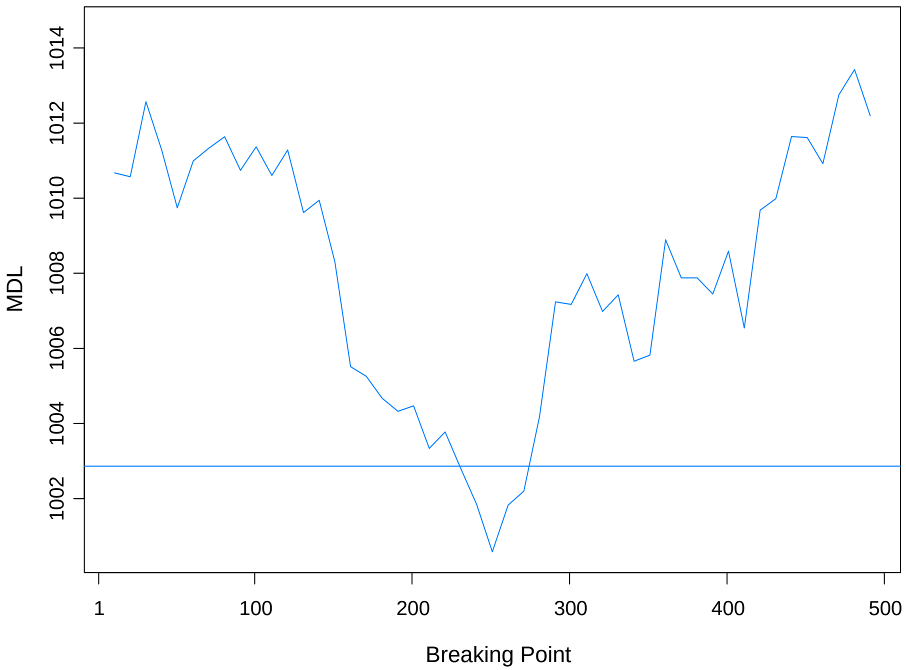
Goal: Optimize an *objective function* over $(m, \tau_1, \ldots, \tau_m)$.

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

Count Data Example

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



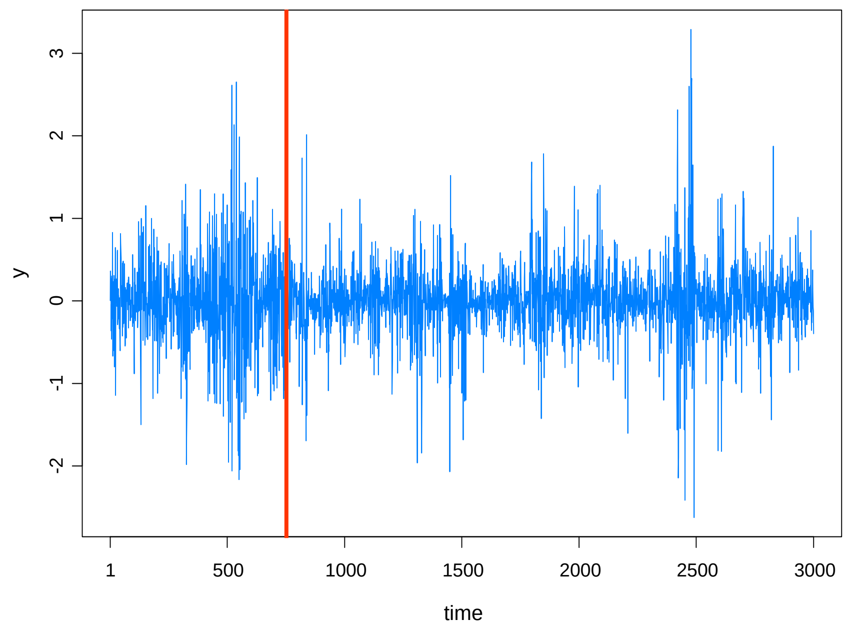


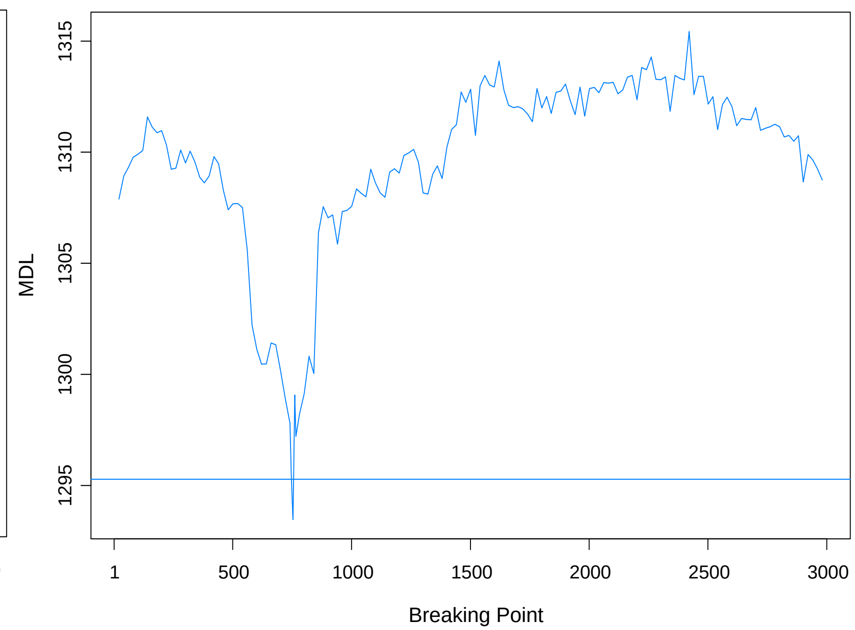
True model:

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

SV Process Example

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



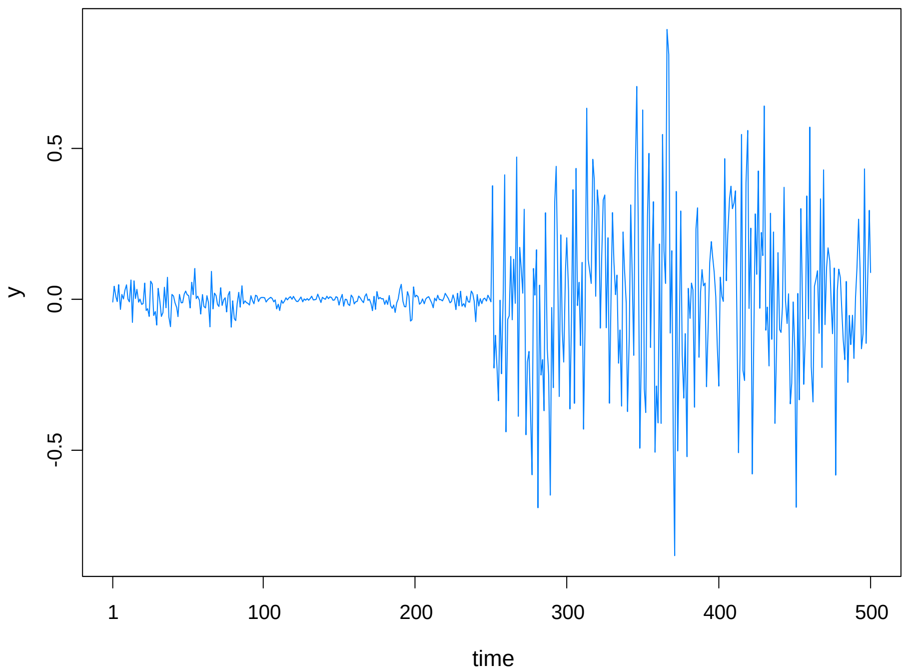


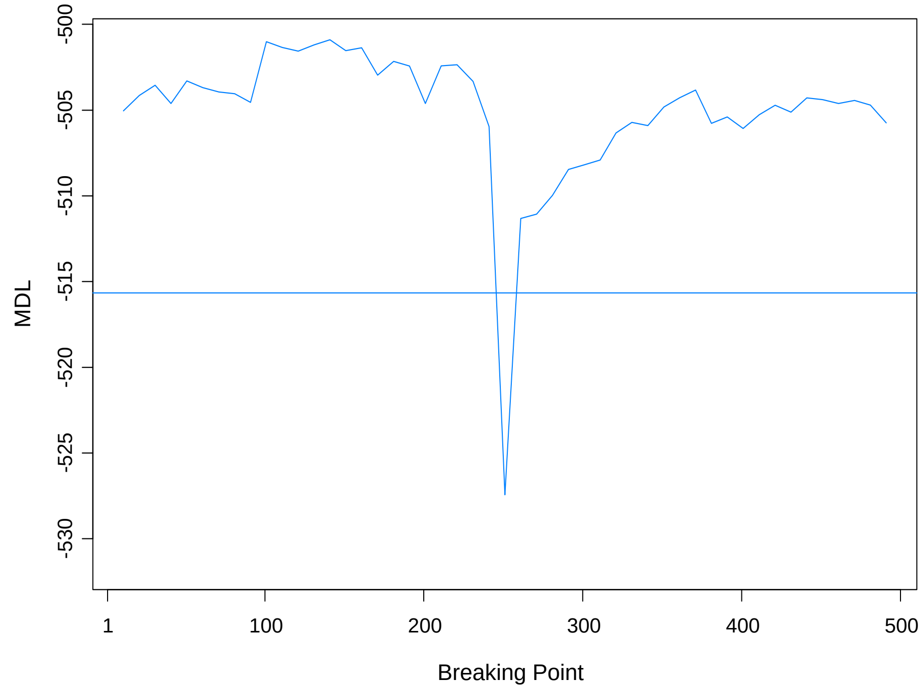
True model:

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

SV Process Example

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





True model:

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

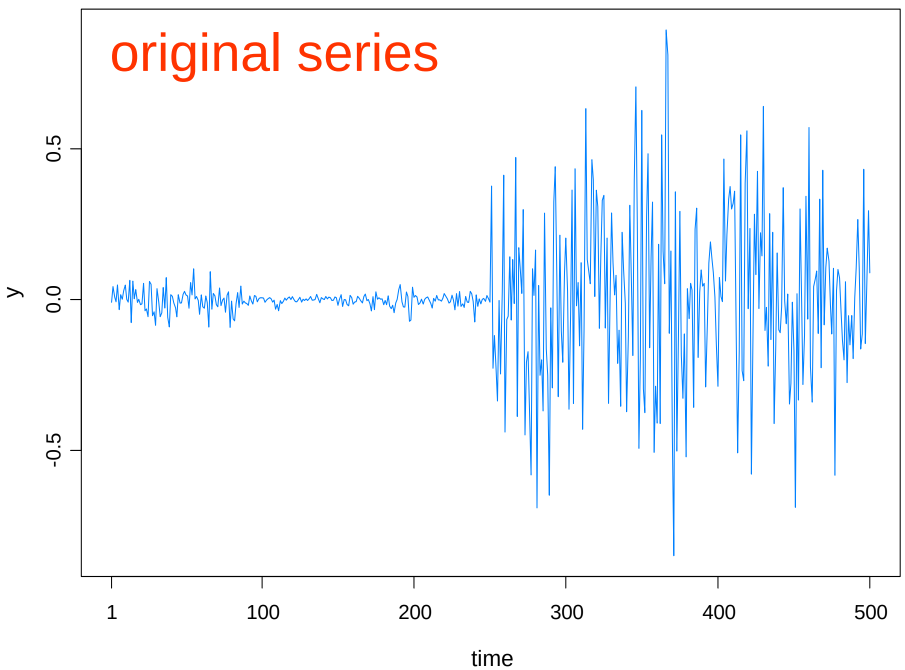
SV Process Example-(cont)

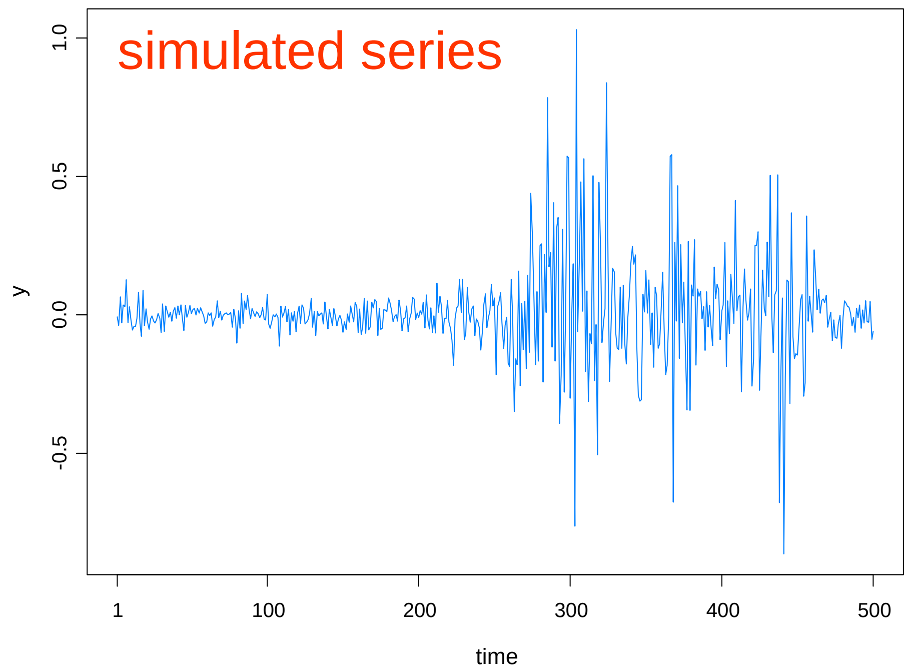
True model:

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

Fitted model based on no structural break:

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

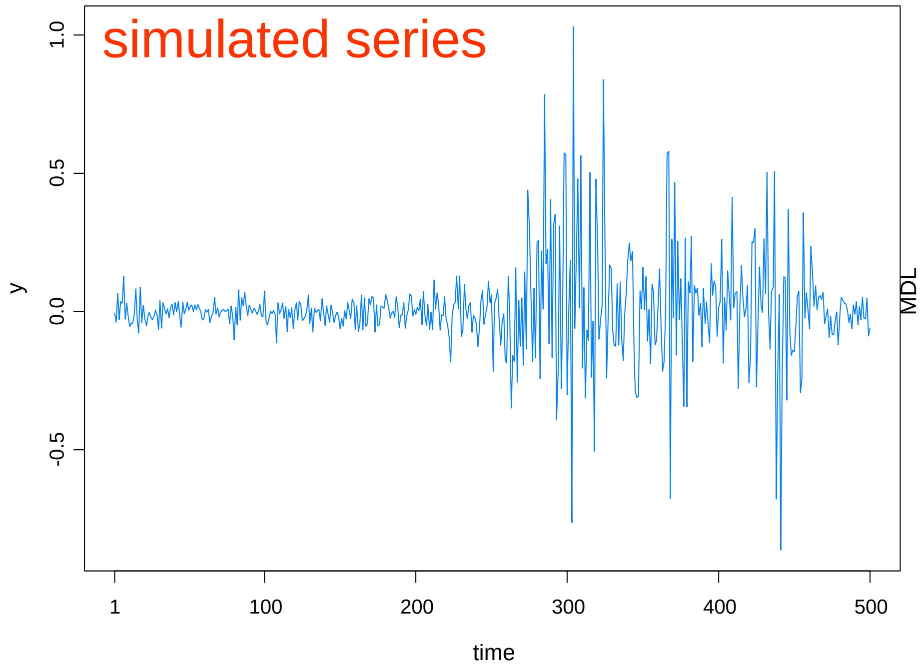


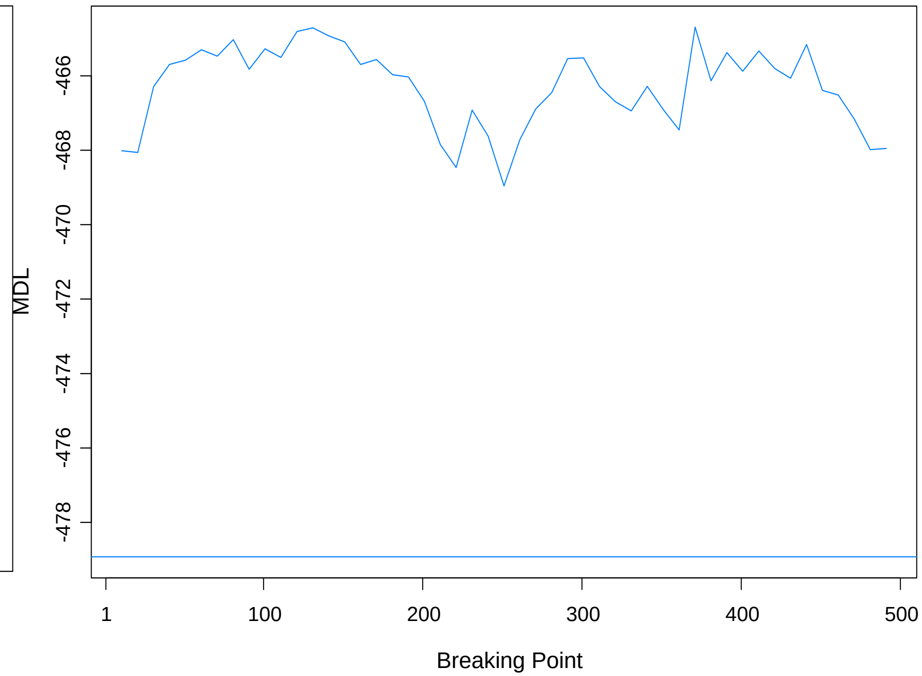


SV Process Example-(cont)

Fitted model based on no structural break:

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





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.