Structural Break Detection for a Class of Nonlinear Time Series Models

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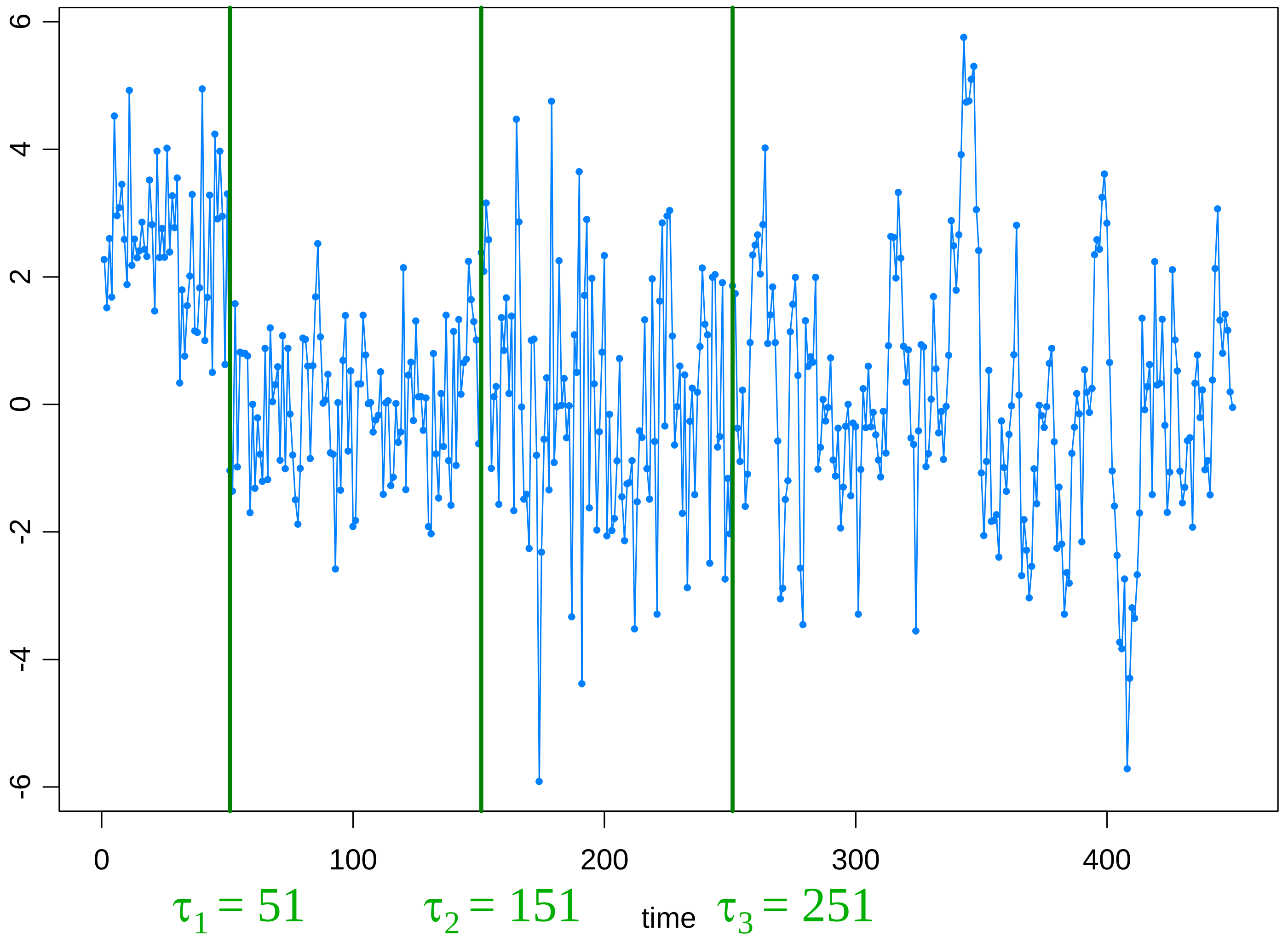
Illustrative Example

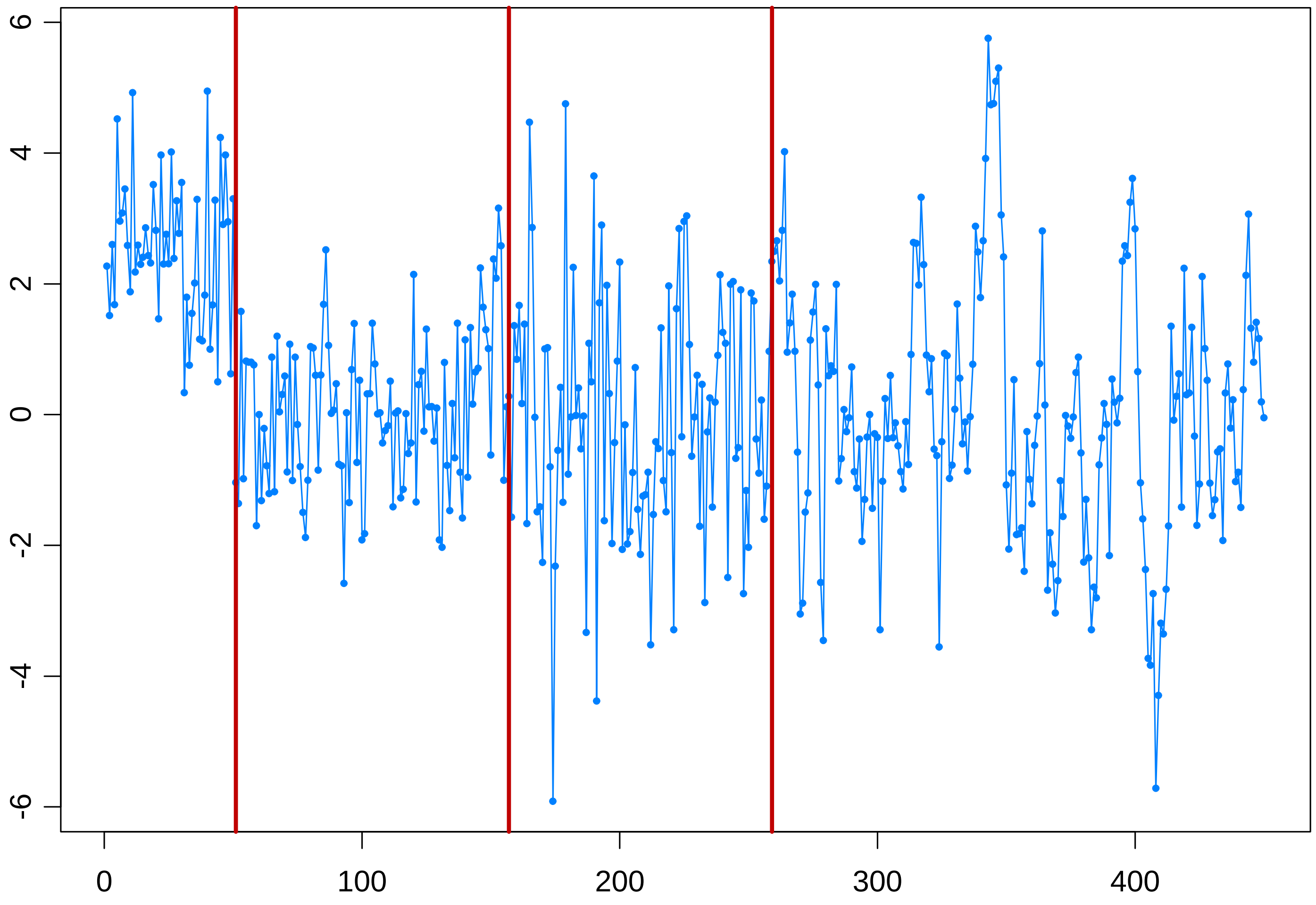
How many segments do you see?



Illustrative Example

Auto-PARM=Auto-Piecewise AutoRegressive Modeling

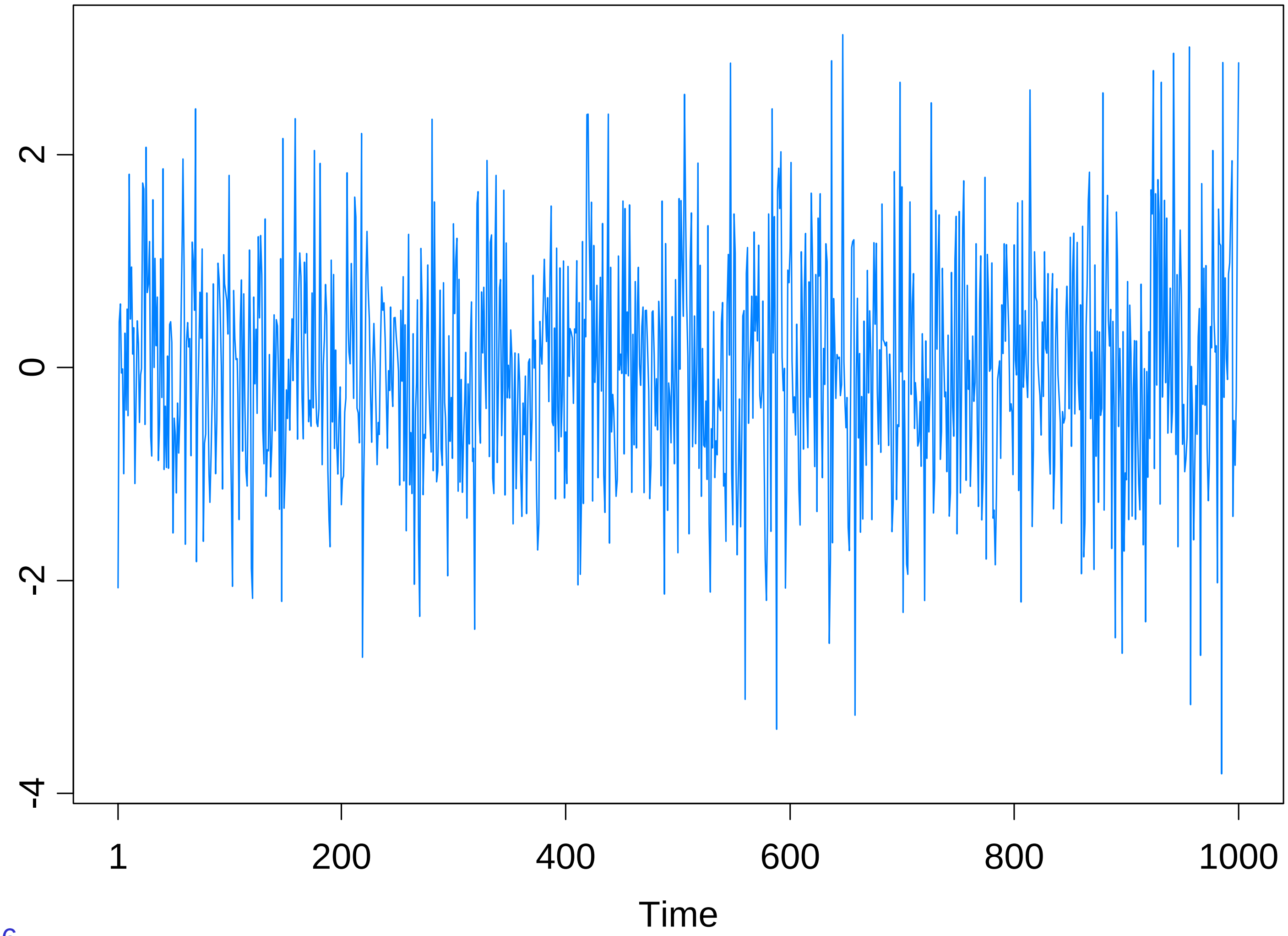
4 pieces, 2.58 seconds.



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

A Second Example

Any breaks in this series?



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    - GARCH
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- Simulation results for GARCH and SV models

Examples

1. Piecewise AR model:

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

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

Examples (cont)

2. Segmented GARCH model:

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

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

3. Segmented stochastic volatility model:

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

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

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

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 $y = (y_1, \ldots, y_n)$

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

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

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 $L(\hat{\boldsymbol{F}}|y)$:

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

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

Second term $L(\hat{e} \mid \hat{\boldsymbol{F}})$:

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

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

$$= \log_2 m + m\log_2 n + \sum_{j=1}^{m} \log_2 p_j + \sum_{j=1}^{m} \frac{p_j + 2}{2} \log_2 n_j + \sum_{j=1}^{m} (\log_2(2\pi\hat{\sigma}_j^2) + n_j)$$

Optimization Using Genetic Algorithm

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:

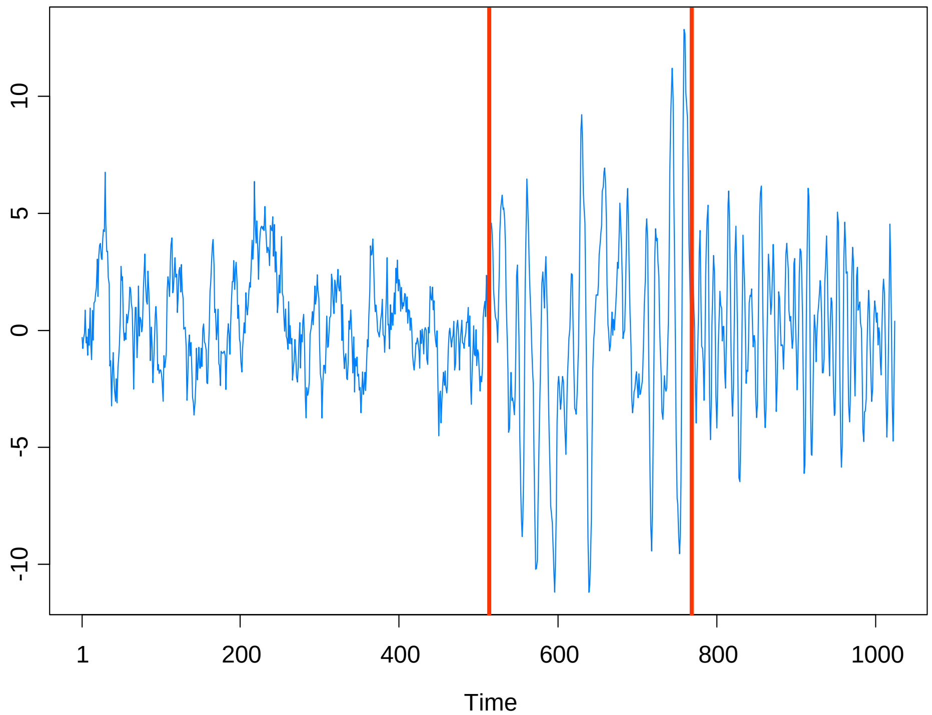
- with probability π_c, *crossover* occurs.
  - two parent chromosomes c_i and c_j are selected at random with probabilities proportional to the ranks of $MDL(c_i)$.
  - k^{th} gene of child is $\delta_k = \delta_{i,k}$ w.p. ½ and $\delta_{j,k}$ w.p. ½
- with probability $1-\pi_c$, *mutation* occurs.
  - 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. $1-\pi_1-\pi_2$.

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).



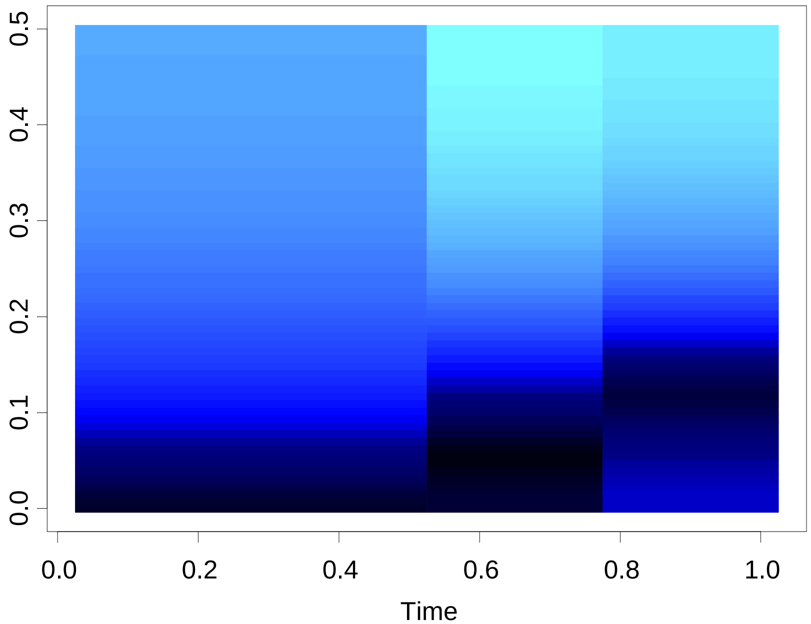
1. Piecewise stat (cont)

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

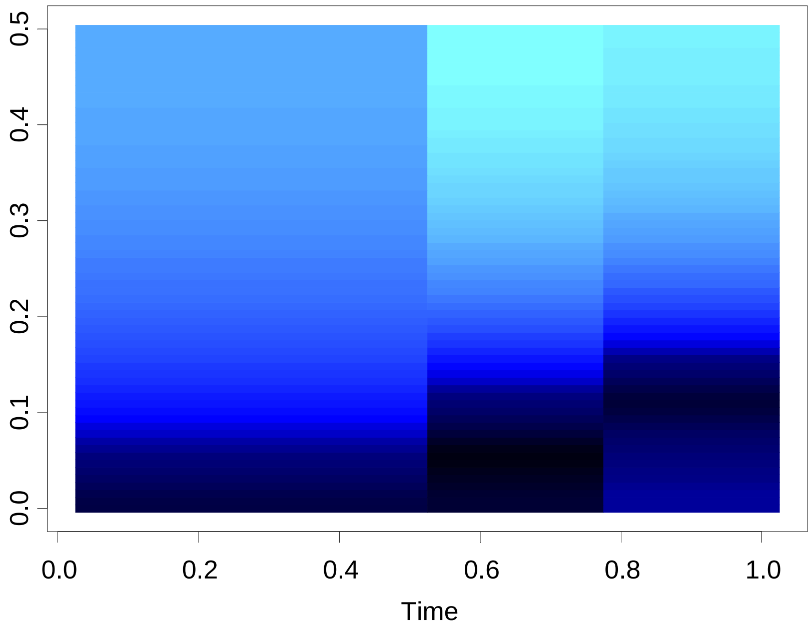
Fitted model:

	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

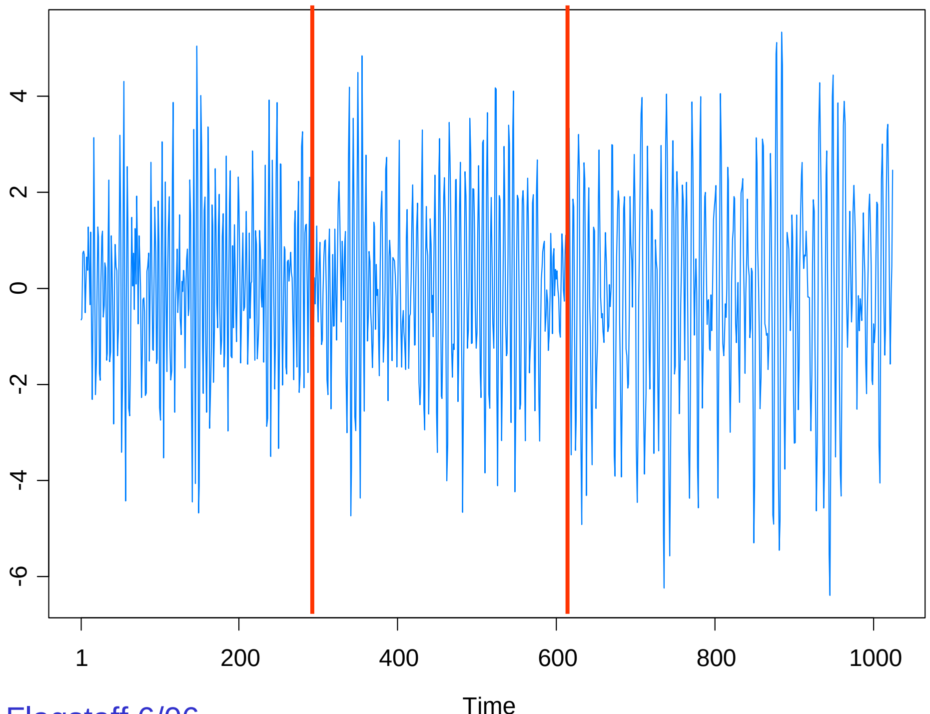


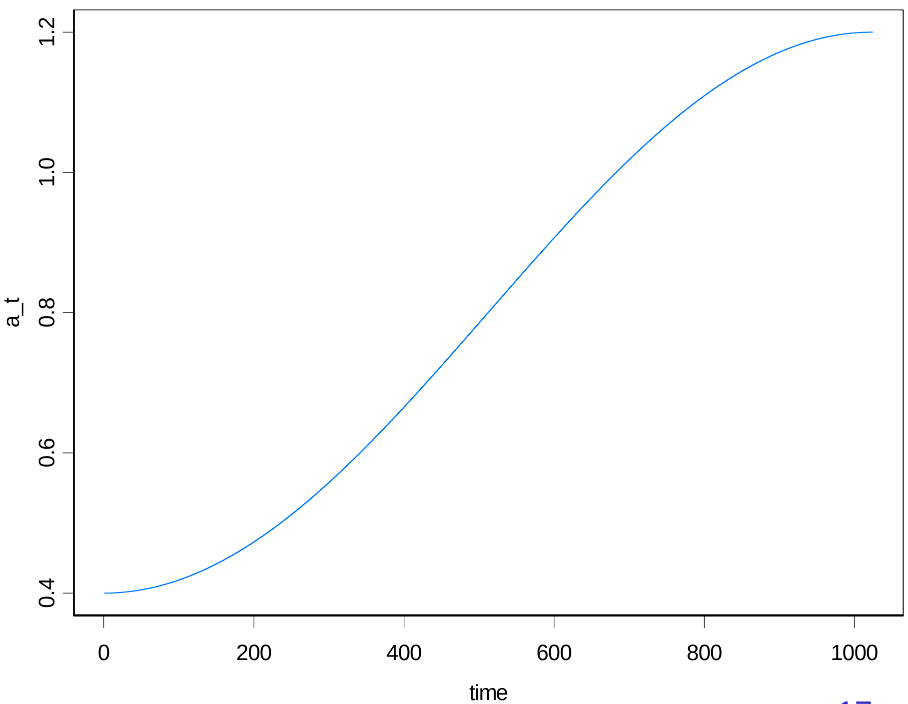
Simulation Examples (cont)

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).





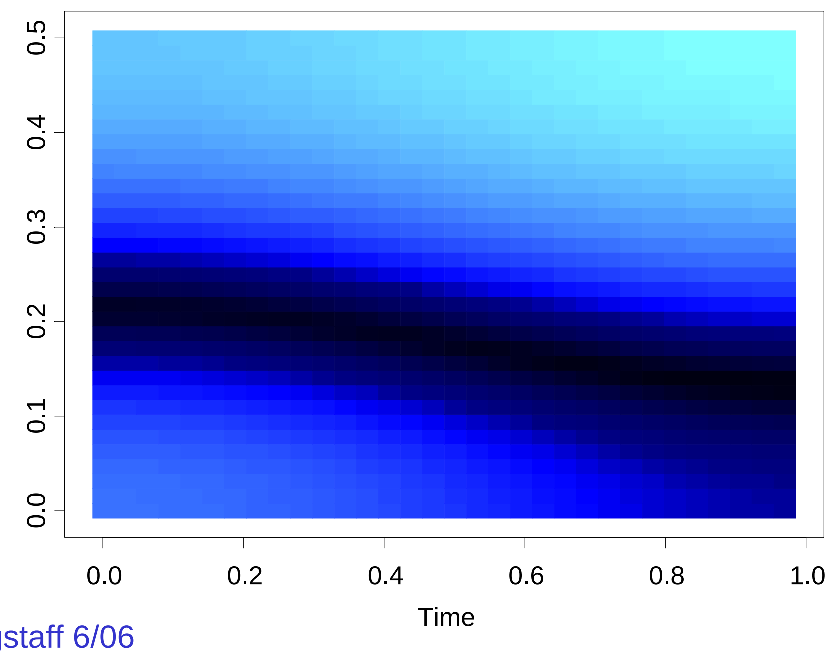
2. Slowly varying AR(2) (cont)

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

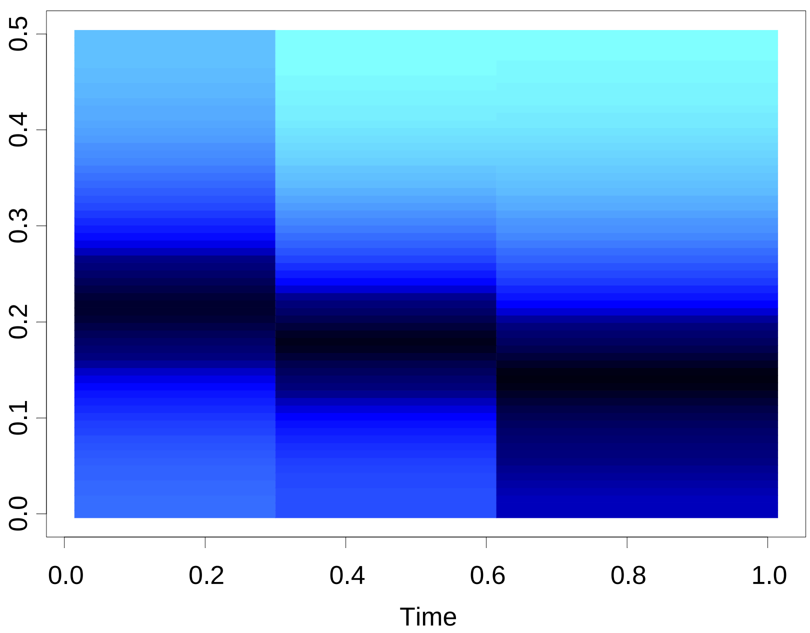
Fitted model:

	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

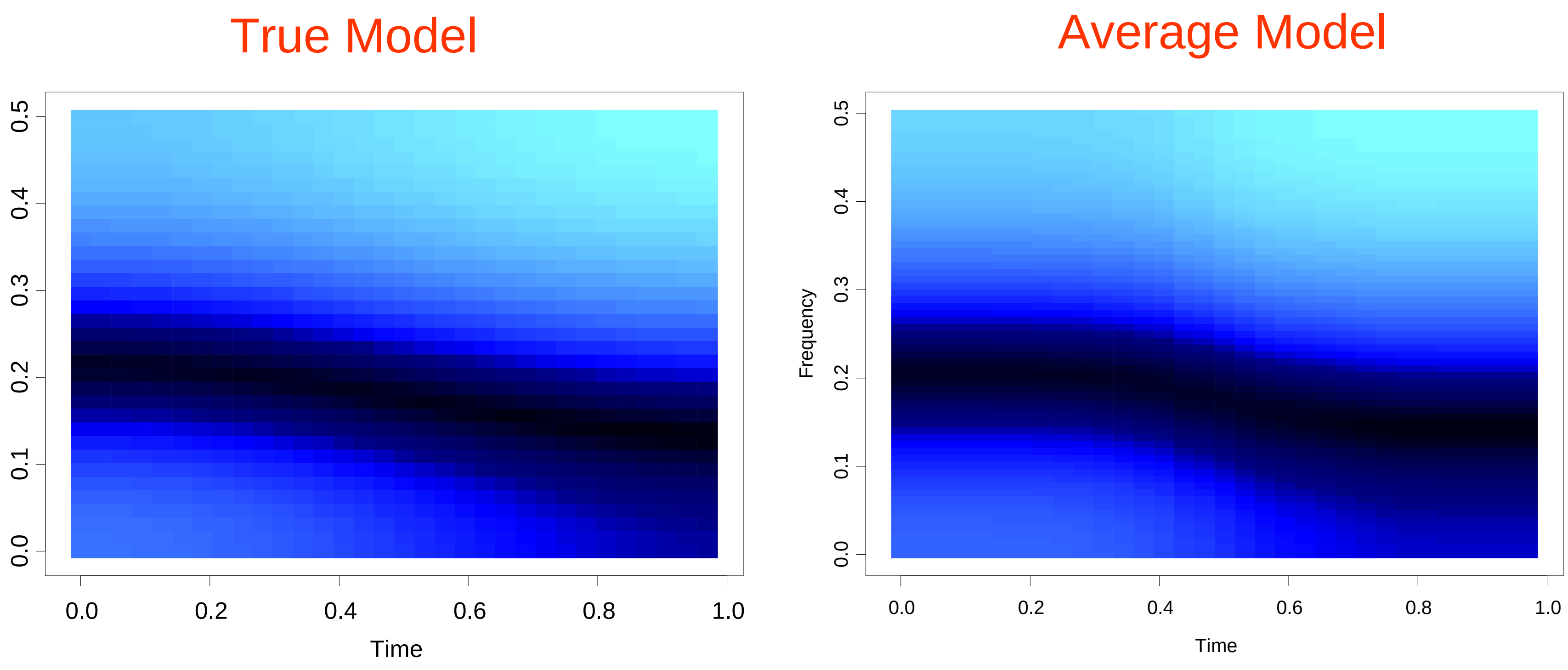


Fitted Model



2. Slowly varying AR(2) (cont)

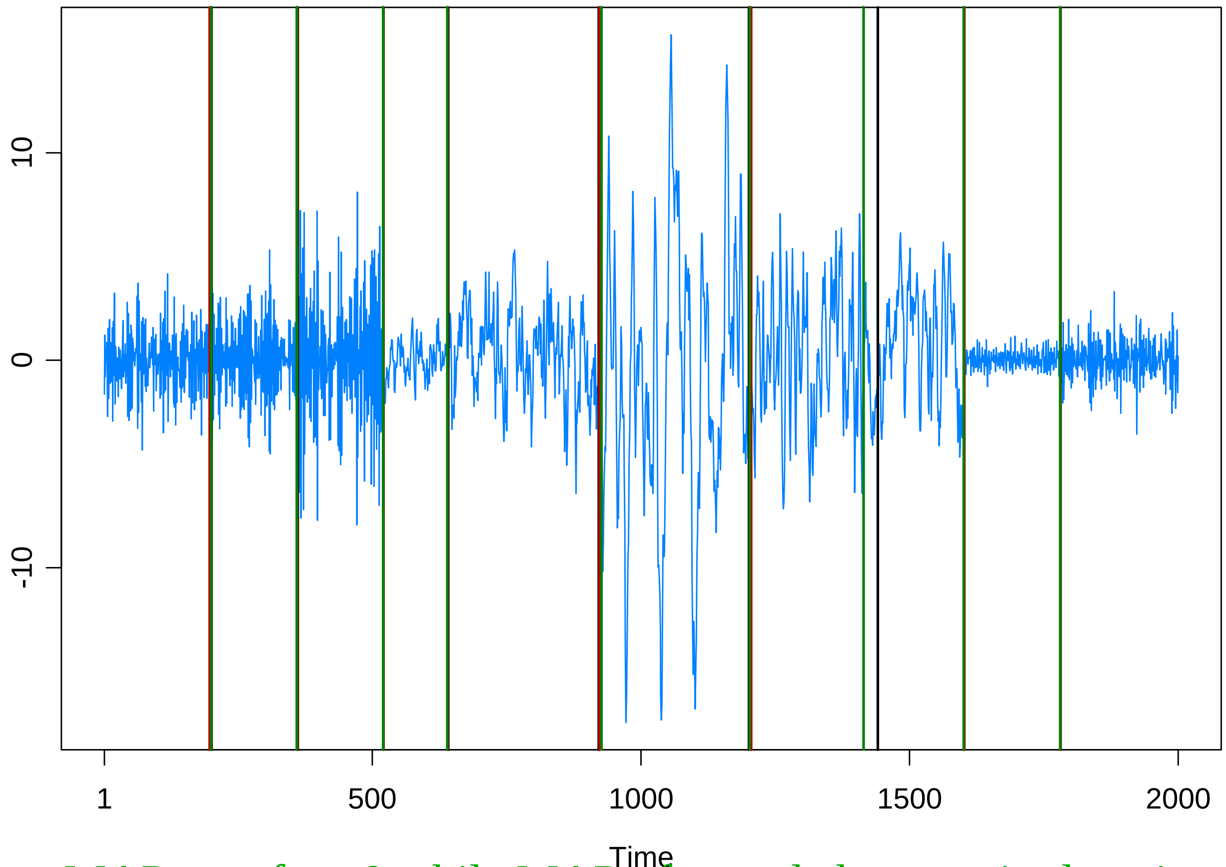
In the graph below right, we average the spectogram over the *GA fitted models* generated from each of the 200 simulated realizations.



Simulation Examples (cont)

3. Simulated data from Fearnhead (2005):

True model has 9 changepoints



black=true

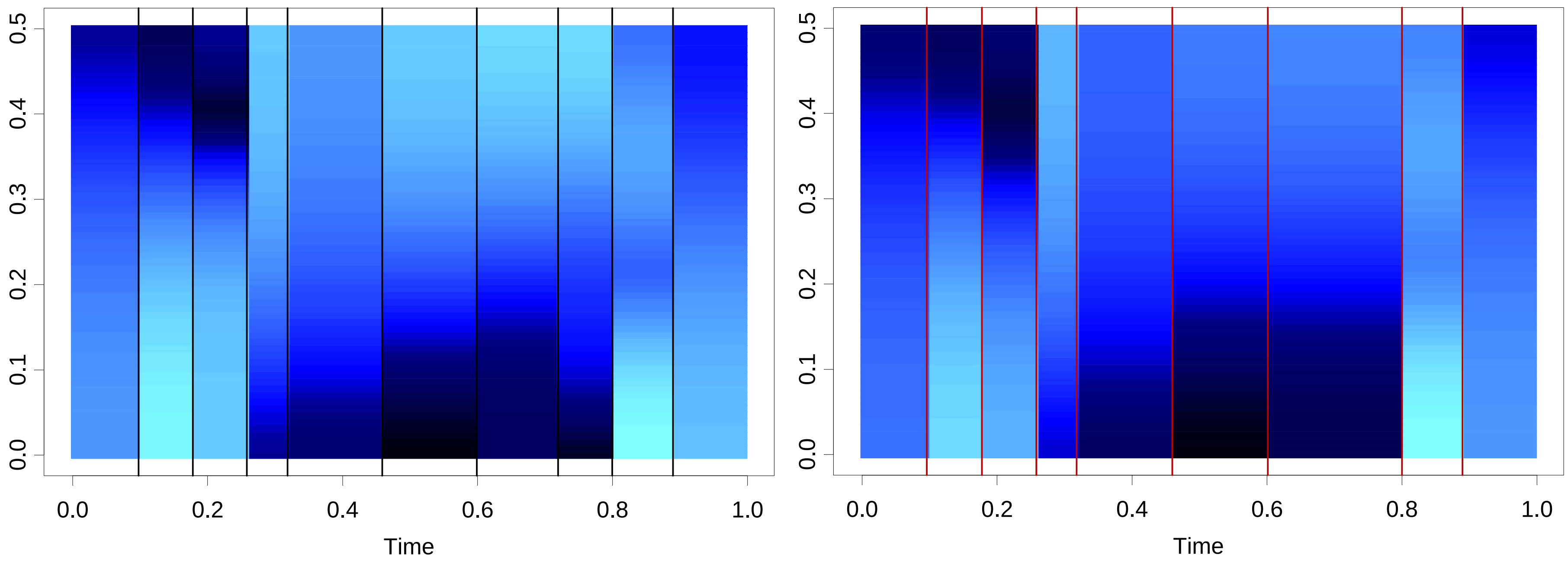
red=APARM

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

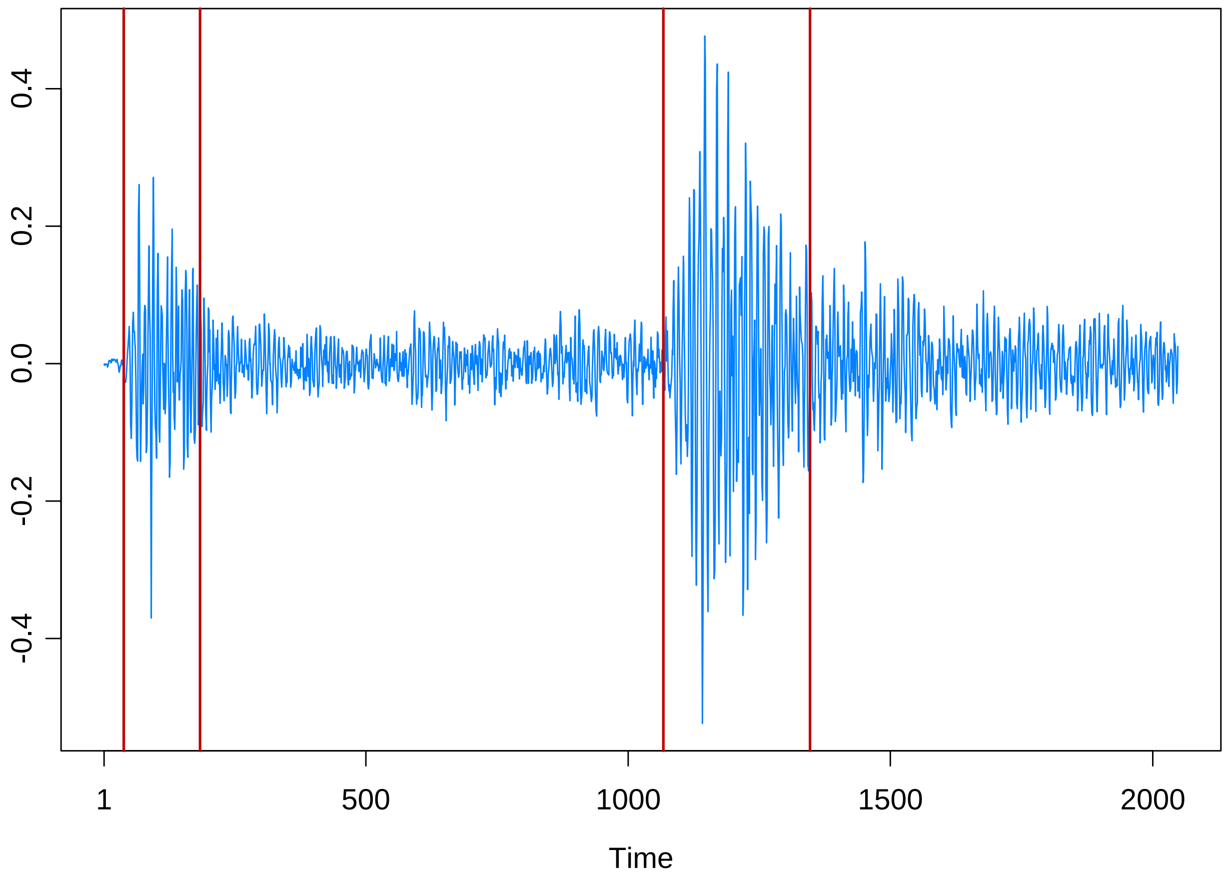
True Model | Fitted APARM Model



Examples

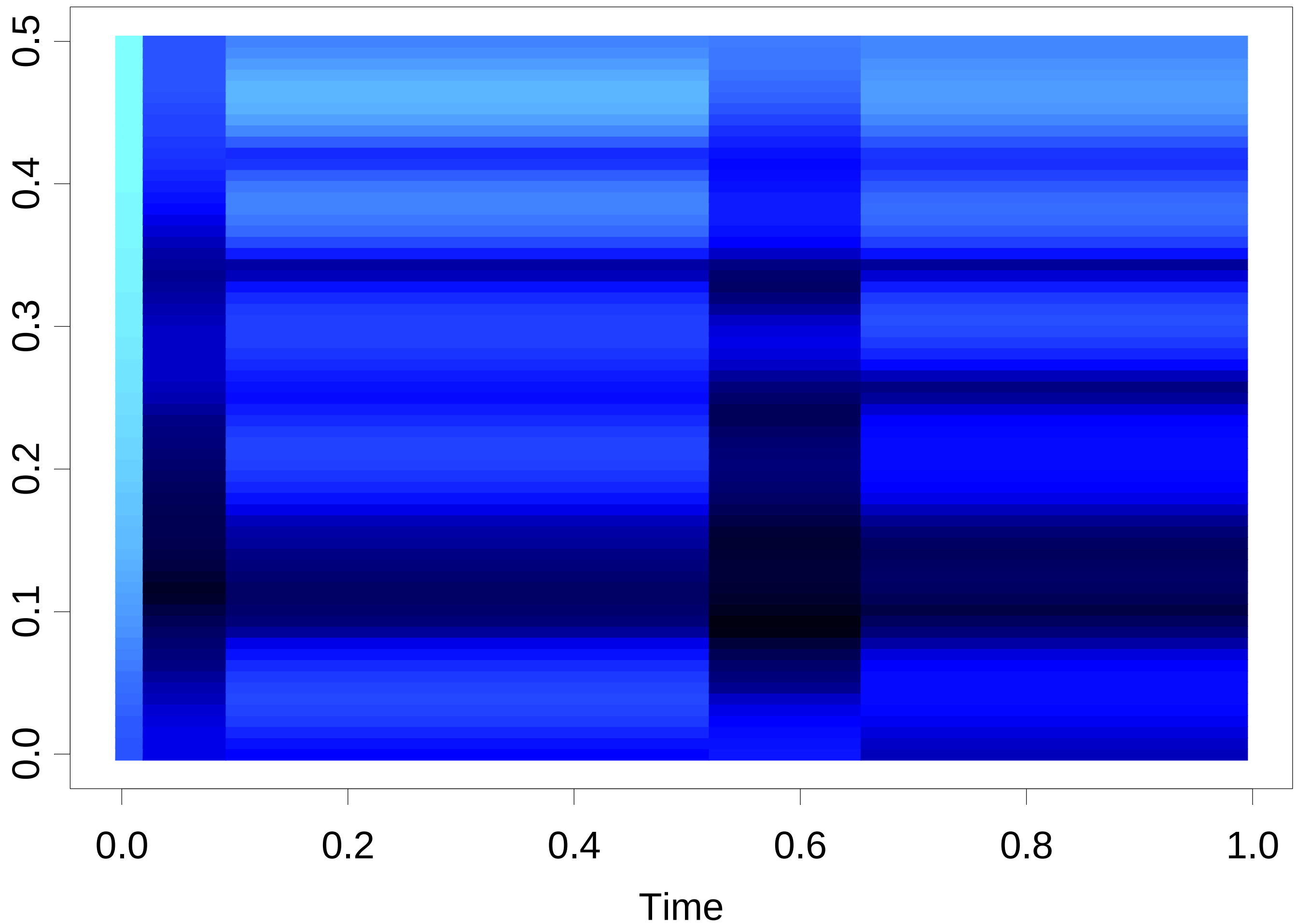
Mine explosion seismic trace in Scandinavia: (Shumway and Stoffer 2000, Stoffer et al. 2005)

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



Examples

AR orders: 1 7 17 13 15

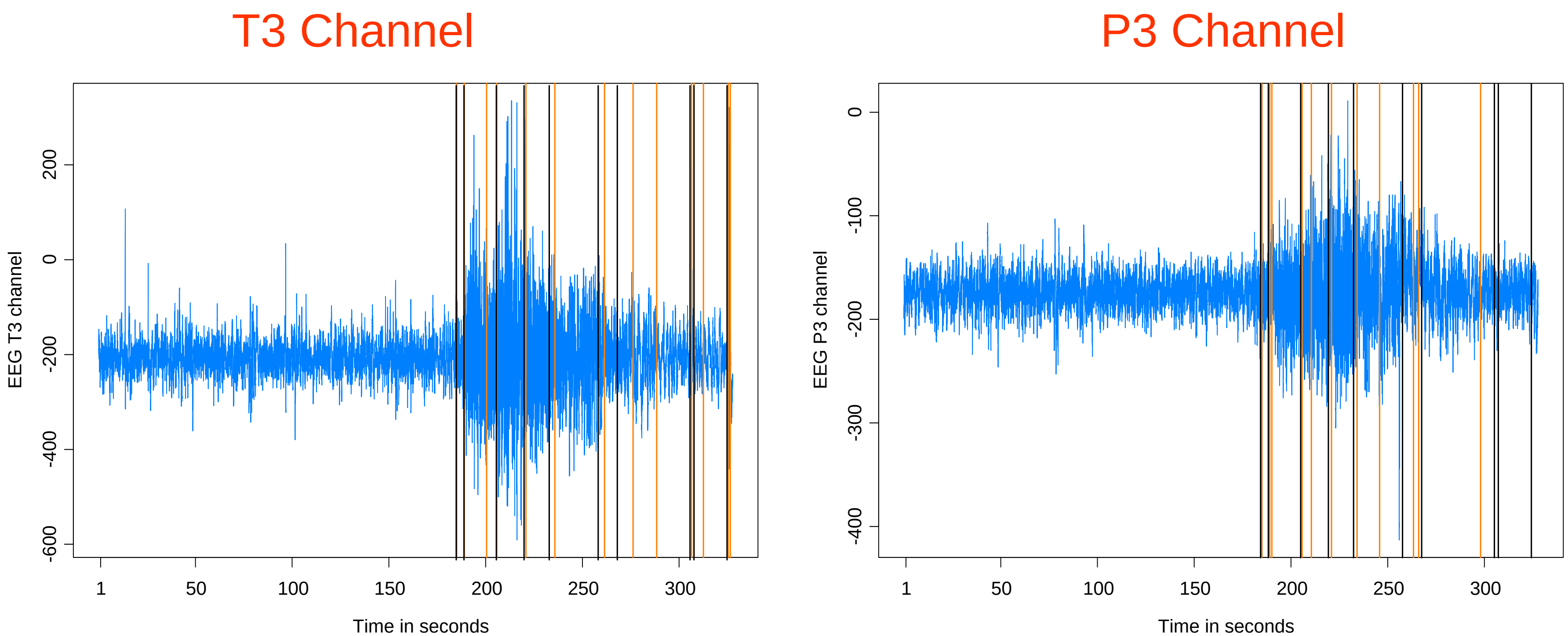


Example: EEG Time series

Data: Bivariate EEG time series at channels T3 (left temporal) and P3 (left parietal). Female subject was diagnosed with left temporal lobe epilepsy. Data collected by Dr. Beth Malow and analyzed in Ombao et al (2001). (n=32,768; sampling rate of 100H). Seizure started at about 1.85 seconds.

GA Univariate results: 14 breakpoints for T3; 11 breakpoints for P3

GA Bivariate results: 11 pieces with AR orders, 17, 1, 2, 6, 15, 2, 3, 5, 9, 5, 4, 1

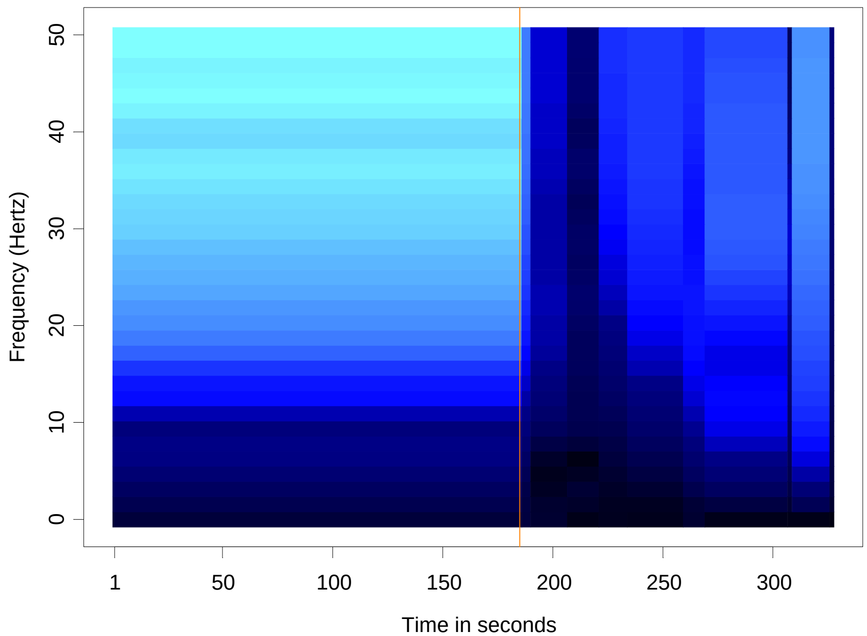


Example: EEG Time series (cont)

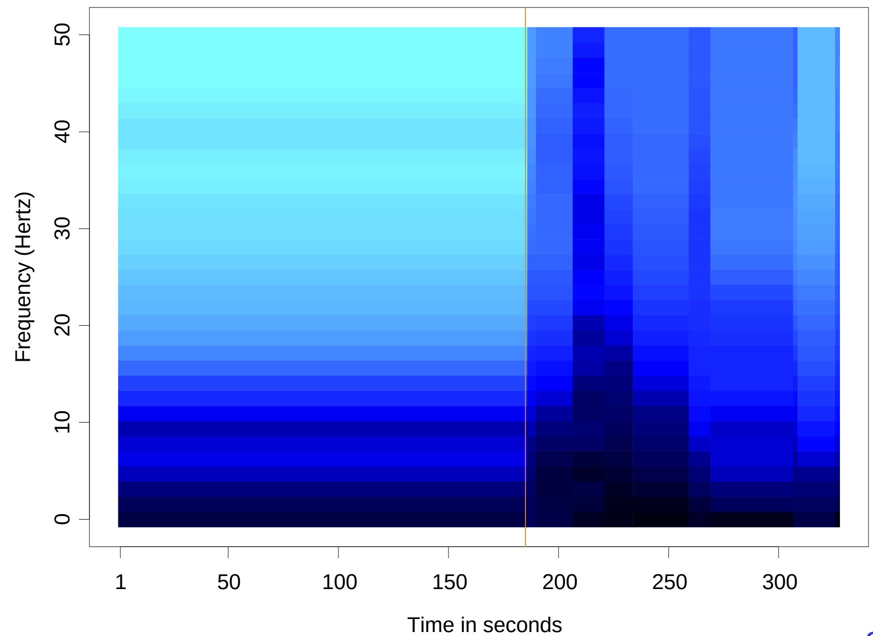
Remarks:

- 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

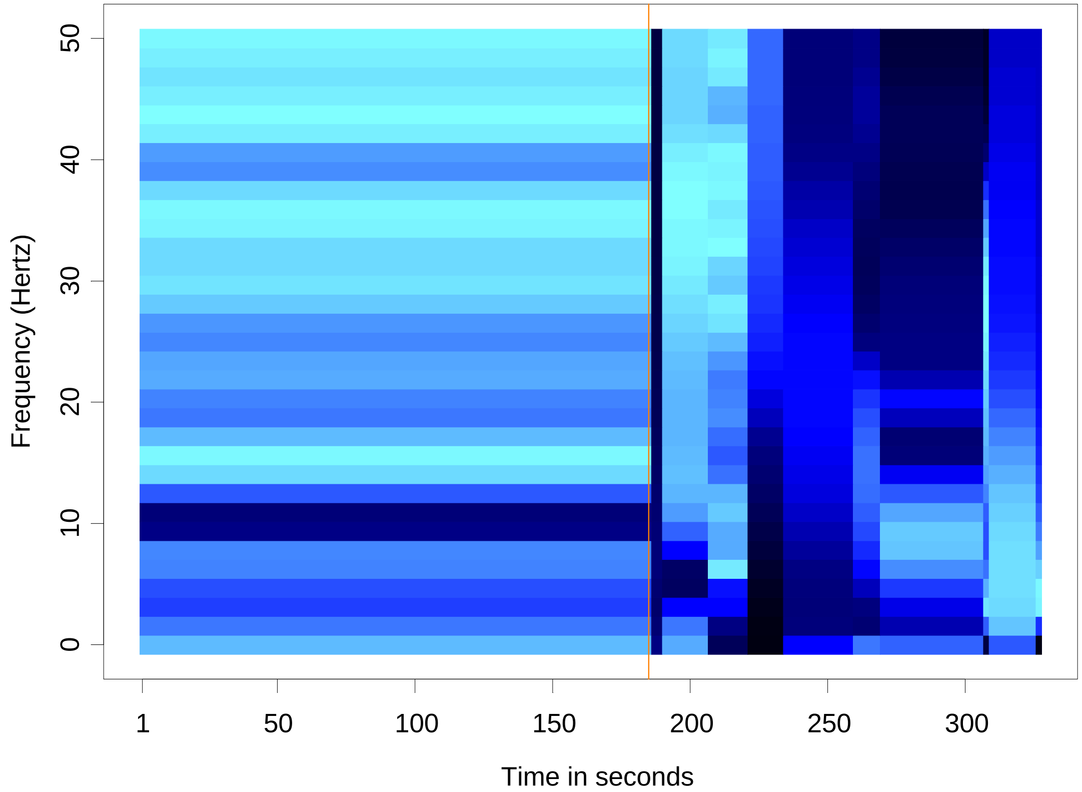


Example: EEG Time series (cont)

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 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 k^{th} epoch

ϕ_k = AR coefficients k^{th} epoch

σ_k = scale in k^{th} epoch

Application to Structural Breaks—(cont)

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

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

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.

Remark: The exact likelihood is given by the following formula

$$L(\psi;\mathrm{y}_n) = L_a(\psi;\mathrm{y}_n)Er_a(\psi),$$

where

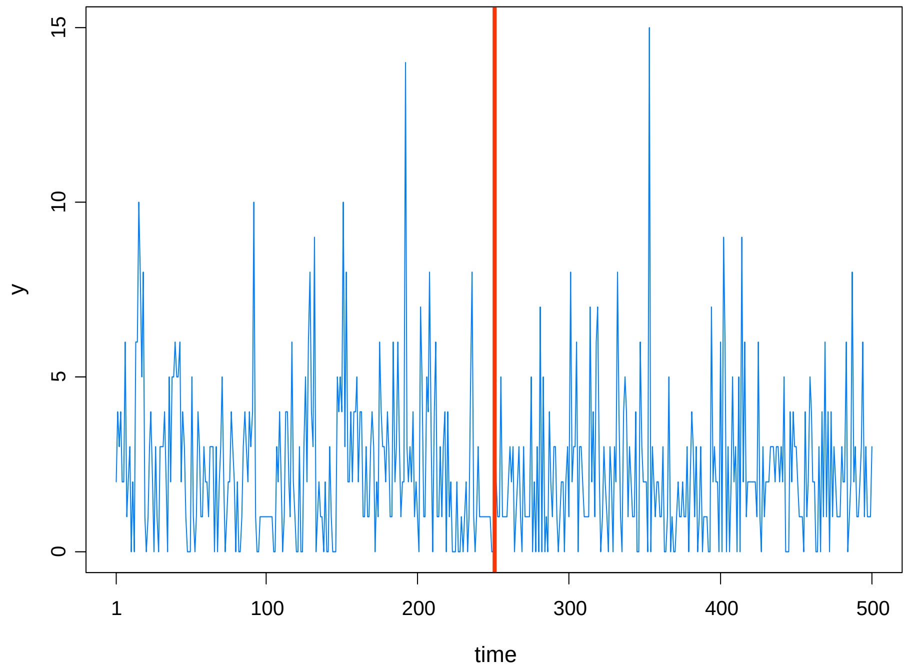
$$Er_a(\psi) = \int \exp\{R(\alpha_n;\alpha^*)\}\, p_a(\alpha_n \mid \mathrm{y}_n;\psi)\, \mathrm{d}\alpha_n.$$

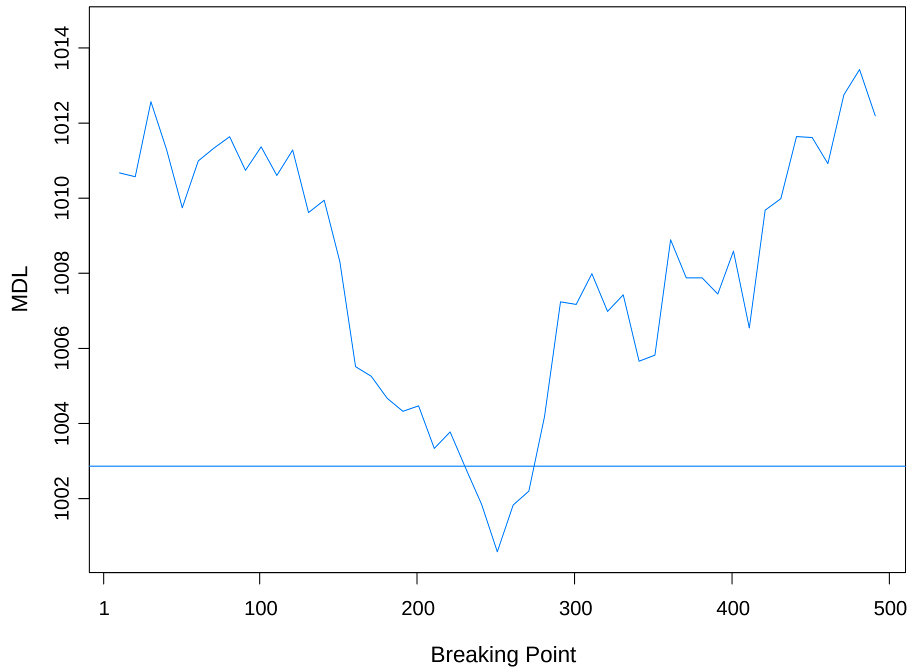
It turns out that $\log(Er_a(\psi))$ is nearly linear and can be approximated by a linear function via importance sampling,

$$e(\psi) \sim e(\hat{\psi}_{AL}) + \dot{e}(\hat{\psi}_{AL})(\psi - \hat{\psi}_{AL})$$

Count Data Example

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



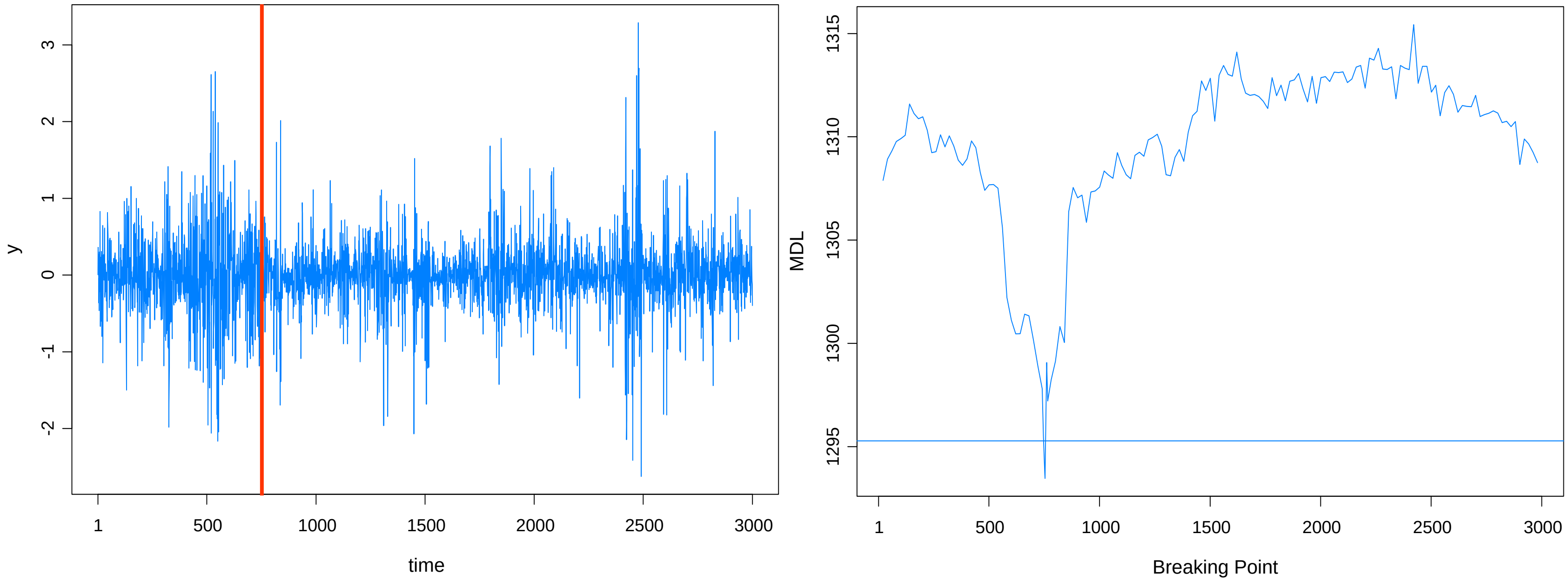


True model:

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

SV Process Example

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

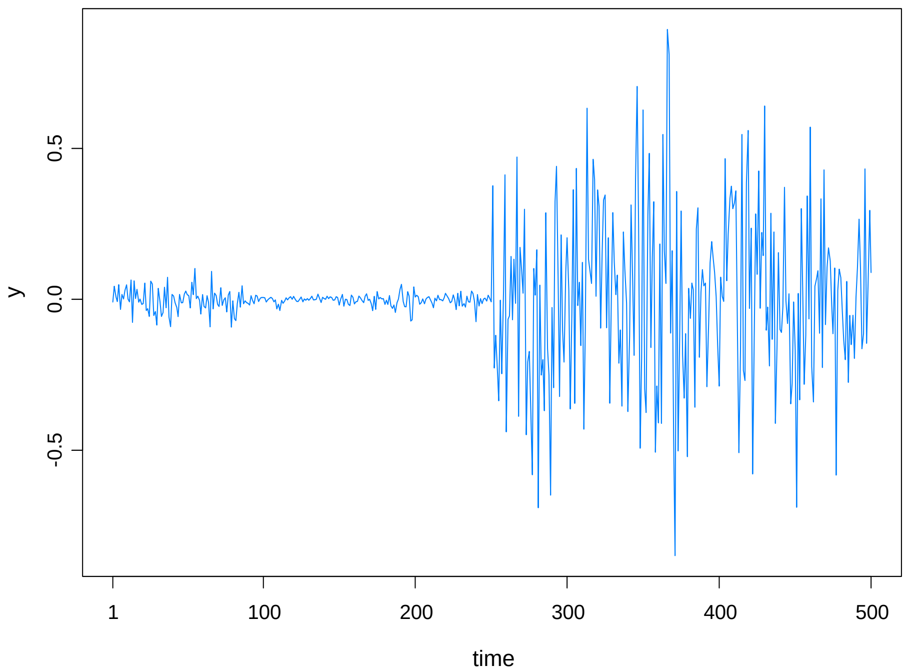


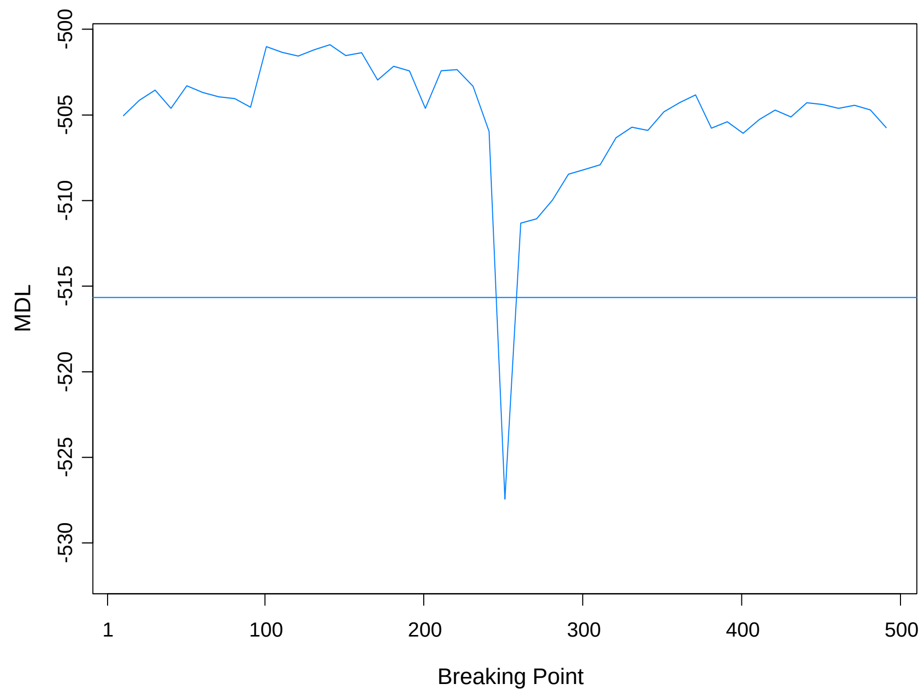
True model:

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

SV Process Example

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





True model:

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

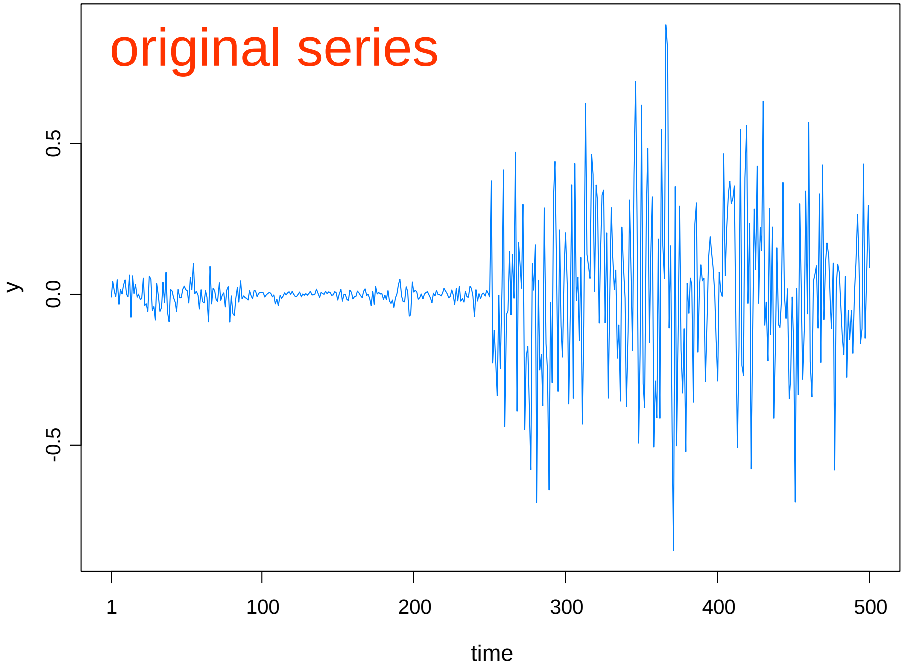
SV Process Example-(cont)

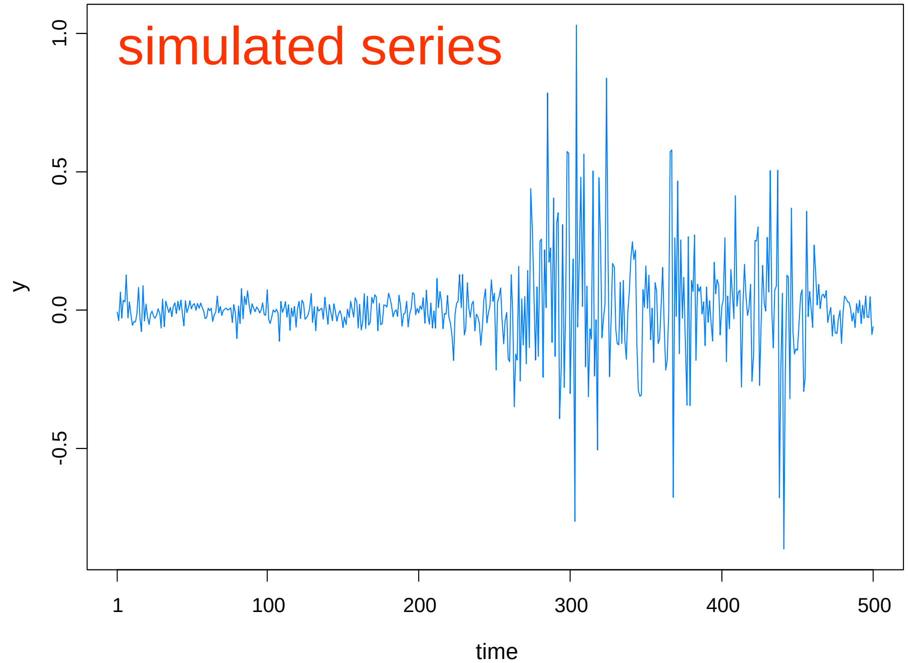
True model:

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

Fitted model based on no structural break:

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

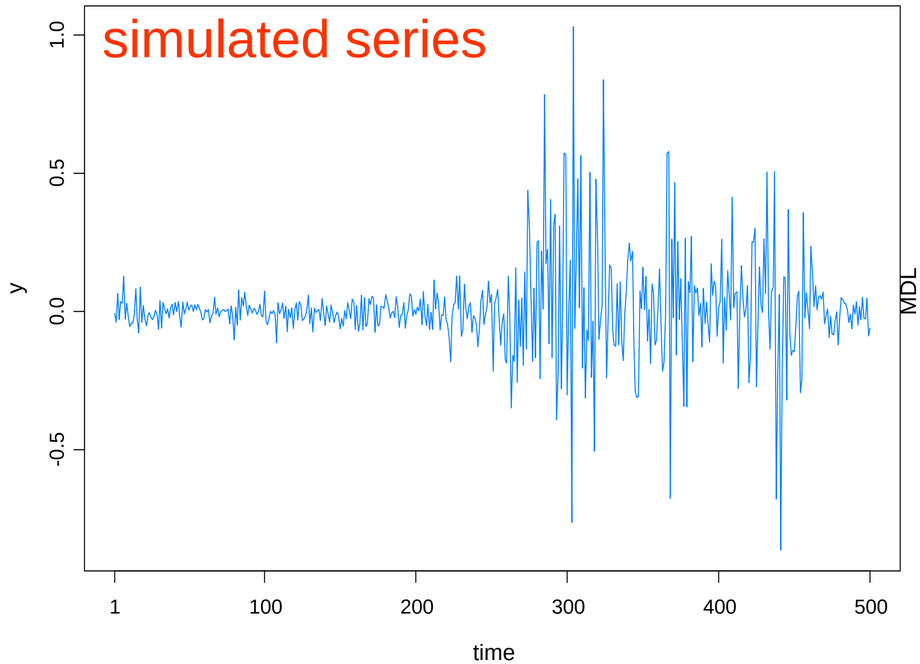


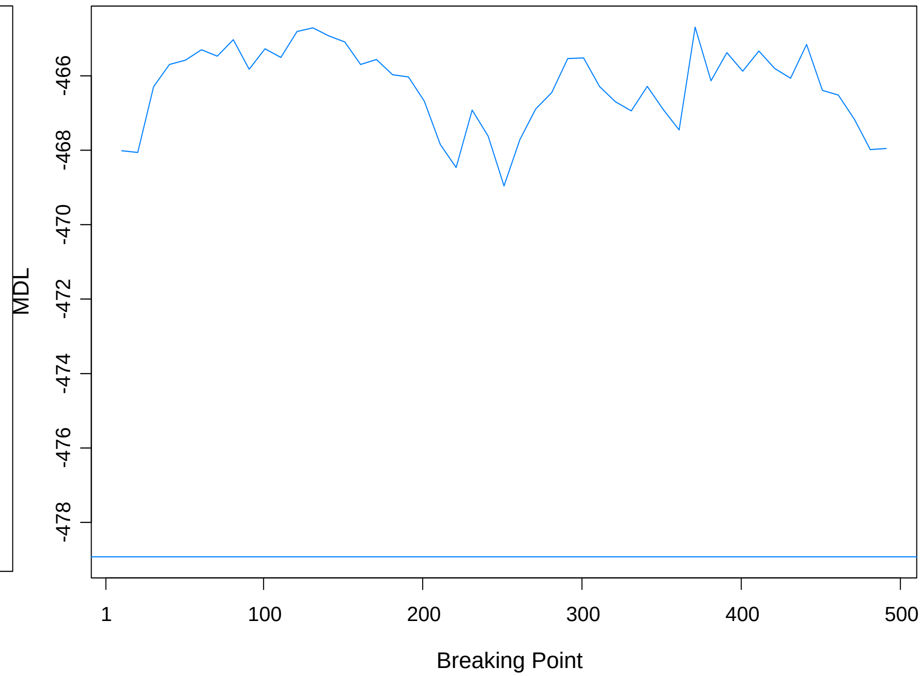


SV Process Example-(cont)

Fitted model based on no structural break:

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