

# Kernseg: A new efficient change-points detection procedure for analyzing biological data

ALAIN CELISSE

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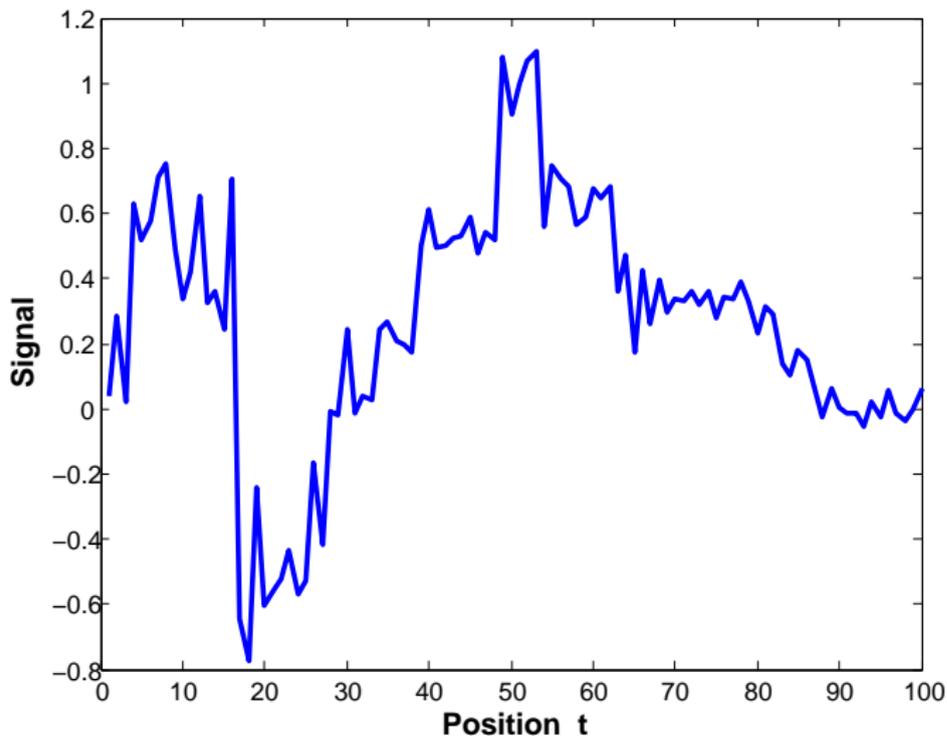
<sup>2</sup>MODAL INRIA team-project

joint work with G. Rigail, M. Pierre-Jean, and G. Marot

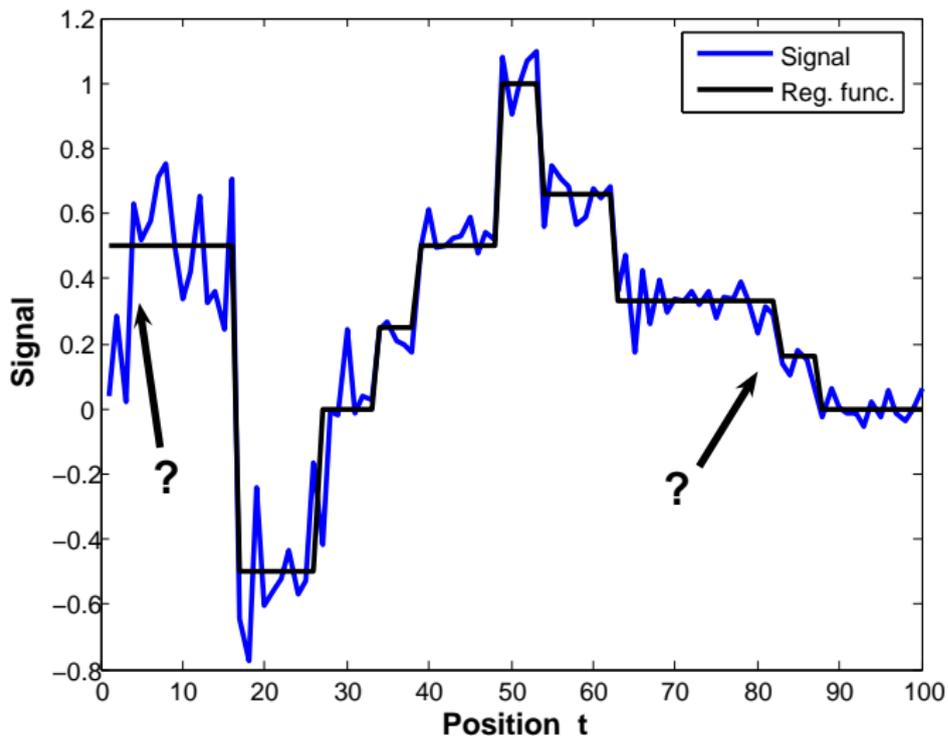
Stat4Bio – LaMME

Évry, April 3rd, 2019

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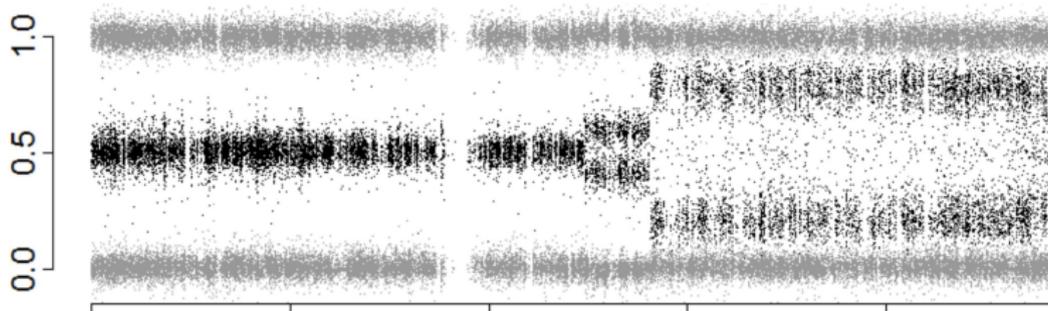


# Detect abrupt changes. . .

## General purposes:

- 1 Detect **changes in** (features of) **the distribution** (not only in the mean)

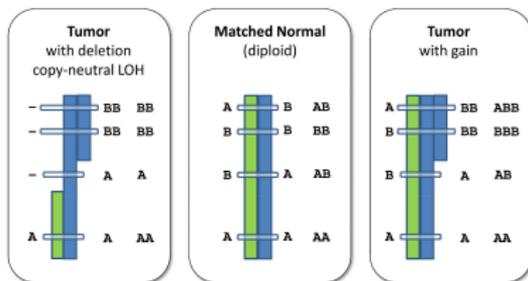
# Example 1: Changes in the distribution



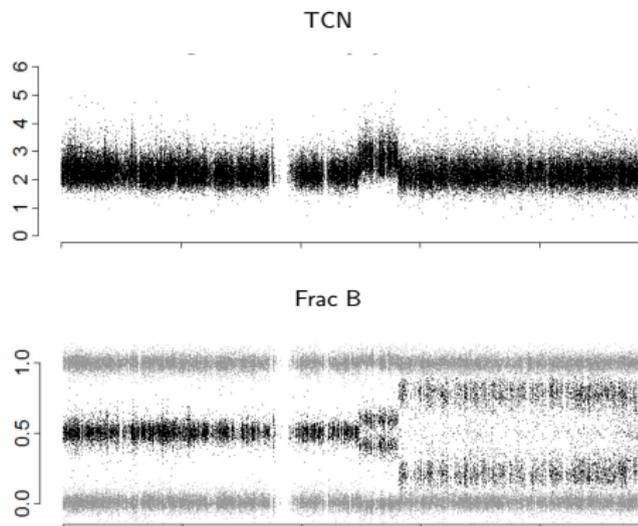
→ Detecting changes in the mean is useless

# Example 1: Changes in the distribution

Total copy number (TCN) and Allele B fraction (Frac B)



$$(\text{Frac } B)_t = \frac{N_{B,t}}{N_{A,t} + N_{B,t}} .$$



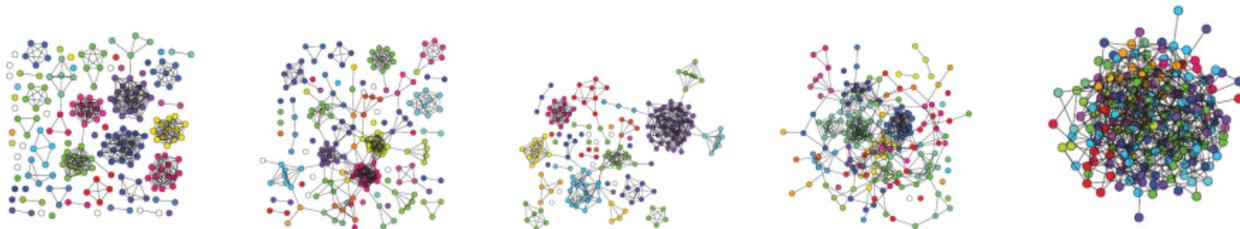
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- 2 **Complex data:**
  - High-dimension: measures in  $\mathbb{R}^d$ , curves, . . .
  - Structured: audio/video streams, graphs, DNA sequence, . . .

# Motivating example 2: Structured objects

Observe networks along the time



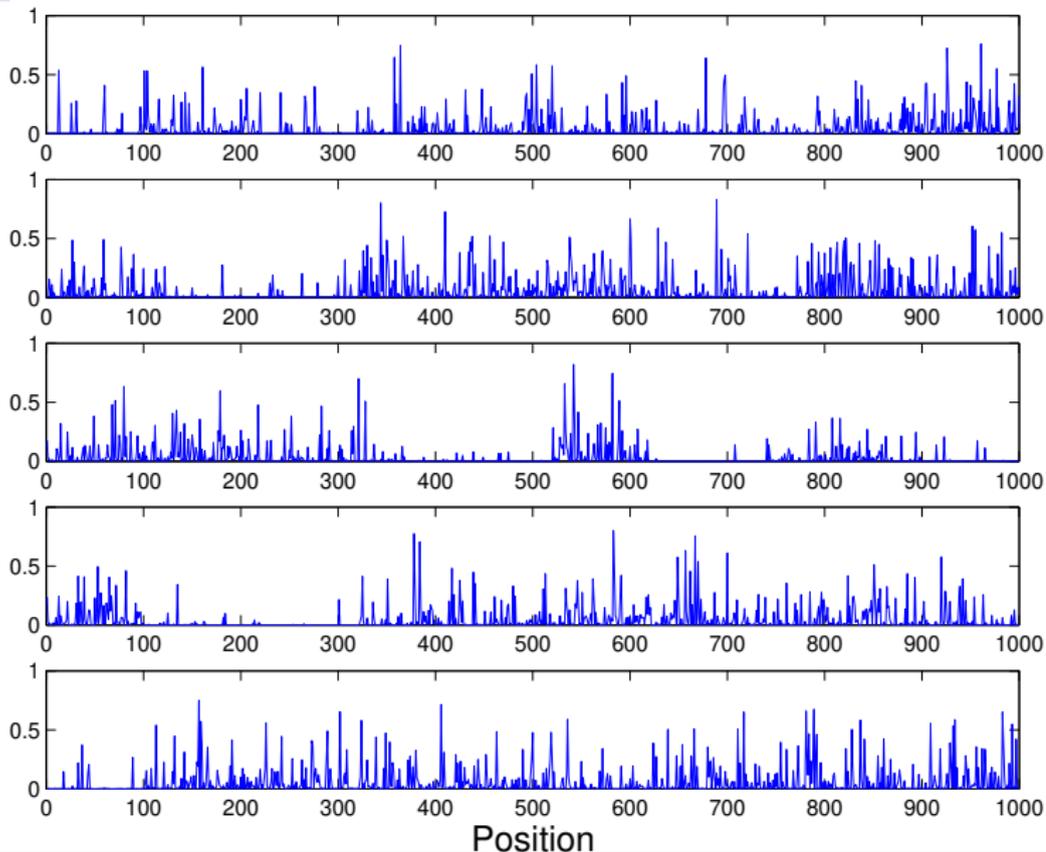
**Goal:**

Detect abrupt changes in some features of the network

**Ex:**

- Each network represented by one histogram
- Columns  $\leftrightarrow$  counts of specific motifs (stars, triangles, ...)

# Motivating example 2: dynamic networks



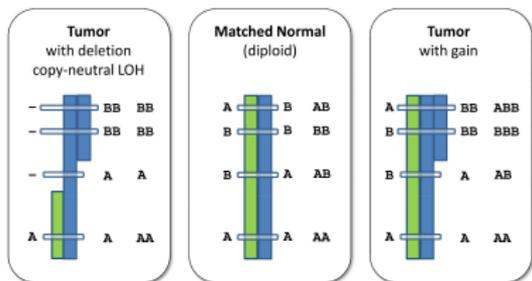
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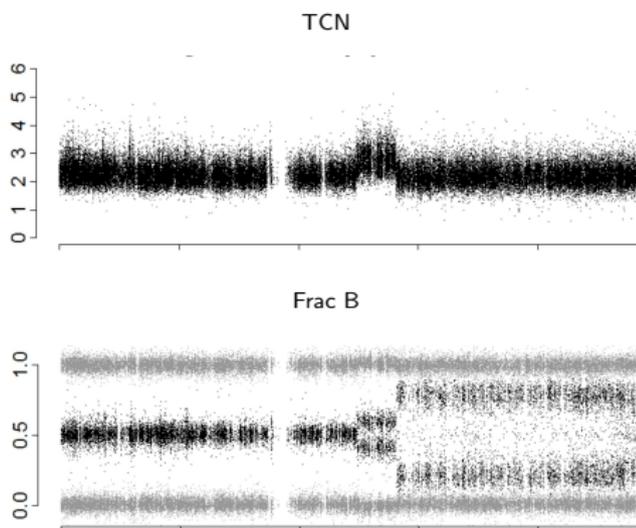
- ① Detect **changes in** (features of) **the distribution** (not only in the mean)
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- ③ **Fusion of heterogeneous data**
  - Deal simultaneously with different types of complex data

# Example 1 (Cont'd): Fusion of TCN and Frac B

Total copy number (TCN) and Allele B fraction (Frac B)



$$(\text{Frac } B)_t = \frac{N_{B,t}}{N_{A,t} + N_{B,t}} .$$



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  - Structured: audio/video streams, graphs, DNA sequence, . . .
- ③ **Fusion of heterogeneous data**
  - Deal simultaneously with different types of complex data
- ④ **Efficient algorithm** allowing to deal with large data sets (“Big data” challenge)

# Outline

- 1 KCP: Kernel change-points detection proc.
- 2 Dyn. programming and reproducing kernels
- 3 Faster approximate algorithm
- 4 How many change-points?  $\rightarrow$  penalty
- 5 Experiments on biological data

## II Kernel change-points procedure

# Basic notations

- Segmentation:  $\tau = (\tau_1, \dots, \tau_D)$

$$\{1, \dots, n\} = [\tau_1, \tau_2[ \cup [\tau_2, \tau_3[ \cup \dots \cup [\tau_{D-1}, \tau_D[ \cup [\tau_D, \tau_{D+1}[$$

with  $\tau_1 = 1$  and  $\tau_{D+1} = n + 1$ .

- $\mathcal{T}_n = \{\tau : \text{segmentation of } \{1, \dots, n\}\}$
- $D_\tau$ : number fo segments of  $\tau$
- $\mathcal{T}_n^D$ : segmentations with  $D$  segments

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# Model selection-based procedure: KCP

## Outline

- 1 For every  $1 \leq D \leq D_{\max}$ ,

$$\hat{\tau}^D \in \operatorname{Argmin}_{\tau \in \mathcal{T}_n^D} \mathcal{R}_{\text{emp}}(\tau) ,$$

- 2 Define

$$\hat{D} = \operatorname{Argmin}_{1 \leq D \leq D_{\max}} \left\{ \mathcal{R}_{\text{emp}}(\hat{\tau}^D) + \text{pen}(\hat{\tau}^D) \right\} .$$

- 3 Final segmentation:

$$\hat{\tau} := \hat{\tau}^{\hat{D}} .$$

## Rks

- $\mathcal{R}_{\text{emp}}(\tau)$  quantifies the mistakes (cost) of  $\tau$
- $\text{pen}(\tau)$ : penalty to be made precise

(Arlot, Celisse, Harchaoui (2018))

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# Cost of a segmentation

## Reproducing kernel

- $X_1, \dots, X_n$ : initial observations (structured objects)  
**Ex:** DNA sequences, networks, texts, ...
- $k(\cdot, \cdot) \rightarrow \mathbb{R}$ : reproducing kernel (sdp, ...)
- $k(\cdot, \cdot)$  similarity measure between “objects”  
**Ex :** Gaussian kernel

$$k_\alpha(x_i, x_j) = \exp \left[ -(x_i - x_j)^2 / h \right], \quad h > 0$$

## Empirical risk

$$\mathcal{R}_{emp}(\tau)$$

$$= \frac{1}{n} \sum_{i=1}^n k(X_i, X_i) - \underbrace{\frac{1}{n} \sum_{\ell=1}^D \left[ \frac{1}{\tau_{\ell+1} - \tau_\ell} \sum_{i=\tau_\ell}^{\tau_{\ell+1}-1} \sum_{j=\tau_\ell}^{\tau_{\ell+1}-1} k(X_i, X_j) \right]}_{=\text{Cost of } [\tau_\ell, \tau_{\ell+1}]}$$

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# Instances of reproducing kernels

- Polynomial kernel:

$$k_{\alpha,c}(x, y) = (x \cdot y + c)^\alpha, \quad c, \alpha \geq 0.$$

- $\chi^2$ -kernel:

$$k_l(p, q) = \exp \left[ - \sum_{i=1}^l \frac{(p_i - q_i)^2}{p_i + q_i} \right].$$

- Combination of kernels:

With  $x = (x_1, x_2)$  and  $y = (y_1, y_2)$ ,  $(\alpha \in [0, 1])$

$$k_\alpha(x, y) = \alpha k_1(x_1, y_1) + (1 - \alpha) k_2(x_2, y_2).$$

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→ Dynamic programming

- 2 Define

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## III Dynamic prog. and reproducing kernels

# Find the best segmentation with $D$ segments

## Dynamic programming (Step 1 in KCP)

- Solving  $\hat{\tau}^D \in \text{Argmin}_{\tau \in \mathcal{T}_n^D} \{\mathcal{R}_{emp}(\tau)\}$ : computationally hard ( $1 \leq D \leq D_{\max}$ )
- General principle:

$$L(D+1; t) = \min_{1 \leq s \leq t-1} \{L(D; s) + C(s, t)\}$$

- $L(D; s)$ : cost of the best segmentation of  $[1, s+1[$  with  $D$  segments
- $C(s, t)$ : cost of segment  $[s, t+1[$
- Outputs the exact solution

## Classical computational complexity

- Time complexity:  $O(n^2)$  (if evaluating  $C(s, t)$  is linear time)
- Space complexity:  $O(n^2)$  (storing the cost matrix)

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# Embedding dynamic programming in the kernel framework

## Main limitations of the naive formulation

$$C(\tau_\ell, \tau_{\ell+1}) = \frac{1}{\tau_{\ell+1} - \tau_\ell} \sum_{i=\tau_\ell}^{\tau_{\ell+1}-1} \sum_{j=\tau_\ell}^{\tau_{\ell+1}-1} k(X_i, X_j)$$

- Computing  $C(\tau_\ell, \tau_{\ell+1})$  is **quadratic**
- A naive formulation of the dyn. prog. is  $O(n^4)$  in time and  $O(n^2)$  in space (if we store the cost matrix  $\{C(i, j)\}_{1 \leq i, j \leq n+1}$ ).

## Improved formulation

- At round  $t$ , only store  $C(\cdot, t) \in \mathbb{R}^n$ .
  - Update  $C(\cdot, t+1)$  from  $C(\cdot, t)$  on the fly.
- Reduced time and space complexity to  $O(n^2)$  and  $O(n)$  resp.

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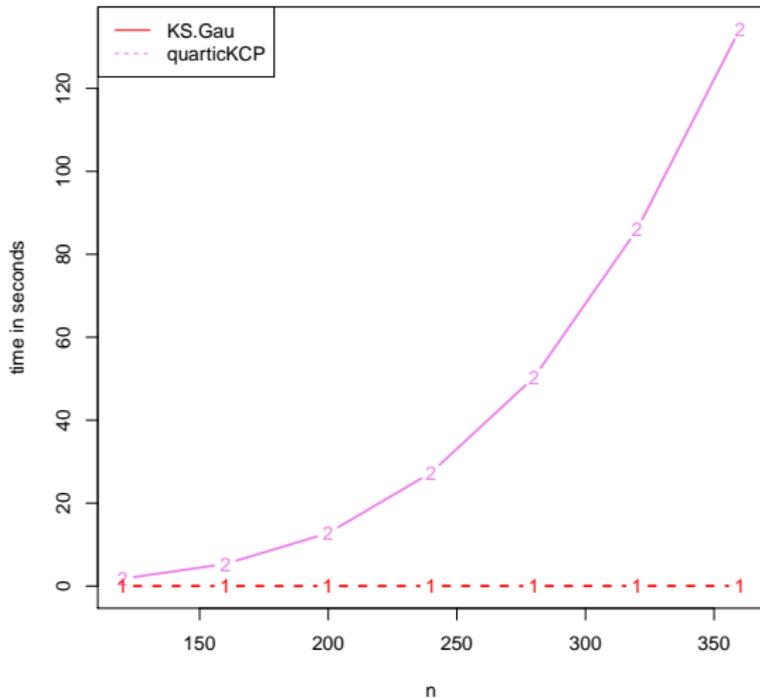
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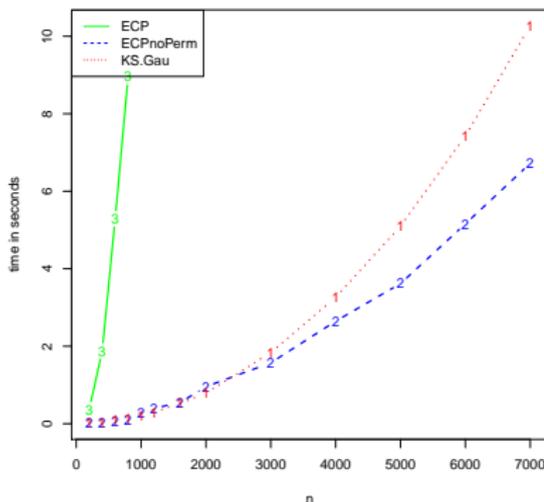
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# Runtime of the improved dyn. prog.: Kernseg

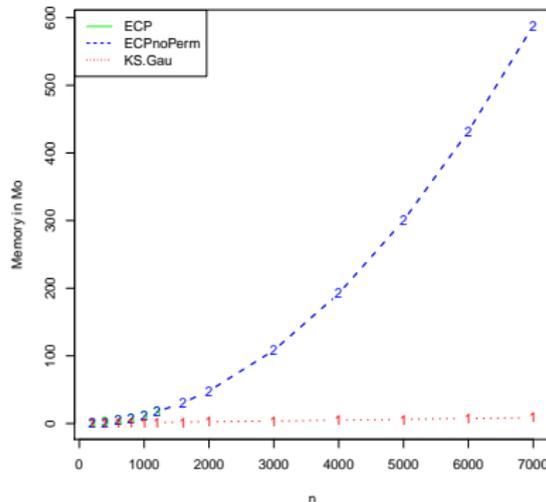


# Comparison Kernseg - ECP ( $D_{\max} = 100$ )

Time



Memory



## Rks:

- ECP: based on a kernel and Binary Segmentation
- Chooses among candidate change-points using permutations

## IIII Faster approx. optimization algo.

# From quadratic-to linear-time cost

## Computational limitation

$$C(\tau_\ell, \tau_{\ell+1}) = \frac{1}{\tau_{\ell+1} - \tau_\ell} \sum_{i=\tau_\ell}^{\tau_{\ell+1}-1} \sum_{j=\tau_\ell}^{\tau_{\ell+1}-1} k(X_i, X_j)$$

- With general kernel, the cost of  $[\tau_\ell, \tau_{\ell+1}]$  is quadratic  
 $\rightarrow n \approx 5 \cdot 10^4$  in less than 2 minutes
- $n \geq 10^6$  not realistic with a  $O(n^2)$  time complexity
- If  $k(x, y) = \langle \phi(x), \phi(y) \rangle_{\mathbb{R}^p}$ , then

$$\sum_{1 \leq i < j \leq s} k(x_i, x_j) = \left\langle \sum_{i=1}^s \phi(x_i), \sum_{j=1}^s \phi(x_j) \right\rangle_{\mathbb{R}^p} = \left\| \sum_{i=1}^s \phi(x_i) \right\|_{\mathbb{R}^p}^2$$

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# Low-rank matrix approximation (Drineas Mahoney (05))

- Gram matrix:  $K = \{k(X_i, X_j)\}_{1 \leq i, j \leq n}$
- $I, J \subset \{1, \dots, n\}$  with  $I = \{1, \dots, n\}$  and  $\text{Card}(J) = p$ .
- $K_{J,J}^-$ : pseudo-inverse of  $K_{J,J}$

Nyström approximation of size  $p$

$$K \approx \tilde{K} = K_{I,J} \times K_{J,J}^- \times K_{J,I}.$$

Then

$$\tilde{K} = Z^T Z, \quad \text{where } Z \in \mathcal{M}_{p,n}(\mathbb{R}),$$

which means that

$$\tilde{k}(x_i, x_j) = Z_i^T Z_j, \quad \text{with } Z_i, Z_j \in \mathbb{R}^p.$$

# Approximate optimization algorithm

## Fast (approximate) procedure (ApKern)

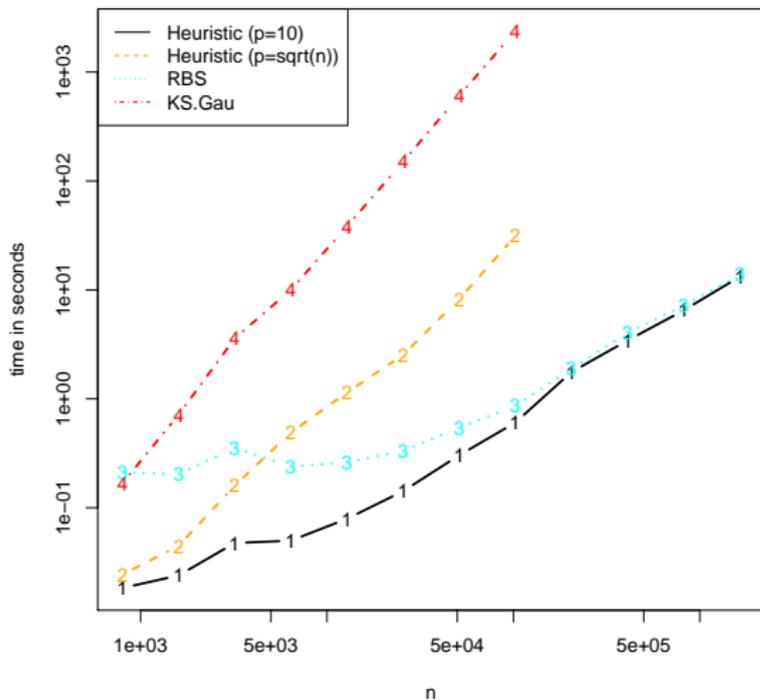
- 1 Approximate  $K \approx \tilde{K} = Z^T \cdot Z$
- 2 Apply Binary Segmentation to the  $Z_i$ s and output a sequence of approximate solutions:

$$\left\{ \hat{\tau}_{BS}^D \right\}_{1 \leq D \leq D_{\max}} .$$

## Computational complexity

- Time:  $O(n \log(n) \vee np^2)$
- Space:  $O(n)$
- Allows for  $n \geq 10^6$

# Comparison ApKern - RBS ( $D_{\max} = 100$ )



## IV How many chgpts? → designing a penalty

# Model selection-based procedure: KCP

## Outline

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→ Model selection result

- 3 Final segmentation:

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# Penalty shape and minimal length

- Arlot, C., Harchaoui (18) proved an oracle inequality for

$$\text{pen}(\tau) = c_1 \frac{D_\tau}{n} + c_2 \frac{1}{n} \log \underbrace{\binom{n-1}{D_\tau-1}}_{=\text{Card}(\mathcal{T}_n^{D_\tau})}$$

- $c_1, c_2 > 0$ : estimated by slope heuristic
- With a constraint on the minimal length  $\ell$  of any segment:

$$\text{pen}_\ell(\tau) = c_1 \frac{D_\tau}{n} + c_2 \frac{1}{n} \log \binom{n - D_\tau(\ell - 1) - 1}{D_\tau - 1}$$

→ Particularly relevant with low signal-to-noise ratio data.

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- Arlot, C., Harchaoui (18) proved an oracle inequality for

$$\text{pen}(\tau) = c_1 \frac{D_\tau}{n} + c_2 \frac{1}{n} \log \underbrace{\binom{n-1}{D_\tau-1}}_{=\text{Card}(\mathcal{T}_n^{D_\tau})}$$

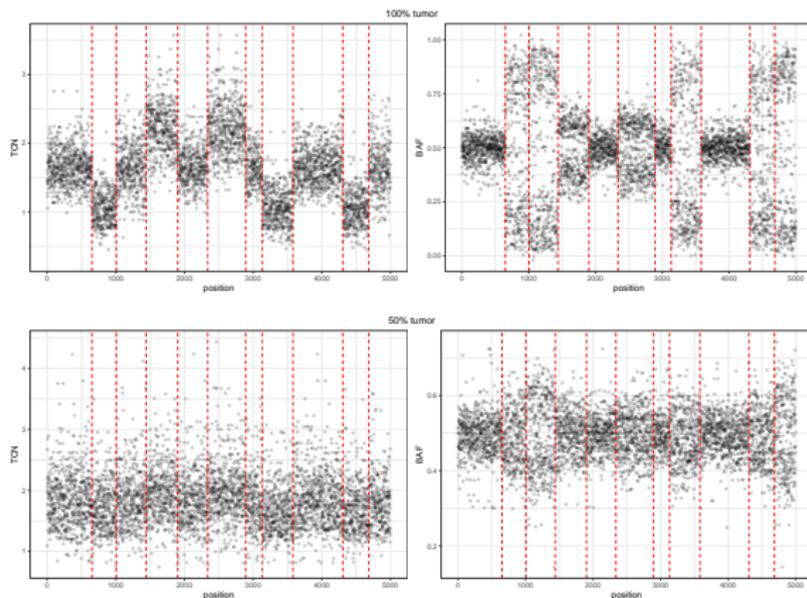
- $c_1, c_2 > 0$ : estimated by slope heuristic
- With a constraint on the minimal length  $\ell$  of any segment:

$$\text{pen}_\ell(\tau) = c_1 \frac{D_\tau}{n} + c_2 \frac{1}{n} \log \binom{n - D_\tau(\ell - 1) - 1}{D_\tau - 1}$$

→ Particularly relevant with low signal-to-noise ratio data.

## ∇ Biological experiments: LOH

# Data from ACNR package (Pierre-Jean, Neuvial (14))



- $n = 5000$ ,  $D^* = 11$ , purity is 100% and 50%
- $k(x, y) = k_{TCN}(x_1, y_1) + k_{BAF}(x_2, y_2)$

# Parameters values and accuracy

## Tuning the kernel parameters

- $k_{TCN}$  and  $k_{BAF}$ : Gaussian kernels  $e^{-\frac{(x-y)^2}{h}}$
- Bandwidth:

$$h = 2 \left( \frac{\hat{\sigma}}{\sqrt{2}} \right)^2, \quad \text{with} \quad \hat{\sigma}^2 = \frac{1}{n/2} \sum_{i=1}^{n/2} (X_{2i} - X_{2i-1})^2$$

## Accuracy measure of the segmentation

- Segmentation  $\tau$  as a matrix  $M^\tau = \{M_{i,j}^\tau\}$  such that

$$M_{i,j}^\tau = \sum_{d=1}^{D^\tau} \frac{\mathbb{1}_{\{\tau_d \leq i < j < \tau_{d+1}\}}}{\tau_{d+1} - \tau_d}$$

- $\|M\|_F = \sqrt{\text{tr}(M^\top M)}$
- 

$$\text{Accuracy}(\tau) = \left\| M^\tau - M^{\tau^*} \right\|_F$$

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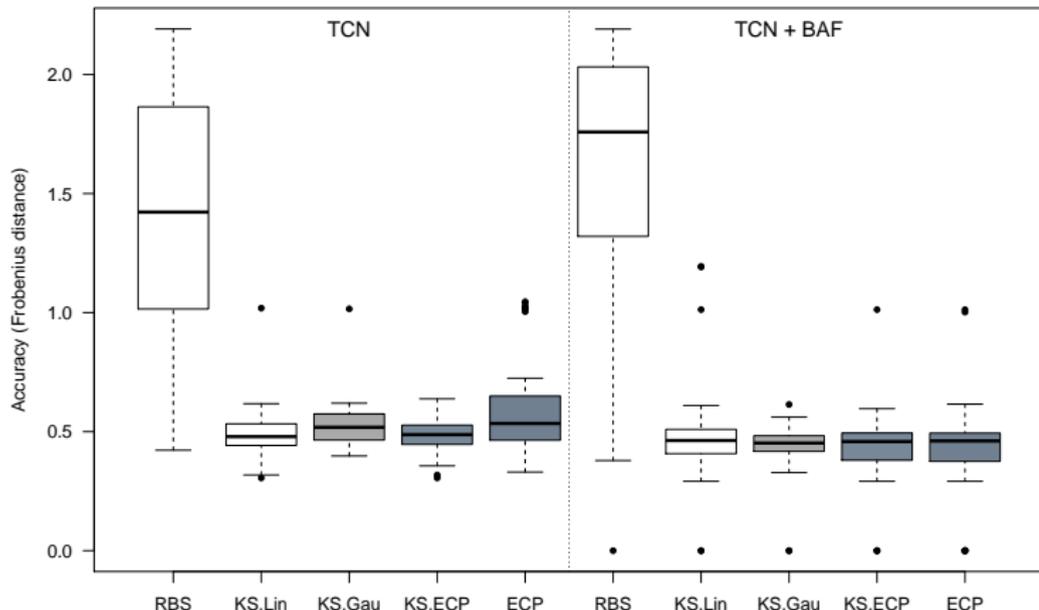
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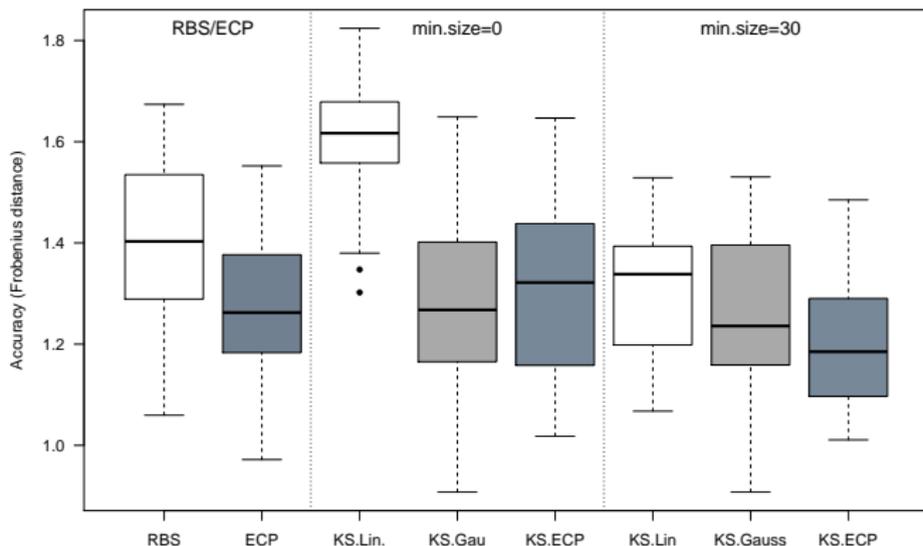
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# Easy case: high purity



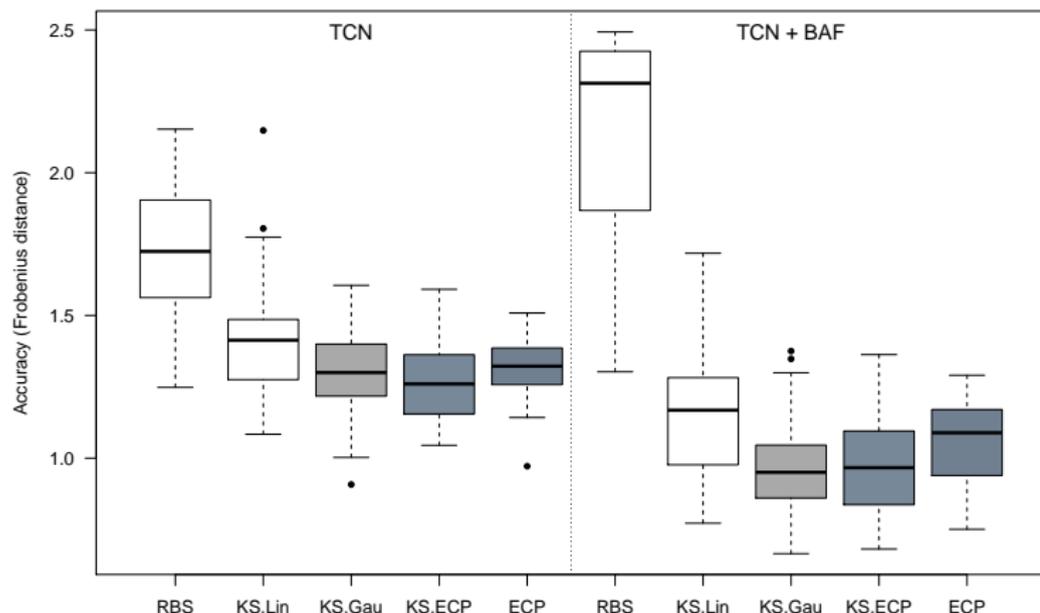
- Accuracy (chpts location) expressed with Frobenius norm
- Everyone works well at  $\hat{D}$  (except RBS)
- (TCN,BAF) not significantly better! (easy case)

# Difficult case (low purity): Minimum length



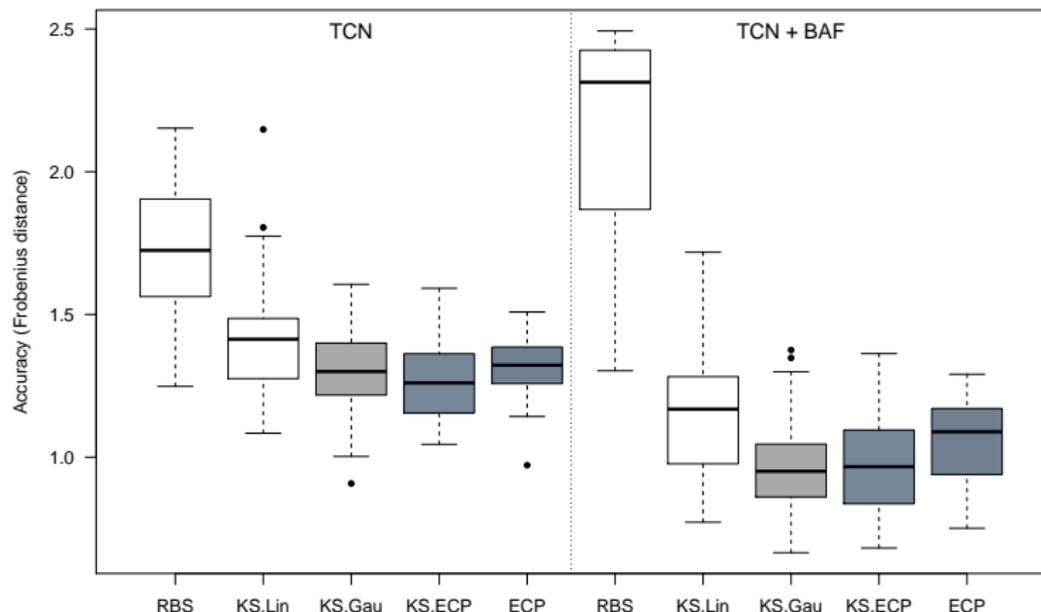
- ECP:  $\ell = 30$  constraint encoded by default
- Global improvement with  $\ell = 30$  (especially for linear kernel)
- Gaussian and ECP kernels: best performance

# Influence of the kernel – joint signal



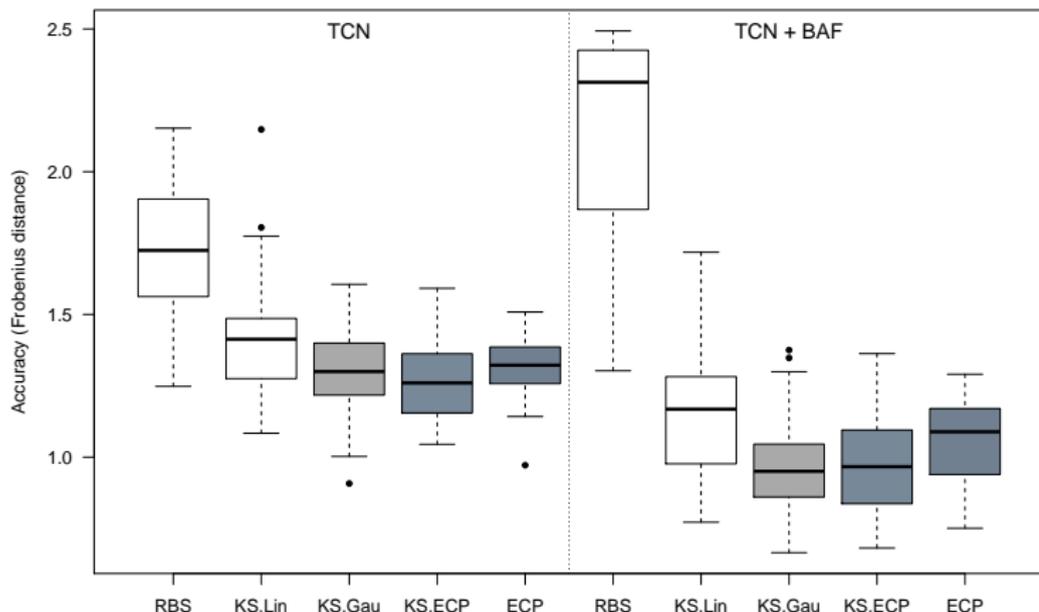
- RBS fails: bad choice of  $\hat{D}$
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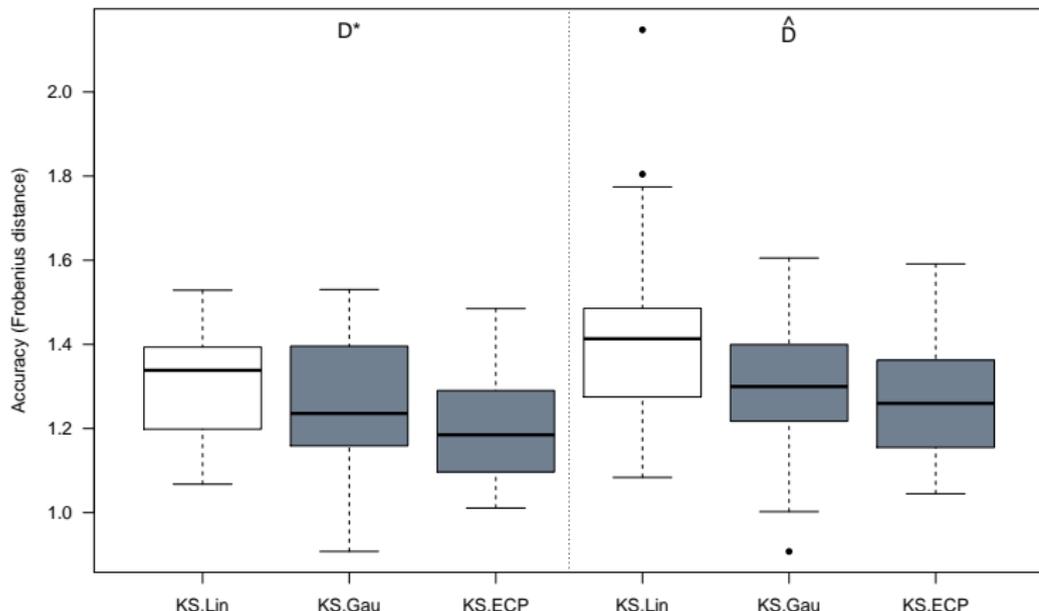
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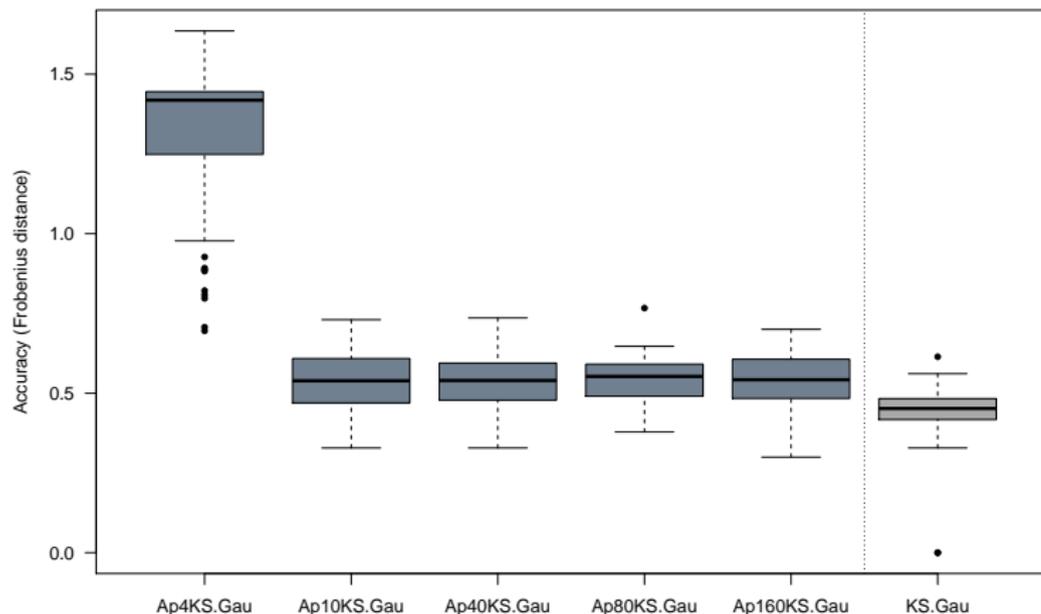
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# Estimated the number of segments quality



- Slight loss of accuracy when estimating
- Does not modify the ranking of kernel-based procedures

# Quality of the approximate procedure (ApKern)



- $p$  has to be large enough ( $p \geq \text{rk}(K)$ )?
- Close to the optimal solution
- Quite stable results w.r.t.  $p$

# Pros/cons of ApKern

## Assets

- Dealing with  $n \geq 10^6$  in a few seconds is possible!
- Enjoys a good accuracy
- Reducing the dimension (low-rank approx.) allows for using any available discrete optimization algorithm (dynamic programming, BS, ...)

## Drawbacks

- Choosing  $p$  (and the  $X_i$ s) remains an open practical question
- No ongoing model selection result to choose the number of segments (Binary Segmentation)

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# Take-home message/discussion

## Recap

- KCP: no (strong) distributional assumption and theoretical guarantees
- Kernseg: R package with an improved complexity
  - Time:  $O(n^2)$  (exact) or  $O(n \log n)$  (approx.)
  - Space:  $O(n)$
- Achieves state-of-the-art performances on biological data generated with the ACNR package (Characteristic kernels)

## Open questions

- Explore other structured objects (dynamic networks, ...)
- Optimize the kernel (approx.): supervised or not
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