Hawkes process as models for some genomic data

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Contents

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Why just DNA ? RNA etc ...

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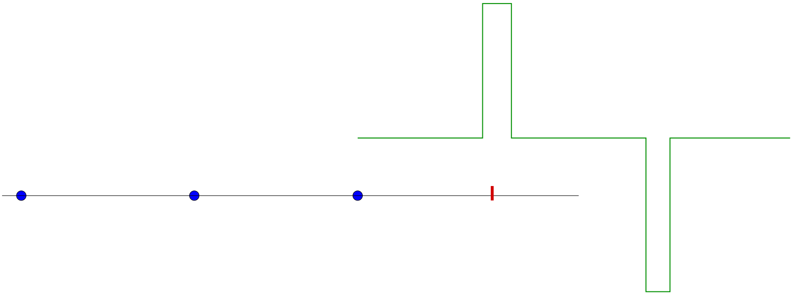

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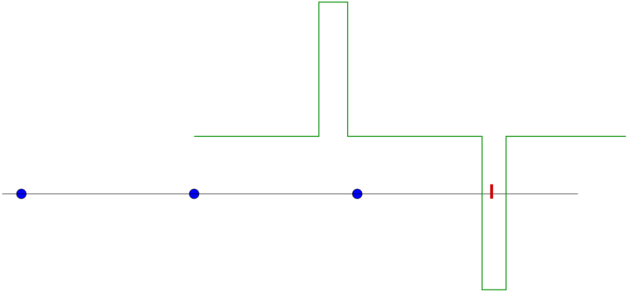

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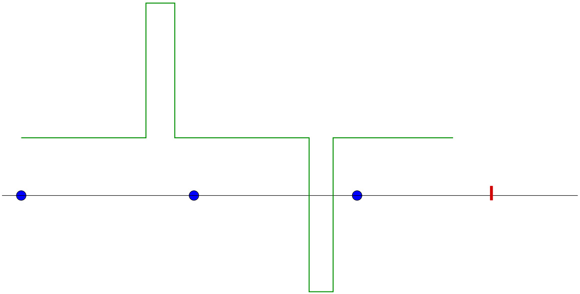

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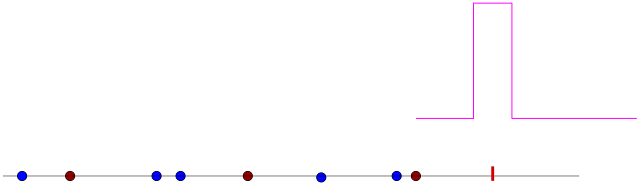

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Maximal sensible interaction distance: 5 000 - 10 000 bases because of the 3d DNA structure

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N_A number of points of N in A, $N_t = N_{[0,t]}$,
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NB : here $\mathbb{R}$ is the DNA strand. The "past" may be interpreted as what has already been read in a prescribed direction (e.g. 5'-3' or 3'-5').

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The intensity $\lambda(t)$ is given by

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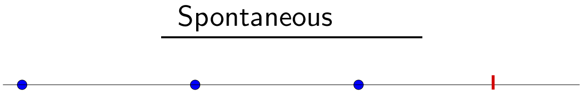

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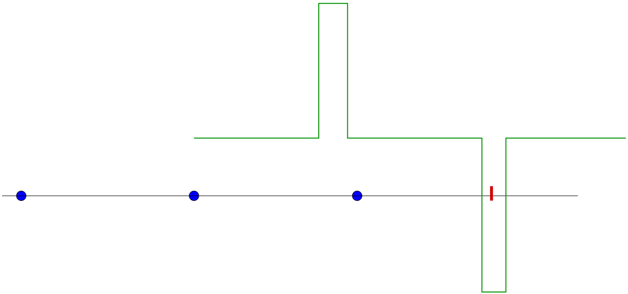
$$\nu \qquad + \quad \sum_{T\in N} h(t-T)$$

Spontaneous Self-exciting



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The most classical case corresponds to $h > 0$ (see Hawkes (1971)) and a stationary version exists if $\int h < 1$. There is also in this specific case a branching / cluster process representation (see Hawkes and Oakes (1974)).

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One can actually consider any 1-Lipschitz modification, there is still a stationary version of it if $\int |h| < 1$ (Brémaud and Massoulié (1996)).

The Hawkes process interaction with itself + an additional interaction

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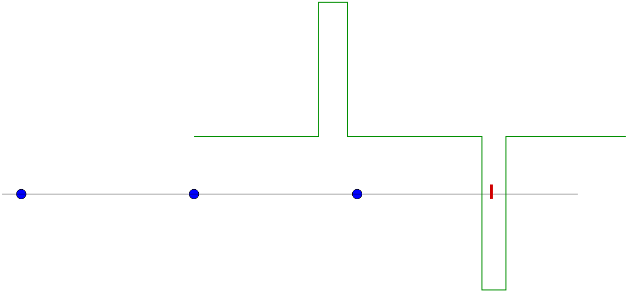
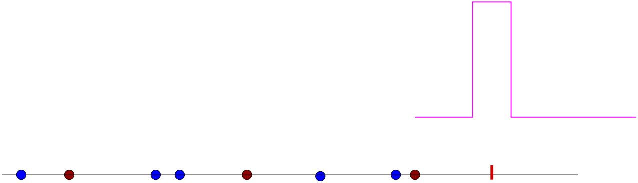


The Hawkes process interaction with itself + an additional interaction

$$\lambda(t) = \underbrace{\nu}_{\text{Spontaneous}} + \underbrace{\sum_{T \in N} h(t - T)}_{\text{Self-interaction}} + \underbrace{\sum_{X \in N_2} h_2(t - X)}_{\text{Interaction with other type}}$$



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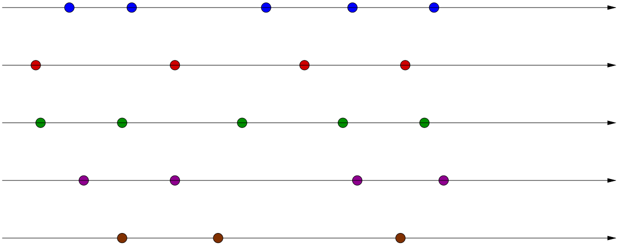
If h is null and if N_2 is fixed (no reciprocal interaction), then N is a Poisson process given N_2.

The multivariate Hawkes process

One observes $N^{(1)}, \ldots, N^{(r)}, \ldots, N^{(M)}$ processes such that



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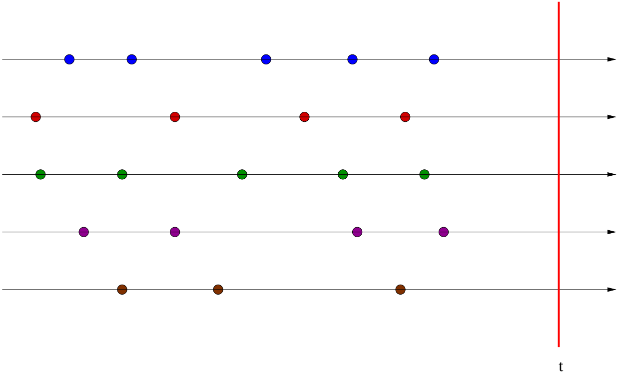

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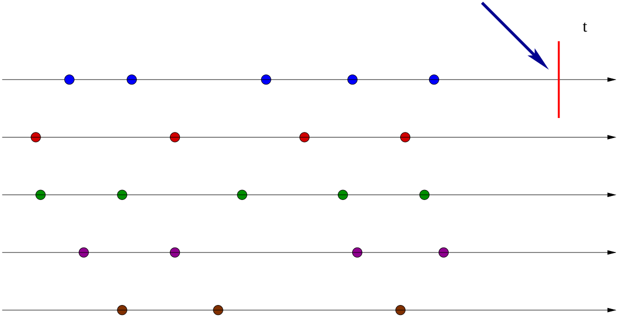

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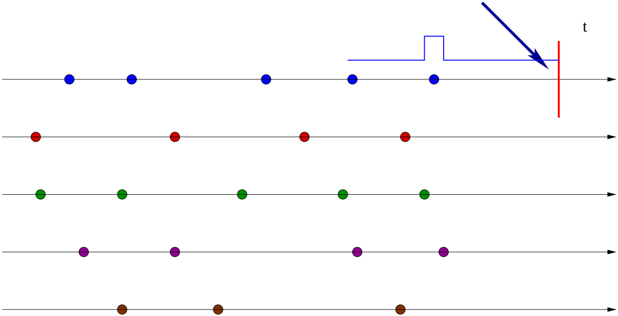

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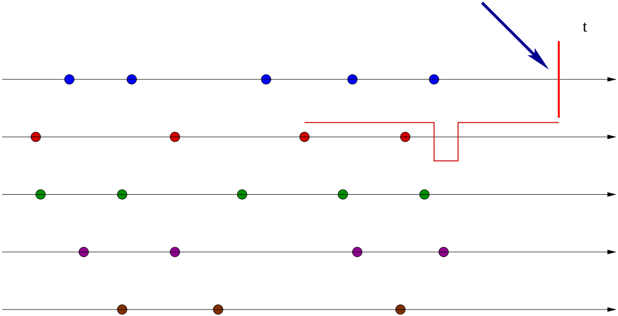

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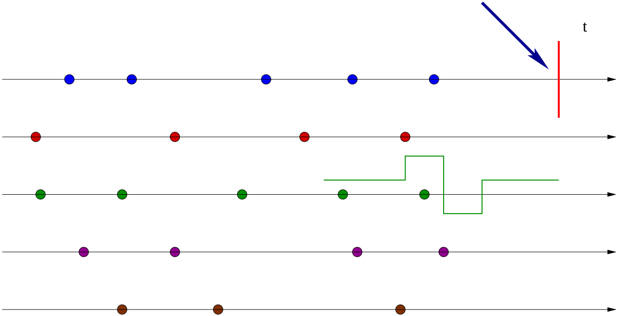

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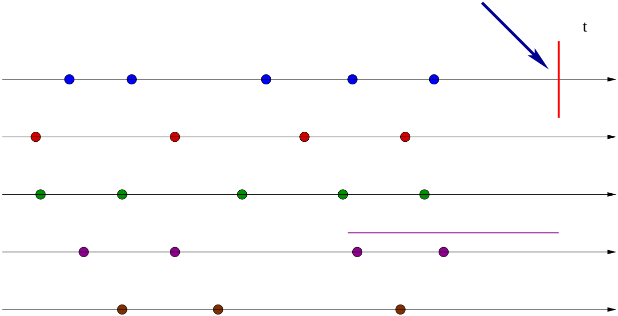

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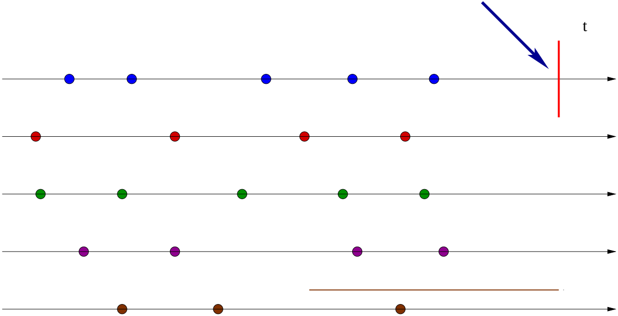

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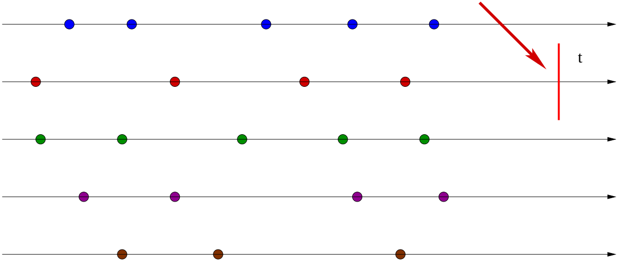

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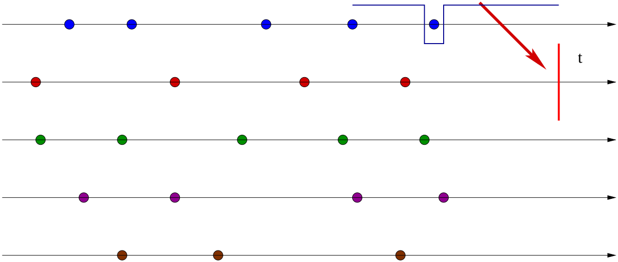

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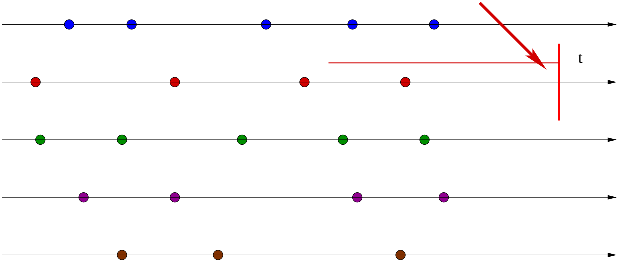

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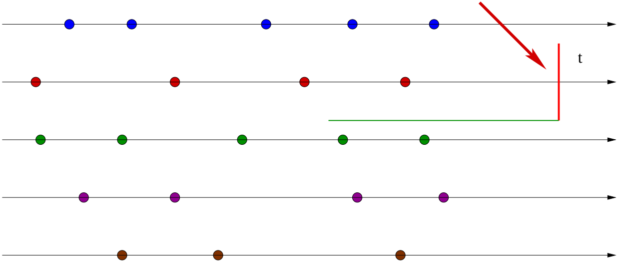

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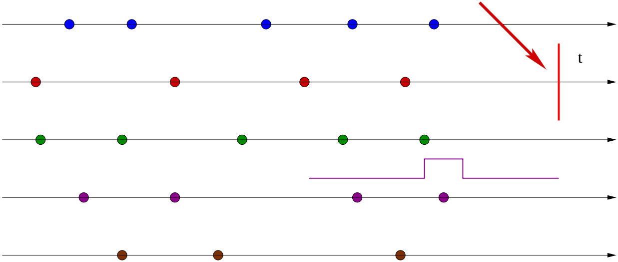

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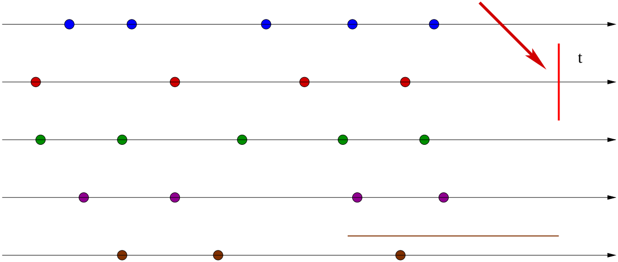

The multivariate Hawkes process(2)

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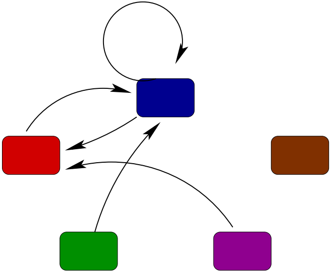

The multivariate Hawkes process(3)

- Only excitation (all the $h_\ell^{(r)}$ are positive): for all r,

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Branching / Cluster representation, stationary process if the spectral radius of $\left(\int h_\ell^{(r)}(t)dt\right)$ is < 1.

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- Exponential

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  Multiplicative shape but no guarantee of a stationary version

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- not necessary to have a stationary version, it depends on the considered asymptotics.
- Consistence, asymptotic normality under smooth conditions, see Ogata and Akaike (1982), Ozaki (1979) or Andersen et al (1993).

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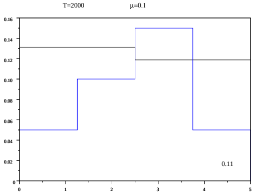
- Only the shape of the intensity is necessary.
- Given the "past" before 0, for one process observed until time T,

$$L_T(\theta) = \int_0^T \ln(\lambda_\theta(t))dN_t - \int_0^T \lambda_\theta(t)dt.$$

- maximizing gives $\hat{\theta}$.
- If several processes or n sample → sum
- not necessary to have a stationary version, it depends on the considered asymptotics.
- Consistence, asymptotic normality under smooth conditions, see Ogata and Akaike (1982), Ozaki (1979) or Andersen et al (1993).
- Even tests of the nullity of $h_\ell^{(r)}$ and access to a graphical model (see Carstensen et al (2010)) .

Model choice



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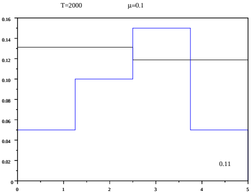

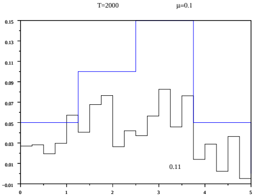

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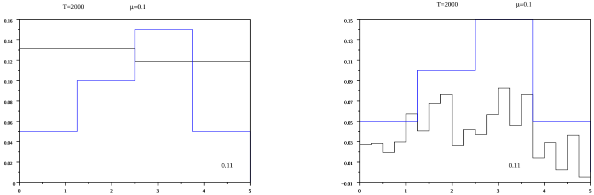

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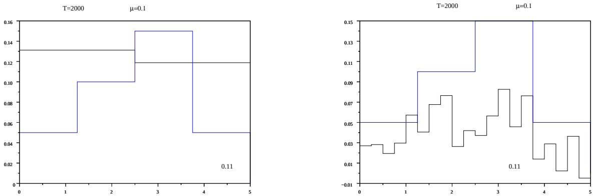

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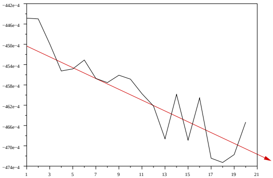

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- Hence no clear access to favoured or avoided distance

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- $\longrightarrow$ penalized model selection (Birgé and Massart, see Massart course in St Flour (2007))
- but also, thresholding or Lasso methods.

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- The meaningful quantity is $\lambda(t)$.

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- We will minimize γ_T for precise shape of intensity candidates.

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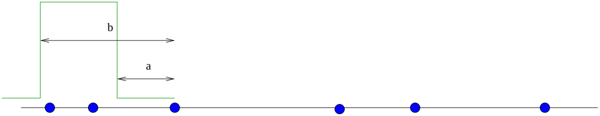

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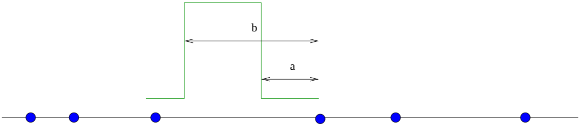

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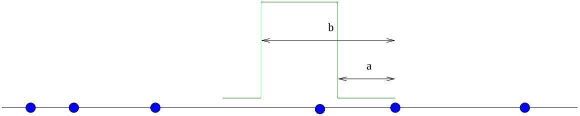

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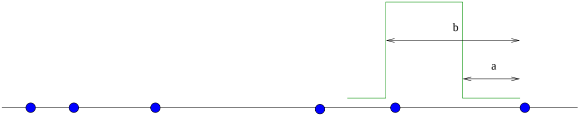

For the simple Hawkes process

- $\mathbb{L}_2 = \left\{ f = (\mu, g) \ : \ \text{Supp}(g) = [0, A], \|f\|^2 = \mu^2 + \int_0^A g^2(x)dx < +\infty \right\}$
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- $\hat{s}_m = \arg\min_{f \in S_m} \gamma_T(f)$. no close formula in general.

Risk study

Only for simple Hawkes process

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- → compromise: the best (or oracle) in a family is the one that minimizes the sum.

Model selection with dimension-based penalty

Joint work with S. Schbath (2010). Only for simple Hawkes process

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- NESTED Regular dyadic partitions constructed on Γ.
- REGULAR Regular partitions until a certain prescribed bandwidth
- IRREGULAR All irregular partitions contructed on Γ.

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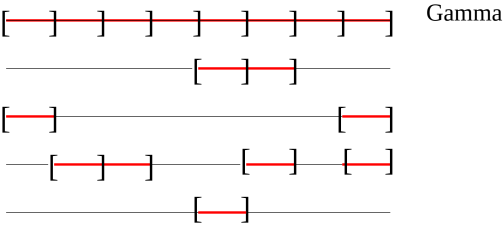

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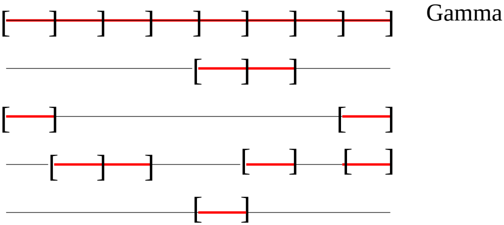

- ISLANDS
  All models included in Γ. The most adapted to the biological question.

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Under technical assumptions, if

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- also adaptive minimax results for Hölder functions.

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- Theoretical penalty not observed, Slope heuristics does not work especially for Islands
- An angle is perfectly clear on the simulations at the correct dimension:

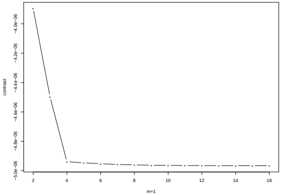
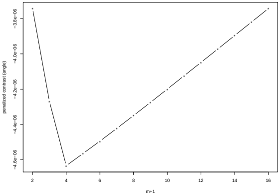
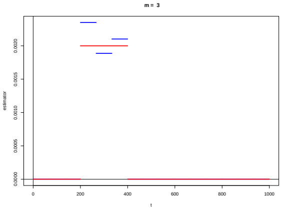
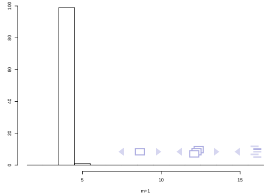
$$-\bar{k} = \frac{\gamma_T(\hat{s}_\Gamma) - \gamma_T(\hat{s}_1)}{|\Gamma| - 1}$$

and

$$\hat{m} = \mathrm{argmin}_{m \in \mathcal{M}_T} \gamma_T(\hat{s}_m) + \bar{k}(|m| + 1).$$

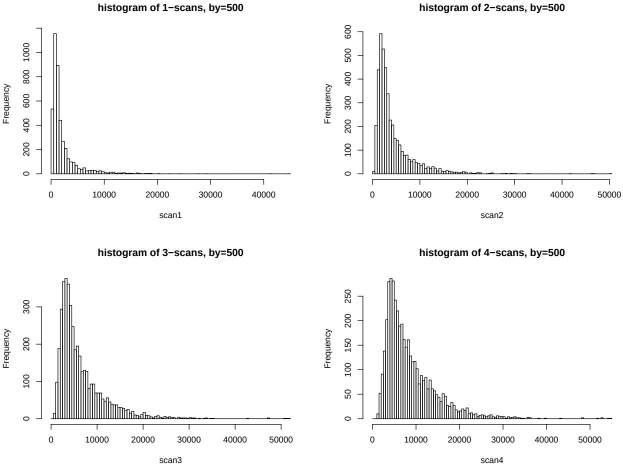
Illustration

Only for simple Hawkes process

Contrast	Penalized contrast
	
Chosen estimator	Selected dimension
	

On real data

Only for simple Hawkes process



Analysis of the positions of the 4290 genes of E. coli

($T = 9288442$, $A = 10000$) (r-scans)

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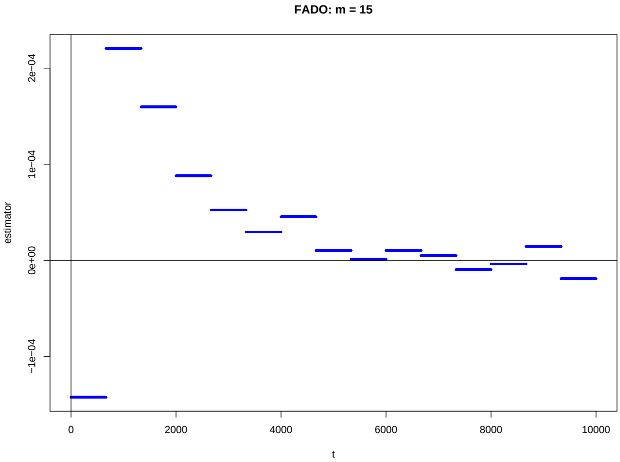

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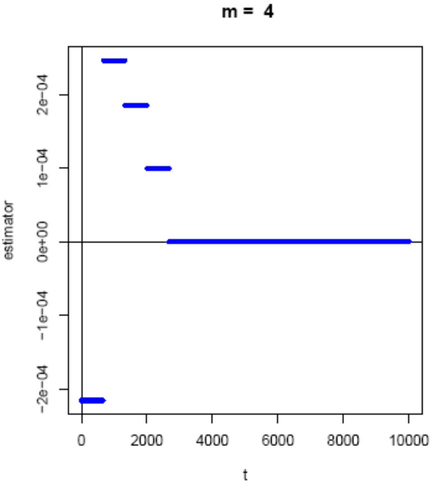

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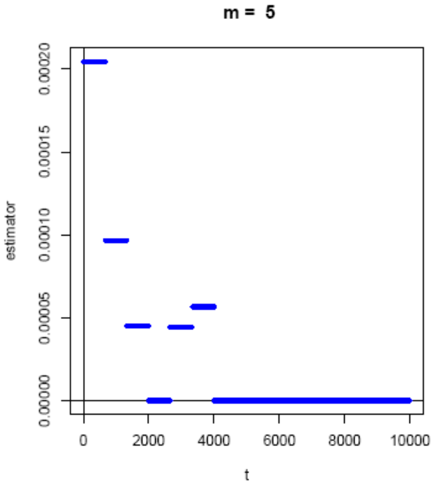

Analysis of the 1036 occurrences of `tataat` for E. coli.

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Disadvantages of the dimension-based penalty method

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- We miss part of the understanding because we do not take external information into account (here interaction `tataat` - genes).

Poissonian Interaction

Work in progress of Laure Sansonnet.

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- A pairwise study of two processes is possible (for instance `tataat` and genes). If h has support in $\mathbb{R}_+$ = very special case of multivariate Hawkes process.

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- Computation quite fast. Precision $>>$ Islands

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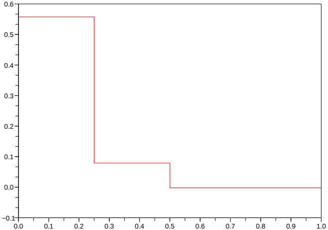
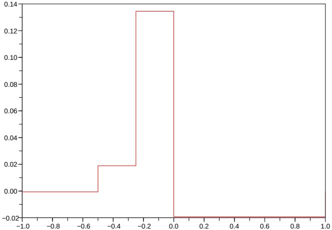
- Crucial to say who are the parents/ the children (it is not symetric!).
- For the moment, one cannot explain the Children position, even with an extra spontaneous apparition.

Poissonian Interaction (2)

Interaction `tataat` - genes.



Parents = `tataat`



Parents = Genes

Full Multivariate Hawkes processes and lasso procedure

Joint Work with N.R. Hansen (Copenhagen) and V. Rivoirard (Dauphine), in progress.

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We want to estimate $s = \left((\nu_r, (h_\ell^{(r)})_{\ell=1,\dots,M})_{r=1,\dots,M} \right)$ in

$$\mathbb{L}_2 = \Big\{ f = \left((\mu_r, (g_\ell^{(r)})_{\ell=1,\dots,M})_{r=1,\dots,M} \right) \ \ / \ \ g_\ell^{(r)} \text{ with support in } (0,A] \text{ and } \|f\|^2 = \sum_r (\mu_r)^2 + \sum_r \sum_\ell \int_0^A (g_\ell^{(r)})^2(x)dx < \infty \Big\}.$$

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Intensity candidate per mark

$\psi_f^{(r)}(t) = \mu_r + \sum_\ell \int_{-\infty}^t g_\ell^{(r)}(t-u)dN_u^{(\ell)}$.

Full Multivariate Hawkes processes and lasso procedure(2)

Least-square contrast (full form)

$\gamma_T(f) = \sum_r \gamma_T^{(r)}(f)$ where

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- $$\gamma_T^{(r)}(f) = -2\mathbf{a}_r^*\mathbf{b}_r + \mathbf{a}_r^*\mathbf{G}\mathbf{a}_r,$$

  where

  - **G** is a random observable matrix, independent of the mark r
  - $\mathbf{b}_r$ is also a random observable vector.

Full Multivariate Hawkes processes and lasso procedure(3)

The Lasso criterion can be expressed independently for each mark.

Lasso criterion

$$\hat{\mathbf{a}}_r = \mathrm{argmin}_{\mathbf{a}_r \in \mathbb{R}^{MK+1}} \{-2\mathbf{a}_r^*\mathbf{b}_r + \mathbf{a}_r^*\mathbf{G}\mathbf{a}_r + 2\mathbf{d}_r^*|\mathbf{a}_r|\}$$

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- Oracle inequality with "high" probability possible....