

Hawkes process as models for some genomic data

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Several examples

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Why just DNA ? RNA etc ...

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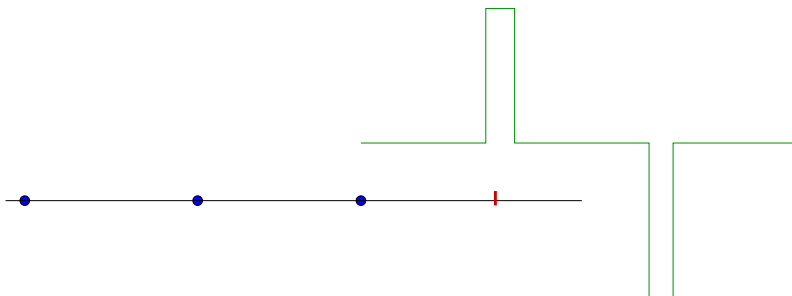
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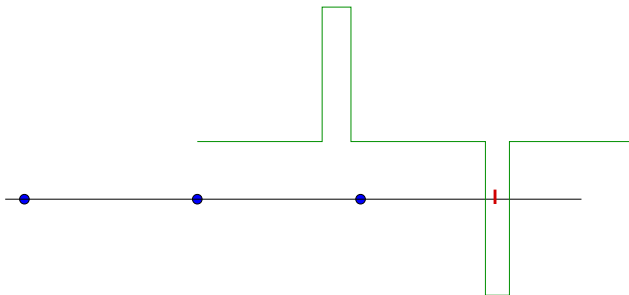
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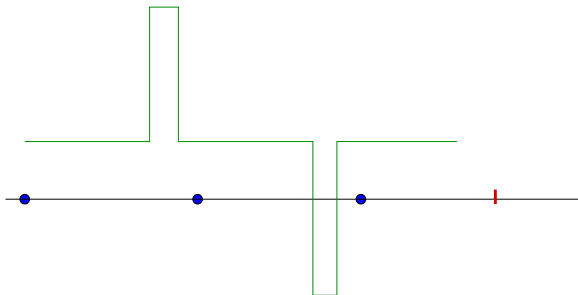
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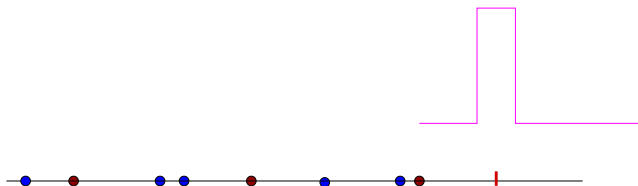
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Maximal sensible interaction distance: 5 000 - 10 000 bases
because of the 3d DNA structure

Point process on the real line

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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').

The simple Hawkes process

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

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$$\nu$$

Spontaneous

A horizontal timeline with three blue dots representing events. A thick black horizontal bar labeled "Spontaneous" is positioned above the first two dots. A red vertical tick mark is located on the timeline to the right of the third dot.

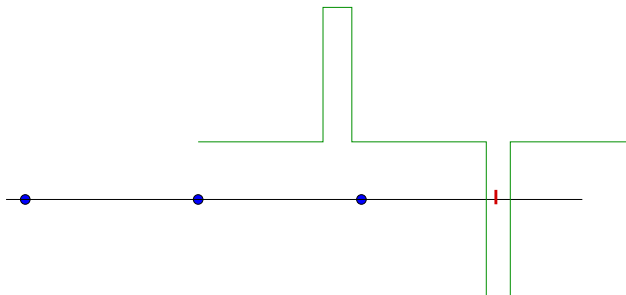
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The most classical case corresponds to $h > 0$ (see Hawkes (1971)) and a stationary version exists if $\int h < 1$. There is also in this specific case a branching / cluster process representation (see Hawkes and Oakes (1974)).

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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)).

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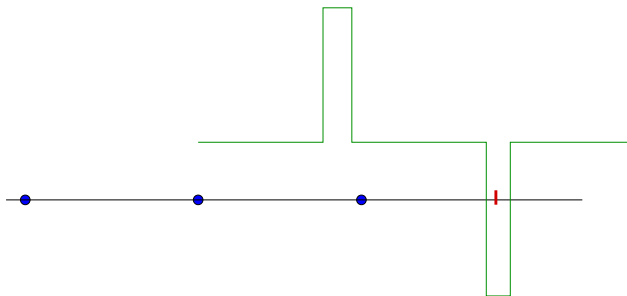
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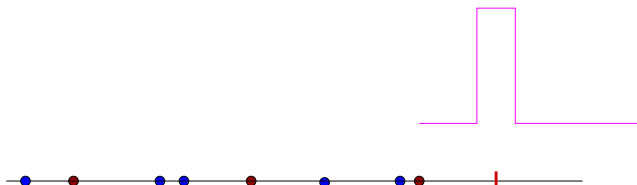
$$\lambda(t) =$$

$$\nu \quad + \quad \sum_{T \in N} h(t - T) \quad + \quad \sum_{X \in N_2} h_2(t - X)$$

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Interaction with other type



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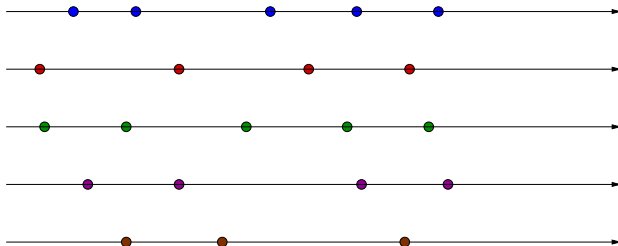
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Interaction with other type

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 $N^{(1)}, \dots, N^{(r)}, \dots, N^{(M)}$ processes such that



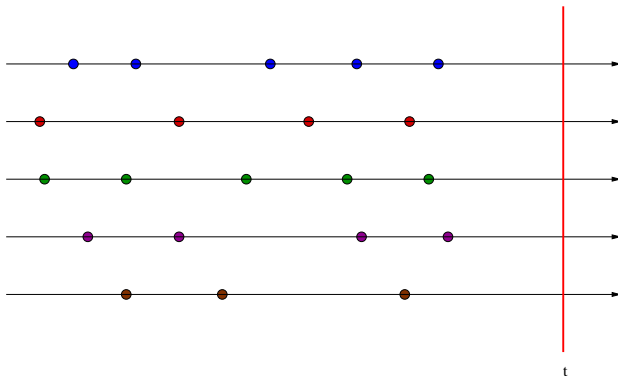
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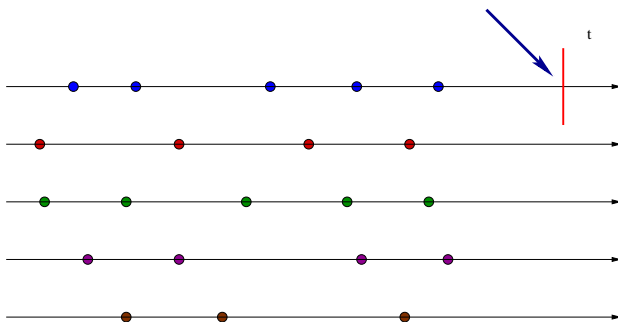
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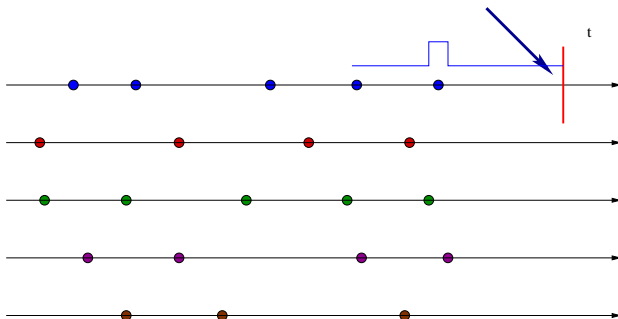
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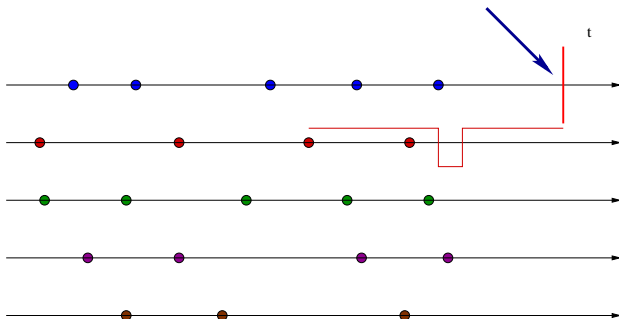
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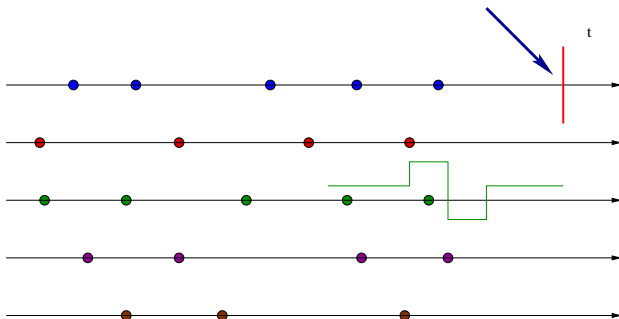
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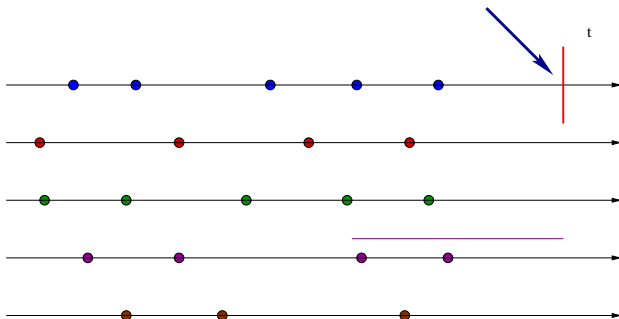
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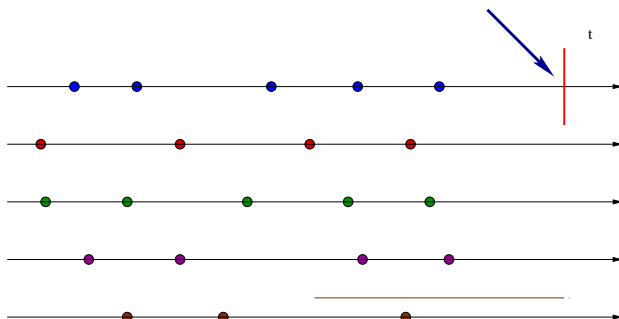
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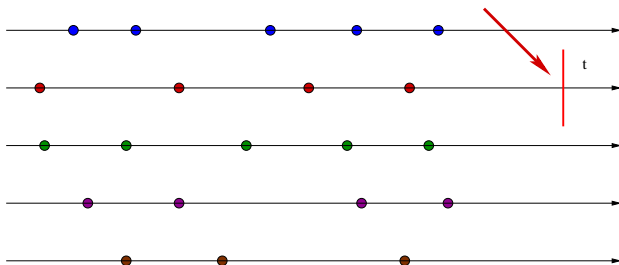
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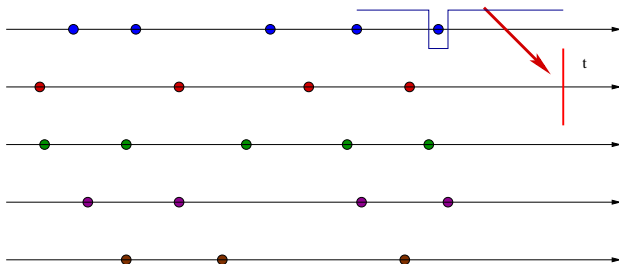
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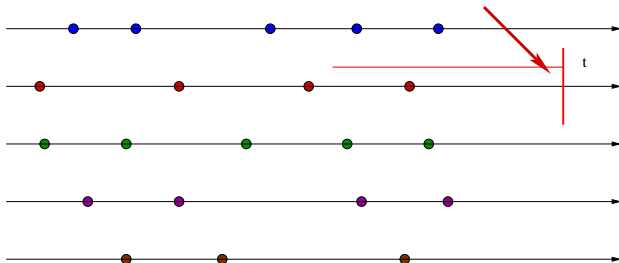
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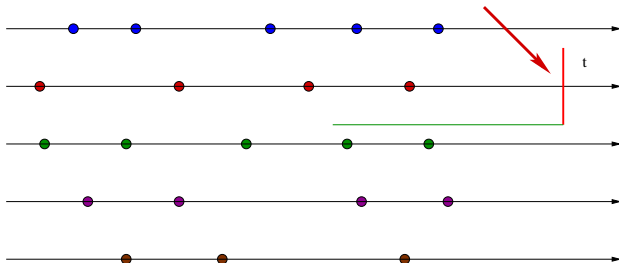
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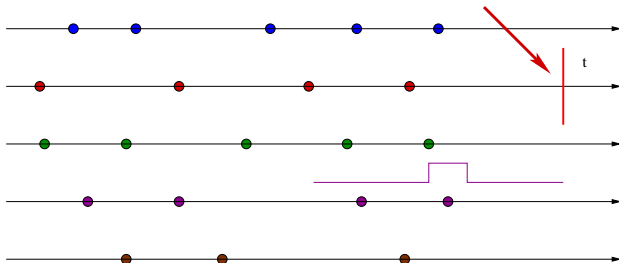
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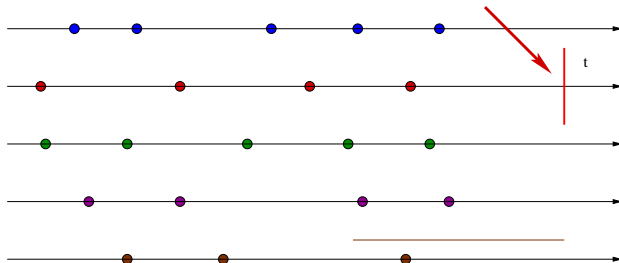
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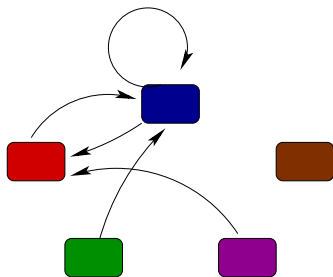


The multivariate Hawkes process(2)

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The multivariate Hawkes process(3)

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Multiplicative shape but no guarantee of a stationary version

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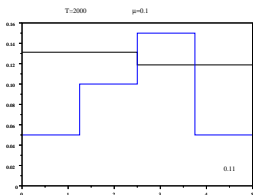
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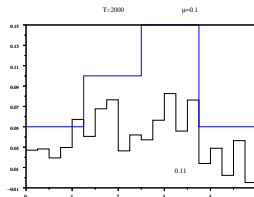
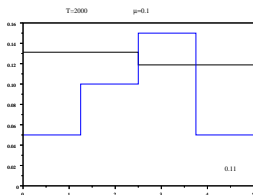
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- Consistence, asymptotic normality under smooth conditions, see Ogata and Akaike (1982), Ozaki (1979) or Andersen et al (1993).
- Even tests of the nullity of $h_\ell^{(r)}$ and access to a graphical model (see Carstensen et al (2010)) .

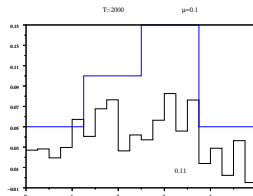
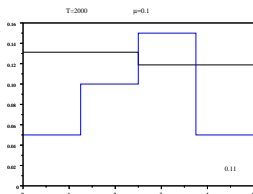
Model choice



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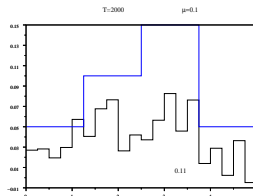
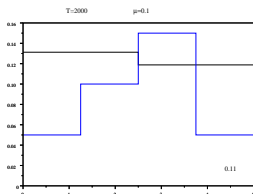


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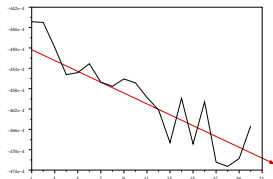


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- Hence no clear access to favoured or avoided distance

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

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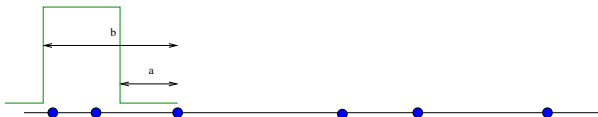
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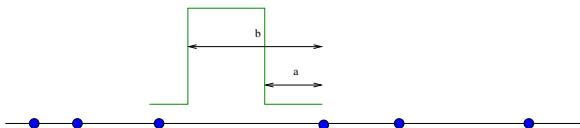
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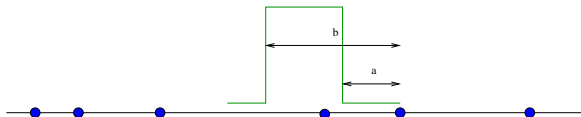
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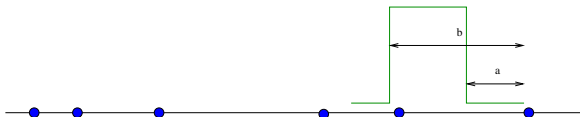
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- $\mathbb{L}_2 = \left\{ f = (\mu, g) : \text{Supp}(g) = [0, A], \|f\|^2 = \mu^2 + \int_0^A g^2(x) dx < +\infty \right\}$
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- $\hat{s}_m = \arg \min_{f \in S_m} \gamma_T(f)$. no close formula in general.

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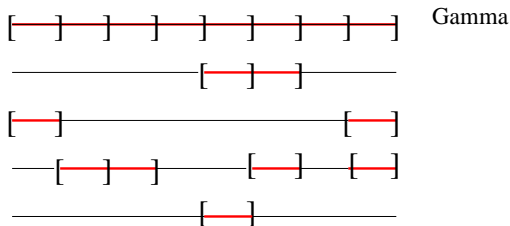
- NESTED Regular dyadic partitions constructed on Γ .
- REGULAR Regular partitions until a certain prescribed bandwidth
- IRREGULAR All irregular partitions constructed on Γ .

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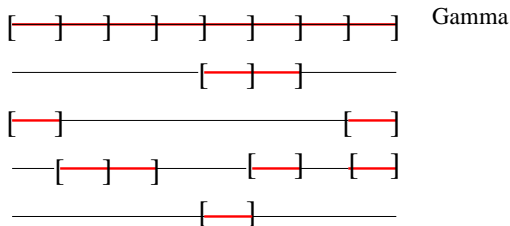


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- ISLANDS

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

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Under technical assumptions, if

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

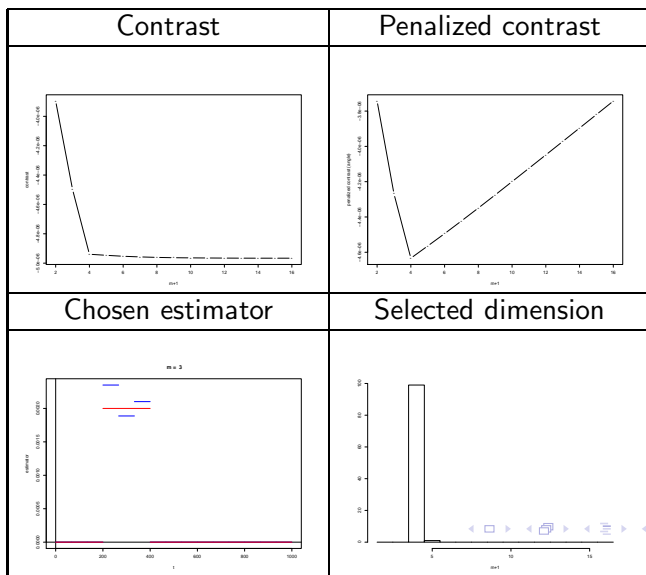
$$-\bar{k} = \frac{\gamma_T(\hat{\sigma}_\Gamma) - \gamma_T(\hat{\sigma}_1)}{|\Gamma| - 1}$$

and

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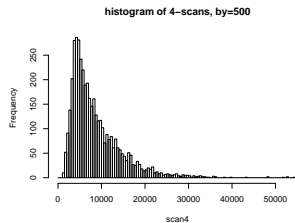
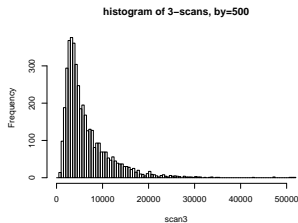
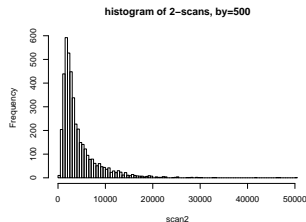
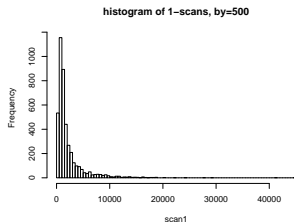
Illustration

Only for simple Hawkes process



On real data

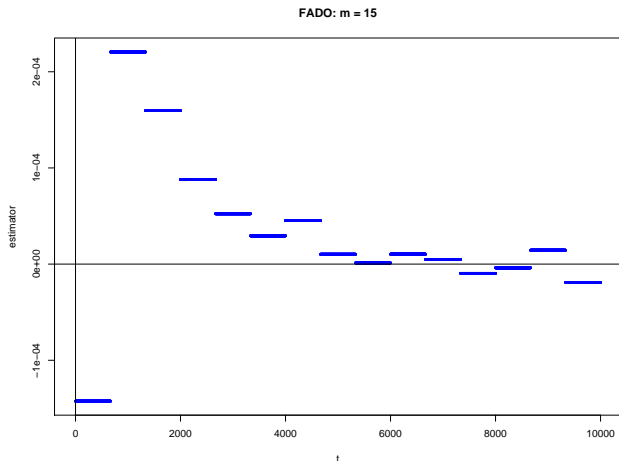
Only for simple Hawkes process



Analysis of the positions of the 4290 genes of *E. coli*
 ($T = 9288442$, $A = 10000$) (r-scans)

On real data

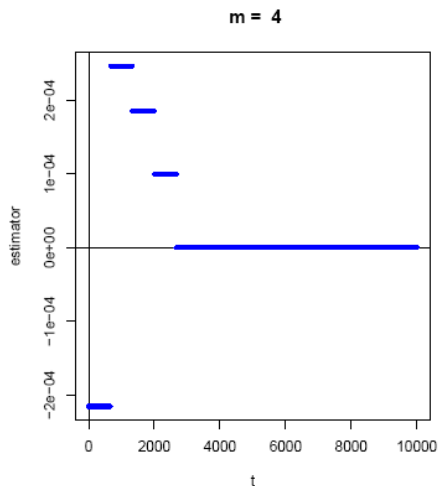
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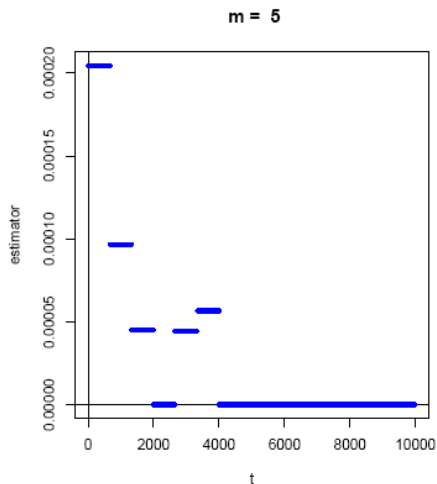
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On real data

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Analysis of the 1036 occurrences of tataaat for E. coli.

($T = 9288442$, $A = 10000$) (Islands)

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

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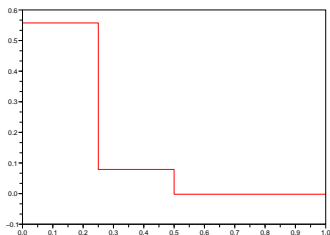
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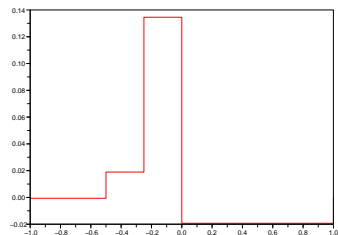
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- For the moment, one cannot explain the Children position, even with an extra spontaneous apparition.

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

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

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Intensity candidate per mark

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

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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

- \mathbf{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

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

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