

Continous Testing for Poisson Processes Intensities

F. Picard^{*}, P. Reynaud-Bouret^o, E. Roquain[‡],

* Laboratoire de Biométrie et Biologie Évolutive, Univ. Lyon 1,
 ° Laboratoire J.A. Dieudonné, Univ. Nice,
 [‡] Laboratoire de Probabilités et Modèles Aléatoires, Univ. Paris 6.

September 2017

Outline

1 Point Process modeling of Genomic features

- 2 Test statistics and associated p-value process
- 3 Two error rates in continuous time
- 4 Simulations
- **5** Application



Observations are random sets of points

• We observe two independent sets of peaks location:

$$N_A = \{T_1, \ldots, T_{n_A}\} \text{ and } N_B = \{T_1, \ldots, T_{n_B}\}.$$

- We model those sets by two heterogeneous Poisson processes with intensity λ_A, λ_B in L²[0, 1].
- For any interval $I \subseteq [0, 1]$,

$$N_A(I)\sim \mathcal{P}\left(\int_I \lambda_A(t)dt
ight) \quad ext{and} \quad N_B(I)\sim \mathcal{P}\left(\int_I \lambda_B(t)dt
ight)$$

Aim

Testing $\lambda_A = \lambda_B$ and detecting zones where $\lambda_A \neq \lambda_B$

Global and local strategies

- The first strategy would be to test {λ_A = λ_B}, but lacks of sensitivity (yes / no answer)
- Scan Statistics : sliding windows and the global Type-I error control \rightarrow Asymptotic expansions of distribution tails
 - \rightarrow No strict testing framework
 - \rightarrow No real interpretation in terms of multiple testing
 - \rightarrow No satisfying FDR control yet

Global and local strategies

- The first strategy would be to test {λ_A = λ_B}, but lacks of sensitivity (yes / no answer)
- Scan Statistics : sliding windows and the global Type-I error control
 → Asymptotic expansions of distribution tails
 - ightarrow No strict testing framework
 - \rightarrow No real interpretation in terms of multiple testing
 - \rightarrow No satisfying FDR control yet
- Our strategy is local testing
 - \rightarrow Non asymptotic, non parametric
 - \rightarrow We provide a complete testing framework
 - \rightarrow We fill the gap between sliding windows and multiple testing
 - \rightarrow We provide a formal definition of the FDR in continuous time

Avé les mains

- Consider an interval $I \in [0,1]$, and suppose that $\lambda_A = \lambda_B$ on I
- Given $N_A(I) + N_B(I) = n(I), N_A(I) \sim \mathcal{B}(n(I), 1/2)$

Avé les mains

- Consider an interval $I \in [0,1]$, and suppose that $\lambda_A = \lambda_B$ on I
- Given $N_A(I) + N_B(I) = n(I), N_A(I) \sim \mathcal{B}(n(I), 1/2)$
- Our strategy is to perform **conditional** testing, given $N = N_A + N_B$.
- $\lambda = \lambda_A + \lambda_B$ becomes a nuisance parameter
- The challenge is to do it for every possible window on [0,1]

Definition of the joint process

- From (N_A, N_B) we define the couple (N, ε)
- $N = N_A \cup N_B$ is the **joint process** of intensity $\lambda = \lambda_A + \lambda_B$,
- and where $\varepsilon = (\varepsilon_T)_{T \in N}$ is a set of marks:

$$\varepsilon_{T} = \begin{cases} +1, & \text{if } T \in N_{A}, \\ -1, & \text{if } T \in N_{B}. \end{cases}$$



PP & Genomic Features Test Stat & *p*-values Error Rates Simulations Application Conclusion

Conditional distribution of the marks

• Conditionally to N, the distribution of the marks is:

$$\mathbb{P}(\varepsilon_T = +1|N) = \frac{\lambda_A(T)}{\lambda_A(T) + \lambda_B(T)}$$

• We introduce notation:

$$orall t \in [0,1], \; heta(t) = rac{\lambda_{\mathcal{A}}(t) - \lambda_{\mathcal{B}}(t)}{\lambda_{\mathcal{A}}(t) + \lambda_{\mathcal{B}}(t)}.$$

• Conditionally to *N*, the distribution of the marks becomes:

$$\varepsilon_{\mathcal{T}}|N \sim 2\mathcal{B}\left(\frac{\theta(\mathcal{T})+1}{2}\right) - 1,$$

Nuisance parameters and conditional testing

• The distribution of the joint process (N, ε) can be re-parametrized:

 $(N,\varepsilon) \sim \mathbb{P}_{\theta,\lambda}$

- λ and θ are unknown under the null, but are not "really" of interest
- We propose procedures that are **conditional to the observed joint process** *N*.

Reparametrization of the test

Conditional to N, the new hypothesis focuses on ε and becomes $\theta = 0$.

An infinite set of local null hypothesis

- We propose a functional testing framework : $\lambda_A = \lambda_B$ or $\theta = 0$.
- The global strategy corresponds to the global null hypothesis.

An infinite set of local null hypothesis

- We propose a functional testing framework : $\lambda_A = \lambda_B$ or $\theta = 0$.
- The global strategy corresponds to the global null hypothesis.
- We consider **local hypothesis**:

$$H_{0,t}: \left\{ heta(t) = 0
ight\}$$
 against $H_{1,t}: \left\{ heta(t)
eq 0
ight\}.$

• The null hypothesis corresponding to

$$\left\{ \forall t \in J, \, \theta(t) = 0 \right\} \Leftrightarrow \left\{ \mathcal{H}_0 \left\{ J \right\} = \bigcap_{t \in J} \mathcal{H}_{0,t} \right\}$$

An infinite set of local null hypothesis

- We propose a functional testing framework : $\lambda_A = \lambda_B$ or $\theta = 0$.
- The global strategy corresponds to the **global null** hypothesis.
- We consider **local hypothesis**:

$$H_{0,t}: \left\{ heta(t) = 0 \right\}$$
 against $H_{1,t}: \left\{ heta(t)
eq 0
ight\}.$

• The null hypothesis corresponding to

$$\left\{ \forall t \in J, \ \theta(t) = 0 \right\} \Leftrightarrow \left\{ \mathcal{H}_0 \left\{ J \right\} = \bigcap_{t \in J} \mathcal{H}_{0,t} \right\}$$

- The global null hypothesis corresponds to \mathcal{H}_0 {[0,1]}.
- The null function on [0,1] is denoted by θ_0 in the sequel.

Error Rates

Local testing with a cartoon



Definition of scanning windows

- We introduce a resolution parameter η that is fixed
- Using the **continuous testing** framework, we perform a whole *continuum* of tests for each interval of length *η* contained in [0, 1].
- We will distinguish sets of points (denoted by *t*) from sets of windows center (denoted by *x*)

$$\forall x \in \mathcal{X}_{\eta} = [\eta/2, 1 - \eta/2], \ I_{\eta}(x) = [x - \eta/2, x + \eta/2]$$

Our multiple testing procedures are based on single tests on $\mathcal{H}_0 \{ I_\eta(x) \}$ for all possible window centers Is continuous testing computationally tractable ?

- Each observation *T_i* has a span *η* and will be used by the testing procedure on [*T_i η*/2, *T_i* + *η*/2]
- There exists a partition τ of \mathcal{X}_η consisting in M intervals and with inner breaks given by

$$au = \left(igcup_{T\in N} \{T - \eta/2\} \cup \{T + \eta/2\}
ight) igcap \mathcal{X}_{\eta},$$

• The set au is chosen as the center of the observed windows

 $]\tau_{m-1}, \tau_m]$ are homogeneous intervals in terms of *composition* $N \cap I_\eta(x)$



Outline

- Point Process modeling of Genomic features
- 2 Test statistics and associated *p*-value process
- 3 Two error rates in continuous time
- 4 Simulations
- **5** Application



Count or position-based statistics

• The easiest possibility is to use the count and the *p*-value is explicit

$$S_{\eta}(x) = N_A(I_{\eta}(x))$$

Count or position-based statistics

• The easiest possibility is to use the count and the *p*-value is explicit

$$S_{\eta}(x) = N_A(I_{\eta}(x))$$

- Does not account for the spatial repartition of points within windows
- Define a statistics based an estimator of:

$$\|\lambda_A - \lambda_B\|_{I_\eta(x)}^2 = \int_{I_\eta(x)} \left(\lambda_A(s) - \lambda_B(s)\right)^2 ds$$

Count or position-based statistics

• The easiest possibility is to use the count and the *p*-value is explicit

$$S_{\eta}(x) = N_A(I_{\eta}(x))$$

- Does not account for the spatial repartition of points within windows
- Define a statistics based an estimator of:

$$\|\lambda_A - \lambda_B\|^2_{I_\eta(x)} = \int_{I_\eta(x)} \left(\lambda_A(s) - \lambda_B(s)
ight)^2 ds$$

• Kernel-based statistics is (n = N([0, 1])):

$$S_{\eta}(x) = \frac{1}{n(n-1)} \sum_{T \neq T' \in N \cap I_{\eta}(x)} K_{h}(T - T') \varepsilon_{T} \varepsilon_{T'}$$

• Small increase in performance in pratice

Conditional testing and the *p*-value process

• We are interested in the distribution of $S_{\eta}(x)$ under $H_0\{I_{\eta}(x)\}$:

$$orall x \in \mathcal{X}_\eta, \; F_{ heta_0,N}(s;x) = \mathbb{P}_{ heta_0}\Big(S_\eta(x) \ge s |N\Big)$$

• Since the intensities are heterogeneous, we rather consider *p*-values (normalize between [0, 1]):

$$\forall x \in \mathcal{X}_{\eta}, \ p_{\eta}(x) = F_{\theta_0, N}\Big(S_{\eta}(x); x\Big)$$

Since S_η(x) is piece-wise constant, (p_η(x))_x is a piece-wise constant process on [0,1].

The *p*-value process with a cartoon



Conditional Monte-Carlo approximation of the *p*-values

• Sample *B* independent draws of i.i.d. Rademacher sets of marks:

$$\varepsilon^b := (\varepsilon^b_T)_{T \in N}, \text{ for } b = 1, ..., B$$

- Label the observed marks such that ε⁰ := (ε_T)_{T∈N}, (first term of a B + 1-sample of marks)
- The conditional distribution given N of the Rademacher process is:

$$\varepsilon_T^b | N \sim 2\mathcal{B}(1/2) - 1,$$

• We obtain the estimated *p*-value process

$$\widehat{p}_\eta(x) = rac{1}{B+1} \left(1 + \sum_{b=1}^B \mathbb{1}_{\left\{S^b_\eta(x) \geq S^0_\eta(x)
ight\}}
ight)$$

This parametrization guarantees that under $H_0\{I_\eta(x)\}$: $\forall \alpha \in [0, 1], \ \mathbb{P}_{\theta, \lambda}(\widehat{p}_\eta(x) \leq \alpha) \leq \alpha.$

Continuous Testing

Outline

- Point Process modeling of Genomic features
- 2 Test statistics and associated p-value process
- 3 Two error rates in continuous time
- 4 Simulations
- **5** Application



Approximation Sets



PP & Genomic Features Test Stat & *p*-values **Error Rates** Simulations Application Conclusion

Acceptation and Rejection Sets

- *u* is a threshold potentially depending on the data.
- A multiple testing procedure is defined by a rejection set:

$$\mathcal{R}_{\eta}(u) := \left\{ x \in \mathcal{X}_{\eta} : p_{\eta}(x) < u
ight\},$$

• The set of accepted windows is denoted by

$$\mathcal{A}_{\eta}(u) := \{x \in \mathcal{X}_{\eta} : p_{\eta}(x) \ge u\}.$$

PP & Genomic Features Test Stat & *p*-values **Error Rates** Simulations Application Conclusion

Acceptation and Rejection Sets

- *u* is a threshold potentially depending on the data.
- A multiple testing procedure is defined by a rejection set:

$$\mathcal{R}_{\eta}(u) := \left\{ x \in \mathcal{X}_{\eta} : p_{\eta}(x) < u
ight\},$$

• The set of accepted windows is denoted by

$$\mathcal{A}_{\eta}(u) := \{x \in \mathcal{X}_{\eta} : p_{\eta}(x) \ge u\}.$$

• $\mathcal{A}_{\eta}(u)$ is an approximation of

$$J_0^\eta := ig\{ x \in \mathcal{X}_\eta \ : \ orall t \in I_\eta(x), heta(t) = 0 ig\}$$

Challenge

How to evaluate the quality of threshold u ?

Continuous Testing

False Positive Windows and the continuous FWER

• The target is the set of false positive windows

 $J_0^\eta\cap \mathcal{R}_\eta(u)$

• Its size can be measured by its Lebesgue measure:

 $\Lambda(J_0^\eta \cap \mathcal{R}_\eta(u))$

• The Family-Wise Error Rate in continuous time can be defined by

$$\mathsf{FWER}^{\eta}_{\theta,\lambda}(u) = \mathbb{P}_{\theta,\lambda}\Big(\Lambda\big(J^{\eta}_{0} \cap \mathcal{R}_{\eta}(u)\big) > 0\Big).$$

False Positive Windows and the continuous FWER

• The target is the set of false positive windows

 $J_0^\eta\cap \mathcal{R}_\eta(u)$

• Its size can be measured by its Lebesgue measure:

 $\Lambda(J_0^\eta \cap \mathcal{R}_\eta(u))$

• The Family-Wise Error Rate in continuous time can be defined by

$$\mathsf{FWER}^\eta_{\theta,\lambda}(u) = \mathbb{P}_{\theta,\lambda}\Big(\Lambda\big(J^\eta_0 \cap \mathcal{R}_\eta(u)\big) > 0\Big).$$

Aim

Calibrate $u^{\alpha} \in [0,1]$ such that $\mathsf{FWER}^{\eta}_{\theta,\lambda}(u^{\alpha})$ is controlled at level α

Conclusion

False Positive Windows and the continuous FDR

• The target is the set of false positive windows

 $J_0^\eta\cap \mathcal{R}_\eta(u)$

• Its size can be measure by its Lebesgue measure:

 $\Lambda(J_0^\eta \cap \mathcal{R}_\eta(u))$

• The False Discovery Rate in continuous time can be defined by

$$\mathsf{FDR}^\eta_{ heta,\lambda}(v) = \mathbb{E}_{ heta,\lambda}\left(rac{\Lambda\left(J^\eta_0\cap\mathcal{R}_\eta(v)
ight)}{\Lambda\left(\mathcal{R}_\eta(v)
ight)}
ight)$$

False Positive Windows and the continuous FDR

• The target is the set of **false positive windows**

 $J_0^\eta\cap \mathcal{R}_\eta(u)$

• Its size can be measure by its Lebesgue measure:

 $\Lambda\bigl(J_0^\eta\cap \mathcal{R}_\eta(u)\bigr)$

• The False Discovery Rate in continuous time can be defined by

$$\mathsf{FDR}^\eta_{ heta,\lambda}(v) = \mathbb{E}_{ heta,\lambda}\left(rac{\Lambda\left(J^\eta_0\cap\mathcal{R}_\eta(v)
ight)}{\Lambda\left(\mathcal{R}_\eta(v)
ight)}
ight)$$

Aim

Calibrate $v^{\alpha} \in [0,1]$ such that $\mathsf{FDR}^{\eta}_{\theta,\lambda}(v^{\alpha})$ is controlled at level α

PP & Genomic Features Test Stat & p-values Error Rates Simulations Application Conclusion

Controlling the FWER in continuous time - 1

• The starting point is that we have for all *u*,

$$\begin{cases} J_0^{\eta} \cap \mathcal{R}_{\eta}(u) \neq \emptyset \\ \end{cases} = \begin{cases} \exists x \in J_0^{\eta} : p_{\eta}(x) < u \\ \\ = \begin{cases} \inf_{x \in J_0^{\eta}} \{p_{\eta}(x)\} < u \end{cases}. \end{cases}$$

- Control the FWER by learning the distribution of the min. *p*-values under the null.
- Consider the conditional α-quantile of the min. *p*-value process on [0, 1]:

$$U^{lpha}_{J^{\eta}_0} = \min\left\{ u \in [0,1] \ : \ \mathbb{P}_{ heta_0}\left(\inf_{x \in J^{\eta}_0} \left\{ p_{\eta}(x)
ight\} \leq u \ \Big| N
ight)
ight\}.$$

Controlling the FWER in continuous time - 2

- But the set of windows J_0^η is unknown: Choose the worst-case scenario
- We compute the quantile of the min. of the *p*-value process on \mathcal{X}_{η} :

$$U_{\mathcal{X}_{\eta}}^{\alpha} = \min \left\{ u \in [0,1] : \mathbb{P}_{\theta_{0}} \left(\inf_{x \in \mathcal{X}_{\eta}} \left\{ p_{\eta}(x) \right\} \leq u \left| N \right. \right) \right\}.$$

- \bullet This ensures the control of the FWER at level α
- This procedure can be extended to step-down approaches.

FWER-Adjusted *p*-value process: the min-*p* procedure

• In practice we would like to use the *adjusted p*-value process:

$$\forall x \in \mathcal{X}_{\eta}, \ q_{\eta}(x) = F_{\theta_0,N}^{\min} \Big(p_{\eta}(x) \Big)$$

• This requires to compute the distribution of the min-p under the null

$$\forall z \in [0,1], \ F_{\theta_0,N}^{\min}(z) = \mathbb{P}_{\theta_0,N}\left(\inf_{x \in \mathcal{X}_\eta} \left\{p_\eta(x)\right\} \leq z \mid N\right)$$

• In practice we control the FWER using:

$$orall x \in \mathcal{X}_\eta, \;\; \widehat{q}_\eta(x) = \widehat{F}^{\min}_{ heta_0,N} \Big(\widehat{p}_\eta(x) \Big)$$

The min-*p* procedure with a cartoon



The weighted BH procedure with a cartoon



Control of the FDR, a heuristic inspired by Blanchard et al.

• For a given threshold v (eventually depending on everything !),

$$FDR_{\theta,\lambda}^{\eta}(\mathcal{R}(v)) = \mathbb{E}_{\theta,\lambda}\left(\frac{\Lambda(J_0^{\eta} \cap \mathcal{R}(v))}{\Lambda(\mathcal{R}(v))}\right)$$

Control of the FDR, a heuristic inspired by Blanchard et al.

• For a given threshold v (eventually depending on everything !),

$$FDR^{\eta}_{ heta,\lambda}(\mathcal{R}(v)) = \int_{J^{\eta}_{0}} \mathbb{E}_{ heta,\lambda}\left(rac{\mathbf{1}_{p_{\eta}(x) \leq v}}{\Lambda(\mathcal{R}(v))}
ight) d\Lambda(x)$$
 (Fubini Th.)

Control of the FDR, a heuristic inspired by Blanchard et al.

• For a given threshold v (eventually depending on everything !),

$$FDR^{\eta}_{\theta,\lambda}(\mathcal{R}(v)) = \int_{J^{\eta}_{0}} \mathbb{E}_{\theta,\lambda}\left(\frac{\mathbf{1}_{p_{\eta}(x) \leq v}}{\Lambda(\mathcal{R}(v))}\right) d\Lambda(x)$$
 (Fubini Th.)

• If one could find a v such that $\frac{\Lambda(\mathcal{R}(v))}{\Lambda(\mathcal{X}_{\eta})} \geq \frac{v}{\alpha}$, then (as if v was deterministic)

$$egin{aligned} & \textit{FDR}^\eta_{ heta,\lambda}(\mathcal{R}(v)) \leq rac{lpha}{\Lambda(\mathcal{X}_\eta)} \int_{J_0^\eta} rac{\mathbb{P}_{ heta,\lambda}\left(p_\eta(x) \leq v
ight)}{v} d\Lambda(x). \ & \leq rac{lpha \Lambda(J_0^\eta)}{\Lambda(\mathcal{X}_\eta)} \leq lpha. \end{aligned}$$

A weighted step-up BH procedure

- Hence one needs the largest v such that $\frac{\Lambda(\mathcal{R}(v))}{\Lambda(\mathcal{X}_n)} \geq \frac{v}{\alpha}$,
- Let τ be the partition that defines the windows:

$$\Lambda\left(\mathcal{R}_{\eta}(\boldsymbol{v})\right) = \sum_{m=0}^{M-1} (\tau_{m+1} - \tau_m) \mathbb{1}_{\{p_{\eta}(\tau_m) \leq \boldsymbol{v}\}}.$$

- Compute the weights $w_m = (au_{m+1} au_m)/(1-\eta)$
- Denote $\{p_m, 1 \le m \le M\} = \{p_\eta(\tau_m), 0 \le m \le M 1\}$ and order this *p*-values in increasing order $p_{\sigma(1)} \le \cdots \le p_{\sigma(M)}$ for an appropriate permutation σ of $\{1, \ldots, M\}$;
- Consider $\widehat{k} = \max\{k \in \{1, \dots, M\} : p_{\sigma(k)} \le \alpha \sum_{l=1}^{k} w_{\sigma(l)}\}$
- Compute V^{α} as $\alpha \sum_{l=1}^{\hat{k}} w_{\sigma(l)}$.

BH-adjusted *p*-value process

Let us denote by (q_η(x))_{x∈X_η} the adjusted *p*-values of the step-up procedure:

$$q_{\eta}(x) = \min_{k: p_{\sigma(k)} \ge p_{\eta}(x)} \left\{ \frac{p_{\sigma(k)}}{\sum_{l=1}^{k} w_{\sigma(l)}} \right\}.$$

- The decision at level α is simply to reject the nulls corresponding to windows I_η(x) with adjusted p-values lower than α.
- We can check that

$$\mathcal{R}_{\eta}(V^{\alpha}) = \{x \in \mathcal{X}_{\eta} : q_{\eta}(x) \leq \alpha\}.$$

Theorem

For the one-sided case with the p-values based on the $N_A(I_\eta(x))$, the FDR of \mathcal{R}^{wBH} is controlled by α .

BH-adjusted *p*-value process

Let us denote by (q_η(x))_{x∈X_η} the adjusted *p*-values of the step-up procedure:

$$q_{\eta}(x) = \min_{k: p_{\sigma(k)} \ge p_{\eta}(x)} \left\{ \frac{p_{\sigma(k)}}{\sum_{l=1}^{k} w_{\sigma(l)}} \right\}.$$

- The decision at level α is simply to reject the nulls corresponding to windows I_η(x) with adjusted p-values lower than α.
- We can check that

$$\mathcal{R}_{\eta}(V^{\alpha}) = \{x \in \mathcal{X}_{\eta} : q_{\eta}(x) \leq \alpha\}.$$

Theorem

For the one-sided case with the p-values based on the $N_A(I_\eta(x))$, the FDR of \mathcal{R}^{wBH} is controlled by α .

Outline

- Point Process modeling of Genomic features
- 2 Test statistics and associated p-value process
- 3 Two error rates in continuous time
- **4** Simulations
- **5** Application



Simulations FWER (homogeneity)



Error Rates

Simulations FDR (homogeneity)



Outline

- Point Process modeling of Genomic features
- 2 Test statistics and associated *p*-value process
- 3 Two error rates in continuous time
- 4 Simulations
- **5** Application



Conclusion

Density of replication origins along chromosome 16



Density of replication origins along chromosome 16



Outline

- Point Process modeling of Genomic features
- 2 Test statistics and associated p-value process
- 3 Two error rates in continuous time
- 4 Simulations
- **6** Application



Perspectives of our work

- We provide a framework to locally compare Poisson processes intensities
- How procedures control the FWER and the FDR in continuous time
- This framework can be extended to one-sided hypothesis, and one-sample testing (homogeneity)
- Provides a new look on scanning statistics (lack of proper definition for FDR)
- Calibration of the windows size η
- Extension to 2D / 3D scans ?