

Détection de ruptures dans les données de séquençage

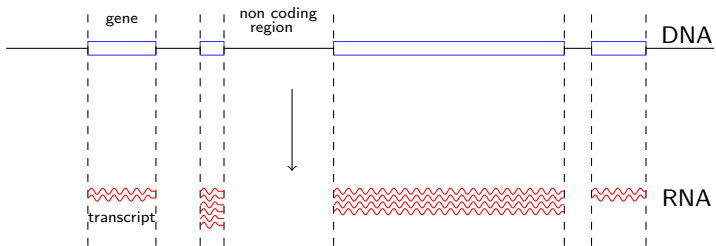
Alice Cleynen

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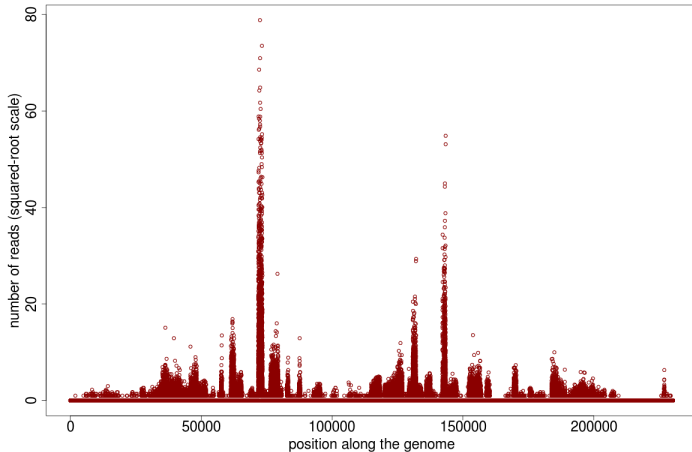
5 Janvier 2017

From DNA to RNA

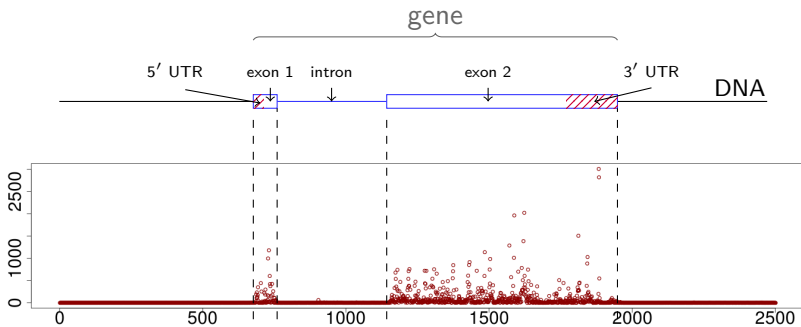


RNA-Seq data

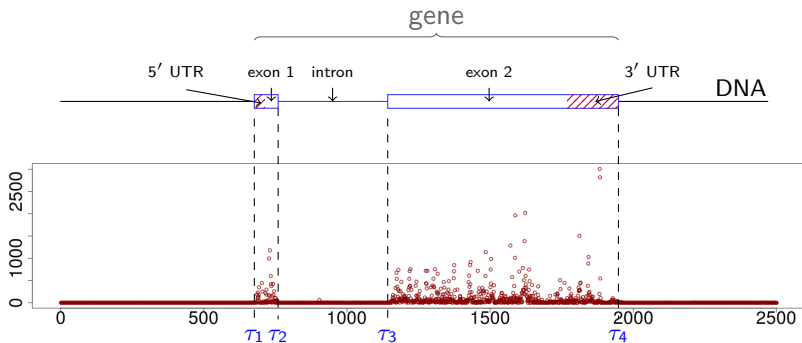
Mapping to the genome



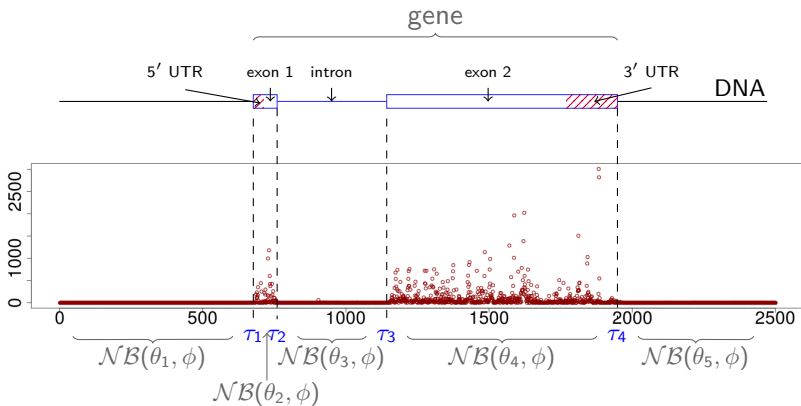
Gene structure



Segmentation Framework

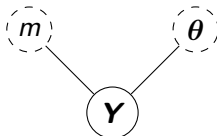


Segmentation Framework



Segmentation Framework

- m a partition of $\{1, \dots, n\}$
 - n = length of profile
 - K = number of segments
 - $m = \{\tau_1, \dots, \tau_{K-1}\}$
 - J a segment of m
- θ = probability parameter of $\mathcal{NB}$
 - $\theta = \{\theta_1, \dots, \theta_K\}$
 - ϕ = overdispersion (known)
- $\forall J \in m, \forall t \in J, Y_t \sim \mathcal{NB}(\theta_J, \phi)$



Optimization framework

Optimal segmentation in K segments ?

- Cost of a segmentation m : $\ell(\mathbf{Y}, m)$
- To be minimized over $\mathcal{M}_K$ of cardinality $|\mathcal{M}_K| = \binom{n-1}{K-1}$
→ exhaustive search intractable

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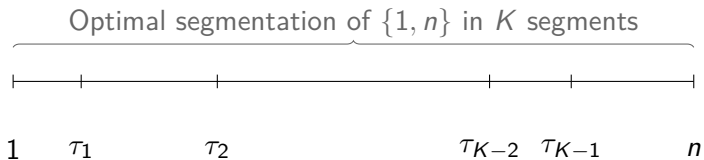
Under a summation assumption:

$$\ell(\mathbf{Y}|m, \theta) = \sum_{r \in m} \ell(Y^r | \theta_r)$$

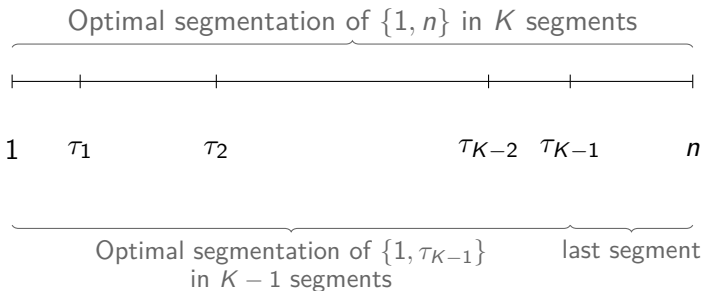
- Dynamic programming algorithm (DPA) provides optimal segmentation in $\mathcal{O}(Kn^2)$

DPA : Bellman (1961); Auger and Lawrence (1989)

How it works



How it works



How it works (with equations)

$C_{k,t}$ = cost of optimal segmentation in k segments up to point t .

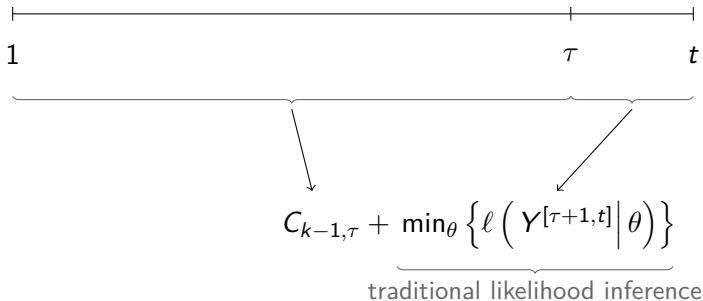


$$\min_{\theta} \left\{ \ell \left(Y^{[\tau+1,t]} \mid \theta \right) \right\}$$

traditional likelihood inference

How it works (with equations)

$C_{k,t}$ = cost of optimal segmentation in k segments up to point t .



(Using summation assumption)

How it works (with equations)

$C_{k,t}$ = cost of optimal segmentation in k segments up to point t .

$$C_{k,t} = \min_{\{k-1 < \tau < t\}} \left\{ C_{k-1,\tau} + \underbrace{\min_{\theta} \left\{ \ell \left(Y^{[\tau+1,t]} \mid \theta \right) \right\}}_{\text{traditional likelihood inference}} \right\}$$

(Using summation assumption)

Choice of K ?

- Standard criteria (AIC, BIC...)
 - theoretically unjustified
 - asymptotic criteria
 - overestimation

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 - Collection of models $\mathcal{S}_m$
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 - Penalized-likelihood estimator
 $\hat{m} = \arg \min_{m \in \mathcal{M}_n} \{ \gamma(\hat{s}_m) + \text{pen}(m) \}$

$$R(s, \hat{s}_{\hat{m}}) \leq C R(s, \hat{s}_{m(s)})$$

Specifications

- true model

$$s(t) = \mathcal{NB}(\theta_t, \phi)$$

- collection of models

$$\mathcal{S}_m = \{s_m \mid \forall J \in m, \forall t \in J, s_m(t) = \mathcal{NB}(\theta_J, \phi)\}$$

- log-likelihood contrast

$$\gamma(s) = - \sum_{t=1}^n \phi \log \theta_t + Y_t \log(1 - \theta_t)$$

- Kullback-Leibler risk

Main Theorem

Let $\mathcal{M}_n$ be a collection of partitions constructed on a partition m_f such that there exist absolute positive constants ρ_{min} , ρ_{max} and Γ satisfying:

- $\forall t, \rho_{min} \leq \theta_t \leq \rho_{max}$ and
- $\forall J \in m_f, |J| \geq \Gamma (\log n)^2$.

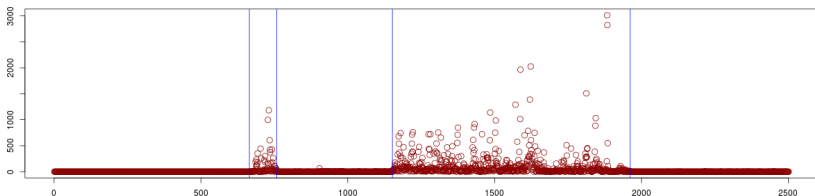
Let $\beta > 1/2\rho_{min}$. If, $\forall m \in \mathcal{M}_n$,

$$\text{pen}(m) \geq \beta |m| \left(1 + 4 \sqrt{1.1 + \log \left(\frac{n}{|m|} \right)} \right)^2 ,$$

$$\mathbf{E} \left[h^2(s, \hat{s}_{\hat{m}}) \right] \leq C \log(n) \inf_{m \in \mathcal{M}_n} \{ \mathbf{E}[K(s, \hat{s}_m)] \} + C(\phi, \Gamma, \rho_{min}, \rho_{max}, \beta, \Sigma).$$

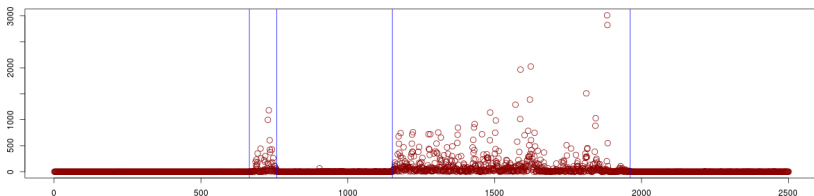
Segmentation procedure

- $K = 5$

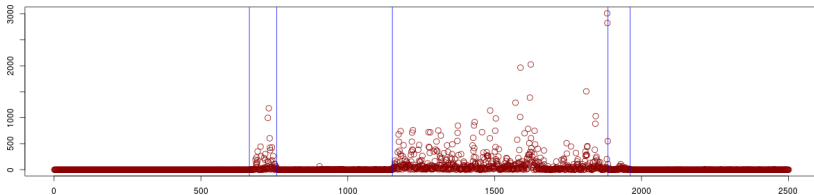


Segmentation procedure

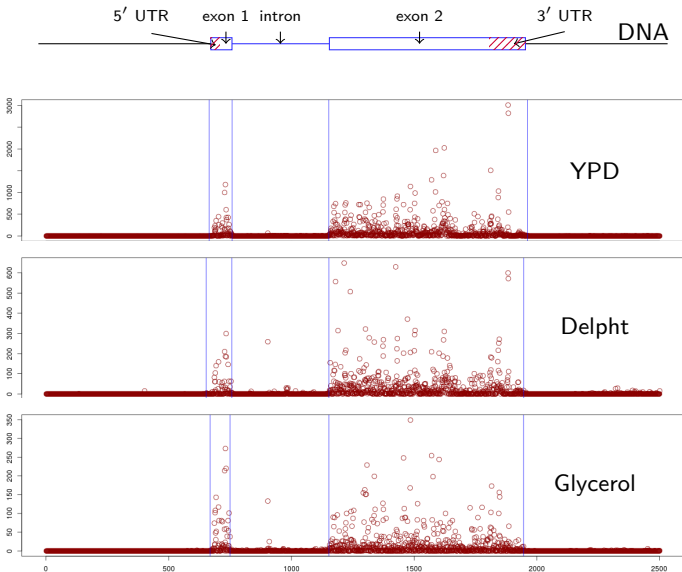
- $K = 5$



- estimated K ($= 6$)

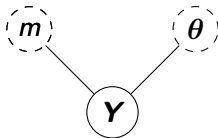


How to compare different conditions ?



Confidence in the segmentation

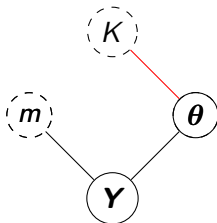
- $\forall J \in m, \forall t \in J, Y_t \sim \mathcal{NB}(\theta_J, \phi)$



Confidence in the segmentation

Rigaill *et.al.* (2012)

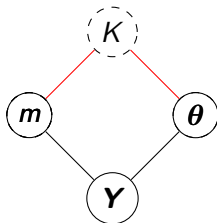
- $\forall i \in \{1, \dots, K\},$
 $\theta_i \sim \text{Beta}(1/2, 1/2)$
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Confidence in the segmentation

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- $m \sim \mathcal{U}(\mathcal{M}_K)$
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Computations

$$\mathbb{P}(Y|K) = \sum_{m \in \mathcal{M}_K} \mathbb{P}(Y, m|K) = \sum_{m \in \mathcal{M}_K} c_K \prod_{J \in m} a_J P(Y_J|J)$$

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Key point: $\forall 1 \leq i < j \leq n+1$,

$$[A]_{i,j} = a_{[i,j]} P(Y_{[i,j]}|[i,j]) = a_{[i,j]} \int \mathbb{P}(Y_{[i,j]}|\theta_{[i,j]}) \mathbb{P}(\theta_{[i,j]}) d\theta_{[i,j]}$$

- $\mathbb{P}(Y|K) = C_K [A^K]_{1,n+1};$

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- $\mathbb{P}(Y|K) = C_K [A^K]_{1,n+1}$;
- $P(\tau_k = t | Y, K) = \frac{[(A)^k]_{1,t} [(A)^{K-k}]_{t,n+1}}{[(A)^K]_{1,n+1}}.$

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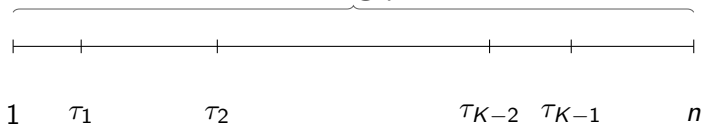
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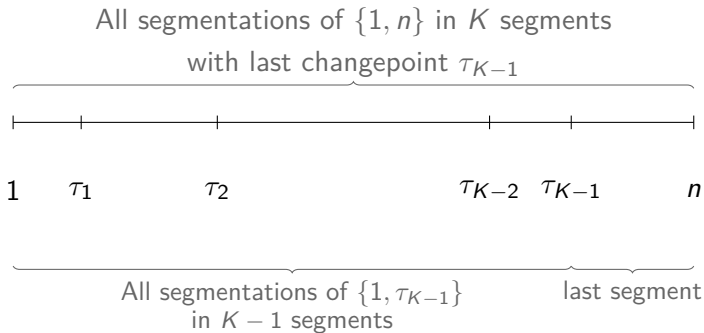
$\mathcal{NB}$ with conjugate prior $\Rightarrow$ exact computations; quadratic time

How it works

All segmentations of $\{1, n\}$ in K segments
with last changepoint τ_{K-1}



How it works



How it works (with equations)

Let $P(k)_{1,t}$ = posterior probability of k segments up to point t .



$$\begin{aligned} & P \left(Y^{[\tau+1,t]} \mid [\tau+1, t] \right) \\ & \underbrace{= \int_{\theta} P \left(Y^{[\tau+1,t]} \mid \theta \right) dp(\theta)} \end{aligned}$$

How it works (with equations)

Let $P(k)_{1,t}$ = posterior probability of k segments up to point t .



The diagram shows a horizontal timeline with three tick marks labeled 1, τ , and t from left to right. A horizontal curly brace spans from 1 to τ , and another horizontal curly brace spans from τ to t . An arrow points from the first brace down to the first term of the equation, and another arrow points from the second brace down to the second term of the equation.

$$P(k-1)_{1,\tau} \times P \left(Y^{[\tau+1,t]} \middle| [\tau+1, t] \right)$$
$$= \int_{\theta} P \left(Y^{[\tau+1,t]} \middle| \theta \right) dp(\theta)$$

(Using factorability assumption)

How it works (with equations)

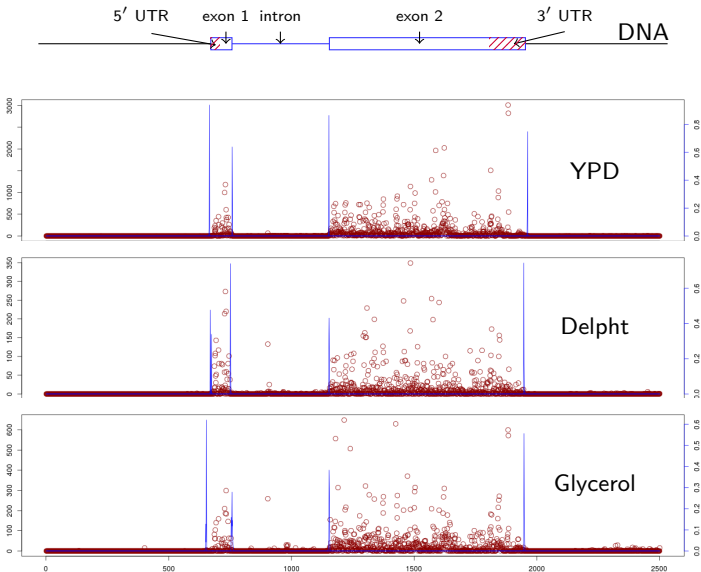
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$$P(k)_{1,t} = \sum_{\{k-1 < \tau < t\}} \left\{ P(k-1)_{1,\tau} \times \underbrace{P\left(Y^{[\tau+1,t]} \mid [\tau+1, t]\right)}_{= \int_{\theta} P\left(Y^{[\tau+1,t]} \mid \theta\right) dp(\theta)} \right\}$$

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How to compare different conditions ?



Model for two profiles

- Series Y^1 and Y^2 with same length n
- Respective (known) number of segments K^1 and K^2 .
- Change-points to compare: $\tau_{k_1}^1$ and $\tau_{k_2}^2$

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$$\rightarrow \Delta = \tau_{k_1}^1 - \tau_{k_2}^2$$

$$P(\Delta = d | Y^1, Y^2, K^1, K^2) = \sum_t P(\tau_{k_1} = t | Y^1, K^1) P(\tau_{k_2} = t - d | Y^2, K^2)$$

Still exact computations, quadratic time

Position of 0 w.r.t. posterior distribution of shift?

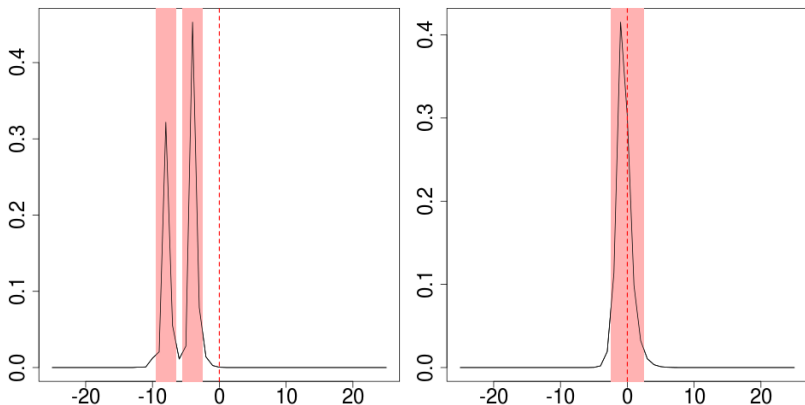


Figure: posterior distribution and 95% credibility intervals of shift

Framework of I profiles

- Series Y^ℓ for $1 \leq \ell \leq I$ $\rightarrow \mathbf{Y}$
- Partitions m^ℓ in K^ℓ segments $\rightarrow \mathbf{m}$ and $\mathbf{K}$
- Parameters θ^ℓ $\rightarrow \boldsymbol{\theta}$
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- $E_0 = \{\tau_{k_1}^1 = \dots = \tau_{k_I}^I\}.$
- $\mathbf{E} = \mathbb{I}\{E_1\} = 1 - \mathbb{I}\{E_0\}.$

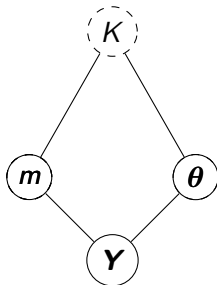
Under the product model,

$$P(\mathbf{Y}|\mathbf{K}) = \prod_{\ell} P(Y^\ell|K^\ell)$$

$$P(E_0|\mathbf{K}) \simeq 10^{-8}$$

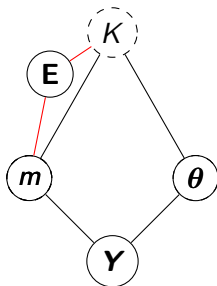
Confidence in the segmentation

- $m \sim \mathcal{U}(\mathcal{M}_K)$
- $\forall i \in \{1, \dots, K\}, \theta_i \sim \text{Beta}(1/2, 1/2)$
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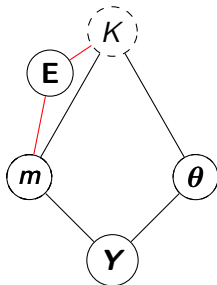
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For instance,

- $\mathbf{m} | \mathbf{K}, E_0 = \mathcal{U}(\mathcal{M}_{n, \mathbf{K}} \cap E_0)$
- $\mathbf{m} | \mathbf{K}, E_1 = \mathcal{U}(\mathcal{M}_{n, \mathbf{K}} \cap E_1)$

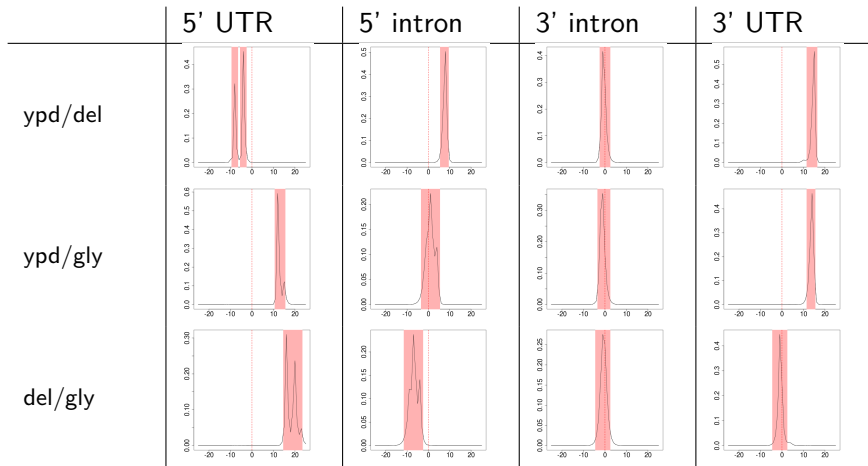
where $\mathcal{M}_{n, \mathbf{K}} = \bigotimes_{\ell} \mathcal{M}_{n, K^{\ell}}$.

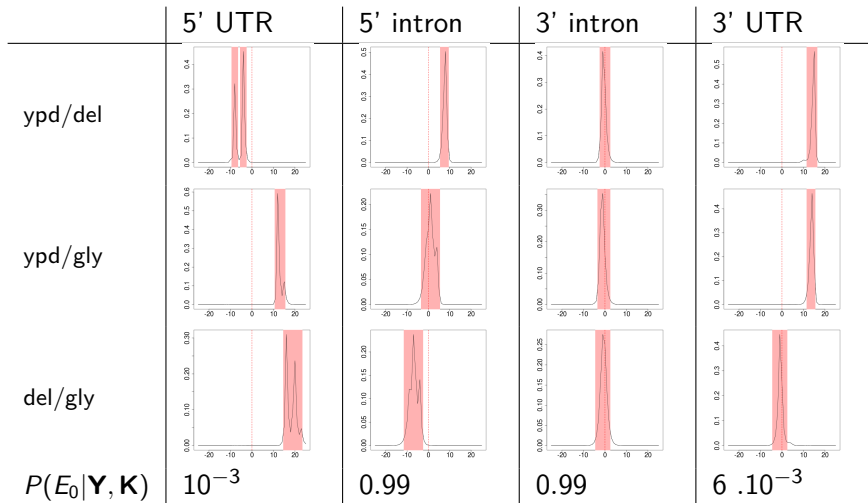


Posterior probability of E_0

$$P(E_0|\mathbf{Y}, \mathbf{K}) = \frac{p_0(\mathbf{K})}{q_0(\mathbf{K})} Q(\mathbf{Y}, E_0|\mathbf{K}) \Big/ \left[\frac{p_0(\mathbf{K})}{q_0(\mathbf{K})} Q(\mathbf{Y}, E_0|\mathbf{K}) + \frac{1-p_0(\mathbf{K})}{1-q_0(\mathbf{K})} Q(\mathbf{Y}, E_1|\mathbf{K}) \right]$$

- $Q(\mathbf{Y}, E_0|\mathbf{K})$ and $Q(\mathbf{Y}, E_1|\mathbf{K})$
 - probabilities induced by product model
 - computed exactly with probability matrices A_ℓ
- $\frac{p_0(\mathbf{K})}{q_0(\mathbf{K})}, \frac{1-p_0(\mathbf{K})}{1-q_0(\mathbf{K})}$
 - weights induced by new model
 - $q_0(\mathbf{K})$ prior under product model; $p_0(\mathbf{K})$ under new model
 - exact computation, and in quadratic time
 - R package EBS





$$P(E_0|\mathbf{K}) = 1/2$$

Illustration: 50 genes with 2 exons

Distribution of the posterior probability of event E_0

a) $p_0(K) = 1/2$

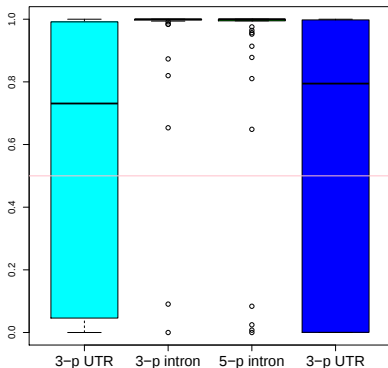
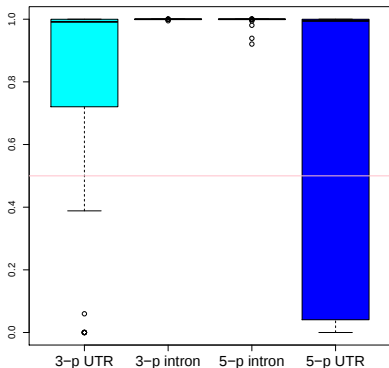


Illustration: 50 genes with 2 exons

Distribution of the posterior probability of event E_0

b) $p_0(K) = 0.9$ for UTRs, $p_0(K) = 0.99$ for introns



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- Stéphane Robin (INRA, AgroParisTech)
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Thank you !