

# Noisy Decompounding With Several Channels Guillaume Garnier



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## Introduction

- All organisms are subject to mutations
- These new traits can change the selective value (fitness) of an individual
  - We call *Fitness* the ability of an individual with a certain genome to survive and reproduce
- How these mutations affect the selective value is a central question in evolutionary biology
- The density of the distribution of these

# Strategy, Tools & Methods

- Strategy: We want to estimate the characteristic function of X : (heuristic) If  $\varphi_X(\xi) \simeq \widehat{\varphi}_X(\xi)$ , then  $f(x) \simeq \widehat{f}(x)$
- ▶ Indeed, the characteristic function  $\varphi_X \rightarrow$  Density f of X:

$$f(x) = \frac{1}{2\pi} \int_{\mathbb{R}} \varphi_X(\xi) e^{-ix\xi} d\xi$$

# **Building the estimator**

▶ We write the characteristic function of the process on a single channel  $Z_t^j$ . For all  $t \in \mathbb{R}_+$ , we have

#### **Numerical Results**

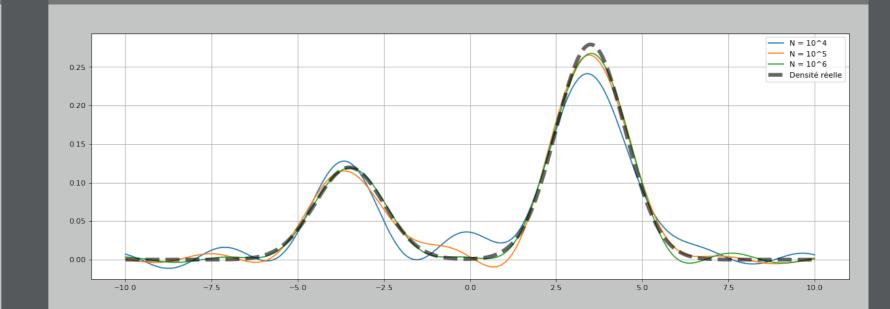


Figure 2:Reconstruction of the  $0.3\mathcal{N}(-3.5,1) + 0.7\mathcal{N}(3.5,1)$  distribution with J channels, corrupted by a Gaussian noise  $\mathcal{J}(0,1)$  with  $J \in 10^4, 10^5, 10^6$ .  $t_1 = 0.1, t_2 = 1, m = 2$ 



## effects is called the **Distribution of Fitness Effect (DFE)**



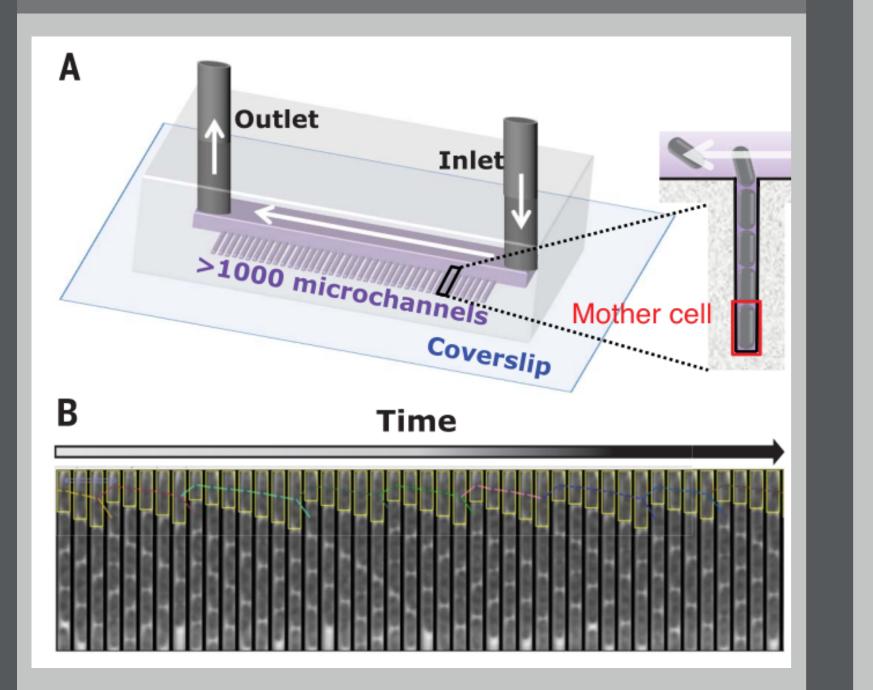


Figure 1:Measurement of the evolution of the fitness of several cell lines over time

Robert et al., 2018

$$\forall u \in \mathbb{R} , \varphi_{Z_t^j}(u) = e^{-\lambda t + \lambda t \varphi_X(u)} \cdot \varphi_{\varepsilon}(u)$$
Consider two different times  $0 < t_1 < t_2$ , then
$$\frac{\varphi_{Z_{t_2}}}{\varphi_{Z_{t_1}}} = e^{-\lambda(t_2 - t_1) + \lambda(t_2 - t_1)\varphi_X(u)}$$

Then

$$\varphi_X(u) = 1 + \frac{1}{t_2 - t_1} (\log \varphi_{Z_{t_2}}(u) - \log \varphi_{Z_{t_1}}(u))$$

It leads us to define

$$\widehat{\varphi}_X^J(u) = 1 + \frac{1}{t_2 - t_1} \left( \log \widehat{\varphi}_{Z_{t_2}}^J(u) - \log \widehat{\varphi}_{Z_{t_1}}^J(u) \right)$$

with

$$\widehat{\varphi}_{Z_{\tau}}^{\,'J}(u) = \frac{1}{J} \sum_{j=1}^{J} i Z_{\tau}^{j} e^{i u Z_{\tau}^{j}}, \ \widehat{\varphi}_{Z_{\tau}}^{\,J}(u) = \frac{1}{J} \sum_{j=1}^{J} e^{i u Z_{\tau}^{j}},$$
$$\log \widehat{\varphi}_{Z_{\tau}}^{\,J}(u) = \int_{0}^{u} \frac{\widehat{\varphi}_{Z_{\tau}}^{\,'J}(z)}{\widehat{\varphi}_{Z_{\tau}}^{\,J}(z)} dz$$

Analytic Analyt

Figure 3:Reconstruction of the Gamma  $\Gamma(3)$  distribution with J channels, corrupted by a Gaussian noise  $\mathcal{J}(0,1)$  with  $J \in 10^4, 10^5, 10^6, 10^7$ .  $t_1 = 0.1, t_2 = 1, m = 3$ 

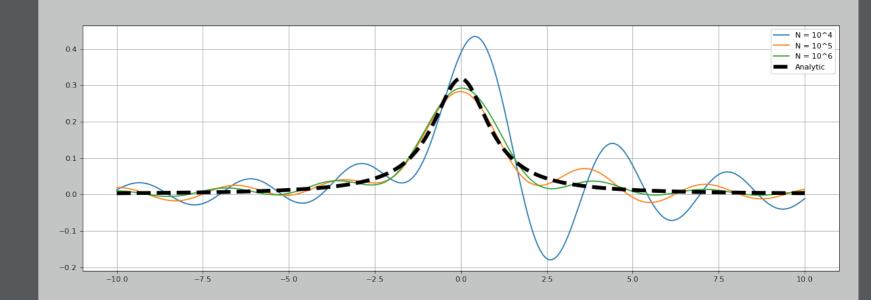


Figure 4:Reconstruction of the Cauchy C(0, 1) distribution with J channels, corrupted by a Gaussian noise  $\mathcal{N}(0, 1)$  with  $J \in 10^4, 10^5, 10^6$ .  $t_1 = 0.1, t_2 = 1, m = 2$ 

**Results: Figure** 

As there is no guarantee that the previous quantities will not explode, a cut-off is added to ensure this.

$$\tilde{\varphi}_X^J(u) = 1 + \frac{1}{t_2 - t_1} \Big\{ \log \widehat{\varphi}_{Z_{t_2}}^J(u) \cdot \mathbb{1}_{|\log \widehat{\varphi}_{Z_{t_2}}^J(u)| \le \ln(J_{t_2})} \Big\}$$

# Model Building

Assumptions :

- 1.  $Z_t^j$  represents the noisy measure of the fitness of the cell in channel  $j \in J$  at time t.
- 2.  $N_t^j$  represents the number of times the cell in channel j has mutated.  $(N_j(t), j \ge 1)$  are *i.i.d* Poisson processes with intensity  $\lambda \in (0, \infty)$ .
- 3.  $X_k^j$  represents the effect of the k-th mutation on the cell in channel j.  $(X_i^j)_{i,j\geq 0}$  are *i.i.d* with density  $f \in L^1(\mathbb{R}) \cap L^2(\mathbb{R})$ .
- 4.  $\varepsilon_t^j$  represents the measurement noise at time t for channel j.  $(\varepsilon_t^j)_{j\geq 0}$  are *i.i.d* and that  $\mathbb{E}(\varepsilon_t^j) = 0.$

 $-\log \widehat{\varphi}_{Z_{t_1}}^J(u) \cdot \mathbf{1}_{|\log \widehat{\varphi}_{Z_{t_1}}^J(u)| \leq \ln(J)} \bigg\}$ 

- We estimate f by Fourier inversion. For any  $m \in (0, \infty)$ ,  $\widehat{f}_{m,J}(x) = \frac{1}{2\pi} \int_{-m}^{m} e^{-iux} \widetilde{\varphi}_{X}^{J}(u) du, x \in \mathbb{R}$ 
  - Here, the choice of m is very important because it defines the frequencies that we keep to apply the inverse Fourier transformation

#### Theorem

For  $t_2 > t_1 > 0$ , we define

$$C_{t_1,t_2}^J = \min\left\{m \ge \mathbf{0} \middle| \mathbf{3}t_2 - t_1 + \sup_{[-m,m]} |\log \varphi_{\varepsilon}(\cdot)| > \ln(J)\right\}.$$

• Theorem : For all reals  $0 < t_1 < t_2$  such that  $t_2 \leq \frac{1}{4} \log(Jt_2)$  $Jt_1 \rightarrow \infty, Jt_2 \rightarrow \infty$  as  $J \rightarrow \infty$  and for any  $m < C_{t_1, t_2}^J$ , the following inequality holds

$$\mathbb{E}\left(||\widehat{f}_{m,J} - f||^{2}\right) \leq ||f_{m} - f||^{2} + \sum_{i=1}^{2} \frac{4e^{4t_{i}}}{J(t_{2} - t_{1})^{2}} \int_{-m}^{m} \frac{du}{|\varphi_{\varepsilon}(u)|^{2}} + \frac{4K_{J,t_{1},t_{2}}}{(t_{2} - t_{1})^{2}} \cdot \left(\frac{\mathbb{E}[X_{i}^{2}]}{Jt_{i}} + \frac{\mathbb{E}[\varepsilon^{2}]}{Jt_{i}^{2}} + 4\frac{m}{(Jt_{i})^{2}}\right).$$

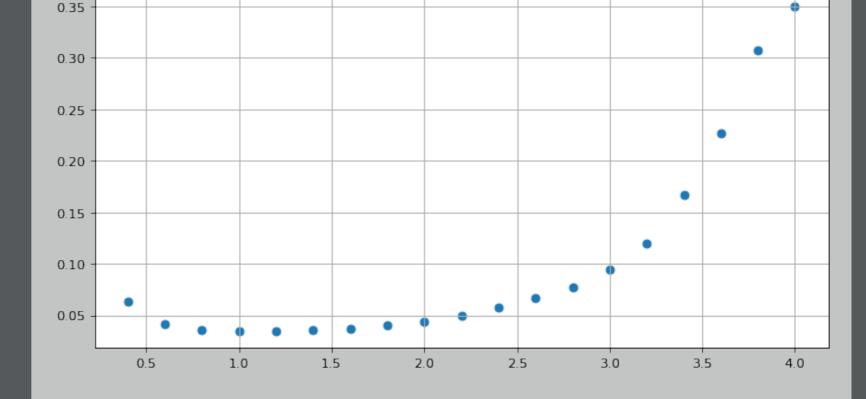


Figure 5: Evolution of the error when  $t_2$  increase

# **Future Work**

- Can we use several times to "aggregate" the estimators and build a new one that is better than all the others?
- Implementation on real dataset
- Our model can be seen under a PDE aspect. Can we reconstruct the DFE from this PDE?

$$\frac{\partial}{\partial t}u(t,x) = -\lambda u(t,x)$$
$$\int_{-\infty}^{\infty} 1 k_{0} {x \choose 1} u(t,x) dx$$

We consider a noisy compound Poisson process:

 $Z_t^j = \left(\sum_{k=1}^{N_t^j} X_k^j\right) + \varepsilon_t^j, \ t \ge 0.$ 

Statement of the problem: Estimate the density of  $X_i$  from observations of  $Z_t$  on each channel  $j \in J$ 

- Combine two classical problems in non-parametric inference.
  - Deconvolution
- Decompounding

where  $K_{J,t_1,t_2}$  depends on  $m, t_2$  and  $\log \varphi_{\varepsilon}(\cdot)$ .

## Discussion

- Our result is asymptotic and ensures that our estimator converges to f when  $J \rightarrow \infty$ .
- In the variance, there is a term  $V \sim \frac{4e^{4t_i}}{J(t_2-t_1)^2}$ .
  - The presence of e<sup>4t<sub>i</sub></sup> means that our estimation is more and more imprecise as we look the sample at a very large time t<sub>2</sub>.
     The presence of (t<sub>2</sub> t<sub>1</sub>) at the numerator means that we cannot take t<sub>1</sub> and t<sub>2</sub> too close to each other.

 $+\lambda \int_{0} \frac{-\kappa_0}{z} \left( \frac{-}{z} \right) u(l, z) dz$ 

#### References

[1] Lydia Robert, Jean Ollion, Jérôme Robert, and al.
Mutation dynamics and fitness effects followed in single cells. *Science*, 359(6381):1283–1286, 2018.

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