Statistical inference for molecules: How many, When and Where?

Frank Werner

joint with

Katharina Proksch and Axel Munk

Statistical Inverse Problems in Biophysics Group Max Planck Institute for Biophysical Chemistry, Göttingen

and

Felix Bernstein Institute for Mathematical Statistics in the Biosciences University of Göttingen







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Outline

1 Introduction to scanning fluorescence microscopy

- 2 Methodology
- **3** Asymptotic theory
- **4** MISCAT Multiscale Inverse SCAnning Test
- 5 Statistical Inference for molecules: Where?
- 6 Conclusion

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Pulsed scanning fluorescence microscopy

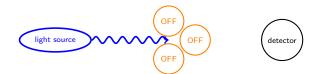
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Pulsed scanning fluorescence microscopy

- \rightarrow For each scanning position s repeat
 - 1 Visible laser pulse focused to *s* (illumination)



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 - 1 Visible laser pulse focused to s (illumination)
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- \rightarrow Until the markers start to bleach (say t times)



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- Recordings are blurred by the so-called **point-spread-function**, which limits the resolution to approximately half the wavelength of the excitation light.
 - However, super-resolution is possible!

Introduction to scanning fluorescence microscopy

Super-Resolution

The Nobel Prize in Chemistry 2014



Photo: Matt Staley/HHMI Eric Betzig Prize share: 1/3



Photo: Wikimedia Commons, CC-BY-SA-3.0

Stefan W. Hell

Prize share: 1/3



Photo: K. Lowder via Wikimedia Commons, CC-BY-SA-3.0

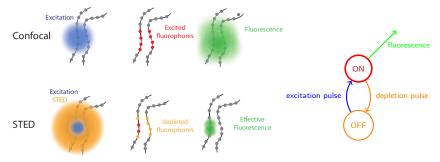
William E. Moerner

Prize share: 1/3

"for the development of super-resolved fluorescence microscopy"

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STimulated Emission Depletion (Hell & Wichmann '94)

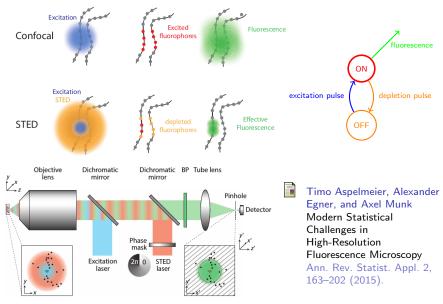


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Statistical inference for molecules

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Methodology

What means Where? mathematically?

 H_1 and H_2 be Hilbert-Spaces of functions, $T : H_1 \rightarrow H_2$ a bounded linear operator and let $f \in H_1$.

Given:

Observations

$$Y_{\mathbf{j}} = Tf(s_{\mathbf{j}}) + \xi_{\mathbf{j}}, \quad \mathbf{j} \in \{1, \dots, n\}^d.$$

• $s_{\mathbf{j}} \in \mathbb{R}^{d}, \mathbf{j} \in \{1, \dots, n\}^{d}$, are the sampling points.

• $\xi_{\mathbf{j}}, \mathbf{j} \in \{1, \dots, n\}^d$, are independent, centered random variables.

Aim:

Identify regions *B* with positive intensity, i.e. $f_{|_B} \neq 0$, at controlled familywise error rate (FWER).

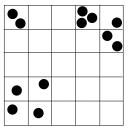
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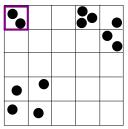
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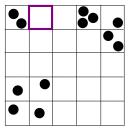
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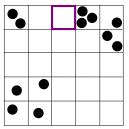
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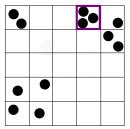
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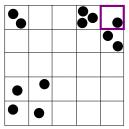
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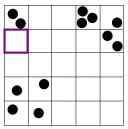
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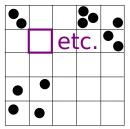
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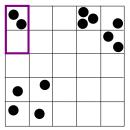
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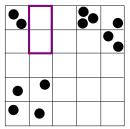
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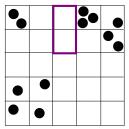
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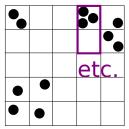
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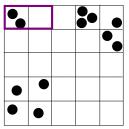
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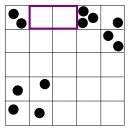
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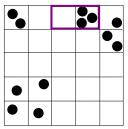
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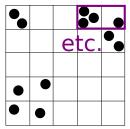
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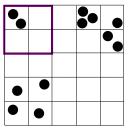
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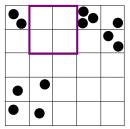
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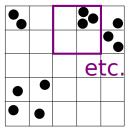
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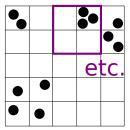
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But: We do not observe f directly, only data related to Tf available. How to get rid of T?

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• For each box *B*, choose a suitable function φ_B with supp $(\varphi_B) \subset B$, $\varphi_B \ge 0$. Then it still holds

$$\langle \varphi_B, f \rangle > 0 \qquad \Rightarrow \qquad f_{|_B} \not\equiv 0$$

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• If $\varphi_B = T^* \Phi_B$, then:

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• The left-hand side can be estimated by $\langle \Phi_B, Y \rangle$ (\rightsquigarrow local test statistic)

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Statistical inference for molecules

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- The left-hand side can be estimated by ⟨Φ_B, Y⟩ (→ local test statistic)
- Consequently, we scan over f by means of $\{\varphi_B\}_B$ by scanning over Tf by means of $\{\Phi_B\}_B$

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Multiscale Scanning in Inverse Problems

• Let $\mathcal{U} = \{\varphi_{i,n}\}_{1 \le i \le N} \subset H_1$ be a dictionary of scanning functions, $\varphi_{i,n} = T^* \Phi_{i,n}$ for all *i* and *n*.

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In this talk ...

... supp $(\Phi_{i,n}) \subseteq [0,1]^d$ for all *i* and *n*, and each index *i* belongs to position $\mathbf{t}_{i,n} = (t_{i,n,1}, \ldots, t_{i,n,d})^T$ and scale $\mathbf{h}_{i,n} = (h_{i,n,1}, \ldots, h_{i,n,d})^T$:

$$\Phi_{i,n}(\mathbf{z}) = \Phi_{\mathbf{h}_{i,n}}\left(\frac{\mathbf{t}_{i,n}-\mathbf{z}}{\mathbf{h}_{i,n}}\right).$$

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$$\Phi_{i,n}(\mathbf{z}) = \Phi_{\mathbf{h}_{i,n}}\left(\frac{\mathbf{t}_{i,n}-\mathbf{z}}{\mathbf{h}_{i,n}}\right).$$

... and we consider the multiscale scan statistic

$$T_n(Y) = \max_i \left[w_{i,n} \left(\frac{\langle \Phi_{i,n}, Y \rangle_{H_2,n}}{\sqrt{\operatorname{Var} \langle \Phi_{i,n}, Y \rangle_{H_2,n}}} - w_{i,n} \right) \right]$$

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Assumptions

• Polynomial growth of the dictionary: For some $\kappa>0$

$$\left|\{\varphi_{i,n}\}_{1\leq i\leq N}\right|=N=O(n^{\kappa}) \quad \text{as} \quad n \to \infty.$$

• Scale restrictions:

$$h_{\min} \gtrsim n^{-1} \log(n)^p$$
 and $h_{\max} = o(\log(n)^{-2}).$

• Moment condition: Suppose that Bennett's Moment condition holds and assume further that

$$\max_{j} \mathbb{E}\xi_{j}^{4} = O(1).$$

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Gaussian Approximation

Gaussian Approximation (Proksch, W., Munk 2018)

If $\Phi_{i,n}/||\Phi_{i,n}||_2$ is uniformly bounded, the moment condition, the polynomial growth of the dictionary and under the scale restrictions, then the ξ_j can be replaced by an i.i.d. field of standard Gaussian rvs $\zeta = (\zeta_j)_{j \in \{1,...,n\}^d}$. More precisely, for

$$M_n(\zeta) = \max_i \left[w_{i,n} \left(\frac{\langle \Phi_{i,n}, \zeta \rangle_{H_2,n}}{\sqrt{\operatorname{Var} \langle \Phi_{i,n}, \zeta \rangle_{H_2,n}}} - w_{i,n} \right) \right]$$

it holds

$$\lim_{n\to\infty}\mathbb{P}_{f=0}(T_n(Y)>q_{1-\alpha}^{M_n(\zeta)})\leq\alpha.$$

Victor Chernozhukov, Denis Chetverikov and Kengo Kato. Gaussian approximation of suprema of empirical processes. *Ann. Statist.*, 2014.

Frank Werner, MPIbpC Göttingen

Limiting distribution (log log-terms are important!)

Under further assumptions on the smoothness γ of $\Phi_{\mathbf{h}_i,n}$, the choice

$$w_{i,n} = \sqrt{2\log(C/\mathbf{h}_{i,n}^{1})} + C_{d} \frac{\log(\sqrt{2\log(C/(\mathbf{h}_{i,n}^{1}))})}{\sqrt{2\log(C/\mathbf{h}_{i,n}^{1})}},$$

with an explicit constant C_d depending on d, γ , and the number of scales leads to a Gumbel extreme value limit:

Limiting distribution (Proksch, W., Munk 2018)

For each suitable C there exists D > 0 such that for any x it holds

$$\lim_{n\to\infty}\mathbb{P}_{f=0}(M_n(\zeta)\leq x)=e^{-De^{-x}}$$

Katharina Proksch, Frank Werner and Axel Munk.

Multiscale Scanning in Inverse Problems.

Ann. Statist., to appear.

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Asymptotic power

Asymptotic power (Proksch, W., Munk 2018)

Under the above assumptions, the power $\mathbb{P}_f(\mathcal{T}_n(Y) > q_{1-lpha}^{M_n(\zeta)})$ is given by

$$\alpha + (1 - \alpha) \Psi \left(\min_{i} \left(\sqrt{2 \log \left(\frac{1}{\mathbf{h}_{i,n}^{1}} \right)} - \frac{\langle \varphi_{i,n}, f \rangle_{H_{1}}}{\sqrt{\mathsf{Var} \left[\langle \Phi_{i,n}, Y \rangle_{H_{2},n} \right]}} \right) \right) + o(1)$$

where $\boldsymbol{\Psi}$ is the tail function of the standard normal distribution.

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• Detection properties depend only on 'local' features $\left< arphi_{i,n}, f \right>_{H_1}$ of f

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- Oracle optimality: the power does not improve by scanning only over the 'correct' ${\bf h}$ (asymptotically)

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Choose dictionary functions φ_{i,n} ∈ R (T^{*}), compute Φ_{i,n}

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by Monte Carlo simulations to obtain the quantile $q_{1-lpha}^{M_n(\zeta)}$

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by Monte Carlo simulations to obtain the quantile $q_{1-\alpha}^{M_n(\zeta)}$

• For each *i* compute $T_i(Y) := \langle \Phi_{i,n}, Y \rangle_{H_2,n}$

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as active

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How to apply the method in practice

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 \rightsquigarrow due to FWER control, all active *i* are 'correct' with prob. $\geq 1 - \alpha$.

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Statistical inference for molecules

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Computational issues

• As long as T and $\{\Phi_{i,n}\}_{i,n}$ are fixed, $q_{1-\alpha}^{M_n(\zeta)}$ can be precomputed.

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 $\mathcal{O}(\#$ scales $\cdot \#$ pixels log (#pixels))

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• In the following examples we apply MISCAT for a dictionary with 28.100.601 elements within less than 20 seconds on a standard laptop (with precomputed $q_{1-\alpha}^{M_n(\zeta)}$).

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Outline

1 Introduction to scanning fluorescence microscopy

- 2 Methodology
- 3 Asymptotic theory

MISCAT - Multiscale Inverse SCAnning Test

5 Statistical Inference for molecules: Where?

6 Conclusion

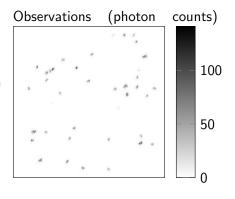
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Statistical Inference for molecules: Where?

Real data example - Setup

- we analyze fluorescent dyes on single DNA Origami
- STED measurements
- each of the two strands can at most hold 12 markers





Data kindly provided by Haisen Ta, Hell Lab, Max Planck Institute for Biophysical Chemistry

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Modeling (recap)

The observations can be modeled by

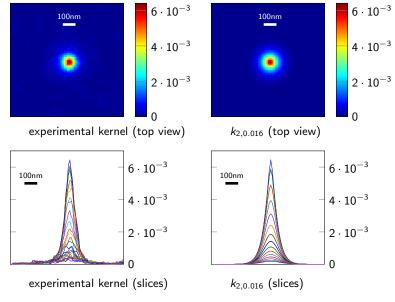
$$Y_{\mathbf{j}} \overset{\text{independent}}{\sim} \operatorname{Bin}\left(t, (f * k)(s_{\mathbf{j}})\right), \qquad \mathbf{j} \in \{1, ..., n\}^{2}$$

- f (s) fluorophore intensity at s
- if c ≤ k * f ≤ C for some constants C, c > 0, all assumptions on the noise are satisfied
- if the Fourier coefficients of k decay polynomially, then desired functions φ_B exist
- we approximate k in the family

$$(\mathcal{F}k_{a,b})(\xi) = (1 + b^2 ||\xi||_2^2)^{-a}, \qquad \xi \in \mathbb{R}^2.$$

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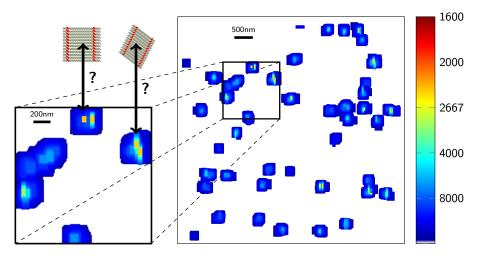
Modeling (cont')



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Statistical Inference for molecules: Where?

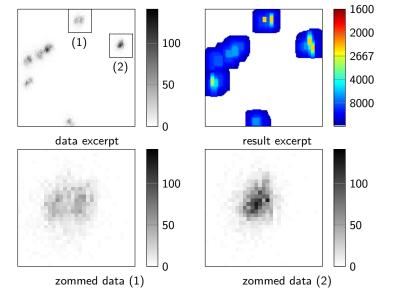
Result



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Statistical Inference for molecules: Where?

Comparison of the result with the data



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Statistical inference for molecules

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Conclusion and outlook

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 - inference on the support w.r.t. a dictionary via testing at controlled family-wise error rate
 - · general limit theory, asymptotic expansion of the power

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Thank you for your attention!

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