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Center for Biomedical Imaging

GLOBALBIOIM
IMAGING AS AN INVERSE PROBLEM MADE EASY

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IMAGING AS AN INVERSE PROBLEM

BIOMEDICAL IMAGING AS AN INVERSE PROBLEM

Biomedically relevant quantity $s \mapsto \mathbf{s}$ ⟶ Process and/or instrument physics $\mathbf{H}$ ⟶ ⊕ ← $\mathbf{n}$ noise, statistical variability ⟶ $\mathbf{y} = \mathbf{H}(\mathbf{s}) + \mathbf{n}$ Measurements / data

- $\mathbf{H}$: (approximate) linearity
  - $\mathbf{H}\{\alpha_1 \mathbf{s}_1 + \alpha_2 \mathbf{s}_2\} = \alpha_1 \mathbf{H}\{\mathbf{s}_1\} + \alpha_2 \mathbf{H}\{\mathbf{s}_2\}$
- $\mathbf{n}$: (approximately) additive statistical variability
- Ill-posed inverse problem: Many $\mathbf{s}$ could lead to the same $\mathbf{y}$

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BIOMEDICAL IMAGING AS AN INVERSE PROBLEM

Biomedically relevant quantity $s \mapsto \mathbf{s}$ ⟶ Process and/or instrument physics $\mathbf{H}$ ⟶ ⊕ ← $\mathbf{n}$ noise, statistical variability ⟶ $\mathbf{y} = \mathbf{H}(\mathbf{s}) + \mathbf{n}$ Measurements / data

- A centuries-old strategy: variational regularization
  - $\mathbf{s}_{\mathrm{rec}} = \arg\min_{\mathbf{s}} \left(\underbrace{\|\mathbf{y} - \mathbf{H}\mathbf{s}\|_2^2}_{\text{data consistency}} + \underbrace{\lambda \mathcal{R}(\mathbf{s})}_{\text{regularization}} \right)$
- Progress:
  - Change $\mathbf{H}$ (e.g., representation $s \mapsto \mathbf{s}$, number of measurements)
  - Change $\mathcal{R}(\cdot)$ (e.g., sparsity, neural networks, statistics)

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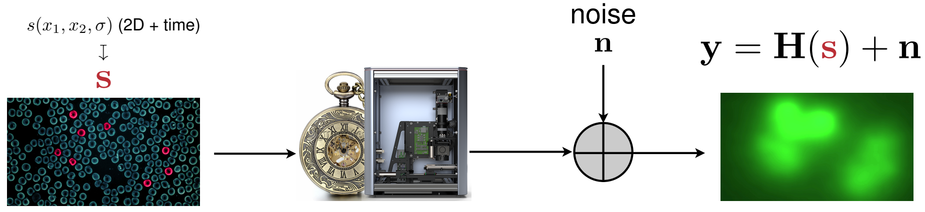
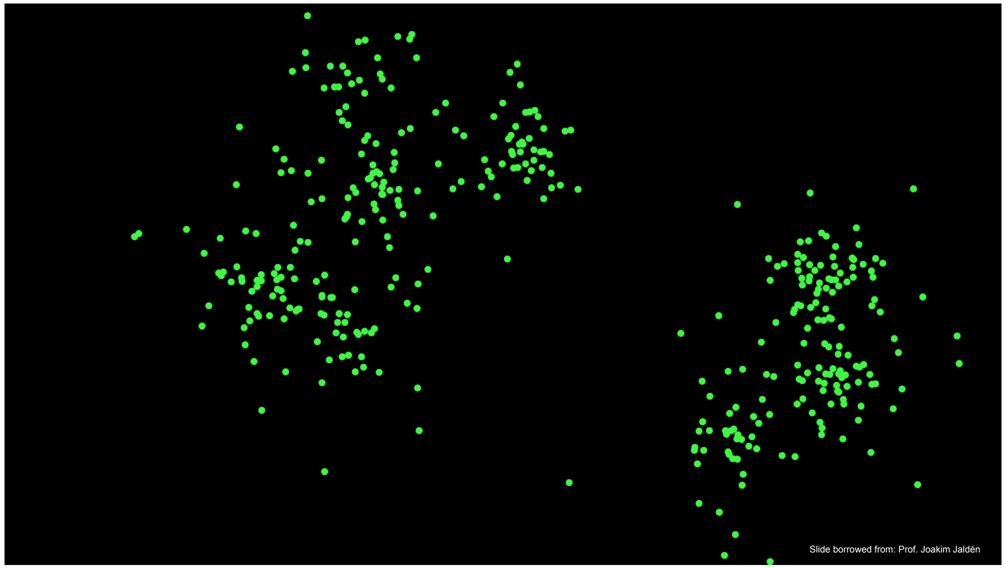
EXAMPLE I: IMMUNOASSAYS

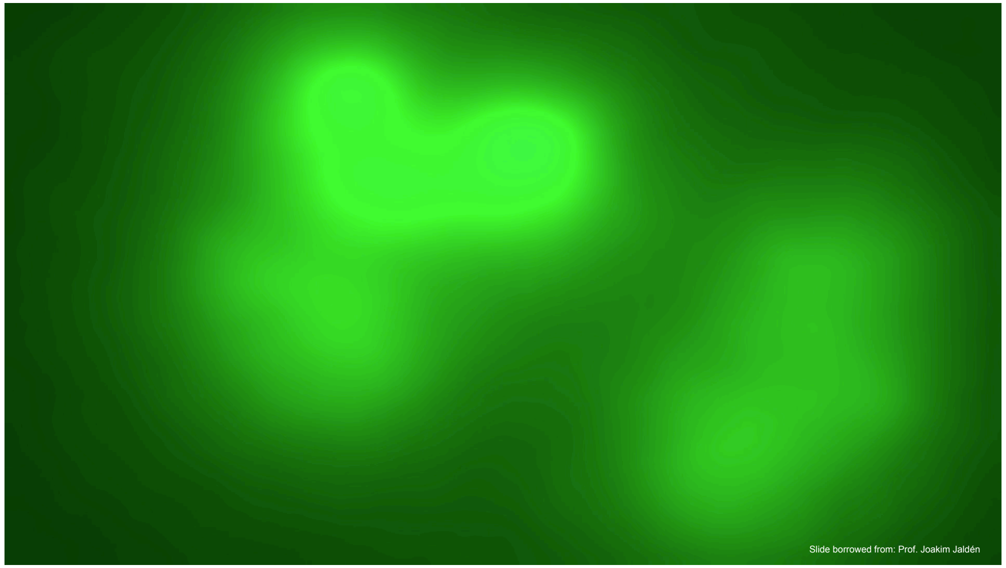
EXAMPLE I

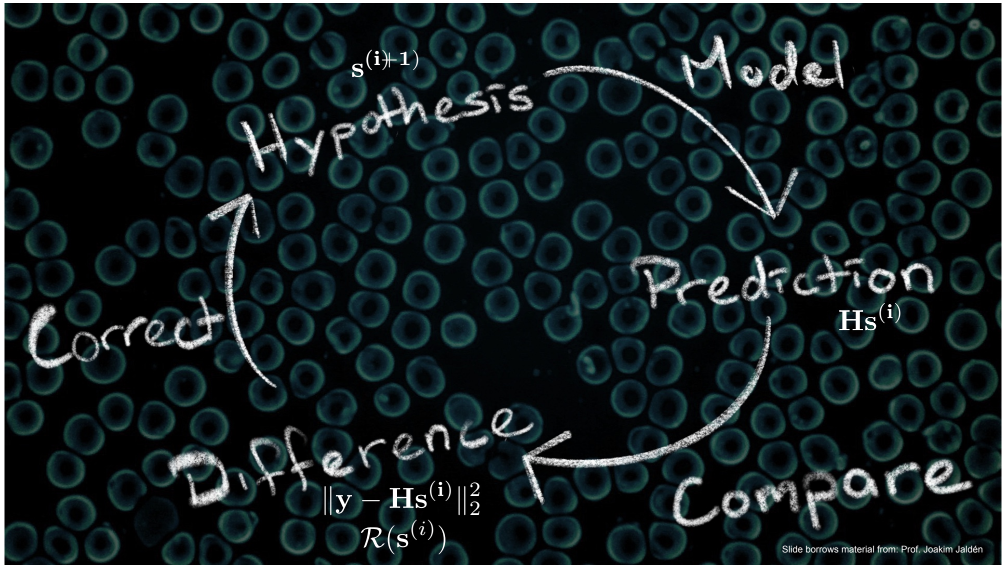
ELISpot and FluoroSpot immunoassays

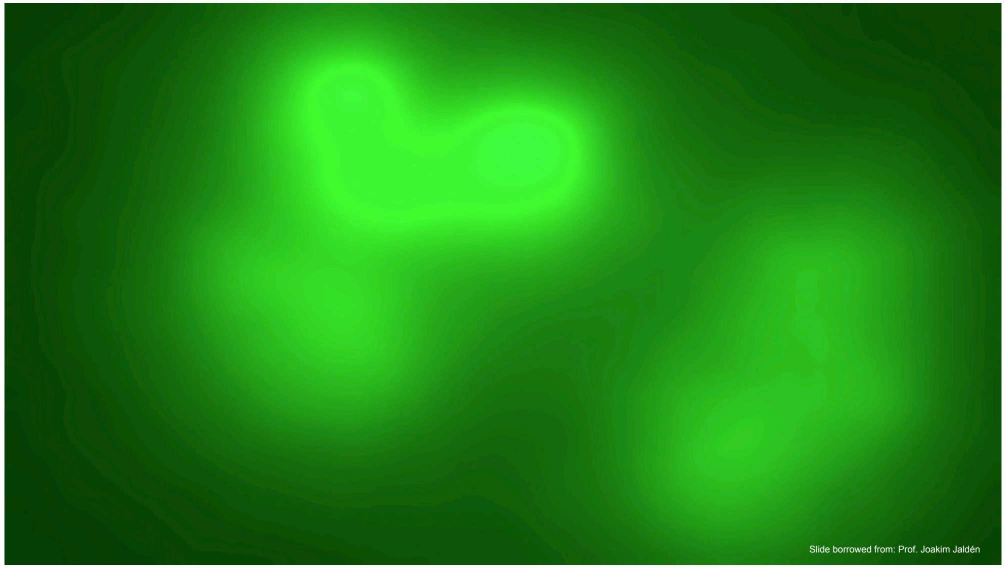


- Vaccine development (very timely)
- 2D $\rightarrow$ 3D









EXAMPLE I

ELISpot and FluoroSpot immunoassays - Physics

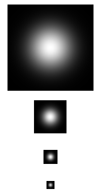
- Reaction-diffusion-adsorption-desorption
  - Inverse diffusion

$$\frac{\partial}{\partial t}c = D\Delta c\,,\ \frac{\partial}{\partial t}\tilde{y} = \kappa_{\mathrm{a}} c\big|_{z=0} - \kappa_{\mathrm{d}}\tilde{y}\,,\ -D\frac{\partial}{\partial z}c\big|_{z=0} = \tilde{s} - \frac{\partial \tilde{y}}{\partial t}\,,$$

$$s(\cdot,\cdot,\sigma) = \frac{\sigma}{D}\int_{\frac{\sigma^2}{2D}}^{T} \tilde{s}(\cdot,\cdot,T-\eta)\,\varphi\left(\frac{\sigma^2}{2D},\eta\right)\mathrm{d}\eta\,.$$

  - Convolutional coding

$$\mathbf{s} = [\mathbf{s}_1, \mathbf{s}_2, \ldots, \mathbf{s}_N]$$

$\mathbf{g}_1$ 

$\vdots$

$\mathbf{g}_N$

$$\mathbf{H}(\mathbf{s}) = \mathbf{g}_1 * \mathbf{s}_1 + \mathbf{g}_2 * \mathbf{s}_2 + \cdots + \mathbf{g}_N * \mathbf{s}_N$$

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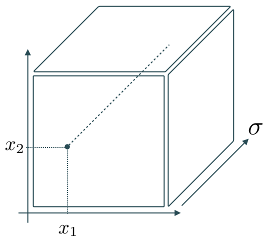
EXAMPLE I

ELISpot and FluoroSpot immunoassays - Mathematics

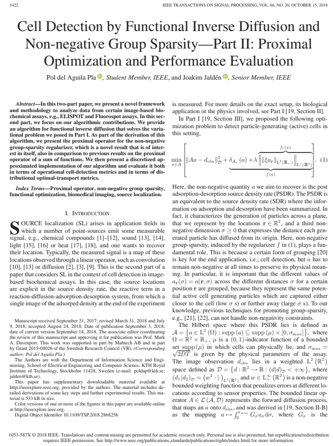
- Group sparsity



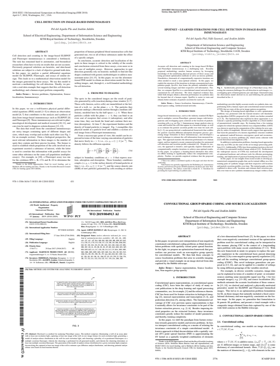
$$\mathcal{R}(\mathbf{s}) = \cdots + \|[\mathbf{s}_1(x_1,x_2), \mathbf{s}_2(x_1,x_2), \ldots, \mathbf{s}_N(x_1,x_2)]\|_2 + \ldots$$
$$= \|\mathbf{s}\|_{2,1}$$


Cell Detection by Functional Inverse Diffusion and Non-negative Group Sparsity—Part I: Modeling and Inverse Problems

Pol del Aguila Pla, Student Member, IEEE, and Joakim Jaldén, Senior Member, IEEE


Cell Detection by Functional Inverse Diffusion and Non-negative Group Sparsity—Part II: Proximal Optimization and Performance Evaluation

Pol del Aguila Pla, Student Member, IEEE, and Joakim Jaldén, Senior Member, IEEE



EXAMPLE II: 3D WIDE-FIELD MICROSCOPY

EXAMPLE II

3D widefield microscopy

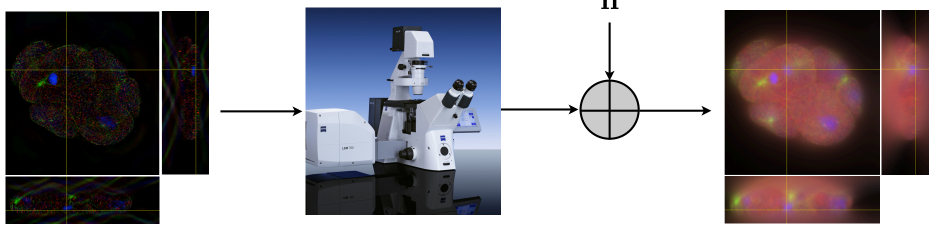
$s(x_1, x_2, x_3, c)$ (3D + 3 fluorophores)

$\updownarrow$

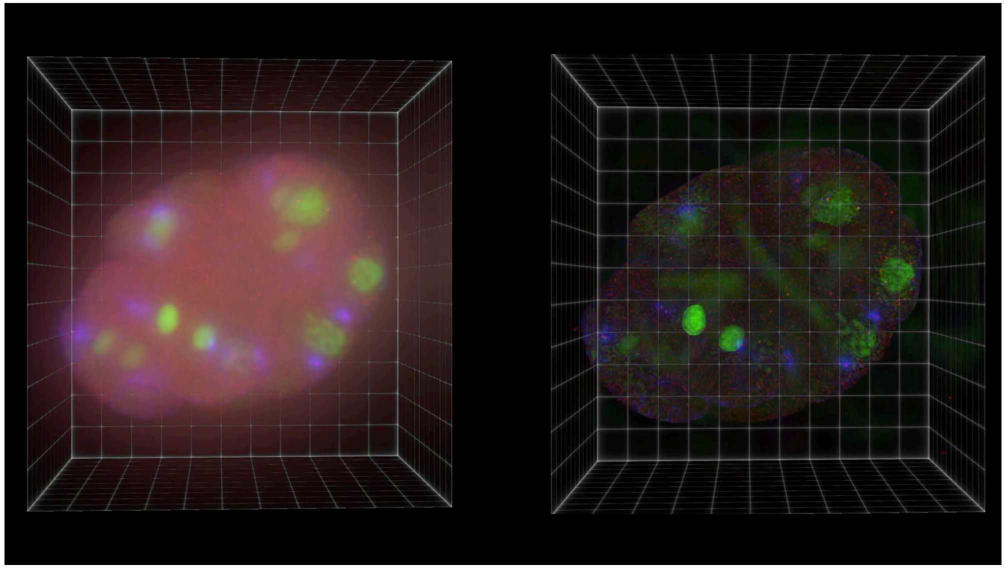
$\mathbf{s}$

noise $\mathbf{n}$

$$\mathbf{y} = \mathbf{H}(\mathbf{s}) + \mathbf{n}$$

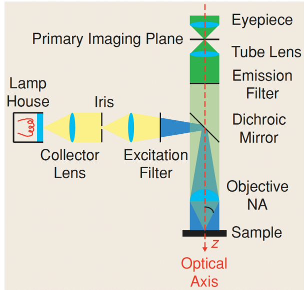


Download the data from: http://bigwww.epfl.ch/deconvolution/bio/ (C. Elegans embryo)



EXAMPLE II

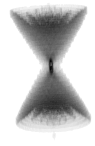
3D widefield microscopy - Physics

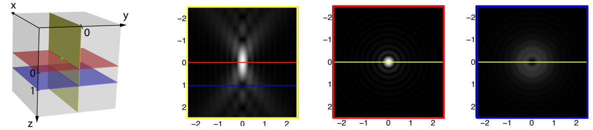


(Vonesch, Aguet, Vonesch, Unser, 2006)

- Diffraction-limited optics
  - Deconvolution / deblurring
  - Convolution: $\mathbf{H}(\mathbf{s}) = \mathbf{h}_{3D} * \mathbf{s}$

$\mathbf{h}_{3D}$



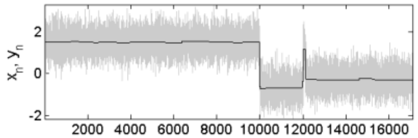


Generate PSFs for microscopes with: bigwww.epfl.ch/algorithms/psfgenerator/

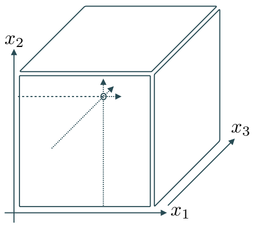
EXAMPLE II

3D widefield microscopy - Mathematics

- Total variation regularization



Wikipedia



- **L**: gradient

$$\mathcal{R}(\mathbf{s}) = \cdots + \|[\Delta_{x_1}\mathbf{s}_1(x_1,x_2,x_3), \Delta_{x_2}\mathbf{s}_2(x_1,x_2,x_3), \Delta_{x_3}\mathbf{s}_N(x_1,x_2,x_3)]\|_2 + \dots$$
$$= \|\mathbf{L}\mathbf{s}\|_{2,1}$$

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A recipe for biomedical imaging:

and even a GUI!

- Learning the physics ($\mathbf{H}$)
  - Linear operators to model most of the usual imaging modalities

    LinOpConv, LinOpXRay, LinOpMatrix, LinOpSDFT, LinOpSum, LinOpSelector
- Learning the maths ($\mathcal{R}$)
  - Linear operators and cost functions for most of the usual regularizers

    LinOpGrad, LinOpHess, CostL1, CostMixNorm21, CostTV, CostKullLeib
- Optimizing and solving the computational aspects

  OptiADMM, OptiChambPock, OptiGradDsct, OptiConjGrad, OptiRichLucy

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A recipe for biomedical imaging:

```
%% Operators
% System matrix / forward operator
% The convolution will be performed in the Fourier domain
H = LinOpConv( fftn( psf ) );
% Regularization operator (to a sparse domain)
% Gradient operator for TV regularization
L = LinOpGrad( var_size );
% Identity operator to impose constraints through regularization
I = LinOpIdentity( var_size );
% Store (noperator outputs
H.memoizeOpts.apply = true; L.memoizeOpts.apply = true;
```

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A recipe for biomedical imaging:

```
%% Cost function
% Least squares data fidelity term
l2_cost = CostL2( [ny, nx, nz], y );
% Operator to extract the 'valid' part of the convolution
% (see zero-padding in the "Load Data" section), i.e.,
% the one to be compared to the data
S = LinOpSelectorPatch( var_size, ...
                        pad_half_size + 1, ...
                        var_size - pad_half_size );
% Compose to create the cost function (inputs will be passed through S and
% then through l2_cost)
least_squares_cost = l2_cost * S;

```

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A recipe for biomedical imaging:

```
%% Regularization
% Mixed norm (group sparisty) to get an isotropic total variation (TV) from
% the gradient
mixed_norm_regularizer = CostMixNorm21( [var_size, 3], 4 );
% Regularization parameter TV
lambda_TV = 2e-6;
% Non-negativity indicator function to preserve physical meaning
nnegativity_regularizer = CostNonNeg( var_size );
```

See more at our ICASSP 2020 tutorial: https://bit.ly/BioImRec-Tutorial

Download the wide-field microscopy data and its reconstruction code (implementation example) at: https://bit.ly/T10-ICASSP2020

Learn more about GlobalBioIm at: https://github.com/Biomedical-Imaging-Group/GlobalBioIm

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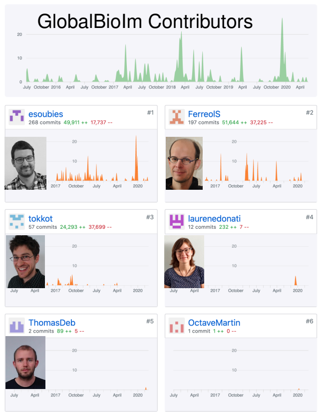
ACKNOWLEDGEMENTS



GlobalBioIm
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THANK YOU FOR YOUR ATTENTION

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