Summary of the ISBI 2013 Grand Challenge on 3D Deconvolution Microscopy

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Thanks to our sponsors!

- ISBI 2013 Grand Challenge Organizers:
  - Stephen Aylward
  - Bram van Ginneken

- Bio Imaging & Signal Processing Technical Committee

- IEEE Signal Processing Society
  - Financial support for awards!

- Funding:
About the organizers

Main organizers:

- Laure Blanc-Féraud
  CNRS
  Sophia Antipolis, France

- Rainer Heintzmann
  Friedrich-Schiller-Universität
  Jena, Germany

- Arne Seitz
  EPFL
  Lausanne, Switzerland

- Michael Unser
  EPFL
  Lausanne, Switzerland

Expert committee members:

- Cédric Vonesch
  EPFL
  Lausanne, Switzerland

- Stamatios Lefkimmiatis
  EPFL
  Lausanne, Switzerland

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  EPFL
  Lausanne, Switzerland

- Stamatios Lefkimmiatis
  EPFL
  Lausanne, Switzerland
Primary goal: promoting cross-fertilization

- **GFP**
  - Biology & Medicine

- **CCD**
  - Optics & Photonics

- **FFT**
  - Signal Processing & Applied Math

- Independent/community-supported developers
- Commercial software providers
- Academic algorithm designers
Overview of the challenge

- **Training**
  - Familiarize participants with data sets, forward model, metrics...
  - Simplified setting

- **Qualification**
  - Determine the performance of proposed methods
  - Larger data, less oracle information

- **Final**
  - ISBI special session
  - Invite participants with best results to present their method
  - Familiarize participants with data sets, forward model, metrics...
  - Simplified setting
## Typology of the phantom data

<table>
<thead>
<tr>
<th>Manifold dimension</th>
<th>Structural class</th>
<th>Mathematical representation</th>
<th>Corresponding biological objects</th>
<th>Stain example</th>
<th>Color channel</th>
<th>λ (nm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Point sources, sub-resolution structures</td>
<td>Dirac distributions, narrow B-splines</td>
<td>Single molecules, vesicles, mitochondria</td>
<td>MitoTracker</td>
<td>Yellow/Orange</td>
<td>600</td>
</tr>
<tr>
<td>1</td>
<td>Curves</td>
<td>Bézier polynomials</td>
<td>Microtubules, actin filaments</td>
<td>GFP</td>
<td>Green</td>
<td>525</td>
</tr>
<tr>
<td>2</td>
<td>Surfaces</td>
<td>Deformable ellipsoidal contours</td>
<td>Cellular or nuclear membranes</td>
<td>DiD</td>
<td>Deep Red</td>
<td>675</td>
</tr>
<tr>
<td>3</td>
<td>Dense volumes</td>
<td>Wide B-splines</td>
<td>Condensing chromatine, DNA</td>
<td>DAPI, Hoechst</td>
<td>Blue</td>
<td>450</td>
</tr>
</tbody>
</table>

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![Diagram](image)
Summary of the forward model

\[ y = Q\left(\mathcal{P}(Tx + b) + \mathcal{N}(0, \sigma^2 I)\right) \]

Notations:
- \( x \): ground-truth fluorophore distribution
- \( T \): block-Toeplitz matrix
- \( b \): background signal (constant vector)
- \( \sigma^2 \): variance of Gaussian noise
- \( Q \): quantization and clipping operator
  \[ Q(x) = \begin{cases} 
  \arg\min_{n \in \mathbb{N}} |x - n| & \text{if } x > 0, \\
  0 & \text{otherwise}
  \end{cases} \]
Simulated micrographs (Maximum-intensity projections)
Simulated micrographs  (Maximum-intensity projections)
Performance Metrics

- **MSE-based Metrics**
  - Increase in signal-to-noise ratio (ISNR)
    
    \[
    \text{ISNR} = 20 \log_{10} \frac{\|y - x\|_2}{\|\hat{x} - x\|_2}
    \]
    
    \(x\): ground-truth
    \(\hat{x}\): affine regressed reconstruction

  - Normalized mean integrated squared error (NMISE)
    
    \[
    \text{NMISE} = \frac{1}{N} \sum_{n=1}^{N} \left[ \frac{T(x - \hat{x})}{[Tx]_n} \right]^2
    \]

- **Structure Similarity Index (SSIM)**
  - Better correlation with human eye perception than SNR
  - Mean-SSIM, Minimum-SSIM (over all slices of the 3D volume)

- **Wavelet sparsity index**
  - Measure of the number of nonzero coefficients in the wavelet domain
Performance Metrics

- Derivative-based metrics
  - Relative total variation error
    \[
    R = \frac{\sum_{n=1}^{N} \| \nabla \hat{x}_n - [\nabla x]_n \|_2}{\sum_{n=1}^{N} \| [\nabla x]_n \|_2}
    \]
  - Relative structure-tensor error
    \[
    R = \frac{\sum_{n=1}^{N} \| [S\hat{x}]_n \| - \| [Sx]_n \|}{\sum_{n=1}^{N} \| [Sx]_n \|}
    \]
  - Relative Hessian-Frobenius error
    \[
    R = \frac{\sum_{n=1}^{N} \| [H\hat{x}]_n \|_F - \| [Hx]_n \|_F}{\sum_{n=1}^{N} \| [Hx]_n \|_F}
    \]

\[
[Sx]_n = G \ast (\nabla x \nabla x^T)
\]

\[
\| [Sx]_n \| = \sum_{k=1}^{3} \sqrt{[\lambda_k]_n}
\]

\[
\| [Hx]_n \|_F = \sqrt{[\lambda_1]_n^2 + [\lambda_2]_n^2 + [\lambda_3]_n^2}
\]
Performance Metrics

- Fourier-based metrics
  - Fourier shell correlation: measures the normalized cross-correlation coefficient between two 3D volumes over corresponding shells in Fourier space
    \[
    \text{FSC}(\omega) = \frac{\sum_{\omega_i \in \omega} \hat{X}(\omega_i) \cdot X^*(\omega_i)}{\sqrt{\sum_{\omega_i \in \omega} |\hat{X}(\omega_i)|^2 \cdot \sum_{\omega_i \in \Omega} |X(\omega_i)|^2}}
    \]
  - Relative energy regain
    \[
    G_R(\omega) = 1 - \frac{\sum_{\omega_i \in \omega} |\hat{X}(\omega_i) - X(\omega_i)|^2}{\sum_{\omega_i \in \omega} |X(\omega_i)|^2}
    \]
  - \( G_R(\omega) = 1 \): spatially frequency domain perfectly reconstructed
  - \( G_R(\omega) = 0 \): no available frequency information
Results (top submissions)
Results (top submissions)
Results (top submissions)

Fourier Shell Correlation

Normalized frequencies

Relative Energy Regain

Normalized frequencies

Normalized frequencies

Normalized frequencies
Results (top submissions)
Results (top submissions)
Results (top submissions)
Summary of the challenge

This year’s awardees (SPS-sponsored prizes):
1. Ferréol Soulez, Lyon University ($500)
2. David Biggs, KB Imaging Solutions ($300)
3. Hiep Luong, Gent University ($200)

Next edition:
- Online submission system to reopen soon
- Take up the challenge & submit your result!
- Best entries will win ISBI 2014 travel grants!
- Visit our website for updates:

bigwww.epfl.ch/deconvolution/challenge