GraspJ - GPU-Run Analysis for STORM and PALM in ImageJ

AFIB - ICFO

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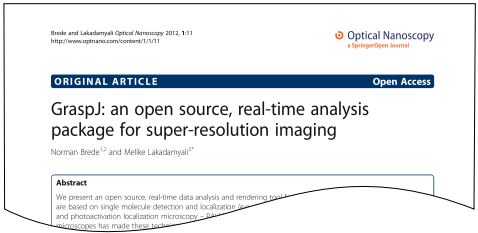
Introducing GraspJ


Brede and Lakadamyali Optical Nanoscopy 2012, 1:1
http://www.opticnano.com/content/1/1/1

Optical Nanoscopy
a SpringerOpen Journal

ORIGINAL ARTICLE Open Access

GraspJ: an open source, real-time analysis package for super-resolution imaging

Norman Brede[1,2] and Melike Lakadamyali[2*]

Abstract

We present an open source, real-time data analysis and rendering tool [illegible] are based on single molecule detection and localization [illegible] and photoactivation localization microscopy [illegible] microscopes has made these techn[illegible]

GraspJ: an open source,real-time analysis package for super-resolution imaging
Norman Brede and Melike Lakadamyali

Was developed by Norman Brede at AFIB as his master thesis. It is thougth:

- As a plugin of ImageJ or FIJI.
- To be able to run in a GPU based system.
- To be able to run in realtime with Labview.
- To be open source.

Dependencies & Modes

ICFO Institut de Ciències Fotòniques

Universitat de Barcelona

Dependencies

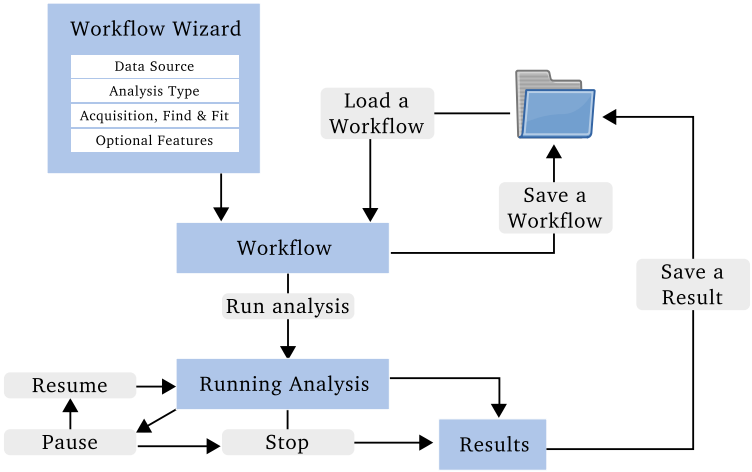
- *Java Virtual Machine (JVM):* needs at least Version 7.
- *OpenCL:* Open Computing Language, allows the possibility to compute in GPUs. Needs compiler and Drivers.

Modes

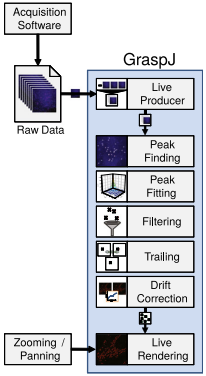
- *Standalone Mode:* Runs indepently from ImageJ/FIJI. Less realtime features. Easier to run.
- *Plugin Mode:* Runs inside ImageJ/FIJI. More realtime features. JVM versions issues.

OpenCL

Common use


Workflow Wizard
Data Source
Analysis Type
Acquisition, Find & Fit
Optional Features
Load a Workflow
Save a Workflow
Workflow
Run analysis
Save a Result
Resume
Running Analysis
Pause
Stop
Results

Workflow details



Norman Brede and Melike Lakadamyali.

- *Live Producer:* creates the packages of frames.
- *Peak Finding:* Peaks are identified based on a threshold.
- *Peak Filtering:* Mean positions are determined
- *Filtering:* Localizations resulting from peak fitting can be filtered.
- *Trailing:* Peaks that appear in close proximity in consecutive frames are trailed together.
- *Drift correction:* Drift is determined by phase correlating consecutive, temporally split high resolution images.
- *Live Rendering:* Final localizations are rendered as Gaussians.

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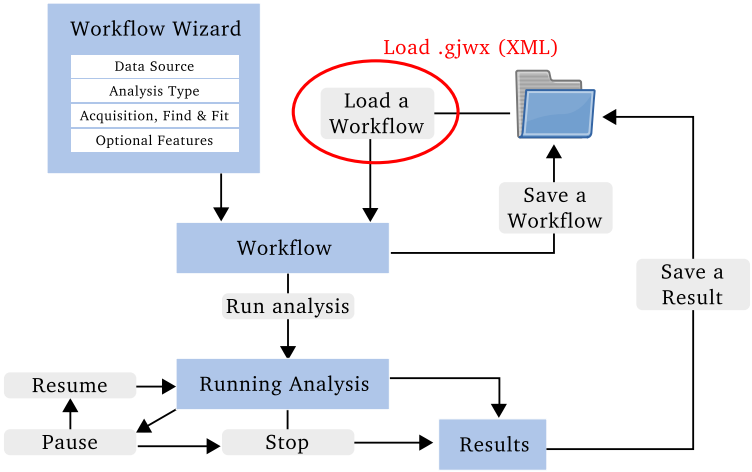
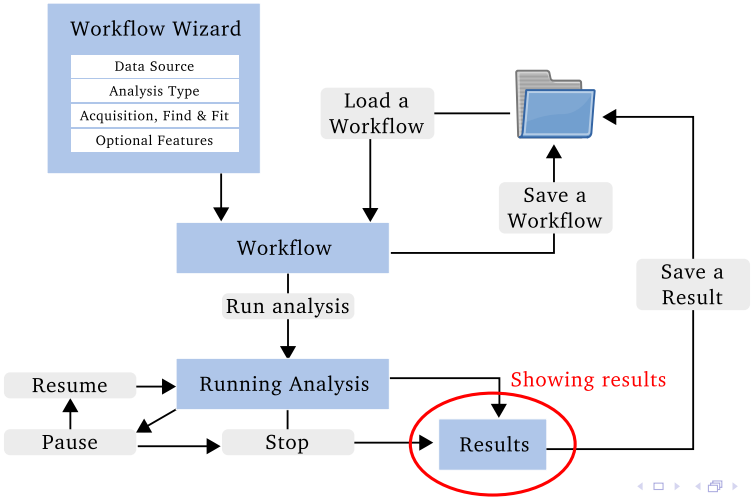
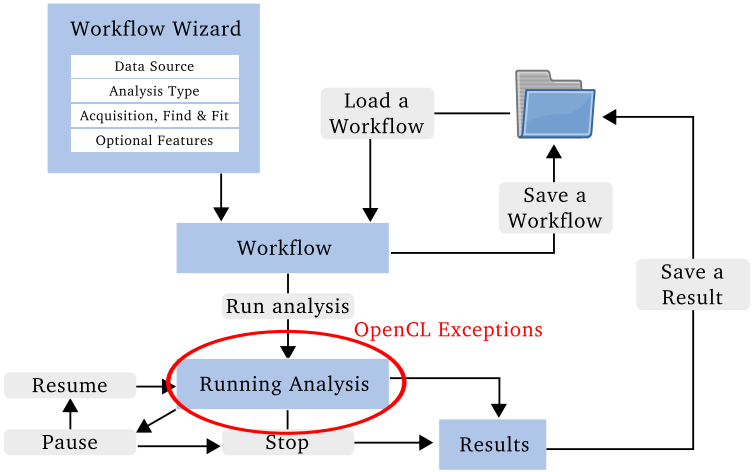
Load Error


Workflow Wizard
Data Source
Analysis Type
Acquisition, Find & Fit
Optional Features
Load .gjwx (XML)
Load a Workflow
Save a Workflow
Workflow
Run analysis
Save a Result
Resume
Running Analysis
Pause
Stop
Results

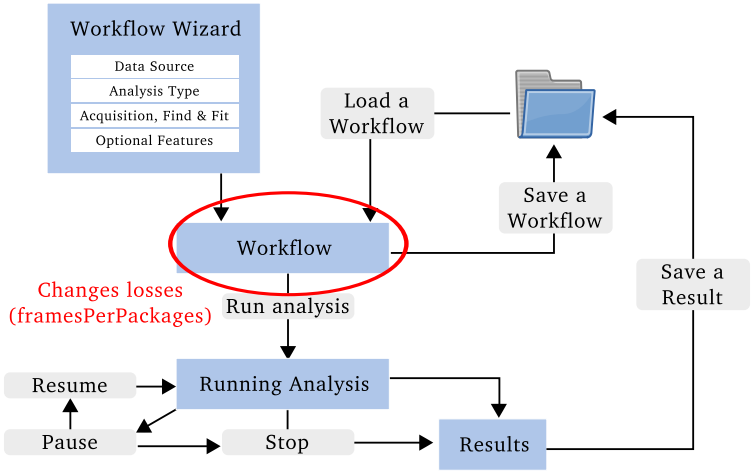
Result Error



OpenCL Exception



Workflow "Mistake"



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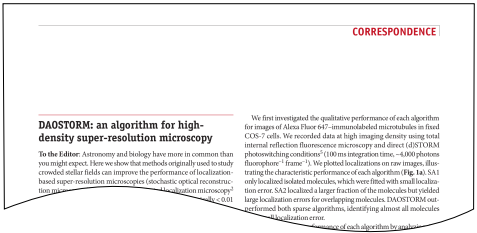
DAOSTORM



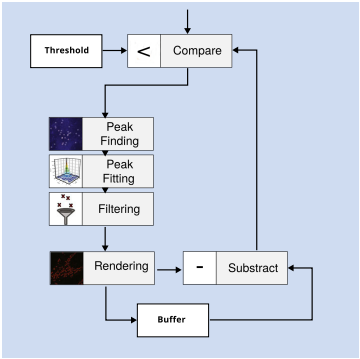
CORRESPONDENCE

DAOSTORM: an algorithm for high-density super-resolution microscopy

To the Editor: Astronomy and biology have more in common than you might expect. Here we show that methods originally used to study crowded stellar fields can improve the performance of localization-based super-resolution microscopies (stochastic optical reconstruction microscopy[1] and photoactivation localization microscopy[2]

We first investigated the qualitative performance of each algorithm for images of Alexa Fluor 647–immunolabeled microtubules in fixed COS-7 cells. We recorded data at high imaging density using total internal reflection fluorescence microscopy and direct ((d)STORM photoswitching conditions[3] (100 ms integration time, ~4,000 photons fluorophore^{-1} frame^{-1}). We plotted localizations on raw images, illustrating the characteristic performance of each algorithm (**Fig. 1a**). SA1 only localized isolated molecules, which were fitted with small localization error. SA2 localized a larger fraction of the molecules but yielded large localization errors for overlapping molecules. DAOSTORM outperformed both sparse algorithms, identifying almost all molecules with localization error.

Was developed forking DAOPHOT II algotrithm from star detections. The basis of the algorithm are:



DAOSTORM: an algorithm for high-density super-resolution microscopy

Seamus J Holden, Stephan Uphoff & Achillefs N Kapanidis