From Images to Knowledge with ImageJ & Friends
virtual conference

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Stephan Preibisch, Stephan Saalfeld, Anna Kreshuk, Pavel Tomancak and Virginie Uhlmann

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Conferences

DECODE for Single Molecule Localization Microscopy

Tutors: Lucas-Raphael Müller (lucasraphael.mueller@gmail.com)
Srini Turaga (turagas@janelia.hhmi.org)
Ulrike Boehm (boehmu@janelia.hhmi.org)
Artur Speiser (arturspeiser@gmail.com)

Session 1:   2020-11-30 13:00 UTC – 2020-11-30 17:00 UTC
Session 2:   2020-12-01 19:00 UTC – 2020-12-01 23:00 UTC

DECODE for Single Molecule Localization Microscopy

Artur Speiser*, Lucas-Raphael Müller*, Ulrike Böhm, Jakob Macke†, Jonas Ries†, and Srini Turaga†

DECODE is a Python and Pytorch based deep learning tool for detecting and localizing fluorophores for the computational reconstruction of super-resolution images from single molecule localization microscopy (SMLM). It has high accuracy for a large range of imaging modalities and conditions, excelling particularly in high density and low signal conditions. On the public SMLM 2016 software benchmark competition, it outperformed all other fitters on 12 out of 12 data-sets when comparing both detection accuracy and localization error, often by a substantial margin. DECODE enables live-cell SMLM data with reduced light exposure in just 3 seconds and to image microtubules at ultra-high labeling density.

DECODE works by training a DEep COntext DEpendent (DECODE) neural network to detect and localize emitters at sub-pixel resolution using synthetic data generated from measured point spread functions. Notably, DECODE also predicts detection and localization uncertainties, which can be used to generate superior super-resolution reconstructions.

DECODE is freely available and packaged for easy use on Google Colab, or for local installation with conda and pip packages [2].

In our tutorial, we will demonstrate how to use DECODE for SMLM on Google Colab, without needing to install any software or download data. The Google Colab notebooks can also be used to analyze one's own data. For interested attendees, we can also demonstrate the easy installation of DECODE on their own CUDA enabled workstations.

Pre-requisites for the tutorial

Only a web browser
Our Google Colab notebooks can be accessed and run with only a web browser (Chrome recommended) with internet access. The tutorial will primarily focus on these notebooks. These notebooks can already be accessed from the github repo [2].

(Optional) Pytorch and DECODE installed on a GPU workstation
However, we will also be happy to help individual users with local installations on their own CUDA compatible GPU workstations (Linux, Windows). For this, we suggest they install DECODE and Pytorch as described in our github repo [2].

Presenters and availability

Lucas-Raphael Müller (Germany, CET / UTC+1)
Srini Turaga (USA, Eastern Time) available to teach at all times of the day
Ulrike Boehm (USA, Eastern Time) available to teach at all times of the day
Artur Speiser (Germany, CET / UTC+1)

References
[1] Artur Speiser*, Lucas-Raphael Müller*, Ulf Matti, Christopher J. Obara, Wesley R. Legant, Anna Kreshuk, Jakob H. Macke†, Jonas Ries†, and Srinivas C. Turaga†, **Deep learning enables fast and dense single-molecule localization with high accuracy** (submitted).
[2] https://github.com/TuragaLab/DECODE