

I2K 2024 Conference - From Images to Knowledge

Thursday, 24 October 2024

† Poster Session #2 (14:00 - 16:30)

[id] title	presenter	board
[81] Unsupervised Denoising for Signal-Dependent and Row-Correlated Imaging Noise	SALMON, Benjamin	01
[111] Fractal: An open-source framework for reproducible bioimage analysis at scale using OME-Zarrs	LÜTHI, Joel	2
[116] METEOR: Enabling precise 3D correlative cryo-FIB milling for high throughput cryo-ET lamella production	HOMBERG, Kevin	3
[117] OptiCell3D: inference of the mechanical properties of cells from 3D microscopy images	YAMAUCHI, Kevin	4
[118] Client-Server Approach for Bioimage Analysis in the Deep Learning Era: Enhancing Extensibility and Accessibility	SUGAWARA, Ko	5
[119] Create web-based OME-Zarr galleries with Zarrcade	ROKICKI, Konrad	6
[120] Potentials and limitations in the application of Convolutional Neural Networks for mosquito species identification using wing images	NOLTE, Kristopher	7
[122] Pycellin: a graph-based framework to analyze cell lineages	XÉNARD, Laura	9
[123] MMV_H4Cells - a cell evaluation napari plugin	KOWITZ, Lennart	10
[124] FISBe: A real-world benchmark dataset for instance segmentation of long-range thin filamentous structures	MAIS, Lisa	11
[125] Integrating Shape and Function: Identifying growth drivers and their morphological expression in Gastric Tumor Organoids.	HASSAN, Maleeha	12
[126] How To Train Your Image Analyst: Perspectives from Upskilled Biologists	TRAVER, Maria	13
[127] Quantifying bacterial dynamics over a wide range of species with TrackMate-Omnipose	ANSELMET, Marie	14
[128] Digital pathology and artificial intelligence-based approaches to characterize the complex interactions between cellular components of the tumor microenvironment and their spatial distribution	VIATORE, Marika	15
[129] **multiview-stitcher: a modular and extensible toolbox for scalable image registration and fusion in python	ALBERT, Marvin	16
[130] DaCapo: a modular deep learning framework for scalable 3D image segmentation	ZOUINKHI, Marwan	17
[131] Mastodon – a Large-Scale Tracking and Track-Editing Framework for Large, Multi-View Images and Extensions for 3D Visualization and Lineage Comparison	ARZT, Matthias HAHMANN, Stefan	18
[132] An AI-based pipeline to extract predictive mechano-features in Triple Negative Breast Cancers	MARTINI, Emanuele TONANI, Mattia	19
[133] Quantifying the Heterogeneity of DNA Interactions in AFM Images	GAMILL, Max	20
[134] A QuPath extension for Data-driven Microscopy	NELSON, Michael S.	21

[135] micronuclAI: Automated quantification of micronuclei for assessment of chromosomal instability	IBARRA-ARELLANO, Miguel A.	22
[136] 3D quantitative image analysis of cell fate acquisition during lateral inhibition	PHAN, Minh-Son	23
[137] Building Foundations for AI-Driven Bioimage Analysis: Infrastructure and Annotation Platforms	MECHTEL, Nils	24
[138] A nextflow-based end to end workflow for decoding of in situ sequencing data	VAKILI, Nima	25
[139] PIXIMI: A web-based deep learning tool for biomedical image analysis	GOGOBERIDZE, Nodar	26
[140] Integrative Open-Source Analysis Pipeline of RNA In Situ Hybridization Immunofluorescence Images	MUHAMMAD RENOLLET, Nur	27
[141] Robust segmentation and measurement of single bacterial cells within a chain	REYES-MATTE, Octavio	28
[142] Robust detection and quantification of beating cells in microscopic 2D videos of cardiomyocytes	NOSOV, Oleksiy	29
[143] Foreground-aware virtual staining for 3D nuclear morphometry	LLANOS, Paula	30
[173] Taggathon on BIII.eu: contributing to a unique database of image analysis tools and workflows	PAUL-GILLOTEAUX, Perrine	31
[144] TOMOMAN•PY - A Python-Based Suite for Handling Large cryo-ET Datasets	ERDMANN, Philipp S.	32
[145] Single protein pinpointing in light microscopy using DNA-PAINT	KOWALEWSKI, Rafal	33
[146] Enabling Access to Bioimage Analysis Tools on University Cluster	KARMAKAR, Ranit	34
[147] AI-powered analysis of histopathological tissues to study of the tumor immune microenvironment	POLIDORI, Rebecca	35
[148] The Human Protein Atlas in OMERO: an accessible dataset for teaching purposes	DORNIER, Rémy	36
[149] Self-supervised learning for sample localization on cryoem grids for tomogram acquisition	M. SÁNCHEZ L., Ricardo	37
[150] Probabilistic Framework for Calibrated Cell Tracking	PAUL, Richard D.	38
[151] BIOP-desktop , a versioned computer for image analysis in life sciences	GUIET, Romain	39
[152] Continuous, interpretable, and transformation-invariant Morphometric for dynamic shape quantification	ROUATBI, Roua	40
[153] Enhancing Synaptic-Resolution Connectomics with an Open-Source AI Ecosystem	MOHINTA, Samia	41
[154] Combining Incremental Deep Learning, Eye Tracking and Virtual Reality for Human-in-the-Loop Cell Tracking: a Progress Report	PANTZE, Samuel	42
[155] Too good to be true: the perils of applying image quality metrics in fluorescence microscopy	CULLEY, Siân	43
[156] Virtual Embryo Zoo: A Web-Based Tool for Embryogenesis Cell Tracking Visualization	HUIJBEN, Teun	44
[157] InstanSeg: a fast, flexible and user-friendly cell segmentation method for brightfield and multichannel images	GOLDSBOROUGH, Thibaut	45
[158] Joined segmentation of nuclei and cells	PÉCOT, Thierry	46
[159] An AI approach for timing analysis of cytokinesis from microscopy data	BONTE, Thomas	47

[160] Investigating DNA damage with Atomic Force Microscopy and TopoStats	CATLEY, Thomas	48
[161] RNA point cloud segmentation for image-based spatial transcriptomics	DEFARD, Thomas	49
[162] Simplified processing for image-based cell profiling with pollen	OUELLETTE, Tom	50
[163] Contextual Segmentation of Large, High-dimensional Medical Images	PORTER, Victoria	51
[164] Leonardo: a toolset to remove sample-induced aberrations in light sheet microscopy images	LIU, Yu	52
[165] Two ways of quantifying inflammation in histopathology slices of the mouse pancreas	THEISS, Maria	53
[168] napari-phasors: Integrating Hyperspectral and FLIM Data Analysis into an Open-Source Bioimaging Framework	LEOMIL ZOCCOLER, Marcelo	54
[113] Enhanced Bacterial Cytological Profiling with super resolution techniques and fluorescent D amino acids	RATCLIFF, Joseph	55
[172] FLUTE: A Python GUI for interactive phasor analysis of FLIM data	STRINGARI, Chiara	56
[192] Data-driven Unsupervised and Sparsely-Supervised Segmentation	KORDASIABI, Sheida	57