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📅 **23-25 October 2024**

📍 **Human Technopole**
Milan

I2K
From Images to
Knowledge 2024

HUMAN TECHNOPOLE

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conference

(time in CET, UTC +1)

Time	Session	Speaker
9:00 - 9:30	**Welcome Coffe & Registration**	
9:30 - 9:45	**OPENING REMARKS**	***Florian Jug*** *(HT)*
9:45 - 10:00	Fiji Progress and Priorities 2024	***Curtis Rueden*** *(University of Wisconsin-Madison)* *Chair: Florian Jug*
10:00 - 10:30	Towards live-cell AI-enhanced Super-Resolution Microscopy	***Ricardo Henriques*** *(IGC - UCL)* *Chair: Florian Jug*
10:30 - 10:45	Shuffle time	
10:45 - 11:45	**WORKSHOP SESSION #1**	
11:45 - 12:00	Shuffle time	
12:00 - 12:30	**Flash Talks**	*Chair: Aubrey Weigel*
	Automated mapping of 3D smFISH gene expression data to electron microscopy	***Elena Bulgakova*** *(EMBL)*
	Machine learning based Evaluation and Enhancement (EVEN) for optical microscopy	***Elena Corbetta*** *(Friedrich-Schiller-Universität Jena)*
	Exploring gene function and morphology using JUMP Cell Painting Consortium data	***Alán Fernando Muñoz González*** *(Broad Institute of Harvard and MIT)*
	A Bayesian solution to count the number of molecules within a diffraction limited spot	***Alexander Hillsley*** *(Howard Hughes Medical Institute)*
	pyCyto: A Pythonic Cytotoxicity Analysis Pipeline	***Jacky Ka Long Ko*** *(University of Oxford)*
	Fractal: An open-source framework for reproducible bioimage analysis at scale using OME-Zarrs	***Joel Lüthi*** *(University of Zurich)*

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Talk	Speaker
Enhancing Synaptic-Resolution Connectomics with an Open-Source AI	**Samia Mohinta** *(University of Cambridge)*
Ecosystem Structure preserving differentiable metric for morphogenetic dynamics	**Roua Rouatbi** *(TU Dresden)*
An Image Analysis Pipeline for Quantifying the Spatial Distribution of Fluorescently Labeled Cell Markers in Stroma-Rich Tumors	**Antoine Ruzette** *(Harvard Medical School)*
Unsupervised Denoising for Signal-Dependent and Row-Correlated Imaging Noise	**Benjamin Salmon** *(University of Birmingham)*
How To Train Your Image Analyst: Perspectives from Upskilled Biologists	**Maria Traver** *(NIH / NIAID)*
TopoStats: taking AFM analysis to new heights	**Laura Wiggins** *(University of Sheffield)*

12:30 - 13:00	Walking time to Triulza Academy
13:00 - 14:00	**LUNCH** @ Triulza Academy
14:00 - 16:30	**POSTER SESSION #1** @ Triulza Academy
16:30 - 17:00	Walking time to HT
17:00 - 18:00	**WORKSHOP SESSION #2**

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9:00 - 9:30	Reconstructing the neuronal wiring diagram of a fruit fly brain	***Sven Dorkenwald*** *(Shanahan Foundation Fellow, Allen Institute) Chair: Anna Kreshuk*
9:30 - 9:45	Shuffle time	
9:45 - 11:15	**WORKSHOP SESSION #3**	
11:15 - 11:45	**Coffee Break** @ Covered Piazza	
11:45 - 12:15	HistoGPT: Generating clinical-grade pathology reports from gigapixel whole slide images	***Tingying Peng*** *(Helmholtz Zentrum München) Chair: Jianxu Chen*
12:15 - 12:30	ZEISS Microscopy Software Ecosystem for Image Acquisition and Analysis	***Francesco Biancardi*** *(ZEISS) Chair: Florian Jug*
12:30 - 13:00	Walking time to Triulza Academy	
13:00 - 14:00	**LUNCH** @ Triulza Academy	
14:00 - 16:30	**POSTER SESSION #2** @ Triulza Academy	
16:30 - 17:00	Walking time to HT	
17:00 - 18:00	**WORKSHOP SESSION #4**	
18:00 - 19:30	**Social Happy Hour** @ HT Restaurant floor	

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9:00 - 9:30	Explorations in embryogenesis	**Hari Shroff** *(HHMI Janelia)* *Chair: Damian Dalle Nogare*
9:30 - 9:45	Shuffle time	
9:45 - 11:15	**WORKSHOP SESSION #5**	
11:15 - 11:45	**Coffee Break** @ Covered Piazza	
11:45 - 12:15	Scalable strategies for a next-generation of FAIR bioimaging	**Josh Moore** *(German Bioimaging)* *Chair: Stephan Saalfeld*
12:15 - 12:30	Shuffle time	
12:30 - 13:30	**WORKSHOP SESSION #6**	
13:30 - 14:30	**LUNCH** @ HT Restaurant floor	
14:30 - 15:00	**WORKSHOP SESSION #7**	
15:00 - 15:15	Shuffle time	
15:15 - 16:00	**Selected Talks**	*Chair: Floran Levet*
	Too good to be true: the perils of applying image quality metrics in fluorescence microscopy	**Siân Culley** *(King's College London)*
	Interpreting Microscopy Images with Machine Learning	**Inês Martins Cunha** *(SciLifeLab, University of Stockholm)*
	OptiCell3D: inference of the mechanical properties of cells from 3D microscopy images	**Kevin Yamauchi** *(ETH Zurich)*
16:00 – 16:30	Sharing the CellMap Approach with a Segmentation Challenge	**Aubrey Weigel** *(HHMI Janelia)* *Chair: Joran Deschamps*
16:30 - 17:00	**Coffee Break** @ Covered Piazza	
17:00 - 18:00	**Panel Discussion**	
18:00 – 18:30	***CLOSING REMARKS***	

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WORKSHOP SESSIONS

SESSION #1

23 Oct 2024 / 10:45 – 11:45

QuPath for Fiji Fans	Peter Bankhead (University of Edinburgh)	HT Auditorium
Leveraging the ImgLib2 / BigDataViewer ecosystem for efficient batch inspection of large bioimage analysis datasets	Christian Tischer (EMBL)	Lower Egg Room
Omega – Harnessing the Power of Large Language Models for Bioimage Analysis	Loic A. Royer (CZ Biohub)	Mezzanine Room
Object Tracking and track analysis using TrackMate and CellTracksColab	Joanna Pylvänäinen (Åbo Akademi University)	PIT.P01.011
clEsperanto: GPU-accelerated image processing library	Stéphane Rigaud (Institut Pasteur)	PIT.P01.026
Width Profile Tools	Volker Baecker (French Institute of Health and Medical Research)	PIT.P02.029
Intermediate napari: from exploratory workflow to widgets	Peter Sobolewski (The Jackson Laboratory)	Upper Egg Room – Big
Automating ImageJ without coding: A hands-on introduction to JIPipe	Ruman Gerst (Hans Knöll Institute)	Upper Egg Room - Small

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WORKSHOP SESSIONS

SESSION #2   *23 Oct 2024 / 17:00 – 18:00*

QuPath for Python Programmers	Allan O'Callaghan (University of Edinbrugh)	HT Auditorium
Advancements in Cell Tracking: The Mastodon Solution for Large-Scale Datasets	Johannes Girstmair (MPI-CBG)	Lower Egg Room
Building Your Own Chatbot for BioImage Analysis	Arrate Munoz Barrutia (Universidad Carlos III de Madrid)	Mezzanine Room
The Spatial Transcriptomics as Images Project (STIM)	Michael Innerberger (HHMI Janelia), Stephan Preibisch (HHMI Janelia)	PIT.P01.011
Segment Anything for Microscopy	Anwai Archit (University of Göttingen), Constantin Pape (University of Göttingen), Luca Freckmann (University of Göttingen), Sushmita Nair (University of Goettingen)	PIT.P01.026
TopoStats: a tool for automated processing and quantification of AFM images	Laura Wiggins (University of Sheffield)	PIT.P02.029
Introduction to Piximi	Nodar Gogoberidze (Broad Institute)	Upper Egg Room – Big
FAIR IPA - A Project Template	Jan Eglinger (Friedrich Miescher Institute for Biomedical Research, FMI), Tim-Oliver Buchholz (Friedrich Miescher Institute for Biomedical Research)	Upper Egg Room - Small

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WORKSHOP SESSIONS

SESSION #3   *24 Oct 2024 / 9:45 – 11:15*

Reproducible Scientific Figure Creation with Fiji/ImageJ and Inkscape	Jan Brocher (BioVoxxel), Jerome Mutterer (IBMP)	HT Auditorium
Open-source bio-image analysis using surface meshes	Clément Benedetti (CNRS)	Lower Egg Room
DaCapo: a modular deep learning framework for scalable 3D image segmentation	David Ackerman (HHMI Janelia), Jeff Rhoades (HHMI Janelia)	Mezzanine Room
PlantSeg 2.0: powerful and user-friendly tissue segmentation	Lorenzo Cerrone (University of Zurich), Qin Yu (EMBL Heidelberg)	PIT.P01.011
Deformable 2D and 3D big data image registration and transformation with BigWarp	John Bogovic (HHMI Janelia)	PIT.P01.026
Introduction to CellProfiler	Paula Llanos (Broad Institute)	PIT.P02.029
Versatile Deep Learning for 2D and 3D Bioimage Analysis with CytoDL	Matheus Palhares Viana (Allen Institute for Cell Science)	Upper Egg Room – Big
Multiplexed tissue imaging: tools and approaches	Agustin Corbat (SciLifeLab), Anna Klemm (SciLifeLab), Frederic Ballllosera Navarro (Stanford University), Jonas Windhager (SciLifeLab), Kristína Lidayová (SciLifeLab)	Upper Egg Room - Small

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WORKSHOP SESSIONS

SESSION #4

An end-to-end image-based spatial transcriptomic pipeline in Nextflow	Stanislaw Makarchuk (Sanger Institute), Tong Li (Sanger Institute)	PIT.P01.011
motile: Multi-Object Tracking with Integer Linear Equations	Anniek Stokkermans (Hubrecht Institute), Carolin Mailin-Mayor (HHMI Janelia)	Mezzanine Room
Accelerating Microscopy Image Annotation with SAMJ Annotator	Arrate Munoz Barrutia (Universidad Carlos III de Madrid)	HT Auditorium
QuPath for Beginners	Fiona Inglis (University of Edinbrugh)	Upper Egg Room – Big
BigStitcher-Spark	Michael Innerberger (HHMI Janelia), Stephan Preibisch (HHMI Janelia), Tobias Pietzsch (HHMI Janelia)	Upper Egg Room - Small
ScaleFEx^{SM},: Single cell feature extraction from large scale datasets	Bianca Migliori (The New York Stem Cell Foundation)	PIT.P02.029
DL4MicEverywhere: Making your deep learning pipelines flexible, shareable, and reproducible	Estibaliz Gómez-de-Mariscal (Instituto Gulbenkian de Ciência), Iván Hidalgo-Cenalmor (Instituto Gulbenkian de Ciência)	PIT.P01.026
Annotation and Visualization of Large 3D Datasets with Paintera	Caleb Hulbert (HHMI Janelia)	Lower Egg Room

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WORKSHOP SESSIONS

SESSION #5

25 Oct 2024 / 9:45 – 11:15

ZEISS arivis: the unique platform for your image analysis	Riccardo Tognato (ZEISS)	HT Auditorium
BiaPy: deep learning based Bioimage Analysis for all audiences	Ignacio Arganda-Carreras (Universidad del Pais Vasco)	Lower Egg Room
Segment Anything using Python for Microscopy Data	Ranit Karmakar (Harvard Medical School)	Mezzanine Room
Tif2Blender: 3D image visualization in Blender	Oane Gros (EMBL)	PIT.P01.011
Recent Advances in ilastik	Benedikt Best (EMBL), Dominik Kutra (EMBL)	PIT.P01.026
Non linear registration of whole slide images with Fiji and QuPath	Olivier Burri (EPFL)	PIT.P02.029
Lazy parallel processing and visualization of large data with ImgLib2, BigDataViewer, the N5-API, and Spark	Tobias Pietzsch (HHMI Janelia), Stephan Saalfeld (HHMI Janelia)	Upper Egg Room – Big
Connecting software tools into reproducible workflows with CellProfiler plugins	Beth Cimini (Broad Institute)	Upper Egg Room - Small

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WORKSHOP SESSIONS

SESSION #6

pymmcore-plus: a pure python way to control your microscope with Micro-Manager	Federico Gasparoli (Harvard University)	HT Auditorium
Introduction to AI4Life and BioImage Model Zoo	Anna Kreshuk (EMBL), Theodoros Katzalis (EMBL)	Lower Egg Room
AI4Life: Empowering BioImaging through the BioEngine	Estibaliz Gómez-de-Mariscal (Instituto Gulbenkian de Ciência), Nils Mechtel (KTH Royal Institute of Technology)	Mezzanine Room
coLoɔ: A Collaborative Board Game for Teaching Co-Localization Analysis	Romain Guiet (EMBL)	PIT.P01.011
Annotating and sharing large images with OME-Zarr and WEBKNOSSOS	Norman Rzepka (Scalable Minds)	PIT.P01.026
Phasor analysis of Fluorescence Lifetime Microscopy data with FLUTE	Chiara Stringari (École polytechnique - Laboratory for Optics & Biosciences)	PIT.P02.029
Using BigTrace for the analysis of curvilinear biological structures	Eugene A. Katrukha (Utrecht University)	Upper Egg Room – Big
Introducing ultrack: cell tracking in python under segmentation uncertainty	Jordão Bragantini (CZ Biohub), Teun Huijben (Chan Zuckerberg Biohub San Francisco)	Upper Egg Room - Small

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WORKSHOP SESSIONS

SESSION #7

25 Oct 2024 / 14:30 – 15:00

QuPath for Groovy Scripters	Léo Plat (University of Edinbrugh)	HT Auditorium
FeatureForest: leveraging foundational models for user guided semantic segmentation	Mehdi Seifi (Human Technopole)	Lower Egg Room
Denoising microscopy images with CAREamics	Joran Deschamps (Human Technopole)	Mezzanine Room
Intro to MemBrain v2: Membrane Analysis in Cryo-ET	Joel Valdivia Ortega (Helmholtz Zentrum München), Lorenz Lamm (Helmholtz Zentrum München)	PIT.P01.011
Exploiting NanoPyx's Liquid Engine to accelerate image analysis pipelines	Bruno Manuel Santos Saraiva (Instituto Gulbenkian de Ciência)	PIT.P02.029
conv-paint: an easy to train interactive pixel classifier for napari	Lucien Hinderling (Institute of Cell Biology - Universität Bern)	Upper Egg Room – Big
Taggathon on BIII.eu: contributing to a unique database of image analysis tools and workflows	Perrine Paul-Gilloteaux (University of Nantes)	Upper Egg Room - Small

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POSTER SESSIONS

@ TRIULZA ACADEMY

SESSION #1

23 Oct 2024 / 14:00 – 16:30

#		
1	Automated Tracking and Analysis of Plasma Membrane Dynamics in TIRF-SIM	Adam Harmanec
2	Morphodynamics of human brain organoid development	Akanksha Jain
3	Exploring gene function and morphology using JUMP Cell Painting Consortium data	Alán Fernando Muñoz González
4	Phenomic data exploration guides drug discovery in a human disease network	Alba Guembe Mülberger
5	BrainGlobe: Accessible software for neuroanatomy of emerging model organisms	Alessandro Felder
6	A Bayesian solution to count the number of molecules within a diffraction limited spot	Alexander Hillsley
7	Quantifying intra-tumoral molecular subtype heterogeneity in MIBC from histological slides using a deep learning approach	Alice Blondel
8	Shaping progress in biomedical image processing with project-based learning	Andreas Kist
9	Iterative Dehazing of Widefield Microscopy Images using Diffusion Models	Anirban Ray
10	A contour-based alignment tool enabling to merge data from live acquisition & immunofluorescence	Anne-Sophie MACE
11	Computational modeling of nanoscale synapse morphology and organization using correlative super-resolution microscopy	Antoine J.-F. Salomon
12	An Image Analysis Pipeline for Quantifying the Spatial Distribution of Fluorescently Labeled Cell Markers in Stroma-Rich Tumors	Antoine Ruzette
13	A Comprehensive Image Analysis Pipeline for Investigating Autism Spectrum Disorder-like Behaviours in Drosophila melanogaster	Arianna Ravera
14	A Cloud-Native Virtual Bioimage Analysis Research Desktop (BARD) for Deployment of Containerised Bioimage Tools on Kubernetes	Arif Khan
15	fsdb - an open-source bioimage analysis and (meta) data management framework	Arnim Jenett
16	Example of a FBIAS project: mutliple fish tracking	Arthur Meslin
17	MicroSplit: Semantic Unmixing of Fluorescent Microscopy Data	Ashesh Ashesh
18	Nellie: Automated organelle segmentation, tracking, and hierarchical feature extraction in 2D/3D live-cell microscopy	Austin E. Y. T. Lefebvre

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POSTER SESSIONS

SESSION #1   *23 Oct 2024 / 14:00 – 16:30*

19	FAIR Image Analysis Workflows	Beatriz Serrano-Solano
20	High-throughput microscopy for deciphering the genetics of cell cycle diversity in wild yeasts	Benedikt Mairhörmann
21	Unsupervised Model Selection Through Test Time Perturbation Consistency	Joshua Talks
22	nlScript: A framework for creating natural-language-based user interfaces	Benjamin Schmid
23	Bilayers - an easy way to make your favorite deep learning tool more user-friendly	Beth Cimini
24	Using deep learning on single-cell images to unlock novel disease signatures and candidate therapeutics	Bianca Migliori
25	Detecting immunological synapses in patient samples through analysis of Imaging Flow Cytometry data	Bram van den Broek
26	Quantification of microtubule-guided peroxisome migration using a hidden Markov chain model	Carl-Magnus Svensson
27	BioImage.IO Chatbot: A Community-Driven AI Assistant for Integrative Computational Bioimaging	Arrate Munoz Barrutia
28	Using Nextflow for scalable and reproducible batch image analysis	Christian Tischer
29	Semi-automatic tracing and analysis of neurons in Brainbow images	Clément Caporal
30	Fiji Progress and Priorities 2024	Curtis Rueden
31	Pollen to pixels: perception of heat stress by machine learning to predict fertility	Daan van den Brink
32	High-throughput in-vivo single-molecule imaging of DNA repair in E. coli	Daniel Thedie
33	Enhancing Image Resolution Through Averaged Autocorrelation Inversion	Daniele Ancora
34	Run-length based mathematical morphology for efficient processing of large 3D images	David Legland
35	Segmentation of budding yeast organelles from bright field time-lapses	Diane Adjavon
36	Discovering explanatory factors of spatial localization with point process models	Dominik Sturm
37	Automated mapping of 3D smFISH gene expression data to electron microscopy	Elena Buglakova

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SESSION #1   *23 Oct 2024 / 14:00 – 16:30*

38	Machine learning based Evaluation and Enhancement (EVEN) for optical microscopy	Elena Corbetta
40	DL4MicEverywhere: Deep learning for microscopy made flexible, shareable, and reproducible	Estibaliz Gómez-de-Mariscal
41	Untangling spaghetti: using BigTrace plugin to analyze 3D filaments in time and space	Eugene A. Katrukha
42	pymmcore-plus: a pure python way to control your microscope with Micro-Manager	Federico Gasparoli
43	Beyond spot detection with spotMAX	Francesco Padovani
44	Deep learning-based classification for label-free microscopy	Franziska Schöb
45	User-oriented tools to characterize epithelia dynamics	Gaëlle Letort
46	Light-Insight: Spatiotemporal profiling of human early brain organoid development.	Gilles Gut
47	Investigating the structural complexities of DNA using high resolution atomic force microscopy	Harriet Read
48	Automating the Neuronal Differentiation of Ntera-2 Cells	Heather McCourty
49	Deep learning enables cross-modality super-resolution for volumetric reconstruction	Hyoungjun Park
50	Interpreting Microscopy Images with Machine Learning	Inês Martins Cunha
51	Cell lineage reconstruction and comparison from light-sheet microscopy image datasets	Ioannis Liaskas
52	pyCyto: A Pythonic Cytotoxicity Analysis Pipeline	Jacky Ka Long Ko
53	Mars, a molecule archive suite for analysis of single molecule properties from bioimages	Karl Duderstadt
54	From pixels to insights: Learning morphological descriptors from cellular ultrastructure	Jonas Hellgoth
55	napari-signal-classifier: Leveraging Interactive Temporal Features Annotation to Classify Signals and Events	Marcelo Leomil Zoccoler
56	Real-time image analysis for feedback control microscopy	Lucien Hinderling
57	TopoStats: taking AFM analysis to new heights	Laura Wiggins

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POSTER SESSIONS

@ TRIULZA ACADEMY

SESSION #2

24 Oct 2024 / 14:00 – 16:30

#	Title	Author
1	Unsupervised Denoising for Signal-Depenedent and Row-Correlated Imaging Noise	Benjamin Salmon
2	Fractal: An open-source framework for reproducible bioimage analysis at scale using OME-Zarrs	Joel Lüthi
3	METEOR: Enabling precise 3D correlative cryo-FIB milling for high throughput cryo-ET lamella production	Kevin Homberg
4	OptiCell3D: inference of the mechanical properties of cells from 3D microscopy images	Kevin Yamauchi
5	Client-Server Approach for Bioimage Analysis in the Deep Learning Era: Enhancing Extensibility and Accessibility	Ko Sugawara
6	Create web-based OME-Zarr galleries with Zarrcade	Konrad Rokicki
7	Potentials and limitations in the application of Convolutional Neural Networks for mosquito species identification using wing images	Kristopher Nolte
10	MMV_H4Cells - a cell evaluation napari plugin	Lennart Kowitz
11	FISBe: A real-world benchmark dataset for instance segmentation of long-range thin filamentous structures	Lisa Mais
12	Integrating Shape and Function: Identifying growth drivers and their morphological expression in Gastric Tumor Organoids.	Maleeha Hassan
13	How To Train Your Image Analyst: Perspectives from Upskilled Biologists	Maria Traver
14	Quantifying bacterial dynamics over a wide range of species with TrackMate-Omnipose.	Marie Anselmet
15	Digital pathology and artificial intelligence-based approaches to characterize the complex interactions between cellular components of the tumor microenvironment and their spatial distribution	Marika Viatore
16	**multiview-stitcher: a modular and extensible toolbox for scalable image registration and fusion in python	Marvin Albert
17	DaCapo: a modular deep learning framework for scalable 3D image segmentation	Marwan Zouinkhi
18	Mastodon – a Large-Scale Tracking and Track-Editing Framework for Large, Multi-View Images and Extensions for 3D Visualization and Lineage Comparison	Matthias Arzt

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@ TRIULZA ACADEMY

SESSION #2

24 Oct 2024 / 14:00 – 16:30

19	An AI-based pipeline to extract predictive mechano-features in Triple Negative Breast Cancers	Mattia Tonani, Emanuele Martini
20	Quantifying the Heterogeneity of DNA Interactions in AFM Images	Max Gamill
21	A QuPath extension for Data-driven Microscopy	Michael S. Nelson
22	micronuclAI: Automated quantification of micronuclei for assessment of chromosomal instability	Miguel A. Ibarra-Arellano
23	3D quantitative image analysis of cell fate acquisition during lateral inhibition	Minh Son PHAN
24	Building Foundations for AI-Driven Bioimage Analysis: Infrastructure and Annotation Platforms	Nils Mechtel
25	A nextflow-based end to end workflow for decoding of in situ sequencing data	Nima Vakili
26	PIXIMI: A web-based deep learning tool for biomedical image analysis	Nodar Gogoberdize
27	Integrative Open-Source Analysis Pipeline of RNA In Situ Hybridization Immunofluorescence Images	Nur Muhammad Renollet
28	Robust segmentation and measurement of single bacterial cells within a chain	Octavio Reyes-Matte
29	Robust detection and quantification of beating cells in microscopic 2D videos of cardiomyocytes	Oleksiy Nosov
30	Foreground-aware virtual staining for 3D nuclear morphometry	Paula Llanos
31	Taggathon on BIII.eu: contributing to a unique database of image analysis tools and workflows	Perrine Paul-Gilloteaux
32	TOMOMAN•PY - A Python-Based Suite for Handling Large cryo-ET Datasets	Philipp S Erdmann
33	Single protein pinpointing in light microscopy using DNA-PAINT	Rafal Kowalewski
34	Enabling Access to Bioimage Analysis Tools on University Cluster /Pre-Processing Quality Control and Image Exploration for Bioimage Analysis: A Novel Python Application	Ranit Karmakar
35	AI-powered analysis of histopathological tissues to study of the tumor immune microenvironment	Rebecca Polidori
36	The Human Protein Atlas in OMERO: an accessible dataset for teaching purposes	Rémy Dornier

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@ TRIULZA ACADEMY

SESSION #2

24 Oct 2024 / 14:00 – 16:30

37	Self-supervised learning for sample localization on cryoem grids for tomogram acquisition	Ricardo M. Sánchez L.
38	Probabilistic Framework for Calibrated Cell Tracking	Richard D. Paul
39	BIOP-desktop , a versioned computer for image analysis in life sciences	Romain Guiet
40	Continuous, interpretable, and transformation-invariant Morphometric for dynamic shape quantification	Roua Rouatbi
41	Enhancing Synaptic-Resolution Connectomics with an Open-Source AI Ecosystem	Samia Mohinta
42	Combining Incremental Deep Learning, Eye Tracking and Virtual Reality for Human-in-the-Loop Cell Tracking: a Progress Report	Samuel Pantze
43	Too good to be true: the perils of applying image quality metrics in fluorescence microscopy	Siân Culley
44	Virtual Embryo Zoo: A Web-Based Tool for Embryogenesis Cell Tracking Visualization	Teun Huijben
45	InstanSeg: a fast, flexible and user-friendly cell segmentation method for brightfield and multichannel images	Thibaut Goldsborough
46	Joined segmentation of nuclei and cells	Thierry Pécot
47	An AI approach for timing analysis of cytokinesis from microscopy data	Thomas Bonte
48	Investigating DNA damage with Atomic Force Microscopy and TopoStats	Thomas Catley
49	RNA point cloud segmentation for image-based spatial transcriptomics	Thomas defard
50	Simplified processing for image-based cell profiling with pollen	Tom Ouellette
51	Contextual Segmentation of Large, High-dimensional Medical Images	Victoria Porter
52	Leonardo: a toolset to remove sample-induced aberrations in light sheet microscopy images	Yu Liu
53	Two ways of quantifying inflammation in histopathology slices of the mouse pancreas	Maria Theiss
54	napari-phasors: Integrating Hyperspectral and FLIM Data Analysis into an Open-Source Bioimaging Framework	Marcelo Leomil Zoccoler
55	Enhanced Bacterial Cytological Profiling with super resolution techniques and fluorescent D amino acids	Joseph Ratcliff
56	FLUTE: A Python GUI for interactive phasor analysis of FLIM data	Chiara Stringari
57	Data-driven Unsupervised and Sparsely-Supervised Segmentation	Sheida R. Kordasiabi

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