Monday, May 8th: Day 1 Defragmentation Training School

Time	Title	Speaker
09:00	Welcome. Overview and logistics	Paula Sampaio, Rocco D'Antuono
09:30	Students introductions	All participants
10:30	Introduction: What is bioimage analysis?	Kota Miura
11:00	Coffee Break	
11:30	Jupyter for interactive cloud computing	Guillaume Witz
12:00	Hands-on session	
13:00	Lunch	
14:00	Cloud-hosted image data storage, visualisation and sharing	Bugra Oezdemir
14:30	Hands-on session	
15:30	Work on your own data (Forming groups and Defining projects)	Rocco D'Antuono, Trainers & Helpers
16:00	Coffee Break	
16:30	OMERO	Petr Walczysko
16:50	Hands-on session 1. OMERO as a data source for workflows in Jupyter, CellProfiler, etc. 2. OME-NGFF examples: Cloud-based workflows 3. Data publications solutions using OMERO and OME-NGFF (e.g., in IDR)	
18:00	End of the day	

Tuesday, May 9th: Day 2 Defragmentation Training School		
Time	**Title**	**Speaker**
09:00	Parallelization and heterogeneous computing: from pure CPU to GPU-accelerated image processing	Marcelo Zoccoler
09:30	Hands-on session	
11:00	Coffee Break	
11:30	Zero code Deep Learning tools for Bioimage Analysis	Daniel Sage, Estibaliz Gomez de Mariscal
12:00	Hands-on session	
13:00	Lunch	
14:00	Analysis of Microtubule Orientation	Thomas Pengo
14:30	Hands-on session	
15:00	CellProfiler for HCS data on the cloud	Nodar Gogoberidze, Anna Klemm
16:00	Coffee Break	
16:30	CellProfiler for HCS - Hands-on	Nodar Gogoberidze, Anna Klemm
17:00	Work on your own data (group work)	Rocco D'Antuono, Trainers & Helpers
18:00	End of the day	

Wednesday, May 10th: Day 3 Defragmentation Training School		
Time	**Title**	**Speaker**
09:00	Metrics and Benchmarking	Martin Maška
10:00	BIAFLOWS: A BioImage Analysis workflows benchmarking platform	Sébastien Tosi, Volker Baecker, and Benjamin Pavie
11:00	Coffee Break	
11:30	BIAFLOWS - Hands-on	Sébastien Tosi, Volker Baecker, and Benjamin Pavie
12:00	Machine and Deep Learning on the Cloud: Classification	Félix Mercier
12:30	Machine and Deep Learning on the Cloud: Segmentation	Ignacio Arganda-Carreras
13:00	Lunch	
14:00	Hands-on session	Félix Mercier, Ignacio Arganda-Carreras
16:00	Coffee Break	
16:30	Work on your own data (group work)	Rocco D'Antuono, Trainers & Helpers
18:00	End of the day	

Thursday, May 11th: Symposium Day 1		
Time	**Title**	**Speaker**
09:00	Welcome & Registration	
09:30	Introduction, overview & logistics	Paula Sampaio
Session 1: **BioImage Data Analysis (Chair: Elnaz Fazeli & Kota Miura)**		
09:40	UFMTrack: Under-Flow Migration Tracker enabling analysis of the entire multi-step immune cell extravasation cascade across the blood-brain barrier in microfluidic devices	Mykhailo Vladymyrov
10:00	Learning cell cycle representations for self-supervised trajectory annotation	Kristina Ulicna
10:20	Image-analysis driven understanding of the mechanisms controlling cell and ECM organisation during tissue fibrosis	Stefania Marcotti
10:30	The Cell Tracking Challenge: 10 Years of Objective Benchmarking	Martin Maška
10:40	Coffee Break	
11:10	ShapoGraphy: a new approach for visualising bioimaging data	Heba Sailem
11:30	NanoPyx - a high-performance Python library for generating and analysing super-resolution microscopy images.	Bruno M. Saraiva
11:40	PoCA: a powerful visualization and quantification software for 3D single-molecule localization microscopy data	Florian Levet
11:50	True 3D Analysis of Human Retinal Inner Limiting Membrane Morphology	Ross Laws
12:00	TechBites: New AI algorithms for Instance Segmentation and new deployment mechanism for AI models inside the ZEISS open software ecosystem	Sebastian Rhode *Zeiss Microscopy*
12:20	**Poster session (extended over lunch)**	
13:00	Lunch	

Session 2: **AI4Life - Deep Learning for Image Data (Chair: Beatriz Serrano-Solano)**		
14:00	Deep learning-based bioimage analysis workflows for all audiences	Ignacio Arganda-Carreras
14:20	Deep learning enabled cellular imaging: making it happen for you	Estibaliz Gomez de Mariscal
14:40	Democratizing Deep Learning-based Segmentation for Microscopy Image Analysis	Constantin Pape
15:00	Short Break	
15:10	Deep learning with sparse annotations in cell image segmentation	Ko Sugawara
15:20	Data Analysis for Super-Resolution Microscopy in nanomedicine	Cristina Izquierdo Lozano
15:30	Arkitekt - Streaming analysis and real-time workflows for microscopy	Johannes Roos
15:40	Coffee Break	
16:10	Open Source Software Lounge (OSSL)	
18:00	End of the day	
20:00	Networking dinner	

Time	Title	Speaker
Friday, May 12th: Symposium Day 2		

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Time	Title	Speaker
Session 3: **Data Management and Infrastructures (Chair: Aastha Mathur)**		
09:00	Image Data Services at Euro-BioImaging: Community efforts towards FAIR Image Data and Analysis Services	Aastha Mathur
09:20	The BioImage Archive: Accelerating bioimage analysis and improving reproducibility	Matthew Hartley
09:40	BioImage: correlated multimodal imaging in life sciences and the problem of big data management for core facilities	Julia Fernandez-Rodriguez
10:00	NFDI4BIOIMAGE: Building information infrastructures for imaging data	Christian Tischer
10:20	FAIR workflows	Beatriz Serrano-Solano
10:40	Cooking great things for FAIR data management and access to reproducible HPC environments	Tatiana Woller
10:50	The BrainGlobe Initiative - Developing Open-Source Computational Neuroanatomy Tools	Adam L. Tyson
11:00	TechBites: Visualization, collaborative annotation, and sharing of large 3D images with WEBKNOSSOS: ScalableMinds	Tom Herold *Webknossos*
11:10	Coffee Break	
11:30	Student presentations	
12:30	**Poster session (extended over lunch)**	
13:00	Lunch	

Session 4: **High-Throughput Imaging Data Analysis (Chair: Hanneke Okkenhaug & Bram van den Broek)**		
14:00	Session Introduction	Chair
14:05	High-content imaging-based serology test for SARS-CoV-2	Lassi Paavolainen
14:25	Live-cell screening of signal transduction pathways using FRET-FLIM	Bram van den Broek
14:45	Fractal: An Open-Source Framework for Processing OME-Zarr High Content Imaging Data	Joel Luethi
15:05	High-throughput image analysis for studying hormonal impact on neurodevelopment through human cortical brain organoids	Alessia Valenti
15:15	Cell phenotyping with Perkin Elmer Operetta® CLS™ and the Harmony high-content analysis software	Véronique Berchet **Perkin Elmer**
15:25	Short Break	
15:45	WhiSCR, a pipeline for analysis of whole-slide immunofluorescence image data using CellProfiler and R	Hanneke Okkenhaug
16:05	User-friendly droplet detection pipelines for high-throughput experiments	Immanuel Sanka
16:15	High content screening from a core facility perspective: from experiments to discoveries	Hugo M. Botelho
16:35	High Content Screening in a Multi-Thematic Research Environment: Examples & Challenges	André Maia
16:55	Final remarks & Wrap-up	
17:10	End of the Symposium	

Invited talks: 20 mins
Selected talks from abstracts: 10 mins
TechBites