Centre for
Cancer Biomarkers
Norwegian Centre of Excellence – University of Bergen

9th ScanPath Network Meeting

Scandinavian Symposium on Translational Pathology

Solstrand, October 29-30, 2025 (Bergen - Norway)

Preliminary Scientific Program – v2

Day 1: Wednesday – October 29, 2025

09:00-10:00	*Registration and Coffee*
10:00-10:15	Welcome and Introduction: **Lars A. Akslen, Carina Strell & Arne Östman**
	Chair session 1: Patrick Micke
10:15-10:45	**Karin Jirström (Lund):** Reshaping pathology to monitor and combat hard-to-treat cancers
10:45-11:00	**Daniel Menges (Trondheim):** The potential of intelligent algorithms for cancer diagnosis and therapy
11:00-11:15	**Maren Høibø (Trondheim):** Digital pathology: segmentation, classification, and compression
11:15-11:30	**Li Yi (Stockholm)**: Targeting astrocyte-driven glioblastoma growth
11:30-11:45	**Markus Heidrich (Lund):** Identifying outcome-determinative tumor microenvironment niches through multi-level spatial clustering in multiplex images
11:45-12:00	**Emmanuel Nwadozi (Uppsala):** Vascular leakage in non-small cell lung cancer
12:00-13:30	*Lunch and poster session*
	Chair session 2: Marit Valla
13:30-14:00	**Trine Tramm (Aarhus):** Tumor infiltrating lymphocytes as a predictive marker for benefit of radiation therapy
14:00-14:15	**Oscar Briem (Lund):** Neutrophils as modulators of the specific immune response in breast cancer
14:15-14:30	**Jon Lømo (Oslo):** Low-grade inflammation in mammary adipose tissue
14:30-14:45	**Jens Henrik Norum (Oslo):** Spatial mapping of immune cells and energy metabolism in DCIS.
14:45-15:00	**Ute Spiske (Trondheim)**: Breast cancer prognostication: Exploring the impact of data type
15:00-15:15	**Arian Askari (Turku):** Patient-derived conditionally reprogrammed cells as predictive models for bladder cancer therapy response
15:15-15:30	**Katiane Tostes (Uppsala)**: Spatial immunophenotyping to predict immunotherapy benefit in lung cancer patients
15:30-16:00	*Coffee & Crosstalk*
	Chair session 3: Carina Strell
16:00-16:30	**Per Uhlén (Stockholm):** Advancing histopathology through volumetric 3D imaging
16:30-16:45	**Mengping Long (Stockholm):** Studies of lung cancer and lung fibrosis using spatial transcriptomics
16:45-17:00	**Ghazal Toussi (Bergen):** Combining PLA and imaging mass cytometry for immune checkpoint signaling
17:00-17:15	**Etienne Platini (Trondheim)**: Transcriptomics and antibody-based proteomics for mapping single-cell profiles of human tissues in health and disease

17:15-17:30	**Artur Mezheyeuski (Barcelona**): TONES: From protocol to stain - standardized, automated, easy
18:30-19:30	*Posters & Prosecco*
19:30	*Dinner*
Day 2:	**Thursday – October 30, 2025**
	Chair session 4: Arne Östman
09:00-09:30	**Charlotte Stadler (Stockholm):** Spatial Proteomics: from translational to future clinical tissue diagnostics
09:30-09:45	**Austin Rayford (Bergen):** Targeting AXL in solid tumor microenvironments
09:45-10:00	**Daniela Costea (Bergen):** Spatial profiling of cancer-associated fibroblast heterogeneity in head and neck cancer
10:00-10:15	**Tessa Lohr (Bergen):** Dual interactions between breast cancer and peripheral neurons: Investigating the role of axon guidance factors
10:15-10:30	**Manuel Carrasco (Bergen):** Adrenergic signals in 3D breast cancer models
10:30-11:00	*Coffee & Crosstalk*
	Chair session 5: Heidrun Vethe
11:00-11:30	**Leena Latonen (Kuopio):** Unravelling prostate cancer drug responses and treatment resistance through proteomics-driven multi-omics
11:30-11:45	**Martin Johansson (Gothenburg):** Lipid droplets as source of novel biomarkers for clear cell renal cell carcinoma
11:45-12:00	**Kirsi Ketola (Kuopio):** Mechanisms of treatment resistance and prediction of prostate cancer therapy response via patient-derived models and high-throughput imaging of live zebrafish avatars
12:00-12:15	**Xinsong Chen (Stockholm):** Joint analysis of breast cancer intratumoral heterogeneity using spatial transcriptomics and computational pathology
12:15-13:45	*Lunch and poster session (check-out at 12:00)*
	Chair session 6: Karin Jirström
13:45-14:15	**Teijo Pellinen (Helsinki):** Spatial multiplex tissue profiling ¬ from discovery to clinic
14:15-14:30	**Maximilian Senftleben (Uppsala)**: Bioimage analysis support on multiplexed image data by SciLifeLab BIIF
14:30-14:45	**Mehrdad Rakaee (Oslo):** Pathology foundation models for molecular and IO prediction
14:45-15:00	**Lassi Paavolainen (Helsinki):** Self-supervised machine learning enables unbiased cancer patient characterization from multiplexed tissue microscopy images
15:00-15:15	**Elisabeth Wetzer (Tromsø)**: Leveraging geometric deep learning and graph visualizations to unravel the tumor microenvironment
15:15-15:30	*Break*
	Chair session 7: Elisabeth Wik
15:30-15:45	**Pekka Ruusuvuori (Turku):** Foundational AI models for histology - Towards generalizable computational pathology
15:45-16:00	**Yujie Xiang (Stockholm)**: AI-based multi-modal prognostic modelling of histopathology images, mRNA expression, and clinical information in >3,000 patients
16:00-16:15	**Luka Tandaric (Bergen):** A multimodal translational approach to ovarian cancer immunotherapy.
16:15-16:30	**Elisabeth Wik (Bergen)**: Breast cancer in the young: Age-related clinical and biological features
16:30-16:45	Closing remarks: **Teijo Pellinen**