

# Central European Nanopore Days 2026

## Monday

**7:30-8:00 Short morning jogging for Long-read day (~5km)**

**9:00 Registration**

**9:00-11:00 Workshop by Sebastian Ganschow (ONT)**

Use of adaptive sampling for panel sequencing (Hereditary Cancer Panel)

**11:30-13:00 Lunch (Panský dvůr)**

**13:00-13:10 Welcome Speech**

**13:10-14:10 Alexander Rotmann + Sebastian Ganschow**

Oxford Nanopore News: Clear Answers Start Here

**14:15-14:30 Mariateresa Mazzetto**

Epigenetic variation of Y-chromosome palindromic regions across human populations revealed by nanopore sequencing

**14:30-15:00 Jory Lietard**

Chemical libraries of long RNA oligonucleotides synthesized by microarray photolithography

**15:00-15:30 Coffee break**

**15:30-15:45 Matěj Lexa**

G-quadruplex annotation and mutational dynamics in long-read based human genome assemblies.

**15:45-16:30 Monika Čechová**

The bioinformatics in the era of complete T2T human genomes Nanopore sequencing

**16:30-16:45 Dániel Vörösvácki**

Genome-wide analysis shows increased LINE-1 retrotransposition in colorectal cancer

**16:45-19:00 Coffee + Posters + Solution Playground**

**Ondřej Brzoň + Andreas Klingenhoff**

Bioinformatic consultation

**19:00-1:00 Dinner, Social Evening (Panský dvůr)**

## Tuesday

**7:30-8:00 Short morning jogging for Long-read day (~5km)**

**8:00-9:30 Morning coffee**

**9:00-9:30 Tan Jey Sern (Vazyme Biotech)**

Molecular tools for NGS

**9:30-9:50 Jan Špaček**

Dissecting transcriptional drivers of acquired valproate resistance in brain endothelial cells using long-read RNA sequencing

**9:50-10:10 Pavel Šenkyřík**

Oxford Nanopore Sequencing as a Tool for Comprehensive Analysis of Fetal Cell-Free DNA

**10:10-11:00 Florian Kraft**

Hype or Hope - Human Long-Read Genome Sequencing in Clinical Practice

**11:00-11:30 Ben Liesfield (Varvis)**

A Perfect Game: End to End Long Read Diagnostics

**11:30-13:00 Lunch (Panský dvůr)**

**13-13:45 Matt Loose**

Rapid diagnostics with Nanopore: CNS and beyond

**13:45-14:00 Filip Pardy**

Unlocking the predictive potential of epigenomics with modified basecalling and trained classifiers

**14:00-14:15 Štěpán Stočes (SEQme)**

The Devil is in the Details: Optimizing Nanopore Workflows Beyond the Defaults

**14:15-15:00 Coffee**

**15:00-15:30 Tábora**

FAQ vs. F\*\*k ups: The Final Frontier Between Wisdom and Blunders

**15:30-15:45 Alexandra Kalmar**

Nanopore sequencing of Hungarian colorectal cancer cases with DNA methylation and single stranded DNA data

**15:45-16:15 Micol Baronio (4bases)**

4bases improving precision medicine through long reads: clinical applications of Nanopore Sequencing

**16:30-18:00 Commented Walk Through the City (UNESCO)**

**16:30-19:00 Coffee + Posters + Solution Playground**

**Ondřej Brzoň + Andreas Klingenhoff**

Bioinformatic consultation

**19:00-1:00 Dinner, PubQuiz (Panský dvůr)**

## Wednesday

**7:30-8:00 Short morning jogging for Long-read day (~5km)**

**8:00-9:30 Morning coffee**

**9:30-9:45 Markéta Jakubíčková**

MethylomeMiner reveals bacterial methylation profiles from nanopore data

**9:45-10:15 Tomáš Strenčanský**

First Evaluation Report of PARADiX - Rapid Diagnostics of Pathogens and their AMR Using Nanopore Sequencing

**10:20-10:40 Pavel Vopálenký**

Uncovering Ap2N-Capped Human tRNAs and Their Fragments with Ap2N-RNA Sequencing

**10:40-10:55 Jana Nekvindová**

First Experiences with the Oxford Nanopore Microbial Amplicon Barcoding Kit for Full-Length 16S and ITS Sequencing in Preterm Prelabor Rupture of Membranes

**11:00-11:30 Workshop evaluation, Prices Lunch to go**



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