

DNASense Nanopore course

Dates announced pending COVID-19 situation

This year the DNASense Nanopore course is held in collaboration with BioXpedia on the picturesque Aarhus waterfront (Incuba – Navitas, Inge Lehmanns Gade 10, 8000 Aarhus C).

Course program

Day 1			
WHEN	WHAT	HOW	WHO
09.00-09.45	Welcome <ul style="list-style-type: none"> Course introduction Practical information DNASense, BioXpedia & participants (who is who) 	Lecture	MTS
09.45-10.00	BREAK / BUFFER		
10.00-10.45	Nanopore basics <ul style="list-style-type: none"> Applications and limitations Platforms Basic principles and components Workflows, kits and multiplexing 	Lecture	RWO
10.45-11.00	BREAK / BUFFER		
11.00-11.45	Quality control <ul style="list-style-type: none"> Essential QC parameters Library scaling Troubleshooting 	Lecture	RWO
11.45-12.30	LUNCH		
12.30-14.00	Rapid DNA sequencing (1/3) <ul style="list-style-type: none"> Principles Flow cell QC Library preparation Flow cell priming and library loading MinKNOW software (GUI) Sequencing QC 	Lecture / Demonstration	RWO
14.00-14.15	BREAK / BUFFER		
14.15-15.45	Rapid DNA sequencing (2/3) <ul style="list-style-type: none"> Library preparation Flow cell priming and library loading Sequencing QC EPI2ME workflows 	Hands-on	MTS/HK RWO
15.45-16.00	Q&A		ALL
18.00-21.00	Social dining and networking (optional)		ALL

Day 2

WHEN	WHAT	HOW	WHO
09.00-09.45	Nanopore amplicon sequencing <ul style="list-style-type: none"> • 16S rRNA sequencing and classifications • Illumina vs. Nanopore • On-site sequencing • Unique Molecular identifiers (UMIs) 	Guest Lecture	MHA
09.45-10.00	BREAK / BUFFER		
10.00-10.45	Rapid DNA sequencing (3/3) <ul style="list-style-type: none"> • Sequencing QC (continued) • Reusing and storing flow cells (flow cell wash) 	Lecture / demonstration	MTS
10.45-11.00	BREAK / BUFFER		
11.00-11.45	Basecalling <ul style="list-style-type: none"> • Files and folders • Introduction to basecalling and Guppy • Pore types, error profiles and benchmarking • Guppy parameters • Demultiplexing and trimming • Quality control • GPU-accelerated basecalling • Remote basecalling • Hardware requirements 	Lecture	RWO HK MTS
11.45-12.30	Lunch		
12.30-13.15	Automation of data processing <ul style="list-style-type: none"> • Introduction to putty (ssh) and X2Go • Bash scripting 101 – set up your first bash script • Data QC and subsetting 	Hands-on	HK MTS RWO
13.15-13.30	BREAK / BUFFER		
13.30-14.00	Genome Assembly (1/2) <ul style="list-style-type: none"> • Illumina vs. Nanopore • Strategies and workflows • Assemblers and compute cost • Polishing of draft assembly • Benchmarking 	Lecture	RWO
14.00-16.00	Genome Assembly (2/2) <ul style="list-style-type: none"> • From script to pipeline • Assembly and polishing • Taxonomic assignments • Stats and benchmarking 	Hands-on	RWO HK MTS
16.00-16.15	Q&A		ALL

Day 3

WHEN	WHAT	HOW	WHO
09.00-09.45	BioXpedia – Biomarker discovery and validation	Guest Lecture	MK
09.45-10.00	BREAK / BUFFER		
10.00-10.45	Danish national SARS-CoV-2 sequencing efforts	Guest Lecture	MA
10.45-11.00	BREAK / BUFFER		
11.00-11.45	Sars-CoV-2 bioinformatics example <ul style="list-style-type: none"> • Genome assembly & QC • SNP calling • Reference database matching 	Hands-on	MTS/HK
11.45-12.30	LUNCH		
12.30-14.00	Extended Q&A and networking Possibility to further discuss your own projects and potential strategies involving long-read sequencing.	Hands-on	ALL
14.00-14.30	Final question round and course evaluation		RWO

Abbreviations: Rasmus Wollenberg (RWO), Henrik B. Kjeldal (HK), Mads T. Søndergaard (MTS), Martin H. Andersen (MHA), Mogens Kruhøffer (MK), and Mads Albertsen (MA).

It is necessary to bring a laptop, and preferably with a SSH client (e.g. PuTTY or MobaXterm) for command line interfacing (CLI) and/or X2Go client for graphical user interfacing (GUI) already installed.