Nordic Alliance for Clinical Genomics

INVITATION

Join the NACG 10th workshop week
Virtual daily lunch sessions
31st May - 4th June 2021

NACG week

This summer the traditional NACG workshop will be organised as a virtual event with daily lunch sessions spread out across the week from May 31-June 4, 2021. Members and other interested parties are welcome to register for the NACG workshops **HERE.**

Workshop outline

For details on sessions see next page.

Time (Oslo GMT+2)	Monday 31st May	Tuesday 1st June	Wednesday 2nd June	Thursday 3rd June	Friday 4th June
12:00	**Opening and keynote** **Genome sequencing in clinical microbiology** Rasmus L Marvig, Center for Genomic Medicine, Rigshospitalet DK	**Digital dynamic consent in clinical genomics** Sharmini Alagaratnam, and Courtney Nadeau, DNV NO	**Somatic variant calling - benchmarking exercise with in-silico spiked-in variants.** Oleg Agafonov, DNV NO, Valtteri Wirta, Clinical Genomics Stockholm, SciLifeLab SE	**Variant interpretation and data sharing** Dag Undlien, OUS NO; Stephen McAdam, DNV NO; and Sharmini Alagaratnam DNV NO	**Clinical diagnostic unsolved cases** Maria Rossing, Center for Genomic Medicine, Centre of Diagnostic Investigations, Rigshospitalet DK
12:30					
13:00	**Automation of sequencing operations and data management** Tony Håndstad, Department of Medical Genetics, OUS NO	**IVDR compliance progress** Cathrine Høgseth Nordhus, Department of Medical Genetics, OUS NO			**Social networking hour** Sharmini Alagaratnam, DNV NO
13:30			END		
14:00	END	END		END	END

Workshop sessions details

Please reach out directly to the contact person(s) as early as possible if you would like to engage more actively in any of the sessions

Topic	Description	Contact person
Keynote Genome sequencing in clinical microbiology	The session will provide an introduction to ***Genome sequencing in clinical microbiology***	Rasmus L. Marvig (rasmus.lykke.marvig@regionh.dk)
Automation of sequencing operations and data management	While most labs automate the execution of their variant calling pipeline, the further operational aspects of data management are often handled by manual procedures, cron jobs and many diverse scripts. As data management and analyses increase in complexity, an adequate level of automation is needed. In this session, we learn how some of the larger labs automate their operations and also learn about a specific open-source event-based system that can be particularly suited to the task. Target audience: All bioinformaticians and others interested in operations, automation and data management	Tony Håndstad (tonyha@extern.uio.no)
Digital dynamic consent in clinical genomics	Join us for an interdisciplinary, interactive workshop where we will explore challenges in consent across the clinical genetics landscape, identify common focus areas and share potential approaches to moving towards a more dynamic and digital reality. Target audience: Anyone and everyone working within clinical genetics who collect, manage and/or need consent, either directly or indirectly, for their work.	Sharmini Alagaratnam (Sharmini.Alagaratnam@dnv.com) & Courtney Nadeau (Courtney.David.Nadeau@dnv.com)
IVDR compliance progress	All actors in the field of medical genetics will have to comply with the new European Medical Devices (MDR) and In-Vitro Diagnostics Medical Device Regulation (IVDR) by May 2021 and May 2022 respectively. In this session Nordic laboratories will share the status of their efforts to secure compliance to the new regulations. The goal of the session is to compare the different laboratories' approaches to these regulations and to identify areas where the NACG members can work together to address challenges. Topics to be addressed are formats for collaboration, use of open source code, factory developed test arguments and market surveillance. Target audience: Labs or those interested in developing or deploying their own pipelines or software for genetic diagnostics.	Cathrine Høgseth Nordhus (cahnor@ous-hf.no)
Somatic variant calling - benchmarking	The adoption of molecular diagnostics based on NGS technologies is challenging from a quality assurance perspective. In contrast to	Valtteri Wirta (valtteri.wirta@scilifelab.se) & Oleg Agafonov (oleg.agafonov@dnvgl.com)

exercise with in-silico spiked-in variants.	more established assays, the often broad contents and technically complex workflows commonly seen in NGS diagnostics mean that assay validation and verification is difficult. In comparison to the identification of germ-line variation, somatic variation imposes an extra layer of difficulties due to several factors: (i) most tumour samples are comprised of an unknown fraction of both normal and tumour cells (tumour purity); (ii) the ploidy of cancer cells is unknown; (iii) due to the subclonal evolution the cancer cell population could be heterogeneous. In this session, we aim to gather best practices of somatic variant calling and subsequent variant filtering through a benchmarking exercise, for which we use deep sequenced, highly characterized reference with in-silico spiked-in variants in a set of oncogenes Target audience: Laboratories that perform clinical NGS-based oncology testing (Illumina, WES or gene panels).	
Variant interpretation and data sharing	The results from a pre-workshop variant sharing and variant interpretation benchmarking exercise focusing on hereditary cancer and retinopathy variants will be shared and discussed. Opportunities for extending these efforts to somatic variants will also be discussed. Target audience: Everyone involved in variant classification	Dag Erik Undlien (UXDAUN@ous-hf.no)
Clinical diagnostic unsolved cases	The session will cover case presentations from various clinicians &/or bioinformaticians on clinical diagnostic unsolved cases. If you have an interesting case you would like to share, please contact Maria Rossing and/or register your interest in contributing in the registration form. Target audience: Everyone involved in the processes around clinical diagnoses and solving of cases	Maria Rossing (caroline.maria.rossing@regionh.dk)
Social networking hour	We will be using Spatial.chat for our closing social event, to virtually recreate the bar at the end of a successful meeting. This app allows you to informally meet new participants and catch up with familiar faces. Try it here beforehand, and we're looking forward to seeing you all there!	Sharmini Alagaratnam (Sharmini.Alagaratnam@dnv.com)

About NACG

The Nordic Alliance for Clinical Genomics is an independent, non-governmental, not-for-profit, Nordic association open for organizational and individual members.

Our overall mission is to work together and learn from each other to lift performance standards. We aim at responsible sharing of trustworthy data for improved diagnosis and treatment, and as a resource for research.

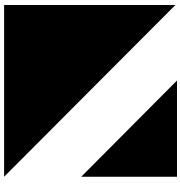
Our goals are to

- Facilitate the **responsible sharing** of genomic data, bioinformatics tools, sequencing methods and best practices for interpretation of genomic data.
- **Enhance quality** of genomic data and processes and explore methodologies to provide assurance.
- Understand **legal barriers** to the implementation of personalised medicine and to engage with key stakeholders that influence these barriers
- Develop **demonstration projects** that challenge perceived legal barriers that limit responsible and ethical sharing of genomic and health data.
- **Build bridges** between research and clinical communities, technologies and practices to foster innovation

To learn more about the Nordic Alliance for Clinical Genomics and how to become a member please visit our website at https://nordicclinicalgenomics.org/ or contact us at post@nordicclinicalgenomics.org.

Workshop reports from previous events, NACG papers and governing documents are available at https://nordicclinicalgenomics.org/resources

NACG is collaborating closely with the Nordic Permed Law network; a network of lawyers in the Nordic region who work with questions related to precision medicine and new medical technology. Information, publications and events can be found at https://www.nordicpermedlaw.org/



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