PRELIMINARY AGENDA

Agenda for Nordic Alliance for Clinical Genomics workshop #13

Transportation / logistics (exact times will be confirmed)

8.45 Bus departure from Stockholm City terminal
9.00 Bus departure from Arlanda
9.15 Bus departures from Arlanda

DAY I	January 19	Lead
9.00	Registration and coffee + visit to sponsors booths	
10:00	Welcome address	Dag Undlien, Valtteri Wirta
10.15	**Invited keynote speaker** *Anna Lindstrand (Department of Clinical Genetics, Karolinska University Hospital)*	Valtteri Wirta
	45 min + 15 min questions	
11.15	**National updates relating to development in national programs in genomic medicine, precision diagnostics and precision medicine**	Valtteri Wirta
	10 min per country (Finland, Sweden, Norway, Denmark, Iceland)	
12:15	**Lunch**	
TRACK 1 - MOLECULAR SCIENCES		
13:30	**Rapid-fire session on knowledge sharing**	Janna Saarela
	Brief presentations (5+2 min) on essentially any topic relevant to NACG activities (does not have to be on the theme of the workshop). Also event sponsors may present new products and services. The purpose is to disseminate information regarding new tools, workflows, clinical cases etc. The session is in the beginning of the workshop to facilitate follow-up discussion during breaks and other social events.	
15:00	Coffee break + visit to sponsors booths	

15:30	Maximizing the use of short-read sequencing data: **Session I - Structural variation and different reference genomes**	Jesper Eisfeldt
	This session addresses structural variation and includes use of emerging reference genomes, including T2T and/ graph genomes. The session also covers use of tools supporting visualisation and interpretation of structural variation data. Clinical cases with interesting structural variations can be presented. Short-read data in combination with long-read data can also be presented.	
16:30	Coffee break + visit to sponsors booths	
17:00	Maximizing the use of short read seq data **Session I - Structural variation and different reference genomes - Continuation**	Jesper Eisfeldt
18:00	Time on your own – relax, sauna or free time	-
19.30	Pre-dinner drink and social activity	Anna Lyander
20:00	Dinner	-
DAY II		
09:00	**The future of clinical genomics**	Anders Lind
	Interactive session where we explore where the field is heading, focussing on new technology, its applications and implications. How should NACG develop to prepare for the future? *This is a new session on the NACG ws agenda.* *<u>Agenda</u>* *Summary from the scalable IT environment session.* *Five brief view points (3 min) from selected attendees of the ws + questions from the audience via menti/other tool.* *Panel discussions with presenters (replies to questions)* *Reflections - topics for future workshops (menti)*	
	TRACK 1 - BIOINFORMATICS	
	TRACK 2 - CLINICAL INTERPRETATION	
10:00	Maximizing the use of short read seq data: **Session II (Track 1) - Add-on analyses on top of conventional WGS**	Anders Jemt

	This session includes tools addressing repeat expansions, custom callers such as SMN1/2, mobile elements, mitochondrial analyses etc.	
10:00	Maximizing the use of short read seq data **Session II (Track 2) - Filtering / prioritisation strategies**	Morten Duno, Eirikur Briem
	This session addresses conventional filtering or ranking strategies for variant prioritisation prior to clinical interpretation, as well as use of augmented and artificial intelligence-based approaches for variant prioritisation. Also multiomics-based strategies for linking information between RNA and DNA layers can be included.	
11:00	Coffee break + visit to sponsors booths	
11:30	Maximizing the use of short read seq data: **Session II (Track 1) - Add-on analyses on top of conventional WGS - Continuation**	Anders Jemt
	Maximizing the use of short read seq data **Session II (Track 2) - Filtering / prioritisation strategies - Continuation**	Morten Dunno, Eirikur Briem
12:30	Lunch	
13:30	Maximizing the use of short read seq data - **Session III (Track 1) - Multiomic analyses**	Anders Jemt
	This session explores use of additional data layers to support identification disease causing variants in rare disease patients. For example, use of RNA sequencing to support prioritisation of non-coding DNA variants.	
	Session III (Track 2) - Re-analysis strategies	TBC
	This session discusses under what clinical circumstances previously unsolved cases are subjected to bioinformatic re-analysis and interpretation, as well as technical means facilitating such re-analysis at scale. Also ethical perspectives can be included.	
14:45	**Summary & farewell, announcement of next WS** Coffee break + visit to sponsors booths	Valtteri Wirta, Dag Undlien
15.30	Bus departures	