Scientific Programme

NGS Data after the Gold Rush 6-8 May 2014, Norwich, United Kingdom

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Conference Programme

Day 1	NGS: State of the Art, Current Challenges & Applications Chair: Ana Conesa
08:30-09:00	Registration and Coffee
09:00-09:30	Welcome from Vicky Schneider & Dr Erik Bongcam-Rudloff
09:30-10:00	Plenary Lecture: "NGS, then, now and in the future", Matt Clark
10:00-10:30	Coffee Break & poster set-up
10:30-11:00	SeqAhead: NGS data analysis network across countries and projects, Erik Bongcam-Rudloff
11:00-11:30	Using NGS to answer biological questions, Björn Usadel
11:30-12:00	NGS scaling up: A retrospective from the Norwegian Sequencing Centre, Robert Lyle
12:00-13:00	Lunch
13:00-13:30	NGS for studying viruses "beyond the consensus", Jan Kim
13:30-14:00	Towards sustainability in Bioinformatics training, Judit Kumuthini
14:00-14:15	Selected oral presentation: Added value of whole-genome sequence data to genomic predictions, Marco Bink
14:15-14:30	Selected oral presentation: Molecular Signalling in interaction between Potato, Potato virus Y and colorado Potato beetle, Kristina Gruden
14:45-15:30	Coffee Break and Poster Presentations
15:30-16:00	Training in computational skills, Aleksandra Pawlik
16:00-16:30	NGS in Functional Genomics: Where are we now and its impacts, Ana Conesa

Day 2	NGS: State of the Art, Current Challenges & Applications Chair: Aleksandra Pawlik
09:00-09:30	Morning Coffee
09:30-10:00	Coding & Best Practice in Programming: Why it matters so much in the NGS era, Lex Nederbragt
10:00-10:30	GWAS, where are we now?, Ashley Farlow
10:30-11:00	Scaling Galaxy for Big Data, Dave Clements
11:00-11:30	Coffee Break & poster set-up
11:30-12:00	Sex, deep sequencing and microRNAs, Antonio Marco
12:00-13:00	Lunch
13:00-13:15	Selected Oral Presentation: Transcription microvariability detection by NGS, Fleur Leenen
13:15-13:30	Selected oral presentation: From BIG data to RELEVANT data: Application of ribo- seq technology for understanding gene expression, Pavel Baranov
13:30-13:45	Selected oral presentation: KmerStream: a Streaming Algorithms for k-mer Abundance Estimation, Pall Melsted
13:45-14:15	NGS data management and analysis for hundreds of projects: Experiences from Sweden, Ola Spujuth
14:15-15:00	Coffee Break
15:00-15:15	Selected oral presentation: High-throughput Sequencing of the Immunoglobulin Heavy Chain Repertoire of Transgenic Humanized Rats Reveals Convergent Antibody Signatures, Claude Muller
15:15-15:30	Selected oral presentation: Analyzing RNA-seq data with RNASeqHUI, Claudia Angelini
15:30-16:00	NGS in Pathogen Genomics: It's impact and applications, Claudio Donati
16:00-16:30	Impact and sustainability of hands-on training in the analysis of NGS data, Gabriella Rustici
16:30-17:15	Closing remarks & What's Next, Erik Bongcam-Rudloff

Day 3	SeqAhead Management Committee Meeting
08:30-09:00	Morning Coffee
09:00-09:15	Welcome, Introduction and overview of the day, Vicky Schneider
09:15-09:30	Approval of minutes and matters arising from last meeting
09:30-10:00	Update from the Action Chair Status of Action, including participating countries
10:00-10:20	Promotion of gender balance and of Early Stage Researchers (ESR) STSM status and new applications
10:20-10:30	Annual Progress Conference in Malta
10:30-11:00	Coffee Break
11:00-11:40	Follow up of MoU objectives a. WG reports (5 mins each) b. Progress report on the third years workshops (5 mins) c. Publication of State-of-the-art Reports (5 mins) d. Maintaining lists of publications and projects on the website (5 mins)
11:40-12:50	Scientific Planning for last year of the action a. Scientific strategy: WG activity during the last year b. Action Budget Planning c. Long-term planning (including anticipated locations and dates of future activities) d. Dissemination planning (publications and outreach activities)
12:50-13:00	Summary of Management Committee Decisions, close meeting and confirm location and date of next meeting
13:00-14:00	Lunch