Programme of the SeqAhead MC Business Meeting and Scientific Meeting

Monday		**November 7 - Management Committee (MC) business meeting - By invitation only**
12:00	12:15	Welcome and lunch at COST office
		• *Welcome by local organizer (Jacques van Helden)* • *Welcome by the chair (Erik Bongcam)*
12:15	14:00	Lunch
14:00	18:00	MC (Management Committee) business meeting
		Auditorium room (COST office, 15th floor) • *Introduction by the chair Erik Bongcam-Rudloff* • *WG presentations by the WG chairs* *WG1: Technology watch for new developments - Ralf Herwig* *WG2: Development of an Action Plan for NGS bioinformatics to cope with challenges for ERA - Andreas Gisel* *WG3: Design, implementation, and incorporation of software solutions - Eija Korpelainen* *WG4: Generic informatics topics - Veli Makinen* *WG5: Development of a strategic dissemination and education program for NGS bioinformatics - Jacques van Helden* • *Discussion of common aims* • *Discussion programme COST Action year 2* • *Discussion training school and workshop in Uppsala* • *Alliances:* *Sylvie Hermouet: BM0902: Network of experts in the diagnosis of myeloproliferative disorders (MPD)*
Tuesday		**November 8 – Scientific program meeting**
		Scientific program meeting *Auditorium room (COST office, 15th floor)*
09:00	10:20	Session 1 - Facilities
09:00	09:20	Robert Lyle. The Norwegian Sequencing Centre (NSC)
09:20	09:40	Kjell Petersen. NGS research and service at the CBU
09:40	10:00	Laurent Falquet. The Vital-IT HPC and the Swiss-Prot group
10:00	10:20	Ning Li. BGI: combination of sequencing and bioinformatics strategy
10:20	11:00	Coffee break
11:00	12:00	Session 2 – Various

11:00	11:20	Matthias Steinbrecher. Innovation and Trends with In-Memory Technology
11:20	11:40	Jean Imbert. HTS Science and Technology Watch Tour
11:40	12:00	José Ramón Valverde. NGS data analysis: the user POV
12:00	14:00	Lunch + posters
14:00	16:00	Session 3 - Tools and applications
14:00	14:20	Frank Picard. Bioinformatics developments for NGS data analysis at PRABI
14:20	14:40	Ana Conesa. NOIseq: a RNA-seq differential expression method robust for sequencing depth biases
14:40	15:00	Eric Rivals. A combinatorial and integrated method to analyse RNA-seq reads
15:00	15:20	Jacques van Helden. RSAT peak-motifs: fast extraction of transcription factor binding motifs from full-size ChIP-seq datasets
15:20	15:40	Luca Pireddu. The Seal suite of distributed software for high-throughput sequencing
15:40	16:00	Keijo Heljanko. Scalable Cloud Computing Solutions for Next Generation Sequencing Data
16:00	16:30	Coffee break
16:30	17:30	Session 3 - Tools and applications (continued)
16:30	16:50	Andreas Gisel. smallRNA data analysis.
16:50	17:10	Eija Korpelainen. Chipster 2.0: User-friendly NGS data analysis software with built-in genome browser and workflow functionality
17:10	17:30	Petr Baldrian. Exploration of environmental metagenomes and metatranscriptomes: current possibilities and limitations in data analysis
17:30	18:15	Discussions: Challenges and perspectives
20:00	22:00	Dinner
Wednesday		**November 9 - Work group meetings**
09:00	09:20	Introduction by Erik Bongcam
09:20	11:30	Split meeting (parallel sessions)
		• *WG1: Technology watch for new developments - Ralf Herwig* • *WG2: Development of an Action Plan for NGS bioinformatics to cope with challenges for ERA - Andreas Gisel* • *WG3: Design, implementation, and incorporation of software solutions – Eija Korpelainen* • *WG4: Generic informatics topics - Veli Makinen* • *WG5: Development of a strategic dissemination and education program for NGS bioinformatics - Gert Vriend*
11:30	12:30	Conclusion
12:30		End of the meeting