ESF
Next-Generation Sequencing Meeting

Leiden, The Netherlands: August 29-September 1, 2010

Date	8:30-9:00	9:00-12:30	12:30-13:30	13:30-17:00	17:00-19:00
08/29/10		Registration from 12:00	Registration	Hands-on workshops	
08/30/10	Coffee	Registration & Oral session 1	Lunch	Oral session 2	Posters & Drinks
08/31/10	Coffee	Oral session 3	Lunch	Oral session 4	Posters & Drinks
09/01/10	Coffee	Oral session 5	Lunch	New Technology Sponsored Talks	

On 8/31/10 there is also dinner from 19:00 in Restaurant Building 2

Program color code: Keynote speakers Selected researchers Selected young researchers

Day 2, August 30, 2010

8:30-9:00 Welcome coffee 8:00-11:00 Registration

Oral Session 1a: From old to new: evolution and archaeology
Chair: Peter de Knijff

8:55-9:00 Welcome talk: **GertJan van Ommen**
9:00-9:30 Evolutionary insights from the 1000 Genomes Project: **Chris Tyler-Smith**, The Wellcome Trust Sanger Institute, Hinxton, UK
9:30-9:50 Ancient DNA research without PCR: the power of single molecule sequencing: **Eveline Altena**, Leiden University Medical Center, Leiden, NL
9:50-10:20 Hunting the Molecular Past: **Eske Willerslev**, Ancient DNA and Evolution Group, Department of Biology, Univ of Copenhagen, Denmark

10:30-11:00 coffee

Oral Session 1b: Gene expression and regulation, part I
Chair: GertJan van Ommen

11:00-11:30 Evolution of transcriptional control in mammals: **Mike Wilson**, Cancer Research UK, Cambridge Research Institute Department of Oncology, University of Cambridge, UK
11:30-11:50 Nucleolar association of DNA: **Marek Gierlinski**, University of Dundee, Dundee, UK
11:50-12:10 Pol II ChIP-seq as a measure of gene transcription rate: **Michal Mokry**, Hubrecht Institute, Utrecht, NL
12:10-12:30 Linking genomic variation to differences in transcriptomes: **Marieke Simonis**, Hubrecht Institute, Utrecht, NL

12:30-13:30 Lunch

Oral Session 2: Gene expression and regulation, part II
Chair: Edwin Cuppen

13:30-14:00 Tag-based transcript sequencing: Comparison of SAGE and CAGE: **Matthias Harbers**, DNAFORM Inc., Japan
14:00-14:20 The small transcriptome of prostate cancer: **Elena S. Martens-Uzunova**, Erasmus MC, Rotterdam, NL
14:20-14:40 Next generation sequencing-based mRNA profiling of total blood in a large human cohort: **Peter-Bram 't Hoen**, Leiden University Medical Center, Leiden, NL
14:40-15:00 RNA-Seq in Ensembl: **Simon White**, Wellcome Trust Sanger Institute, Hinxton, UK

15:00-15:30 coffee

15:30-16:00 Mapping and quantifying mammalian transcriptomes by RNA-Seq: **Barbara Wold**, Division of Biology, California Institute of Technology, USA
16:00-16:20 Tracing the derivation of embryonic stem cells from the inner cell mass by single cell RNA-Seq analysis: **Raimo Tanzi**, Life Technologies, USA
16:20-16:50 Next-generation systems genetics: **Edwin Cuppen**, Hubrecht Institute, Utrecht, NL

17:00-19:00 Poster viewing & Drinks

Day 3, August 31, 2010

8:30-9:00 Welcome coffee

Oral Session 3: Re-sequencing and diagnostics, part I

Chair: Xavier Estivill

9:00-9:30 Bacterial metagenomics: **Sacha van Hijum**, NIZO food research, Ede; Radboud University Medical Center, Nijmegen; and TIFN

9:30-9:50 Benefit of high throughput sequencing in virus discovery: **Michel de Vries**, Academic Medical Center of the University of Amsterdam, Amsterdam, NL

9:50-10:10 Multiplexed targeted genomic enrichment and next-generation sequencing for efficient mutation discovery: **I.J Nijman**, Hubrecht Institute, Utrecht,NL

10:10-10:30 Multiplexed amplicon sequencing of the breast cancer genes BRCA1 & 2: opportunities, challenges and limitations: **Kim de Leeneer**, CMGG, University Hospital Ghent, Gent, BE

10:30-11:00 coffee

11:00-11:30 The next generation of human genetics: **Debbie Nickerson**, Dept. of Genome Sciences, Univ of Washington, Seattle

11:30-11:50 Disease gene identification by exome sequencing: **Alexander Hoischen**, Radboud University Nijmegen Medical Centre, Nijmegen, NL

11:50-12:20 The 'next' of next-generation sequencing; diagnostic applications: **Joris Veltman**, Radboud University Nijmegen Medical Centre, Nijmegen, NL

12:30-13:30 Lunch

Oral Session 4: Current and Future Challenges

Chair: Ivo Gut

13:30-14:00 Alignment and assembly: **Ewan Birney**, EBI, Hinxton, UK

14:00-14:20 Reconstructing complex plant genomes using NGS data: **Erwin Datema**, Wageningen University, Wageningen, NL

14:20-14:40 Context dependency in Illumina sequencing: **Irina Abnizova**, Wellcome Trust Sanger Institute, Hinxton, UK

14:40-15:00 Direct comparison of highly multiplexed pre-barcoded microarray and solution-based genomic enrichment of human samples: **Magdalena Harakalova**, University Medical Center Utrecht, Utrecht, NL

15:00-15:30 coffee

15:30-16:00 Storage and archiving: **Guy Cochrane**, EBI, Hinxton, UK

16:00-16:20 The vision of the Genomic Standards Consortium in today's ultra high-throughput sequencing era: **Peter Sterk**, Wellcome Trust Sanger Institute, Hinxton, UK

16:20-16:50 READNA - 4 Generations of Nucleic Acid Analysis: **Ivo Gut**, Centre Nacional d'Analisis Genomics (CNAG), Barcelona, Spain

17:00-19:00 Poster viewing & Drinks

19:00 Dinner

Day 4, September 1, 2010

8:30-9:00 Welcome coffee

Oral Session 5: Re-sequencing and diagnostics, part II

Chair: Joris Veltman

9:00-9:30 Fast forward: genomic technologies and research ethics: **Jeantine Lunshof**, Faculty of Health, Medicine and Life Sciences, Maastricht University, NL

9:30-9:50 Exome sequencing identifies WDR35, encoding an IFT-A protein, as a novel gene involved in Sensenbrenner syndrome: **Christian Gilissen**, Radboud University Nijmegen Medical Centre, Nijmegen, NL

9:50-10:10 Exome sequencing combined with linkage-based gene prioritization strategy for identification of autosomal dominant mutations in multiplex autism families: **Martin Poot**, University Medical Center Utrecht, Utrecht, NL

10:10-10:30 Mate-pair sequencing reveals de novo and inherited chromosomal rearrangements in a family trio: **Wigard Kloosterman**, University Medical Center Utrecht, Utrecht, NL

10:30-11:00 coffee

11:00-11:30 Getting more comprehensive understanding of human genetic variation: **Ruiqiang Li**, Beijing Genomics Institute, Shenzhen, China

11:30-11:50 Finding the causal variant in a region of genetic association: **Allan F McRae**, Queensland Institute of Medical Research, Brisbane, AU

11:50-12:20 Using next-generation sequencing to understand human genome structural variation: **Evan Eichler**, Univ of Washington, Seattle, USA

12:30-13:30 Lunch

New Technology Sponsored Scientific Talks

Chair: Johan den Dunnen

13:30-13:55 Rapid preparation of targeted resequencing libraries from genomic and FFPE-extracted DNA using microfluidic PCR: **Fiona Kaper**, R&D team, Fluidigm

13:55-14:20 Single molecule real-time nucleic acid sequencing-by-synthesis using Quantum-dot (Qdot(R)) nanocrystal DNA polymerases with FRET-based detection: **Manfred Lee**, Genetic Systems, Life Technologies, Carlsbad CA, USA

Closing discussion

14:20-14:30 Results of survey among European NGS users: **Terry Vrijenhoek**, Radboud University Nijmegen Medical Centre, Nijmegen, NL

14:30-15:15 Round table discussion on NGS in Europe - **ERA-Instuments**

15:15-15:30 Closing and Awards: **Johan den Dunnen**

15:30-16:00 coffee

16:00 All ends