

Posters you find at the NORBIS meeting

1.

Epistasis Analysis Reveals Distinct Roles of Non-homologous End Joining Factors in Human HAP1 Cells

Mengtan Xing, NTNU

2.

Copy Number Variation detection tool for Targeted Sequencing data

Ashish Kumar Singh, NTNU

3.

Strain engineering strategies of genome-scale reconstruction of *Streptomyces coelicolor*

Tjaša Kumelj, NTNU

4.

In vivo vs In vitro – A comparison of prostate cancer cell lines and tissue using FunHoP

Kjersti Rise, NTNU

5.

Parent-of-Origin-Environment Interactions in Case-Parent Triads With or Without Independent Controls

Miriam Gjerdevik, University of Bergen

6.

Metabolically Define Breast EMT and HER2-induced Malignancy via Global LFQ and SILAC Proteomic Approaches

Qiong Wang, NTNU

7.

Comparing protein and proteoform networks for functional analysis

Luis Francisco Hernández Sánchez, University of Bergen

8.
Identifying small peptides in mass spectrometry samples
Bram Burger, University of Bergen

9.
ELFI: Engine for Likelihood-Free Inference.
Kusti Skytén, University of Oslo

10.
Methylation in mtDNA
Romain Guitton, University of Bergen

11.
The interplay between SUMO-dependent gene repression and c-Myb-dependent gene activation
Roza Berhanu Lemma, University of Oslo

12.
Urinary phosphoproteome analysis to differentiate aggressive and indolent prostate cancer
Trung Tran, University of Oslo

13.
A map of direct TF-DNA interactions in the human genome
Marius Gheorghe, University of Oslo

14.
Deep Bayesian regression models
Aliaksandr Hubin, University of Oslo

15.
TAME-SEQ: AN EFFICIENT SEQUENCING APPROACH TO CHARACTERIZE HUMAN PAPILLOMAVIRUS GENOMIC VARIABILITY AND CHROMOSOMAL INTEGRATION
Sonja Lagström, Akershus University Hospital and Cancer Registry of Norway

16.

Development of protein quantification methods for therapeutic proteins and their modification using peptide and protein labeling techniques in combination with liquid chromatography and mass spectrometry

Christina Johannsen, University of Oslo

17.

Early Signatures of Lung Cancer in Serum RNAs

Sinan Ugur Umu, Cancer Registry of Norway

18.

Detection of small non-coding RNA biomarkers in prediagnostic testicular germ cell tumour serum.

Joshua Burton, Oslo Met

19.

Multi-omics approaches to alkylation base modifications

Sarah Martin, NTNU

20.

Environmental epigenetics: methylome analysis in testicular cancer

Marcin Wojewodzic, Cancer Registry of Norway

21.

Transcriptome changes in retinal cultures after starvation

Turkuler Ozgumus, University of Bergen

22.

Getting to the root cause of Alzheimer's disease – tracing molecular events in cell populations during disease progression in mouse models of Alzheimer's disease

Lene Christin Olsen, NTNU

23.

A dynamic landscape of super-enhancers during mouse development

Aziz Khan, University of Oslo

24.

Characterization of mutations that dysregulate driver microRNAs in cancer

Jaime Castro-Mondragon, University of Oslo

25.

hGSuite HyperBrowser: Hierarchical genomic data analysis

Diana Domanska, University of Oslo

26.

Efficient multivariate approach for bacterial GWAS using preselection screening

T. TIEN MAI, University of Oslo

Numerically, we show that Elastic-Net with a pre-selection step out-performs other state-of-the-art methods in bacterial GWAS.

27.

Benchmarking machine learning methods for pattern prediction and recovery in antibody sequences

Rahmad Akbar, University of Oslo

28.

Contemporary Directions in Likelihood-Free Inference

Owen Thomas, University of Oslo

29.

Characterization of population specific variation in non-coding genomic regions and application to Type 2 diabetes

Yafei XING, University of Oslo

30.

High throughput platform for investigating gene regulation networks of Type 2 Diabetes

Siqing Liu, University of Oslo

31.

De novo identification of well hopping fragments (ex-amp duplicates) in Illumina patterned flow cells using suprdUPr

Arvind YM Sundaram, University of Oslo

32. A functional link between FOXA1 and SUMO
Ankush Sharma – University of Oslo