

NTNU Bioinformatics Network Meeting

Biological networks – from genes to populations

December 8th 2014

Suhm-huset - Øya – Trondheim

- 08.45-09.00** **Registration**
- 09.00-09.15** **Welcome**
- 09.15-09.40 Åsmund Flobak – Dept. of Cancer Research and Molecular Medicine - NTNU
Computational modeling and simulations to predict combinatorial drug responses
- 09.40-10.05 Morten Beck Rye - Dept. of Cancer Research and Molecular Medicine – NTNU
Tissue heterogeneity and data integration in prostate cancer
- 10.05-10.35** **Break (coffee, fruit)**
- 10.35-11.00 Lene C. Olsen – Dept. of Cancer Research and Molecular Medicine – NTNU
What's up in the grid cells
- 11.00-12.00 **Keynote - [Steve Horvath](#)** - Human Genetics and Biostatistics - UCLA Program on Genomics and Nutrition
When is hub gene selection better than standard meta-analysis?
- 12.00-13.15** **Lunch**
- 13.15-13.40 Berit Johansen – Dept. of Biology – NTNU
Diet composition, biology and health
- 13.40-14.05 Marit H. Stafsnes - Dept. of Biotechnology – NTNU
Deep phenotyping using Mass Spectrometry based Metabolomics and Fluxomics
- 14.05-14.30 Pankaj Barah – Dept. of Biology - NTNU
Can regulatory genomics explain climate adaptation and genome evolution in plants?
- 14.30-14.50** **Break (coffee)**
- 14.50-15.15 Eivind Almaas - Dept. of Biotechnology - NTNU
Constraint-based metabolic modeling to investigate omics data
- 15.15-15.40 Jarle Tufto – Dept. of Mathematical Sciences - NTNU
Quantitative genetics and evolutionary responses to changing environments
- 15.40-15.45** **Closure**