Newsletter

from FUGE Mid-Norway

www.ntnu.no/fuge

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Editorial

Since the near complete version of the human genome was reported in 2004, sequencing technology has been improved immensely. Now entire subject-specific genomes can be sequenced in a few weeks, and the first cancer-clone-specific genome was presented in Nature last year. DNA from acute myeloid leukemia cells was sequenced and compared to the patient's own skin cell genome. When, or whether, whole genome sequencing will be a standard diagnostic tool in our health care system, is still unknown. However, what this illustrates is the unforeseen rapid speed of technological development. There is a prize of US$ 10 mill out there for the first who can sequence 100 human genomes in 10 days for US$ 10.000 or less per genome. If sequencing technology development continues at the same speed, that prize will be claimed before long. Nevertheless, accumulating sequence data without doing functional genomics (FUGE) is much like acquiring books in an unintelligible language. Only through FUGE activities can sequence data give meaningful information. Therefore, putting genome data into context is more important than ever. And, importantly, that's the fun part: to understand what the words mean.

Best regards, Magne Børset
Leader FUGE Mid-Norway committee

PNAS' Cozzarelli Prize in Biological Sciences for 2008

Pål Sætrom and Ola Snøve have been awarded PNAS Cozzarelli Prize in Biological Sciences for 2008 together with researchers from Beckman Research Institute of the City of Hope, Daniel H. Kim and John J. Rossi. The award was given with background in a article published in PNAS October 21, 2008:

"MicroRNA-directed transcriptional gene silencing in mammalian cells"

The paper adresses the question whether microRNA can regulate gene expression in the nucleus. For the first time, the authors provide evidence for an endogenous pathway for microRNA-directed transcriptional gene regulation in the nucleus of mammalian cells.

FUGE Mid-Norway offers its congratulations to this excellent publication and the PNAS Cozzarelli prize in Biological Sciences for 2008.

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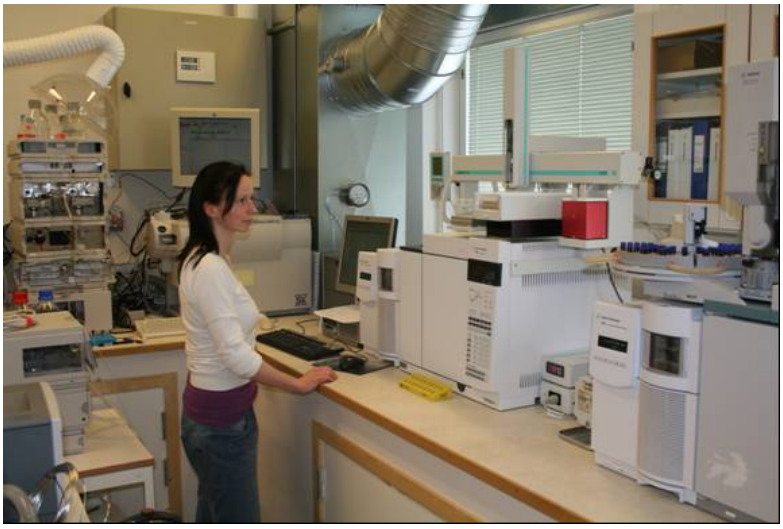
Trondheim Metabolomics Center

In Mid-Norway several research groups have formed the basis of Trondheim Metabolomics Center (TMC). The two most important techniques in metabolomics are mass spectrometry (MS) and nuclear magnetic resonans (MR) (For more information about the methods please see Hollywood et al., 2006). The aim of TMC is to have a joint strategy for MR and MS metabolomics. This will make the researchers international competitive through development of new technologies and methodology for metabolite analyses of all kinds of biological samples. In addition, they have a joint agenda of teaching students metabolomics through a PhD subject in metabolomics.



PhD student Stina K. Lien working on the "gold standard" work horse in Metabolomics - one of the four Agilent GC-MS instruments in the MS lab.

The MS lab

The MS part of TMC is located at the joint MS-laboratory of Department of Biotechnology, NTNU and SINTEF Materials and Chemistry, Department of Biotechnology. The leaders of this part of TMC are Per Bruheim (NTNU) and Håvard Sletta (SINTEF). The MS-laboratory is currently equipped with 4 GC-MS and 9 LC-MS instruments. To cover the major classes of metabolites they have established three core Metabolomics methods: 2 GC-MS and 1 LC-MS. Hence, they can easily analyse for changes in the composition of amino acids, organic acids, sugar and sugar alcohols, vitamins, sugar phosphates and other phospho-metabolites, nucleotides and nucleosides in the metabolome.

The MS technique has been used in a research project on how to optimise antibiotic production in a bacterium. When a bacteria starts to produce antibiotics it slows down its proliferation, and as a consequence its metabolite profile changes. By using a systems biological approach, combining gene expression and metabolite profiles, the production of antibiotics may be optimised based on the information of MS and microarray analysis.

Metabolomics is one of the last introduced 'OMIC technologies in functional genomics.

Metabolomics is the "systematic study of the unique chemical fingerprints that specific cellular processes leave behind" - (B. Daviss, *The Scientist*, 19[8]:25-28, 2005).

The MR lab

Ingrid Gribbestad is the leader of the MR part of TMC. Gribbestads lab has established High-resolution magic angle spinning (HR-MAS) MR spectroscopy. This is an *ex vivo* technique that can be applied to intact tissue for obtaining a detailed picture of tissue biochemistry.

The ex vivo technique is unique in the way that it don't destroy the tissue. Hence, the samples analysed by MR spectroscopy may also be analysed genetically or pathologically. Gribbestad and her coworkers have used a combination of MR spectroscopy, genetic analyses and pathological analysis in their research on breast cancer. By linking different type of analysis they have found that HR MAS MR spectroscopy can be a tool in breast cancer diagnosis, treatment regime planning and treatment monitoring. Clinical MR metabolomics of biofluids is currently being established, headed by Tone Bathen.

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Funds to buy services from the FUGE platforms

FUGE mid-Norway congratulate

Jan Egil Afset , Bjørn Munro Jenssen, Hans E. Krokan, Helena Bertilsson, Odrun Gerderaas, Åsa A. Borg, Jens Rohloff, Anna Kusnierczyk, Astrid Lægreid, Marit W. Anthonsen, Tore Brembu, Geir Bjørkøy, Helga Ertesvåg

with the allocated funds for the purchase of platform services.

Travel and Service funds:

FUGE mid-Norway congratulate

Ane Kjersti Vie / Bin Liu , Anna Kusnierczyk, Åsa Borg, Ishita Ahuja, Kirsti Kvaløy, Kristin Nørsett, Trond Kortner

with the allocated funds for travels.

FUGE mid-Norway congratulate

Atle Bones, Kristian Hveem, Geir Slupphaug og Arne Sandvik

with the allocated funds for service contracts.

News from NFR
(The Research Council of Norway)

The FUGE-NFR web page has been re-designed and is constantly updated with news related to functional genomics.
(Link to FUGE-NFR).

Summary of news from NFR:

- **FUGE-forskere med kreftgjennombrudd**
- **To millioner til bioprospektering**
- **Dypdykk i marine gener**

Seminars

Seminar by Dr Lena Wester Rosenlöf
June 12 at 11.15 - 12.00, Realfagsbygget, R3
Title: "Functional genomic strategies to study nuclear and mitochondrial genes associated with complex autoimmune diseases"

Seminar by Prof. Stefano Ciurli
June 9 at 12.15 in K3-039 - Kjemibygget
Title “Functional genomics of metal sensing and trafficking: the importance of intrinsic unfolded proteins”.

For more information about the FUGE seminars please see here.

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Course in writing applications

FUGE Mid-Norway invited Knut Røe from Røe kommunikasjon AS to hold a today-seminar with focus on how to write good applications. Knut Røe was employed by NRK for 24 years as a reporter, editorial manager and channel manager. In addition he has written textbooks in journalism and communication and started Røe Kommunikasjon AS in 1997.


Knut Røe I Røe Kommunikasjon AS

The main focus of the course was how to write an application in order to evoke the evaluator's interesse in the application.

The course was structured so that the participants received personal feedback on a personal application soon to be submitted. The participants received feedback on their applications from both Knut Røe and Stewart Clark, an English translator, and the participant's themselves. In addition, an experienced evaluator, professor Berit Johansen, was invited to the course. She gave the participants the opportunety to ask questions to understand how an evaluator evaluates an application.

With only 5 participants, the course was a great opportunety to get personal feedback on their own writing. Much of the feedback was given on the introduction in the application in order to catch the evaluators' interest from the start.

The take home message of the course was that it is important with a good opening that catches the reader's interest. Thereafter, you may give the scientific details that are needed to explain the project.

Many of the participants is about to submit their applications in June. We are looking forward to see how many of those who will be granted money in the fall.

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