

# Newsletter/Core facilities

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from The Faculty of Medicine

[www.ntnu.edu/dmf/core-facilities](http://www.ntnu.edu/dmf/core-facilities) | [janne.ostvang@ntnu.no](mailto:janne.ostvang@ntnu.no)

## Genomics Core Facility

**The Genomics Core Facility (GCF) supports your research needs for high-throughput genomics. Do you want to look at whole genome gene expression, genotyping or DNA/RNA sequencing? The Genomics Core Facility may provide you with information on how to plan and perform your wet lab experiment, or how to collect human or animal samples, before high-throughput genomics is performed by the core.**

“The latest implemented technique at GCF is state-of-the-art high throughput sequencing (HTS) technology. This winter we received a brand new Illumina HiSeq2500 machine that allows us to carry out a variety of studies such as de novo sequencing, whole genome or targeted resequencing, complete exome sequencing, whole genome transcriptome profiling, ChIP-Seq to detect transcription binding sites across the genome, and metagenomic sequencing of microflora genomes”, says scientific leader Arne Sandvik.



Photo: Geir Mogens

The staff at GCF is excited to provide the users with this novel sequencing technology, and they expect that this investment will recruit new users to the core facility. “Due to the advanced equipment our users do not carry out hands-on analysis on our instruments themselves, but they preorder the service. Having the service performed by qualified staff. This ensures that the results from sequencing or other high-throughput genomics analysis is of excellent quality”, says the core manager Vidar Beisvåg. The staff is used to handle valuable DNA/RNA samples to ensure that they are not degraded as the analysis is carried out.

We want to support and offer services to all good scientific projects that can benefit from the genomics technology available at our core. For that matter, it is important for GCF to provide basic bioinformatics support as well as the genomics technology. The core manager Vidar Beisvåg points out that: “Although we provide basic bioinformatics support, the user needs to interpret the results according their own biological questions”. If you have little or no experience with genomics, the staff at GCF will be happy to discuss possible experiment setups, and help assess whether your project may benefit from different genomics methods. More information about the core may be found here:<http://www.ntnu.edu/dmf/gcf>



Norwegian University of  
Science and Technology

# Status GCF spring 2013

GCF currently offers a variety of genomics based DNA/RNA analysis. Our most “popular product/service” during 2012, was the Illumina Cardio-Metabo SNP Chip and Illumina Infinium HumanExome SNP Chip service, where we performed analysis on approximately 10 000 samples from the HUNT biobank. Illumina offers a variety of standard SNP chips containing from app. 200 000 – 4 000 000 SNPs per chip analyzed with our Illumina HiScann instrument. Illumina also offers an option to add custom designed SNPs to some of their standard chips or to make a complete custom chip. One large project has used this option, a research group at the Department of Biology designed their own “grey sparrow” SNP chip and this is probably the first time worldwide such analyses have been performed. This project nicely shows the flexibility of the Illumina SNP system.

Regular global gene expression analysis using Illuminas Infinium Gene Chips was also extensively used in 2012, GCF analyzing approximately 1 800 human/mouse samples during the year.

During the first 6 months of 2013 a large number of samples (approximately. 7 000) will be analyzed using the Illumina Infinium HumanExome SNP Chip, and most likely also several custom SNP chip related projects. Moreover, there will be a relatively large number of projects/samples run on regular global gene expression chips, but during the year some of the RNA analysis will probably be switched to high throughput sequencing (HTS) technology (RNASeq). GCF has recently installed a state-of-the art Illumina HiSeq instrument for high throughput sequencing, and we are now able to offer a wide variety DNA and RNA sequencing services. The Illumina HiSeq System employs proven, reversible terminator-based sequencing by synthesis using their latest TruSeq chemistry to provide massively parallel sequencing. With the ability to generate up to 600Gb of high accuracy-data per run, the Illumina platform allows high-quality analysis of large and complex sample sets, spanning from whole genome and exome sequencing through whole transcriptome to microRNA analysis.

An important intention for GCF is to offer a good, integrated bioinformatics service related to the chip and HTS services. GCF therefore wishes to be involved as early as possible in project planning to ensure a good study design and optimize the analyses as much as possible.

Extended information about GCF services can be found at the GCF web page: <http://www.ntnu.edu/dmf/gcf> . Please do not hesitate to contact us if you have any question related to our genomics service.

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Photo: Geir Mogens

## Official opening of Unit of Comparative Medicine (UCM)

**The official opening of UCM will take place on 24<sup>th</sup> of April.**

Even though the animal facility (Unit of Comparative Medicine) for a long time has been operating like a core facility, the facility will finally be implemented as one of the Faculty of Medicine's core facilities from 1<sup>st</sup> of May. More information about the opening ceremony, that will take place at the 24<sup>th</sup> of April, will be announced at Innsida (NTNU) and will be sent to all users of the facility in a separate invitation.

### Information day for core facilities

During the opening event, we will also provide you with information about five other core facilities at the Medical Faculty (NTNU): Bioinformatics Core Facility, Cellular and Molecular Imaging Core Facility, Genomics Core Facility, MR Core Facility, Proteomics and Metabolomics Core Facility.

In addition we will have a live online presentation of our booking system for new users.

## Imaris Open Day, 26<sup>th</sup> April

Imaris is visualization and analysis software for 3D and 4D microscopy data sets. CMIC users have access to this software on a workstation in Gastro, 3<sup>rd</sup> floor (IKM). <http://www.bitplane.com/go/products/imaris>

An introduction to Imaris will be given by Dr. Delisa Garcia, Scientific Liaison and Sales Representative, Bitplane AG

Seminars in the morning will cover various imaris functions, how they work and some applications (open for everyone). Practical session in the afternoon to discuss with users how to achieve the analysis they want with Imaris (for registered users only)

More info and registration on CMIC website:  
<http://www.ntnu.edu/dmf/cmhc>

Imaris website: <http://www.bitplane.com/go/products/imaris>

**VACANCY at Cellular and molecular Imaging Core facility (CMIC):**  
<http://www.jobbnorge.no/job.aspx?jobid=91714>

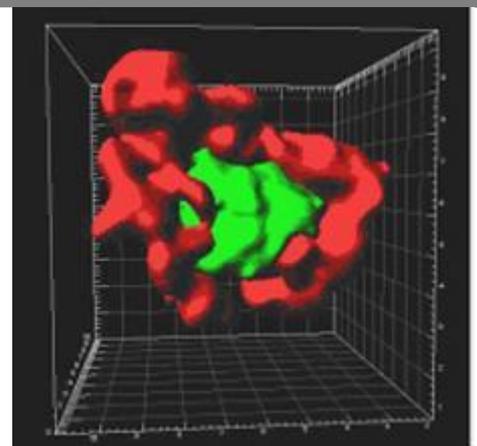


Photo: Harald Huseby