Newsletter/Core facilities

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from The Faculty of Medicine

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Innføring av Totalkostmodellen

-hvordan berøres bruken av kjernefasilitetene?

Our aim is that the newsletter should be written in English. We apologize, the first article in this newsletter are written in Norwegian to ensure a correct communication of the total cost model.

De fleste har hørt at totalkostmodellen (TDI-modellen) innføres fra 1.1.2015, og at med den kommer begrepet leiested. En kjernefasilitet regnes som et leiested – så hvordan skal brukere av kjernefasilitetene forholde seg til innføringen av leiested? Vi vil gi dere informasjon om hvordan innføringen skjer ved Det Medisinske Fakultet sine kjernefasiliteter og hva dere må tenke over i denne prosessen.

Hva er TDI-modellen?

I 2007 kom det et krav fra Kunnskapsdepartementet om at alle kostnader skal synliggjøres i Bidrags- og Oppdragsprosjekter (BOA)[1]. Vi har foreløpig ikke hatt noen gode verktøy for å kunne gjøre dette, men i 2012 utviklet U&H sektoren en nasjonal modell for beregning av totale kostnader i forskningsprosjekter: **TDI-modellen**. TDI står for Tid, direkte- og indirekte kostnader. Modellen skiller mellom direkte og indirekte kostnader hvor det som kalles for **leiested** er en ny faktor under direkte kostnader. Et leiested menes her med: «Felles infrastruktur hvis driftskostnader synligjøres særskilt og fordeles forholdsmessig mellom de prosjekter og aktiviteter som anvender infrastrukturen». **En kjernefasilitet er en type leiested**. I 2013 ble det også utarbeidet retningslinjer for hvordan man finner de totale kostnadene for et leiested og beregner priser for bruk[2]. NTNU har en egen wiki-side[3] som gir mere detaljer om TDI-modellen, og tilhørende satser og budsjetteringsmaler.

For dere som skal bruke kjernefasiliteter, er det viktig å hente informasjon om priser som er utarbeidet i henhold til retningslinjene for leiested, slik at dere kan budsjettere med leiestedskostnader i prosjektsøknader.

Tabell 1. Kostnader som er lagt inn i bidrags- og oppdragspriser for leiested.

Bidragspris	Oppdragspris
Arealkostnader	Laboratorier/verksteds kostnader
Avskrivingskostnader internfinansiert utstyr	Avskrivingskostnader internfinansiert utstyr
	Avskrivingskostnader eksternfinansiert utstyr
Felles driftsmidler (Kjemikalier, materiell, vedlikeholdskontrakter etc.)	Felles driftsmidler (Kjemikalier, materiell, vedlikeholdskontrakter etc.)
Teknisk støttepersonell (lønnskostnad og indirekte kostnad)	Teknisk støttepersonell (lønnskostnad og indirekte kostnad)
	Fortjeneste påslag (minst 5%)

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[1] KDs rundskriv 20-07

[2] Rapport fra ei nasjonal arbeidsgruppe på oppdrag fra Universitets- og høgskolerådet, 1. oktober 2013

[3] https://innsida.ntnu.no/wiki/-/wiki/Norsk/Beregne+kostnader+i+forskningsprosjekt

Husk å legge inn kostnader for leiested/kjernefasiliteter i årets søknader!

Prislister for totale kostnader ved kjernefasilitetene finnes på kjernefasilitetenes hjemmesider. Husk å bruke prislisten for 2015 ved utarbeidelse av budsjett for søknader i 2014.

Følgende retningslinjer gjelder for søknader om Bidragsprosjekter
Totale kostnader skal synliggjøres i alle søknader om bidragsprosjekter.

- I søknader til Forskningsrådet kan totale leiestedskostnader legges inn **uten** egeninnsats så fremt utlysningen ikke begrenser muligheten til å få dekket slike kostnader. Behovet for bruk av leiested må begrunnes i søknaden.

- I søknader til finansieringskilder som ikke dekker leiestedskostnader fullt ut, skal totale leiestedskostnader likevel synligjøres i søknaden. En andel av kostnadene defineres som egeninnsats i søknaden. Kjernefasiliteten vil på fullmakt fra ansvarlig institutt fastsette omfanget av egeninnsatsen. Søker må selv ta kontakt med kjernefasiliteten for å få oppgitt egeninnsatsen. Samtidig må kjernefasiliteten informeres om omfanget av egeninnsatsen som legges inn i hver enkelt søknad.

Følgende retningslinjer gjelder for søknader om Oppdragsprosjekter
Totale kostnader skal legges til grunn i alle søknader om oppdragsprosjekter, inkludert totale leiestedskostnader. Det er ikke anledning til å legge inn egeninnsats eller skjule kostnader i søknader om oppdragsprosjekter. I tillegg til totale kostnader, skal det legges på en fortjenestemargin på minimum 5 % på prosjektkostnaden (i hht. statsstøtteregelverket). Våre leiestedpriser inkluderer en fortjeneste margin på 5 %.

GOD PÅSKE

BioCore updates

The Society for Bioinformatics in Northern Europe (SocBiN) and the Norwegian Bioinformatics Platform / ELIXIR Norway welcome you to Bioinformatics 2014. The conference provides an open atmosphere and a social meeting place for scientist across nations, with a focus on bioinformatics and related topics. Keynote lectures will be held by well-known experts within bioinformatics such as: Eugene V. Koonin, Frank O. Glockner, Gary Stormo, Jun Liu and Steve Pettifer. For more information about the programme and keynote speakers please see: https://www.bioinformatics2014.no/

Please note the deadlines: Early Bird and abstract registration: 7 April 2014

Promec updates

The latest implemented instruments at PROMEC are the Orbitrap Elite/Qexactive mass spectrometers. These are run in-line with nanoflow UHPLC separation of peptides and allow identification and quantification of thousands of proteins in complex samples as well as analysis of post-translational modifications. Presently most protein analyses are run on these instruments, whereas analysis of small molecules are conducted on the ABI 5000 and 5500 instruments.

New methods recently implemented are targeted protein quantification by MRM as well as label-free protein quantification. The latter method does not depend on isotopic labelling of samples or internal standards and can be used for virtually any sample type. A novel method has also been established for quantitation of oxidized cysteines in proteins. The spectrum of damaged/modified DNA bases that can be quantitated now includes the epigenetic marks 5-methylC and 5-hmeC as well as uracil, 8-oxoG and a variety of alkylated bases.

In addition a wide range of modifications found in RNA can be quantified. In total >50 DNA/RNA modifications can now be quantified.

In April 2014, a Microscale thermophoresis instrument from NanoTemper was installed, allowing measurement of binding constants between proteins, nucleic acids and smaller ligands. Here, the proteins or nucleic acids to be analyzed are first labelled with a fluorophore. Alternatively GFP-tagged proteins can be expressed in cells and analyzed in cell lysates.

Finally, PROMEC has purchased 5 licenses of the Ingenuity Pathway Analysis (IPA) suite. This is the most commonly used commercial software for analysis of biological pathways using expression data from e.g proteome profiling, microarrays or sequencing. Licenses can be leased by customers on a monthly basis and introductory training can be provided by the core facility.

Genomics Core Facility updates

High Throughput Sequencing available at GCF

Sequencing is the process of determining the order of nucleotide bases (A, C, T, and G) within a stretch of DNA. Sequencing the entire complement of DNA, or genome, of many animal, plant, and microbial species is indispensable for basic biological and medical research. GCF has an Illumina HiSeq2500 instrument and offers sequencing and data analysis service for characterizing the genome, epigenome, and transcriptome.
Illumina currently offers an extensive collection of library preparation methods related to characterizing the genome, epigenome, and transcriptome. A detailed description of the Illumina “sequencing by synthesis” method and library preparation methods can be found at this web page:
http://res.illumina.com/documents/applications/sequencing-technology-poster.pdf

DNA Sequencing

Characterize genes, regions, or entire genomes with proven solutions for whole-genome or targeted sequencing, including exomes, amplicons, and *de novo* studies. More information about DNA sequencing can be found at this web page: http://www.illumina.com/applications/sequencing/dna_sequencing.ilmn

RNA Sequencing

Revolutionize gene expression profiling and transcriptome analysis with RNA sequencing. Align reads across splice junctions to identify isoforms and fusions. Quantify both rare and common transcripts. Derive precise strand information, and sequence low-quality or FFPE samples. More information about RNA sequencing can be found at this web page: http://www.illumina.com/applications/sequencing/rna.ilmn

Epigenetic Sequencing

Analyze epigenetic modifications and obtain the most complete view of gene regulation mechanics. Examine CpG methylation, histone modifications, chromatin structure, DNA-protein interactions or transcriptome profiling with a broad portfolio of sequencing tools.
http://www.illumina.com/applications/epigenetics/chip_seq.ilmnhttp://www.illumina.com/applications/epigenetics/sequencing_based_methylation_analysis.ilmn

Questions?

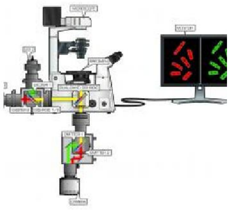
If you have any questions related to High Throughput Sequencing projects or GCF`s service, please visit our web page (http://www.ntnu.edu/dmf/gcf) or contact GCF manager Vidar Beisvåg at email (vidar.beisvag@ntnu.no) or by phone (728 25345). We will be happy to help you to plan and accomplish your next HTS related project.

Cellular and Molecular Imaging Core Facility updates

CMIC has grown substantially since its start-up in spring 2012. As of today, 195 people are using all the various microscopes and sample preparation instruments in the Histology lab, EM lab and Confocal lab, as well as ordering services, such as immunohistochemical staining. This made it possible to invest in a new DAKO Autostainer which was needed in the Histology lab.

In addition, an adjustment to the spinning disk confocal microscope makes this instrument ready to be used by all of you studying fast processes in cells expressing GFP and mCherry or comparable tags. The confocal lab has installed a new EVOS fluoresence microscope for monitoring of cell cultures and time-lapse imaging. This summer, CMIC will install a state of the art confocal microscope with sensitive detectors ideal for live cell imaging and also the possibility of Super Resolution Microscopy, and a TIRF microscope for imaging events in and close to the plasma membrane.

For more info and detailed descriptions of our microscopes, filter sets, objectives etc:
https://www.ntnu.edu/dmf/cmic



Electron microscopy, recent developments and perspectives
Advanced microscopy offers many tools to answer the molecular contribution to biological processes in living cells and tissue. Within the CMIC a solid basis is now available to apply correlative microscopic techniques, which means that we can study molecular interactions and localization in live cells and tissues at different spatial scales in combination with electron microscopy: i.e. dynamics and high resolution of the same sample. In the EM team we have recently applied a new and very sensitive immunocytochemical labeling technique. With this method we can detect extremely low concentrations of antibodies in a specimen. The method includes silver and gold precipitates that will give high contrast labelling; the so called Gold substituted silver peroxidase (GSSP). Proteins are notorious for their unpleasant behavior; often at risk of misfolding, aggregating or simply damaged which leads to cellular stress and disease. With the new GSSP technique we will be able to detect proteins at the smallest scale.

Cellular and Molecular Imaging Core Facility updates

Within the EM facility there are a number of interesting projects going on that apply scanning EM to study Mycobacteria and biofilm by Ernest Wilson, supervised by dr. Magnus Steigedal. Another project involves the study of tiny marine worms (1-3 mm in length) and revises their classification and phylogeny by Dr. Maria Capa. Rajesh Raju is studying polymer complexes by means of transmission EM. The polymers are aimed to carry lipogels to be used in drug delivery systems.

Next to these projects are the ongoing pathology requests for screening patient material from tissues like heart, liver, kidney and skin.

May 1, a new Ph.D. student (Nina Berggaard) will start her project on the ultra-structural analysis of grid cells, a special type of neuron that is involved in orientation and direction selectivity, you will see more about this topic in the near future.

The electron micrograph shows a wormlike creature between two nuclei of granule cells in the brain of a mouse. The worms most likely come from non-sterile drinking water. Photo Nan Skogaker.

MR Core Facility updates

The MRI environment including the MR Core Facility moved its office space to a newly renovated office space in MTFS 3rd floor South. Finally the MR research environmental at DMF is co-located in a shared office environment which we have waited for a long time. We are very happy about this, and you are very much welcome to visit us.

In January 2014 the software package with our two 600MHz High Resolution MRI scanners was upgraded to Topspin 3.2. In addition, new protocols and SOP procedures for quantitative and qualitative runs on biological fluid samples was set up. These new protocols in combination with our modern and specialized magnets are considered the international gold standard for research in the metabolomics field. This makes the core facility able to further increase international cooperation in the search for new biomarkers. We are proud to deliver NMR facilities in world class here at NTNU.