# Workshop on Exome-seq data analysis and visualization

This will be a very useful and timely opportunity to learn how to perform variant detection with next generation sequencing data in practice. Both PhD students and senior scientists are welcome. No prior experience is needed to follow the workshop.

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| **Time** | November 21-22, 2012 |
| **Place** | Kontinkangas Campus, Seminar room 134 B and Room KT285 |
| **Credits** | 0.5 ECTS |
| **Organizers** | Biocenter Oulu Doctoral Programme and DNA sequencing and expression center |
| **Information** | Minna Männikkö, Biocenter Oulu, Institute of Health Sciences<br>Aapistie 5 / P.O. Box 5000, 90014 University of Oulu Finland<br>Tel. +358-(0) 294 -485751<br>Email: minna.mannikko@oulu.fi<br>URL: http://www.biocenter.oulu.fi/ |
| **Registration** | Required for the Workshop, which is limited to 30 participants.<br>Registrations by email to Minna Männikkö by November 14, 2012 |

## PROGRAMME

### 1. General presentations and coffee

(No registration required)

**November 21, 09:15 – 10:15**
Seminar room 134B (Aapistie 5A)

**Reija Laitinen**, Illumina: Illumina solutions for exome sequencing
**Merlin Hu**, COO, BGI-Europe: The development and current scientific research of BGI

### 2. Workshop

(Registration! Max. 30 participants)

**November 21, 10:30 – 16:00 and**
**November 22, 09:00 – 14:00**
Room KT285 (Aapistie 5B)

**Lecturers:**
**Eija Korpelainen**, Bioinformatician and Product manager at CSC - IT Center for Science
**Jarno Tuimala**, Biostatistician at Finnish Red Cross Blood Service.

**Content:**
- Introduction to Chipster
- Quality control and filtering reads (FastQC, PRINSEQ, FASTX)
- Alignment to reference genome (BWA)
- Manipulation of BAM files (SAMtools)
- Variant calling and filtering (SAMtools, GATK)
- Manipulation of VCF files (VCFtools)
- Variant annotation
- Visualization of aligned reads and variants in genomic context (Chipster genome browser)

***The workshop is sponsored by BGI-Europe and Illumina.***