The OMICs course

	Mon 8/5	Tue 9/5	Wed 10/5	Thu 11/5	Fri 12/5
09:00	**1)** **Eirik Frengen:** * **Introduction & Overview** * **Information about "student assignments**" * "**Genome anatomy**" * **Genetic variation** * **Monogenic disorders** (lectures, "Green auditorium, Bygg 25, Ullevål")	**3)** **Yvonne Böttcher**: **"Multifactorial diseases/GWAS/disease assosiation"** "GWAS obesity": monogenic vs. polygenic/common obesity; gene-environment interactions; fat distribution, T2D; array based 5m DNA methylation; epigenome-wide analyses; pyrosequencing. These topics will be addressed together with an overview about the literature (lectures, "Green auditorium, Bygg 25, Ullevål")	**5)** **Manuela Zucknick:** **"Statistical principles behind three basic data analysis tasks in omics"** 1) Screening for "interesting" features (e.g. differential gene expression) -> Multiple testing, gene group tests and pathway analyses 2) Data visualisation and dimension reduction; "unsupervised learning" -> Cluster analysis and heatmaps, principal component analysis 3) Prediction and classification of patients based on omics data; "supervised learning" -> Introduction to some popular prediction methods, correct assessment -> of prediction performance (lectures, "Green auditorium, Bygg 25, Ullevål")	**7)** **Vessela Kristensen:** **"Genomics – from germ line to somatic genetic and epigenetics"** SNPs and CNV -Normal genetic variation and disease GWAS/sequencing Genotype-phenotype associations Phenotypic changes in disease: usefulness for classification, prognosis and treatment response prediction At mRNA level mRNA arrays/RNAseq DNA copy number alterations DNA methylation/ DNA methylation arrays/vs sequencing miRNA/lncRNA regulation arrays/vs RNAseq DNA somatic mutations, dissemination the immunogenicity of somatic mutations. (lecture, "Auditorium 1, Kreftsenteret, Ullevål")	**13)** **Johannes Hov:** **"Introduction to metagenomics and the gut microbiome in health and disease"** Case/problem: Understanding the role of the gut microbiome in a chronic inflammatory disease Study designs (cross-sectional, longitudinal, interventions): discussion Metagenomics: - Choice of biological material - Phylogeny and databases - 16S rRNA-based sequencing - Complete metagenomic sequencing - Imputation methods - Analytical approach (overview) (lectures, "Auditorium 1, Kreftsenteret")
10:00				**8)** **Sigve Nakken:** **"DNA sequencing concept: tumor versus control"** Bioinformatics: from raw data to variants (pipelines) Background noise: oxidation, contamination etc. (lecture, "Auditorium 1, Kreftsenteret")	
11:00		**4)** **Tuula Nyman:** **"Proteomics lecture 1"**: experiment planning, different workflows including some basics on how mass spectrometry is used in proteomics, main applications (lectures, "Green auditorium")		**9)** **Katja Elgstøen** **Metabolomics** (lecture, "Auditorium 1, Kreftsenteret")	**Initiation of the student assignments: Each student gets 7 min to present a project plan & 3 min for feedback from the teachers.** (Auditorium 1, Kreftsenteret)
12:00	**Lunch**	**Lunch**	**Lunch**	**Lunch**	**Lunch**
12:30		**Tuula Nyman:** **"Proteomics lecture 2":** (lectures, "Green auditorium")		**10)** **Alex Rowe:** **Integration of omics data** (statistics & bioinformatics) (lecture, "Auditorium 1, Kreftsenteret")	
13:30	**2)** **Magnus Vigeland**: "**Identification of disease-causing variants with exome sequencing data**" (Hands-on analysis of WES data in the PC room: "PC-stue, 1.etg", Bygg 25")	**Tuula Nyman**: Protein identification, quantitative proteomics experiments, some post-translational modification (Hands on analysis of proteomics results in PC room: "PC-stue, 1.etg", Bygg 25")	**6)** **Robert Lyle:** **"High Throughput Sequencing (HTS)**" Transcriptomics/RNAseq/ncRNA/miRNA Epigenetics (lectures, "Green auditorium")	**11)** **Stig Ove Bøe:** **"The Human Cell Atlas project"** "The Human cell atlas project"- a project aimed at identifying and mapping all types of cells in the human body. Technological advances in defining cell types and/or states at the single cell level. Use of high content imaging for analysis of gene function at the single cell level. (lecture, "Auditorium 1, Kreftsenteret")	Continue the student assignments: Each **student gets 7 min to present a project plan & 3 min for feedback from the teachers.** The students will write a small project as a home exam, which should include a discussion on strengths and weaknesses of the selected approach. This will be submitted two weeks after the course.
14:30-16				**12)** **Tobias Kaufmann, Dennis van der Meer and Ida E. Sønderby:** **"Connectomics – Imaging genetics"** Introduction to principles, strengths and challenges in brain imaging Brain networks and their disruptions in severe mental illness Neurodevelopmental and neurodegenerative perspectives Linking connectomics with genetics: the role of genes in connectivity Methods keywords: multivariate statistics, data driven analysis, machine learning for classification and prediction, independent component analysis, multimodal fusion, network analysis/graph theory, polygenic risk (lectures, "Auditorium 1, Kreftsenteret")	