

# **Project 3 – Integrative Genomics (IG)**

Objective: To give a presentation of about 40-90 minutes duration at the end of the week covering the key aspects of the integrative genomics, which is the combined analysis of data from multiple sources/levels.

The questions and contents below are meant as motivators and need not be followed. Since we give several lectures on IG, you should probably try to give a new angle in the presentation or focus on a few new and exciting publications. You could also supply with very good publications on epigenomics, transcriptomics, proteomics, metabonomics and phenomics? Population variation is excluded, since that is covered in Project 1.

## **The Big Questions Are:**

- What are the key classes of data (OMICS)?
- What is the inherent variation within one level?
- Which classes are often combined in analysis?
- What are the main benefits of combination?
- Which models are used to analyze them?

## **Maximal Contents of Presentation:**

What are the discussed data types?

What are their dimensions?

What do say about the underlying quantities that are of interest.?

How variable are they

## **Recommended literature**

Davies, Rafnar, Hellenthal and Hein (2009) “Integrative Genomics and Functional Explanation” downloadable from <http://www.stats.ox.ac.uk/research/genome/publications>

**Epigenomics:** Meissner et al. (2008) “Genome-scale DNA methylation maps of pluripotent and differentiated cells” Nature 454.766-70.

**Transcriptomics:** Emilson et al. (2008) “Genetics of Gene Expression and its effect on Disease” Nature 452.423-30.

**Proteomics:** Cox and Mann, (2007) “Is Proteomics the New Genomics?” Cell 130.,395-8

**Metabonomics:** Sreekumar et al. (2009) “Metabolomic profiles delineate potential role for sarcosine in prostate cancer progression” Nature 457. 910-15

**Phenomics:** The Mouse Phenotype Database Integration Consortium Mammalian (2007) Integration of mouse phenome data resources Genome 18, 157 163