**Semana de Bioinformática, Bioestadística, Análisis de Supervivencia**
**Del 2 al 8 de mayo de 2010**
**Claudia Rangel-Escareño**

1) Application of Di-base sequencing to SNPs detection in the AB SOLiD™ system

Single nucleotide polymorphisms (SNPs) are single nucleotide variations of DNA base pairs that can be used as genetic markers in disease studies. SNPs are also thought to be key enablers in realizing the concept of personalized medicine. Next generation DNA sequencing technology like Applied Biosystems SOLiD™, generates sequence data at a super large scale up to 4Gb in a single run. In the meanwhile, this creates computational challenges and one of the top ones is the sequence alignment process as it intends to map individual sequence read (lengths 25, 35 or 50) to a reference genome. The SOLiD™ system uses a 2-base encoding algorithm that represents a single data point using two adjacent bases that are meant to detect SNPs with higher accuracy. Single nucleotide may be changed in which case we have substitution, or can be removed having a deletion or also added leading to insertions to polynucleotide sequence.

2) Learning and Inference in Computational Systems Biology

Reverse engineering of biochemical networks remains an open problem in systems biology. Several methods have been proposed for this purpose with a wide variety of approaches. These have evolved in recent years to become what we now call Computational Systems Biology. The main idea is to link modelling of the interactions of system components with the huge volume and diversity of contemporary cellular and molecular data, such as high-throughput microarray data. This talk is an overview of some of the different probabilistic and machine learning approaches focused on the development of statistical and computational methods for the analysis of such data.

3) Genomic Medicine: An integration of post-genomic technologies with Human Disease Susceptibility, Diagnosing, Prescribing and Predicting

Gene expresión microarrays, genotyping arrays and next generation secuencing are some of the post-genomic technologies available for human genome research. I will talk about each one of these technologies, when and how they should be used as well as the mathematical and statistical complexity of their data analisis.