

AVVISO DI SEMINARIO

Il giorno mercoledì **2 marzo 2016** alle ore 14.30, presso l'Aula Magna M. Bonsembiante, dell'Edificio Pentagono, si terrà un seminario, aperto a tutti, dal titolo:

Bioinformatics of High-throughput DNA sequencing

tenuto dal prof. Anders Krogh, Department of Biology, University of Copenhagen.



New technologies for DNA sequencing are revolutionizing research in many complete the life sciences. Not only is it possible to sequence areas of genomes at an unprecedented rate, but also use sequencing for gene genotyping, expression analysis (RNA-seq), mapping of protein DNA (ChIP-seq), study binding in of ecosystems (metagenomics), and manv applications. other Computational needed analvze methods are to the data large amounts of from these experiments. In this talk, will first one ot discuss mapping of DNA reads to a reference genome, which is the most common first task. Special care must be taken, when dealing with T will short reads and present а mapping method that builds on а basis. will probabilistic Т then present а fast and sensitive method for taxonomic classification of metagenomic reads. which compares reads translated to proteins using a Burrows-Wheeler index.

Per eventuali informazioni rivolgersi al prof. Piero Fariselli (<u>piero.fariselli@unipd.it</u>, interno: 2895)