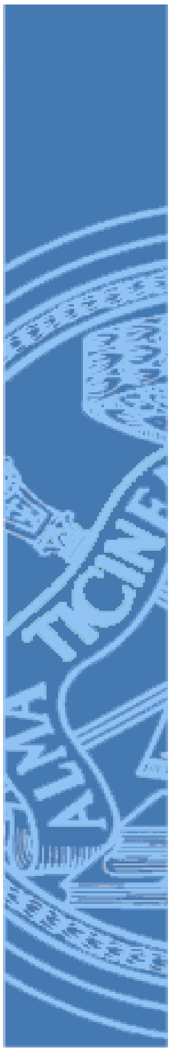
Università degli Studi di Pavia

Dottorato di Ricerca in Bioingegneria e Bioinformatica



Computational methods for NGS analysis of methylation

Alberto Riva

Associate Scientist - DiBiG director
Interdisciplinary Center for Biotechnology Research
University of Florida

Venerdì 28/03/2014 ore 15.30

Aula seminari

(ex-dipartimento di Informatica e Sistemistica)

One of the most exciting and innovative applications of NGS is the genome-wide analysis of DNA methylation. DNA methylation is a major form of epigenetic modification, affecting regulation of gene expression and RNA processing. At a higher level, methylation is linked with development and disease processes. In this seminar we will describe two different strategies for the analysis of DNA methylation using NGS techniques. The first one is based on bisulfite conversion followed by next-gen sequencing (e.g. Illumina). This method combines single base-pair resolution with genome-wide coverage at low costs. The second method is based on the use of SMRT sequencing (PacBio), that provides a direct reading of the methylation status of each sequenced base. Both methods require ad-hoc computational tools and analysis techniques, that are still largely under development. We will present the basic principles of the two methods and some of the computational tools being developed in our group for the analysis of patterns of methylation from the resulting data.

I dottorandi e gli interessati sono caldamente invitati a partecipare

Organizzatore
Prof. R. Bellazzi

Coordinatore del dottorato
Prof. R. Bellazzi

Per informazioni:
marco.tornielli@unipv.it

DIPARTIMENTO DI INGEGNERIA
INDUSTRIALE E DELL'INFORMAZIONE
Via Ferrata 1 – 27100 PAVIA

Scuola di Dottorato in Scienze dell'Ingegneria