Digital Signal Processing of Quantitative Genomic Data

CITTARO D, BUCCI G, MULLER H
Istituto Italiano di Tecnologia, ISI-GenOmics - Center of Genomic Science of IIT@SEMM, Milano

Motivation
Recent advances in genomic research allowed for the efficient collection of a wide variety of quantitative genomic data. One of the most popular protocol to collect such data is chromatin immunoprecipitation followed by array hybridization or tag sequencing (ChIP-chip and ChIP-seq). This approach has been applied to analyze heterogeneous phenomena, such as transcription factor bindings, histone modifications, or even replication forks. Analysis of such phenomena is typically performed using dedicated softwares, which are tuned to recognize specifically sized effects. In order to introduce a more general analysis framework, we applied well-known digital signal processing (DSP) techniques to quantitative genomic data.

Results
We developed dspchip, a python application that implements some common DSP procedures and allows the analysis of quantitative genomic data. dspchip includes a number of signal preprocessing steps and feature recognition capabilities as well. We show that a DSP approach is flexible enough to analyze different genomic features.

Availability
http://code.google.com/p/dspchip

Contact email
davide.cittaro@iit.it