



**FEBS 2018 Advanced Course**  
***The molecular basis of diseases: Can we infer phenotypes from protein variant analysis?***  
***Bologna (Italy), 23-25 May 2018***

**Info and registration:**

<https://genomeanalysis2018.febsevents.org/>

**Extended application deadline: 22 April 2018**

The workshop aims at presenting the state-of-the-art of computational methods for genome interpretation and collects expert scientists from both experimental biomedicine and computational biology.

NGS techniques allow detection of the differences in genetic sequences and in gene expression that can be associated to different phenotypes, and statistical methods can estimate a significance level for each association. However, the exploitation of genetic association data requires elucidation of how variations affect the structure of macromolecules and their interaction patterns.

Proteins, their stability and their relationships in interactomes will be the central topic. Furthermore, a particular regard will be given to the regulation at the transcriptional and translational levels, as derived from epigenomic and ribosome profiling data.

The format of the workshop allows extensive interaction among students and lecturers and offers to young researchers the possibility of presenting their work at poster sessions and with short selected talks.

***Course Organizers:***

Pier Luigi Martelli - *University of Bologna, IT*

Mauno Vihinen - *Lund University, SE*

***Invited Speakers***

Yana Bromberg - *Rutgers University, New Jersey, USA*

Søren Brunak - *University of Copenhagen, DK*

Emanuele Buratti - *International Center for Genetic Engineering and Biotechnology, Trieste, IT*

Gianni Cesareni - *Tor Vergata University, Rome, IT*

Montserrat Corominas - *University of Barcelona, ES*

Piero Fariselli - *University of Padova, IT*

Laura Furlong - *University Pompeu Fabra, Barcelona, ES*

Zoya Ignatova - *University of Hamburg, DE*

Marianne Rooman - *Free University of Brussels, BE*

Alfonso Valencia - *Barcelona Supercomputing Center, ES*

Sundar Venkataraman - *European Bioinformatics Institute, Hinxton, UK*

Mauno Vihinen - *Lund University, SE*

***Sessions***

May 23, 2018 - *Sequencing different levels of complexity (genomes, transcriptomes, epigenomes, transcriptomes): perspectives and data analysis challenges*

May 24, 2018 - *Inferring the effect of variations on protein structure, stability and interactions.*

May 25, 2018 - *From sequences to phenotype: is it possible to dissect the complexity of the relationship?*