

# Computational and Translational Methods for Cancer Genomics



*Tuesday May 29, 2018*

Sala Ulisse, Accademia delle Scienze – Via Zamboni 31, Bologna

## *Session I: Translational approaches*

10:00 – 10:10	Opening
10:10 – 11:00	<b>Christine Nardini</b> , Karolinska Institute (Sweden) Epigenomics and cancer – methylation as a marker in oncology.
11:00 – 11:20	Coffee Break
11:20 – 12:10	<b>Fatima Al-Shahrour</b> , CNIO, Madrid (Spain). Identifying druggable cancer dependencies for personalized medicine.
12:10 – 13:00	<b>Roberta Maestro</b> , CRO, Aviano Italy Genomics of soft tissue sarcomas.

## *Session II: Computational methods and tools*

14:30 – 15:20	<b>Fabio Vandin</b> , University of Padova (Italy) Computational methods to discover significant mutations in cancer genomes.
15:20 – 16:10	<b>Pietro Lio'</b> , University of Cambridge (UK) Combining logic and machine learning in cancer diagnosis.
16:10 – 16:30	Coffee Break
16:30 – 17:20	<b>Hannah Carter</b> , UC San Diego (USA) Are tumors predictable? Inherited immune variation constrains tumor evolution.
17:20 – 17:30	Closing Remarks