Bioinformatics and High Throughput Sequencing

2011

22^{nd} of March

Venue: Institut Pasteur, Paris

More information :
http://www.lirmm.fr/~rivals/HTS-2011

Registration :
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- **9h00 – Opening**

- **9h10 – 9h45 *Sophie Coutant***, Univ. Rouen, France
  Exome Variations Analyzer
- **9h50 – 10h50 *Ali Mortazavi***, CalTech, Pasadena, USA
  Self-organizing maps for analysis and mining of functional genomic data

- **10h50 – 11h20 Break**

- **11h20 – 12h00 *Leena Salmela***, Helsinki University, Finland
  Correction of sequencing errors in a mixed set of reads
- **12h00 – 12h45 *Jacques van Helden***, Univ. Libre de Bruxelles, Belgium
  RSAT peak-motifs: fast extraction of transcription binding motifs from full-size ChIP-seq datasets

- **12h45 – 14h15 Break**

- **14h20 – 14h55 *Philippe Gayral***,
  Institut des Sciences de l'Evolution, Montpellier, France
  Reference-free transcriptome assembly in non-model organisms from next generation sequencing data
- **14h55 – 15h45 *Francesca Ciccarelli***,
  Bioinformatics & Evolutionary Genomics, IFOM-IEO Campus, Milan, Italy
  Genomic Instability and the Evolution of Cancer

- **15h45 – 16h15 Break**

- **16h20 – 17h00 *Ana Conesa***,
  Centro de Investigación Príncipe Felipe, Valencia, Spain
  Differential expression with RNASeq: length and depth does matter
- **17h00 – 17h35 *Pierre Peterlongo***, IRISA, Rennes
  Biological information is in the reads
- **17h35 – 17h50 *Rick Tearle***,
  Complete Genomics, Mountain View, California, USA
  Complete Human Genome Sequencing of 40 Samples across 9 Different Populations

- **17h50 – 18h00 Closure**