

# RNA-Seq Workshop for the Bioinformatician



UNIVERSITÀ DEGLI STUDI  
DI MILANO

Università' degli Studi di Milano

June 11, 2014: from 9:00 to 17:30

Location: *Settore Didattico in via Celoria 20, Milano*  
rooms G13 (morning) and 307 (afternoon)



**Why:** High throughput RNA-Sequencing analysis is far from routine and cannot be done effectively by off-the-shelf tools. Instead, many considerations must be made to process and normalize the data in order to be more effective than their predecessor: microarrays. The RNA-Seq analyst must obtain expert and specialized skills and must delve deeply to learn the necessary secrets of the field. For example which aligners work as advertised and which do not. And most importantly the many issues that arise with feature quantification and normalization. The standard pipelines will show you how to normalize for read depth, feature length, and possibly GC content; however they ignore other crucial factors that can introduce extreme variance into the data, which can result in an underpowered statistical analysis.

**For whom:** Bioinformaticians, bioengineers and statisticians, familiar with Unix, who may be responsible for setting up and/or running the computational pipelines that take raw data all the way through to high level analysis.

**By whom:** *Gregory Grant* and *Elisabetta Manduchi* have been working in Bioinformatics at the University of Pennsylvania since 1998. Dr. Grant is Director of Bioinformatics at the Institute for Translational Medicine and Therapeutics (ITMAT) and Dr. Manduchi is Research Project Manager at the Computational Biology and Informatics Lab (CBIL).

**What:** We will discuss the nature of the data (with focus on Illumina data) and then we will delve into alignment, normalization and quantification issues. We will not take the standard push-button approach, but will instead look deeper into the issues that make every study a special case, with the aim of getting more out of the data than the lowest hanging fruit. This is a practical workshop which will provide down-to-earth material and hand-on experience. You will learn how to perform the analyses on compute clusters (either local or cloud). Our software is freely available.

Full day hands-on workshop: €100 (lunch, coffee break and computers included)  
Info for registration and details: <http://bioinf.itmat.upenn.edu/workshop/milan/>

**Contact:** *Cristina Battaglia*, Dipartimento BIOMETRA, Università degli studi di Milano. tel: 0250330421 e-mail: [cristina.battaglia@unimi.it](mailto:cristina.battaglia@unimi.it)

