

**RNA Analysis  
Bologna University, 2015**

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**OBJECTIVES**

In this course, I will start by introducing mainstream next generation sequencing methods. I will then discuss how these methods can be used to sequence, or re-sequence large genomes. I will then introduce RNA-Seq and the systematic sequencing of cell transcriptomes, along with the many challenges it entails, such as gene modeling and isoform quantification. I will then introduce the notion of multiple genome alignment and review existing methods, including some developed in our group. The course will then be focused on Long Non Coding RNAs. I will introduce the latest ENCODE results on this new class of transcripts and present the challenges of homology based annotation for Long Non Coding RNA. Some methods available for this task will be described, including the pipeline we developed for the ENCODE companion paper on Long Non Coding RNAs. We will see how this pipeline, and similar tools, can be deployed to produce homology-based annotation of newly sequenced genomes.

Next Generation Sequencing  
RNASeq  
Short Reads Mapping  
Short Read Mapping  
Pairwise Dynamic Programming  
Secondary Structure Prediction  
Secondary Structure Prediction  
Blast Algorithm  
Searching Non Coding RNAs  
Multiple Sequence Alignment Algorithms  
The T-Coffee Algorithm  
Multiply Aligning Non Coding RNAs.