



UNIVERSITÀ  
DEGLI STUDI  
DI PADOVA



VENICE ASIAGO 2016

DATE: 25<sup>th</sup> August 2016

TIME: 11:00 – 12:00

LOCATION: University of Padua, Bo Palace, Archivio Antico

## ***Transcriptional landscape of the genome***

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### **ABSTRACT**

During and after the completion of the sequence of the human genome in 2003, major efforts have been devoted to interpret the significance of DNA sequences in terms of presence of protein-coding genes embedded and scattered along the 24 different chromosomes forming the human repertoire.

The picture established from these studies was that the human genome contains some 30.000 protein-coding genes, a number that appeared probably insufficient to explain all the activities that the roughly 37 trillions of cells, which make up a human body, do exert in a strictly controlled manner, during the individual life. The concept of “protein-coding gene” was so established that the remaining, non-coding genome, was unhappily indicated as “Junk DNA”.

Other large-scale genomic projects aimed at establishing how much of the DNA was transcribing RNA molecules, apart from genes, rapidly designed the picture that junk DNA is instead largely transcribed into RNA molecules of very different sizes and function albeit not copied into protein molecules. This “RNA world” is populated by different families of short and long molecules that have been classified with different acronyms such as snoRNA, snRNA, miRNA, circRNA, lncRNA, etc.

The lecture will introduce the concept of the actual “pervasive” transcription of the human DNA that has emerged from several studies aimed at deciphering the RNA content of different organs, tissues and cells of human body. The different classes of regulative RNA molecules will be described, explaining the knowledges that have been gained in the biogenesis, action and interaction of the different types of non-protein-coding RNAs in the regulation of gene and cell functions.

### **FURTHER READINGS**

Will be provided during the lecture.