

## **Program FP7 GEUVADIS and ENGAGE satellite meeting on RNA-seq**

**Title:** Introduction to RNA-seq technology

**Date:** Sunday, May 29, 11:40 – 13:10

**Venue:** RAI, Amsterdam, The Netherlands, room number (Room: G106-107)

**Organisers:** Peter A.C. 't Hoen (Leiden University Medical Center), Stephen Montgomery, Thomas Giger (UNIGE)

**Participation is free of charge for everyone, no subscription needed**

### **Topic**

This satellite will introduce different aspects of RNA-seq technology and data analysis and highlight several applications in clinical and preclinical research. It is aimed at biomedical researchers who are considering the use of RNA-seq technology in their research and would like to learn about the practicalities of RNA-seq experiments.

RNA-seq refers to next generation sequencing (NGS)-based transcriptome profiling. In contrast to microarray-based expression profiling, RNA-seq provides a comprehensive inventory of all mRNAs in a cell or tissue, including splice isoforms and variants with alternative transcription start or polyadenylation sites. Moreover, allelic imbalance in the expression levels can be assessed. Given its greater specificity and sensitivity, it is also gradually replacing microarray technology for the quantitative analysis of gene expression and the identification of differentially expressed genes.

Like for other NGS applications, we are still faced with major challenges in the analysis of RNA-seq data. Some of the challenges will be discussed during the meeting.

*This satellite meeting has been organized and sponsored by the EU-funded projects GEUVADIS and ENGAGE.*

### **Confirmed Speakers**

- 11.40-12.00 Peter A.C. 't Hoen (LUMC) – introduction to RNA-seq technology
- 12.00-12.20 Stephen Montgomery (UNIGE) – experimental design and quality control
- 12.20-12.40 Angela Gonçalves (EBI) – challenges in RNA-seq data analysis
- 12.40-13.00 Roderic Guigo (CRG) – preclinical and clinical application of RNA-seq
- 13.00-13.10 Questions and answers