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Free webinar: Performance assessment of RNA sequencing and expression arrays for transcriptome analysis in cancer research

Discover how transcriptomics and machine learning can improve tumor classification

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RNA sequencing and expression arrays are transcriptomics techniques used to quantify transcribed genes and their isoforms. This live presentation compares the performance of RNA-Seq and arrays for the differential analysis of normal lung epithelium tissue and squamous cell carcinoma lung tumors.

Tuesday, March 6, 2018	
Europe	5:00 p.m. CET
North America	8:00 a.m. PT
	11:00 a.m. ET
GMT	4:00 p.m.

In this webinar, Dr. Petr Nazarov will explain:

- Results of platform comparison for protein-coding and long noncoding genes
- Biases observed in RNA-Seq and expression array platforms
- How deconvolution of transcriptomics data followed by machine learning can improve tumor classification

Webinar title:	**Performance assessment of RNA sequencing and expression array for transcriptome analysis in cancer research**
Presenter:	**Petr Nazarov, PhD**
	Research Scientist, Bioinformatics and Modelling Group, Proteome and Genome Research Unit, Department of Oncology, Luxembourg Institute of Health
	Dr. Nazarov has produced over 30 publications on biostatistics, machine learning, and genomics. His recent work focuses on characterizing transcriptional variations in the peritumoral tissue environment of pancreatic cancer, as well as tumors originating from the

lungs, colon, skin, and brain. His current research leverages deconvolution of transcriptomic signals from heterogeneous tumors to improve cancer classification.

Thermo Fisher Scientific
168 Third Avenue
Waltham, MA 02451
United States
thermofisher.com

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