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Metagenomics : beyond the horizon of current implementations and methods

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Publications

- S. Y. Anvar, L. Khachatryan, M. Vermaat, M. van Galen, I. Pulyakhina, Y. Ariyurek, K. Kraaijeveld, J. T. den Dunnen, P. de Knijff, P. A. C. 't Hoen, and J. F. J. Laros
Determining the quality and complexity of next-generation sequencing data without a reference genome
Genome Biology, 2014 15:555 doi 10.1186/s13059-014-0555-3
- L. Khachatryan, M. E. M. Kraakman, A. T. Bernards, and J. F. J. Laros
BacTag - a pipeline for fast and accurate gene and allele typing in bacterial sequencing data
BMC Genomics, 2019 20:338 doi 10.1186/s12864-019-5723-0
- L. Khachatryan, R. H. de Leeuw, M. E. M. Kraakman, N. Pappas, M. te Raa, H. Mei, P. de Knijff, and J. F. J. Laros
Taxonomic classification and abundance estimation using 16S and WGS - a comparison using controlled reference samples
Forensic Science International: Genetics, 2020 46:102257
doi 10.1016/j.fsigen.2020.102257
- L. Khachatryan, S. Y. Anvar, R. H. A. M. Vossen, and J. F. J. Laros
Reference-free resolving of long-read metagenomic data
bioRxiv 2019 <https://doi.org/10.1101/811760>

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Curriculum vitae

Lusine Khachatryan was born on February 15th 1990 in Jermuk, USSR (currently Armenia). She moved together with her family to Svoboda, Kursk district, Russia in early 1994. She graduated with honours from Svoboda secondary general education school in 2007. Same year she was admitted to Lomonosov Moscow State University (the School of Bioengineering and Bioinformatics). During first three years in University she was working as a bioengineer intern in the Belozersky Institute of Physiochemical Biology (Moscow, Russia) investigating the fragmentation of Potyvirus A coat protein by plant caspase-like protein and learning to create genetically modified plants using *Agrobacterium*-mediated transformation. In a year of 2010 Lusine was one of the 10 students selected for one-month bioinformatics internship in Leiden University Medical Center (Leiden, The Netherlands), after which she decided to continue her scientific career as bioinformatician. She spent one year as an bioinformatics intern in the Institute for Genetics and Selection of Industrial Microorganisms (Moscow, Russia) studying the binding sites of transcriptional factors specific for bidirectional promoters with different tissue expression pattern. Her MS project was dedicated to design and *in – silico* validation of serotype-specific polymerase chain reaction for human rhino- and enteroviruses and was performed as a collaboration between Lomonosov Moscow State University (Moscow, Russia) and Leiden University Medical Center (Leiden, The Netherlands). She graduated from Lomonosov Moscow State University with honours in 2012, her MS thesis work was specifically acknowledged by the University defence committee. In August 2012 Lusine continued her academic career as a PhD student in the department of Human Genetics in Leiden University Medical Center (Leiden, The Netherlands). Her PhD research was dedicated metagenomics - new and rapidly developing branch of molecular microbiology. Particularly, she developed several approaches and investigated the limits of various already existing methods for metagenomics analysis regarding different types of sequencing data. This work resulted a number of publications and was presented at many national and international conferences. From September 2018 Lusine is hired as a Scientist in R&D facility of Philip Morris International (Neuchatel, Switzerland) where she is working on improving the anal-

ysis pipelines for metagenomic and metatranscriptomic data as well as investigating the changes of microflora in health and disease.