Ligia Monica Mateiu

Central Support – Bioinformatics Unit
Department of Molecular Genetics, VIB
University of Antwerp
MD degree, University of Medicine and Pharmacy, Timisoara (Romania), 1999
MSc in Epidemiology and Statistical Genetics, University of Pavia, 2000
PhD in Medical Genetics (Statistical Genetics), University of Alberta, 2006

Current Position

2014 Research Associate
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Keywords
Bioinformatics - RNA sequencing - NGS technologies - data analysis - big data processing - data integration

Science

My work is mainly focused in primary (i.e. data pre-processing, QC), secondary (i.e. alignment to reference data, alignment diagnostics) and tertiary (i.e. differential gene expression, gene co-expression, gene regulation, variant calling, data visualization) data analysis from RNA sequencing experiments. These multistep analysis procedures are using command line tools combined in a dynamic workflow to serve the current research projects. The optimization of this workflow involves many challenges need to addressed: extremely large data sets, multiple reference data, data visualization in multiple ways, annotation using the most recent and accurate Internet resources, reduced number of samples in family data, etc. I'm working towards the integration of RNA-seq data analysis into GenomeComb tool and further automatization in line with GSF and research groups requests.
As part of the Bioinformatics team, I'm working with the MASTR assays and I'm involved in the data management projects for the department.

Publications

Zamani Esteki M., Dimitriadou E., **Mateiu L**, Melotte C., Van der Aa N., Kumar P., Das R., Theunis K., Cheng J., Legius E., Moreau Y., Debrock S., D'Hooghe T., Verdyck P., De Rycke M., Sermon K., Vermeesch J.R., Voet T. Concurrent Whole-Genome Haplotyping and Copy-Number Profiling of Single Cells. American Journal of Human Genetics 2015 (PMID: 25983246)(I.F.10.99)

Voet T., Kumar P., Van Loo P., Cooke S.L., Marshall J., Lin M.L., Zamani Esteki M., Van der Aa N., **Mateiu L.**, McBride D.J., Bignell G.R., McLaren S., Teague J., Butler A., Raine K., Stebbings L.A., Quail M.A., D'Hooghe T., Moreau Y., Futreal P.A., Stratton M.R., Vermeesch J.R., Campbell P.J. Single-cell paired-end genome sequencing reveals structural variation per cell cycle. Nucleic Acids Research 2013 (PMID: 23630320)(I.F.: 8.08)

Ramos A., Santos C., **Mateiu L.**, Gonzalez Mdel M., Alvarez L., Azevedo L. and Amorim A., Aluja MP.Frequency and pattern of heteroplasmy in the complete human mitochondrial genome. PLoS One 2013 (PMID: 24098342) (I.F.: 3.53)

Van der Aa N., Cheng J., **Mateiu L.**, Esteki M.Z., Kumar P., Dimitriadou E., Vanneste E., Moreau Y., Vermeesch J.R. and Voet, T. Genome-wide copy number profiling of single cells in S-phase reveals DNA-replication domains. Nucleic Acids Research 2013 (PMID: 23295674) (I.F.: 8.08)

Ramos A., Barbena E., **Mateiu L.**, Gonzalez MM. , Mairal J., Lima M., Montiel R. , Pilar Aluja M. , Santos C. Nuclear insertions of mitochondrial origin: database updating and application in cancer studies. Mitochondrion 2011 (PMID: 21907832)(I.F.: 3.52)

Ramos A., Santos C., Barbena E., **Mateiu L**., Alvarez L., Nogues R., Pilar Aluja M. Validated primer set that prevents nuclear DNA sequences of mitochondrial origin co-amplification: a revision based on the New Human Genome Reference Sequence (GRCh37). Electrophoresis 2011 (PMID: 2142517)(I.F.: 3.16)

Mateiu L., Rannala B. Bayesian Inference of Errors in Ancient DNA Caused by Postmortem Degradation. Molecular Biology and Evolution 2008 (PMID: 18420593) (I.F.: 14.31)

Mateiu L., Rannala B., Inferring Complex DNA Substitution Processes on Phylogenies Using Uniformization and Data Augmentation. Systematic Biology 2006 (PMID: 16551582) (I.F.: 11.53)