

Dr. Efthymios Motakis

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Overview of my professional profile

I received my Ph.D. in Statistics in January 2008 from the School of Mathematics, Faculty of Science, University of Bristol, UK. Since February 2007 I have been professionally working on gene expression data analysis, biomarker discovery, modeling associations between biological and clinical data, survival analysis, machine learning methods, non-parametric curve fitting, signal processing and object tracking. I am expert in statistical methods development using R. I have 3 years of teaching experience (M.Sc. level).

Past Employment: February 2007 - July 2012

- Senior Postdoctoral Fellow, Genome and Gene Expression Data Analysis Division, Center of Computational Biology, Bioinformatics Institute, A*STAR, Singapore (April 2010-July 2012)
- Postdoctoral Fellow, Genome and Gene Expression Data Analysis Division, Center of Computational Biology, Bioinformatics Institute, A*STAR, Singapore (January 2008 - March 2010)
- Postdoctoral Fellow, Division of Computational and Mathematical Biology, Genome Institute of Singapore, A*STAR (February 2007 - December 2007)

Education

- Ph.D. in Statistics (January 2008), School of Mathematics, Faculty of Science, University of Bristol, United Kingdom. My Ph.D. thesis is entitled "Multiscale Approaches for the Statistical Analysis of Microarray Data (with an application to 3D Vesicles Tracking)".
- M.Sc. in Statistics (June 2002): Department of Statistics, Athens University of Economics, Greece (1st Semester), Biostatistics Center, Catholic University of Leuven, Belgium (2nd Semester)
- B.Sc. in Statistics (February 1999): Department of Statistics, Athens University of Economics, Athens, Greece

Areas of Research Interest & Peer-Reviewed Publications:

- **Microarray Data analysis:** Statistical methods for quality control, data gaussianization, data calibration, batch effect correction, differential expression, correlation analysis and multivariate inference.

1. Diraison F., Motakis E., Parton L.E., Nason G.P., Leclerc I. and Rutter G.A. (2004). Impact of Adenoviral Transduction With SREBP1c or AMPK on Pancreatic Islet Gene Expression Profile: Analysis With Oligonucleotide Microarrays, *Diabetes*, 53, S84-S91.
2. Motakis E., Nason G., Fryzlewicz P. and Rutter G. (2006). Variance Stabilization and Normalization for One-Color Microarray Data Using a Data-Driven Multiscale Approach, *Bioinformatics*, 22, 2547-2553.
3. Motakis E., Nason G.P. and Fryzlewicz P. (2005). The DDHFM Package. Manual of Data-Driven Haar-Fisz Package, CRAN Project (<http://cran.r-project.org/web/packages/DDHFM/index.html>).
4. Toh S.H., Prathipati P., Motakis E., Keong K.C., Yenamandra S.P., Kuznetsov V.A. (2011). A robust tool for discriminative analysis and feature selection in paired samples impacts the identification of the genes essential for reprogramming lung tissue to adenocarcinoma, *BMC Genomics*, 12(Suppl 3): S24.

- **Modeling associations between clinical (survival) and biological (gene expression) data:** Statistical methods development for the analysis of patients' cohorts (gene expression and survival data). Biological gene signature estimation using univariate, multivariate and machine learning models.

1. Motakis E., Ivshina A.V. and Kuznetsov V.A. (2007). Identification of essential genes and gene pairs associated with survival time of cancer patients, BIOCOMP 2007, 753-759.
2. Kuznetsov V.A., Motakis E. and Ivshina A.V. (2008). Low- and High- Aggressive Genetic Breast Cancer Subtypes and Significant Survival Gene Signatures, IJCNN 2008, 4151-4156.
3. Motakis E., Ivshina A.V. and Kuznetsov V.A. (2009). A data-driven method of identification of essential genes and gene pairs associated with survival time of cancer patients, IEEE Engineering in Medicine and Biology, 28, 58-66.
4. Motakis E. and Kuznetsov V.A. (2009). Genome-scale identification of survival significant genes and gene pairs, Proceedings of the World Congress on Engineering and Computer Science 2009 Vol I, WCECS 2009, 20-22 October 2009, San Francisco, USA.
5. Grinchuk O., Motakis E. and Kuznetsov V.A. (2009). Identification of complex sense-antisense gene module on 17q11.2 associated with breast cancer aggressiveness and patients survival, Proceedings of the World Academy of Science, Engineering and Technology, Vol 58, October 2009, Venice, Italy.
6. Grinchuk O., Motakis E. and Kuznetsov V.A. (2010). Complex sense-antisense architecture of TNFAIP1/POLDIP2 on 17q11.2 represents a novel transcriptional structural-functional gene module involved in breast cancer progression, BMC Genomics, 11(Suppl 1):S9

- **Multiscale signal processing, signal denoising, non-parametric estimation:** Non parametric curve fitting and clustering for macrostate identification from molecular dynamics simulations

1. Zhou* W.Z., Motakis* E., Fuentes G. and Verma C. S. (2012). Macrostate Identification from Biomolecular Simulations through Time Series Analysis. Journal of Chemical Information and Modeling, 52(9), 2319-2324. *(equal contribution) [highlighted by A*STAR Research, Nature Publishing Group]*
2. Low D.H.P. and Motakis E. (2013). deltaGseg: Macrostate estimation via molecular dynamics simulations and multiscale time series analysis, Bioinformatics, 29 (19), 2501-2502 *(corresponding author)*

- **CAGE Data analysis:** Statistical methods for quality control, differential expression, correlation analysis and multivariate inference.

1. Motakis E., Guhl S., Ishizu Y., Itoh M., Kawaji H., de Hoon M., Lassmann T., Carninci P., Hayashizaki Y., Zuberbier T., Forrest A.R.R., Babina M. and the FANTOM consortium (2014). Redefinition of the human mast cell transcriptome by deep-CAGE sequencing, Blood, to appear.
2. Forrest A.R.R. et al. (2014). A promoter-level mammalian expression atlas, Nature, to appear.

Patents

- Kuznetsov V.A. and Motakis E. (2010). Title of invention: A method for identification, prediction and prognosis of cancer aggressiveness. US Patent. International Application Number: PCT/SG2010/000078. Publication Number: WO/2010/104472.
- Motakis E., Ivshina A.V., Kuznetsov V.A. (2010). Title of invention: Identification of biologically essential genes and gene pairs and methods employing the identified genes and gene pairs. US Patent. International Application Number: PCT/SG2010/000080. Publication Number: WO/2010/104474