

Personal information

Surname/First name Medvedeva Yulia
E-mail ju.medvedeva@gmail.com
Date of birth 16.11.1977
Nationality Russian
Gender Female
Research interests Epigenomics, transcriptomics, regulation of transcription in animals, comparative genomics, evolutionary biology, system biology, data mining

Research experience

Date Sep. 2013 - now
Position Postdoc grade B
Institute Institute of Personal and Predictive Medicine of Cancer
Group name Regulatory genomics
Leader Dr. Tanya Vavouri
Responsibilities - Analysis of histone modifications induced by changes in DNA methylation changes

Date July 2011- July 2013
Position Postdoctoral Research Fellow
Department Computational Bioscience Research Center (CBRC)
Computer, Electrical and Mathematical Sciences and Engineering Division
University King Abdullah University of Science and Technology (KAUST)
Responsibilities - Development of methods and pipelines for the enhanced recognition of industrially important enzymes from metagenomic data
- Study of the effects of DNA methylation on transcription factor binding sites (hypothesis generation, design of computational experiments, statistical analysis)
- Study of genetic and epigenetic differences between promoters of coding and long noncoding genes (hypothesis generation, statistical analysis)
- Development of a database of human transcriptional factor binding sites (data curation, database structure design)
- Motif analysis
- Co-supervising PhD and Master's students

Date Dec. 2010-Jun. 2011
Position Researcher
Department Laboratory of System Biology and Computational Genetics
Research institute Vavilov Institute of General Genetics
Russian Academy of Sciences
Responsibilities - Development of a statistical method and a pipeline for the search of new modulon members in E. coli
- Analysis of the mutation rates in methylated cytosines within and out of the CpG islands
- Supervising a Master's student

Date Apr. 2006- Jun. 2011

Position Junior researcher
Department Laboratory of Bioinformatics
Research institute Institute of Genetics and Selection of Industrial
Microorganisms
Responsibilities - Statistical analysis of CpG islands properties
- Development of statistical methods for genome-wide
intervals comparison
- Administrative work, including grant proposals

Date Jul. 2003- Nov. 2005
Position Technician
Department Laboratory of molecular basis of oncogenesis
Engelhard Institute of Molecular Biology
Russian Academy of Science

Education and degrees

Dec. 2010 Ph.D. in computational molecular biology
“Features of CpG islands in intra- and intergenic regions of
human genome”
Sep. 2008 – Jun. 2010 Bauman Moscow State Technical University
Informatics and Control Systems
Bachelor with Honor
Nov. 2006 – Nov. 2008 PhD program
Research Institute for Genetics and Selection of Industrial
Microorganisms
Sep. 1995 – Jun. 2003 Lomonosov Moscow State University
Department of Psychology
Specialist

Additional training

Jul. 7-9, 2013 Illumina Genomic Shotgun library preparation training
King Abdullah University of Science and Technology, Saudi
Arabia
Oct. 4-23, 2010 Evolutionary biology
Lomonosov Moscow State University, Department of
Biology, Russia
Jul. 5-17, 2010 Bioinformatics and Comparative Genome Analysis
Institut Pasteur Paris, France

Honors and awards

Jul, 2012 SABIC postdoctoral fellowship (1 year) for the project:
«Improved recognition of industrially important enzymes:
application to the metagenomic data from Red Sea samples»
Jul., 2011 SABIC postdoctoral fellowship (1 year) for the project:
«Enzyme Discovery from Microbiome Studies of Red Sea»
Oct., 2008 Travel fellowship for participation in the 3th ESF
Conference on Functional Genomics and Disease,
Innsbrook, Austria
Mar., 2008 Travel fellowship for participation in the RECOMB
conference, Singapore, Singapore

Professional skills

Computational Linux, Perl/shell scripting, MySQL, R, Bioconductor, Weka
Machine learning techniques, statistics

Experimental Motif finding, TFBS prediction, NGS data analysis
qPCR, NGS: DNA extraction, library preparation

Professional activities

Reviewer Frontiers in Statistical Genetics and Methodology
Current Genomics

List of publications

1. A.R.R. Forrest, H. Kawaji, M. Rehli, J.K. Baillie, M.J.L. de Hoon, V. Haberle, T. Lassmann, I.V. Kulakovskiy, M. Lizio, M. Itoh, R. Andersson, C.J. Mungall, T.F. Meehan, S. Schmeier, N. Bertin, M. Jørgensen, E. Dimont, E. Arner, C. Schmidl, U. Schaefer, **Y. A. Medvedeva**, C. Plessy, M. Vitezic, J. Severin, C.A. Semple, Y. Ishizu, M. Francescato, et al. (2014) A promoter level mammalian expression atlas. *Nature*. 507(7493):462-70.
2. **Y.A. Medvedeva**, A. Khamis, I.V. Kulakovskiy, W. Ba-Alawi, Md.S.I. Bhuyan, H. Kawaji, T. Lassmann, M. Harbers, A.R.R. Forrest and V.B. Bajic (2014). Effects of cytosine methylation on transcription factor binding sites. *BMC genomics*. 26;15(1):119.
3. Lomakin YA, Zakharova MY, Stepanov AV, Dronina MA, Smirnov IV, Bobik TV, Pyrkov AY, Tikunova NV, Sharanova SN, Boitsov VM, Vyazmin SY, Kabilov MR, Tupikin AE, Krasnov AN, Bykova NA, **Medvedeva YA**, Fridman MV, Favorov AV, Ponomarenko NA, Dubina MV, Boyko AN, Vlassov VV, Belogurov Jr AA, Gabibov AG. (2014) Heavy-light chain interrelations of MS-associated immunoglobulins probed by deep sequencing and rational variation. *Mol Immunol*. pii: S0161-5890(14)00023-6.
4. Pardo LM, P.Rizzu, M.Francescato, M.Vitezic, G.G.Leday, J.Sanchez, A.Khamis, H.Takahashi, W.D. van de Berg, **Y.A.Medvedeva**, M.A. van de Wiel, C.O. Daub, P.Carninci, P.Heutink (2013) Regional differences in gene expression and promoter usage in aged human brains. *Neurobiology of Aging* pii: S0197-4580(13)00023-7.
5. Kulakovskiy IV, **Medvedeva YA**, Schaefer U, Kasianov AS, Vorontsov IE, Bajic VB, Makeev VJ. (2013) HOCOMOCO: a comprehensive collection of human transcription factor binding sites models. *Nucleic Acids Res*. Jan;41(Database issue):D195-202.
6. Permina EA, **Medvedeva YA**, Baeck PM, Hegde SR, Mande SC, Makeev VJ. (2013) Identification of self-consistent modulons from bacterial microarray expression data with the help of structured regulon gene sets. *J Biomol Struct Dyn.*, 31(1):115-24.
7. Favorov A, Mularoni L, Cope LM, **Medvedeva Y**, Mironov AA, Makeev VJ, Wheelan SJ. (2012) Exploring massive, genome scale datasets with the GenometriCorr package. *PLoS Comput Biol*. May;8(5):e1002529.
8. Kamanu FK*, **Medvedeva YA***, Schaefer U, Jankovic BR, Archer JA, Bajic VB. (2012) Mutations and binding sites of human transcription factors. *Front Genet.*, 3:100 (*shared first authors).
9. Kulakovskiy IV, Belostotsky AA, Kasianov AS, Esipova NG, **Medvedeva YA**, Eliseeva IA, Makeev VJ. (2011) A deeper look into transcription regulatory code by preferred pair distance templates for transcription factor binding sites. *Bioinformatics*, Oct 1;27(19):2621-4.
10. Klimova E., Mande S, **Medvedeva Iu**, Makeev V, Hedge S, Permina E (2011). Using the operonic gene pairs for establishing the threshold for correlation coefficient of differently expressed genes. *Biofizika*, Nov-Dec;56(6):1062-4.
11. **Medvedeva YA**, Fridman MV, Oparina NJ, Malko DB, Ermakova EO, Kulakovskiy IV, Heinzl A, Makeev VJ. (2010) Intergenic, gene terminal, and intragenic CpG islands in the human genome. *BMC Genomics*. Jan 19;11:48.
12. **Medvedeva IuA**, Kulakovskii IV, Oparina NIu, Favorov AV, Makeev VIu (2010) Asymmetry of the GC content in vicinity of transcription starts (with participation of polymerase PolII) and its correlation with location of adsorption sites of protein SP1 on DNA, *Biofizika*. Nov-Dec;55(6):976-85.
13. **Y. Medvedeva**, A. Favorov, N. Oparina, I. Kulakovskiy, V. Makeev (2010) Clusters of transcription start sites in human genomes exhibit a biased orientation of Sp1 binding

site towards the template strand. *New Biotechnology*, 27:S1, 2010, S23.

14. Hedge, S., E.A.Permina, **Y.A.Medvedeva**, S.C.Mande and V.J.Makeev (2010). Improved modulon identification from bacterial gene expression data using operon-based correlation reference set. *New Biotechnology*, 27:S1, S45.

15. **Y.A. Medvedeva** (2012) Algorithms for CpG Islands Search: New Advantages and Old Problems. *Bioinformatics - Trends and Methodologies*, ISBN 978-953-307-282-1, ed. by M.A. Mahdavi