CURRICULUM VITAE

Nikolay Samusik

Born: 22.02.1986 in Leningrad, USSR
Nationality: Russian Federation
Marital status: married
Language skills: Russian (mother tongue), English (fluent), German (fluent)
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EDUCATION

September 2007 – February 2012	PhD in Systems Biology. Title *Dr. rer. med,* awarded ***summa cum laude*** by the Medical Faculty, Technical University of Dresden, Germany
October 2006 – August 2007	Specialist retraining course in computer science, Saint-Petersburg State University, Department of Mathematics and Mechanics
September 2003 – July 2007	Bachelor of Science in Biology. Certificate awarded with honors by Department of Biology of Saint-Petersburg State University, St. Petersburg, Russian Federation **GPA 3.92** (4.92 in Russian scale)

STANDARD TESTS:

GRE General	Math 800/800, Verbal 440/800, Analytical writing 4.0/6.0.
TOEFL IBT	108/120 (28,26,26,28)

EMPLOYMENT RECORD

September 2007-present	**Affiliation:** Max Planck Institute of Cell Biology and Genetics. **Address:** Pfotenhauerstr 108, 01309 Dresden. **Website:** www.mpi-cbg.de **Position:** PhD Student **Supervisor:** Prof. Dr. Marino Zerial. **PhD Thesis title:** Reconstruction of functional networks from multiparametric high-throughput screens. **Job description:** Development of knowledge mining tools for multiparametric phenotypic screening data, analysis and interpretation of multiparametric high-throughput screens. Studies of novel functional components and design principles of the endocytic systems. **Key Achievements:** • Development of VT-shift, a novel density-based algorithm for robust clustering of multivariate profiles (Samusik et al, in

	Preparation) • Development of a model-based scoring method Phenoscore that significantly improves the hit selection in clusters by selecting the profiles based both on their strength and specificity to the general cluster profile • Development of methods for cluster quality assessment and prioritization that use protein-protein interaction and gene annotation information • Development of strategies to integrate chemical and RNAi screening data to predict drug targets • Computational analysis of the image-based genome-wide RNAi screen on endocytosis (Collinet et. al, 2010) • Computational analysis of the chemical screen for inhibitors of mycobacterial infection, prediction of the drug mechanisms of action based on multiparametric phenotypic data (Sundaramurthy et al, [In Preparation]) • Studies of the interplay between endocytosis and cell cycle through integration of diverse RNAi screening data
January 2003 - August 2007	**Affiliation:** Biomedical Center (part time) **Address:** 197110 Pudozhskya ul. 7, Saint-Petersburg **Website:** www.biomed.spb.ru **Position:** Research Technician **Supervisor:** Dr. Andrei Kozlov **Job description:** • Computational search for human tumor-specifically expressed transcripts through the integration of EST and SAGE data. Selected candidate sequences were experimentally validated to be transcribed in a tumor-specific manner. • Functional and evolutionary characterization of validated tumor-specific transcripts • Search for human protein-coding genes that appeared *de novo* in the evolution, correlations between gene evolutionary history and tumor-specific expression • Genome-wide annotation of tumor-specific alternative splicing events
July 2002 - November 2002	**Affiliation:** Center for Emergency and Radiation Medicine of the Ministry of Emergency Situations (part time) **Address:** 194311 Lebedeva ul. 4/2, Saint-Petersburg **Website:** www.arcerm.spb.ru **Position:** Research Technician **Supervisor:** Dr. Sergei Proshin **Job description:** Studies of correlation between human sperm DNA damage and male infertility.
February 2001 - June 2002	**Affiliation:** Laboratory of Lipid Metabolism, Division of Biochemistry, Institute of Experimental Medicine (part time). **Address:** 194071 Professora Popova ul. 16, Saint-Petersburg **Website:** iemrams.spb.ru

	Position: Laboratory trainee **Supervisor:** Prof. A.P. Perevozchikov **Job description:** Studies of regulation of human VLDLR gene expression by GCC-repeat binding proteins.

PROFESSIONAL QUALIFICATIONS

Math and Computer science:

Strong background in mathematics, including linear algebra, theory of probability and statistics. Essentials of Bayesian approach to probability.

Knowledge of graph theory, machine learning techniques including various types of classifiers (SVM, random forests, density-based classifiers), unsupervised classification/clustering, density-based clustering, kernel regression, Bayesian networks, hierarchical temporal memories (HTM).

Programming skills: Very familiar with Java SE and EE (6 years of experience). Practical knowledge of C++, C#, Visual Basic, Python and Groovy. Experience with parallelization via Java RMI and Apache Hadoop (map-reduce). Database design and maintenance skills, good knowledge of SQL. Essential knowledge of R and MATLAB. Skilled in GUI design, collaborative development, Subversion.

Bioinformatics:

Comparative genomics, analysis of phylogenies and sequence selection features. Knowledge of main public resources genomics, transcriptomics, proteomics and gene annotation resources. Experience with SBML, metabolic modeling and simulations.

Molecular biology and genetic engineering:

Trained in modern wet-lab techniques, such as molecular cloning and genetic engineering in plasmids, eukaryotic cell culture, plasmid and siRNA transfection, cDNA preparation, RT-PCR, immunostaining, confocal microscopy. Basic skills in electron microscopy.

Soft skills: Experienced in oral presentations and scientific communication, grant application writing, manuscript preparation.

1. Publications

1. Samusik N, Galvez T, Collinet C, Marsico G, Zerial M and Kalaidzidis Y. VT-shift: robust density-based clustering for systems biology. [In Preparation]
2. Sundaramurthy V, Barsacchi R, Samusik N, Marsico G, Gilleron J, Kalaidzidis I, Meyenhofer F, Bickle M, Kalaidzidis Y and Zerial M. Defining critical host determinants of intracellular mycobacterial survival by high content screening in human primary cells. [In Preparation]
3. Samusik N, Kurkovskaya L, Shilov E, Kozlov A. PBOV1 - a human de novo protein-coding gene with tumor-specific antigen properties. ***PLoS One*** [In Review]
4. Fietz S, Lachmann R, Brandl H, Kircher M, Samusik N, Schröder R, Lakshmanaperumal N, Henry I, Vogt J, Riehn A, Distler W, Nitsch R, Enard W, Pääbo S, Huttner W (2012) Transcriptomes of germinal zones of human and mouse fetal neocortex suggest a role of extracellular matrix in progenitor self-renewal. ***Proc Natl Acad Sci***. [In Press]
5. Collinet C, Stöter M, Bradshaw CR, Samusik N, Rink JC, Kenski D, Habermann B, Buchholz F, Henschel R, Mueller MS, Nagel WE, Fava E, Kalaidzidis Y, Zerial M. (2010) Systems survey of endocytosis by multiparametric image analysis. ***Nature***. 464(7286):243-9.
6. Samusik N, Galachyants Y, Kozlov A. (2011) Analysis of evolutionary novelty of tumor-specifically expressed sequences. ***Russian Journal of Genetics: Applied Research***. 1(2):138-148
7. Samusik N, Kalaidzidis Y, Zerial M. (2009) A method for validation for clustering of phenotypic gene knockdown profiles using protein-protein interactions information. *Proceedings of ECCB-ISMB 2009:* ***BMC Bioinformatics***. 10(Suppl 13)**:**P3
8. Kozlov AP, Galachyants Y, Duhovlinov I, Samusik N, Baranova A, Polev D, Krukovskaja L.L. (2008) Evolutionarily New Sequences Expressed in Tumours. ***Infectious Agents and Cancer***. 1**:**82-9.

Conference posters & abstracts

1. Samusik N, Kalaidzidis Y, Zerial M. *Phenoscore: improved hit selection from phenotypic screens (2011) // ISMB-ECCB2011, July 13-19 Vienna, Austria*
2. Samusik N, Kalaidzidis Y, Zerial M. (2010) VT-shift: a novel density-based clustering algorithm and its applications multivariate biological datasets. // *PSB, Jan 02-07 2011, Big Island of Hawai'i*
3. Samusik N, Kalaidzidis Y, Zerial M. (2009) A method for validation for clustering of phenotypic gene knockdown profiles using protein-protein interactions information // *ISMB-ECCB2009, Stockholm, Sweden*
4. Samusik N, Kalaidzidis Y, Zerial M. (2008) Mean-shift clustering approach to the analysis of phenotypic data of an image-based genome-wide siRNA screen // *European Conference of Computational Biology, 22-26 September 2008: Cagliari, Italy*
5. Samusik ND, Galachyants YP, Kozlov AP; Comparative genomics analysis of human tumor-related transcripts. // Russian Journal of AIDS, Cancer and Public Health (2006) Vol 10, №2: p 54
6. Samusik ND, Galachyants YP, Kozlov AP; EST-based annotation of human tumor-specific alternative splicing. // Russian Journal of AIDS, Cancer and Public Health (2005) Vol 9, №2: p 78
7. Galachyants YP, Samusik ND, Baranova AV, Kozlov AP; Application of computational differential display to search of tumor-specific transcripts. // *Russian Journal of AIDS, Cancer and Public Health (2005) Vol 9, №2: p 53*

AWARDS

1. Student Council Symposium Poster Award at ISMB-ECCB 2009, Stockholm, Sweden

PERSONAL INTERESTS

Hatha Yoga, Tai Chi Chuang/Qi Gong, Travelling, Sports (biking, downhill skiing, diving), Go game (9 kyu), visual design, electronic music authoring