

Lilit Nersisyan, PhD

Curriculum vitae

<i>Full Name:</i>	Lilit Nersisyan	<i>Position:</i>	Researcher
<i>Date of birth:</i>	19.02.1990	<i>Organization:</i>	Bioinformatics Group, Institute of Molecular Biology, NAS Armenia
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Education

PhD, Bioinformatics	2014-2017
<i>Topic:</i> Telomere analysis based on high-throughput multi-omics data	
<i>Supervisor:</i> Arsen Arakelyan, PhD	
<i>Institute:</i> Bioinformatics Group, Institute of Molecular Biology NAS RA	
<i>Defense:</i> University of Leipzig, Germany	
MSc, Computer and Information Science	2011-2013
College of Science and Engineering, American University of Armenia	
MSc, Biotechnology	2010-2012
Dep. of Biotechnology, International Scientific and Educational Center, NAS, Armenia	
BSc, Biophysics	2006-2010
Faculty of Biology, Department of Biophysics, Yerevan State University	

Professional experience

Researcher	Research Group of Bioinformatics Institute of Molecular Biology, NAS RA	2011 – present
Adjunct lecturer	<i>Introduction to Biosciences</i> American University of Armenia	2016 – present
Teaching Associate	<i>Introduction to Algorithms, Quantitative Biology</i> American University of Armenia	2014-2015
Java Developer (remote)	Communiy Health, New York, USA	2012 - 2014
Senior Research assistant	Research Group of Immune Regulation Institute of Molecular Biology, NAS RA	2009-2011

Research fellowships and stays

EMBO Short Term Fellowship	Telomere shortening induced alteration in the epigenome and transcriptome as a cause of stem cell and organismal aging Leibniz Institute on Aging, Jena, Germany	2017 (3 months)
BMBF MycSys	Aberrant pathway function and telomere lengths in Lymphoma Interdisciplinary Centre for Bioinformatics, University of Leipzig, Germany	2016 (3 weeks)
DAAD Short Term Scholarship	Bioinformatics pathway activity analysis of epigenetic regulation of gene expression in cancer and pulmonary diseases Interdisciplinary Centre for Bioinformatics, University of Leipzig, Germany	2015 (4 months)

Research grants and awards

PI, Research Grant (molbio-3818)	<i>Title:</i> PSFC: pathway signal flow calculator The Armenian National Science and Education Fund	2015
1st place innovation award	<i>Topic:</i> Computel: software for computation of mean telomere length from whole genome Next-generation sequencing data ARPA Institute Invention Competition	2015
Google Summer of Code	<i>Project:</i> PSFC: a Cytoscape app for calculating pathway signal flows. Google, Cytoscape, National Resource for Network Biology	2014
Participant, Research Grant (molbio-3507)	<i>Title:</i> Multiclass growing support set algorithm for analysis of high-throughput gene expression data The Armenian National Science and Education Fund	2014
Participant, Research Grant (13YR-1F0022)	<i>Title:</i> Investigation and analysis of shared and specific biomolecular pathways involved in complex human diseases using high-throughput gene expression data “Young Scholars Support Program”, Armenia	2013
Participant, Research Grant (11B-1f014)	<i>Title:</i> <i>In silico</i> structure-function characterization of Familial Mediterranean fever gene product (pyrin): insights into disease pathogenesis State Committee of Sciences of RA	2011

Research and Technical Skills

Programming skills	Java, R, Python
Bioinformatics skills	telomere bioinformatics, pathway and network analysis, high-throughput biological data analysis, NGS data analysis, Hi-C data analysis, protein structure modeling
Wet lab experience	DNA Isolation, PCR-SSP, qrt-PCR, ELISA, Flow cytometry
Languages	Armenian (native), English (fluent), Russian (fluent), German (elementary)

Software packages (core developer)

TMM	Software for assessment of activity of telomere maintenance mechanisms from gene expression data.
Computel	Software for computation of mean telomere length from Whole Genome Next Generation sequencing data.
PSFC	A Cytoscape app for pathway signal flow calculation based on gene expression data, pathway topology and user-defined rules.
CyKEGGParser	A Cytoscape app for parsing and automatic corrections of KEGG pathways, and obtaining tissue-specific and protein-protein interaction based pathways.

Conferences, workshops and trainings

EMBO Conference “From Functional Genomics to Systems Biology”, Heidelberg, Germany	Poster presentation: “A pathway based approach for classification of telomerase positive and ALT cancer cells”	2016
European Conference on Computational Biology (ECCB) , The Hague, Netherlands	Poster presentation: “Analysis of telomere position effect in lung adenocarcinoma cell lines”	2016
EMBO workshop “Molecular mechanisms of ageing and regeneration: From pluripotency to senescence”, Spetses, Greece	Poster presentation: “Association of telomere length dynamics with epigenetic regulation of gene expression”	2016
ERS International Congress, Amsterdam, Netherlands	Oral presentation: “Telomere-associated gene network in lung adenocarcinoma.”	2015
14th Annual Conference ISMB/ECCB, Dublin, Ireland	Poster presentation: “Association of mean telomere length with biomolecular pathway deregulations in lung adenocarcinoma”	2015
2nd International Conference on Knowledge Engineering in BioMedical Informatics and Digital Health, Varna, Bulgaria	Oral presentation: “Pathway signal flow in looped networks”	2015
ERS International Congress, Munich, Germany	Oral presentation: “Methylation associated pathway activity deregulation in lung adenocarcinoma”	2014
EMBO practical course “Bioinformatics and genomes analyses”, Athens, Greece		2014
10th Network Biology Symposium and Cytoscape Workshop, Paris, France	Oral presentation: “A Cytoscape plugin/app for KEGG pathway map parsing, automatic corrections, and reduction of abstractions”	2013
8th Summer School on Biology, Information, and Computation (BCI 2013), Trieste, Italy		2013
FEBS Practical Course “Bioinformatics for the Bench Biologist”, Dubrovnik, Croatia	Poster presentation: “In silico molecular modeling of pyrin – the protein of Familial Mediterranean fever”	2012
Practical workshop “Formal Approaches to Modelling Bio-molecular Networks”, University of Edinburgh, UK	Poster presentation: “ Molecular modeling and docking of pyrin – the protein of Familial Mediterranean fever”	2012

Publications

Book chapters

1. Arakelyan A, Nersisyan L, Hakobyan A. **Application of MATLAB in -Omics and Systems Biology.** Applications from Engineering with MATLAB Concepts, Associate Prof. Jan Valdman (Ed.), ISBN: 978-953-51-2459-7. InTech, Croatia, 2016. DOI: 10.5772/62847.
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Journal articles

1. Arakelyan A, Nersisyan L, *et al.* **Autoimmunity and autoinflammation: A systems view on signaling pathway dysregulation profiles.** PLoS One 2017. 12(11):e0187572.
 2. Nersisyan L, Arakelyan A. **A transcriptome and literature guided algorithm for reconstruction of pathways to assess activity of telomere maintenance mechanisms.** bioRxiv 200535.
 3. Binder H, Hopp L, *et al.* **Genomic and transcriptomic heterogeneity of colorectal tumors arising in Lynch Syndrome.** J. Pathol. 2017.
 4. Nersisyan L. **Integration of Telomere Length Dynamics into Systems Biology Framework: A Review.** Gene Regul Syst Bio. 2016, 10:35-42.
 5. Arakelyan A, Nersisyan L, *et al.* **Cartography of pathway signal perturbations identifies distinct molecular pathomechanisms in malignant and chronic lung diseases.** Front Genet. 2016, 7:79.
 6. Nersisyan L, Löffler-Wirth H, *et al.* **Gene Set- and Pathway- Centered Knowledge Discovery Assigns Transcriptional Activation Patterns in Brain, Blood, and Colon Cancer: A Bioinformatics Perspective.** IJKDB 2016, 4(2):46-49.
 7. Hakobyan A, Nersisyan L, Arakelyan A. **Quantitative trait association study for mean telomere length in the South Asian Genomes.** Bioinformatics 2016, 32(11):1697-700.
 8. Hopp L, Nersisyan L, *et al.* **Epigenetic heterogeneity of B-cell lymphoma: Chromatin modifiers.** Genes 2015, 6(4):1076-1112.
 9. Nersisyan L, Johnson G, *et al.* **PSFC: a Pathway Signal Flow Calculator App for Cytoscape [version 2; referees: 2 approved]** F1000Research 2015, 4:480.
 10. Nersisyan L, Arakelyan A. **Computel: Computation of Mean Telomere Length from Whole-Genome Next-Generation Sequencing Data.** PLoS One 2015. 10(4): e0125201.
 11. Nersisyan L, Samsonyan R, Arakelyan A. **CyKEGGParser: tailoring KEGG pathways to fit into systems biology analysis workflows [v2; ref status: indexed, <http://f1000r.es/45p>].** F1000Research 2014, 3:145.
 12. Arakelyan A, Nersisyan L. **KEGGParser: parsing and editing KEGG pathway maps in Matlab.** Bioinformatics 2013, 29(4): 518-9.
 13. Nersisyan L, Arakelyan A. ***In silico* structure characterization of Familial Mediterranean fever gene product (pyrin).** IPCBEE 2012; 29: 40-44.
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Conference proceedings

1. Nersisyan L., Hakobyan A., Arakelyan A. **Association of telomere length with epigenetic regulation of gene expression.** F1000Research 2016, 5:2159 (poster) (doi: 10.7490/f1000research.1112996.1).
 2. Nersisyan L., Hakobyan A., Arakelyan A. **Telomere-associated gene network in lung adenocarcinoma.** European Respiratory Journal Sep 2015, 46 (suppl 59) doi: 10.1183/13993003.congress-2015.OA3493.
 3. Nersisyan L, Hakobyan A, Löffler-Wirth H, Binder Hans, Arakelyan A. **Association of mean telomere length with biomolecular pathway deregulations in lung adenocarcinoma.** F1000Research 2015, 4(ISCB Comm J):608 (poster) (doi: 10.7490/f1000research.1110351.1).
 4. Hakobyan A, Nersisyan L and Arakelyan A. **Quantitative trait association study for mean telomere length in the South Asian Genomes.** F1000Research 2015, 4(ISCB Comm J):605 (poster) (doi: 10.7490/f1000research.1110349.1).
 5. Nersisyan L, Lusine K, Hakobyan A et al. **A systems view on mining common pathway deregulation profiles in autoimmunity, autoinflammation and inflammation.** F1000Research 2015, 4(ISCB Comm J):604 (poster) (doi: 10.7490/f1000research.1110348.1).
 6. Nersisyan L, Wirth H, Gevorgyan A, Binder H, Arakelyan A. **Methylation associated pathway activity deregulation in lung adenocarcinoma.** Eur Respir J 2014; 44: Suppl. 58, 403.
 7. Arakelyan A, Nersisyan L, Wirth H, Binder H. **Mining common pathway deregulation profiles in lung diseases.** Eur Respir J 2014; 44: Suppl. 58, 2021.
 8. Nersisyan L, Arakelyan A. **3D structure prediction of pyrin-d2 isoform.** 2nd International Conference “Postgenomic methods of analyses in biology, laboratory and clinical medicine: genomics, proteomics, bioinformatics” 2011 (p. 112), Novosibirsk, Russia.
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