

# LILIT NERSISYAN

## CURRICULUM VITAE

### Personal Information

Full Name: Lilit Nersisyan  
Date of birth: 19.02.1990  
  
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### Work Details

Position: Researcher  
Degree: Master of Sciences, PhD student  
Bioinformatics Group,  
Institute of Molecular Biology,  
National Academy of Sciences  
of the Republic of Armenia  
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### Education

2014 - present ***PhD student***  
*Topic: Telomere analysis based on high-throughput multi-omics data*  
*Institute of Molecular Biology NAS RA*

2011-2013 ***Master's degree in Engineering***  
Specialty: Computer and Information Science  
*College of Science and Engineering, American University of Armenia*

2010-2012 ***Master's degree in Engineering***  
Specialty: Biotechnology  
*Department of Biotechnology, International Scientific and Educational Center, NAS RA*

2006-2010 ***Bachelor's degree in Biophysics***  
Specialty: Biophysics  
*Faculty of Biology, Department of Biophysics, Yerevan State University (YSU)*

### Educational scholarships

2011-2013 AUA/Ministry of Education and Science Academic full Scholarship for the academic year 2011-2013.

### Passed standardized exams

March 11, 2013 **iBT – Internet-Based TOEFL**  
*Overall score - 115*

March 10, 2011 **GRE**

Scores: *Quantitative* – 800 (94%), *Verbal* – 570 (80%), *Essay/writing* – 3.5 (26%)

## Professional Experience

2011 Dec – present	<b>Junior Researcher</b> <i>Research Group of Bioinformatics</i> Institute of Molecular Biology, NAS RA
2016 Spring-present	<b>Adjunct lecturer</b> <i>CSE 162 Introduction to Biosciences</i> American University of Armenia
2014 - 2015	<b>Teaching Associate</b> <i>American University of Armenia</i> <i>Introduction to Bioscience (2014-2015), Quantitative Biology (2015),</i> <i>Introduction to Algorithms (2015)</i>
2012 - 2014	<b>Java Developer</b> <i>CommuniHealth, New York, USA</i>
2011 Jan – 2011 Dec	<b>Senior Research assistant</b> <i>Research Group of Bioinformatics</i> Institute of Molecular Biology, NAS RA
2009-2011	<b>Senior Research assistant</b> <i>Research Group of Immunoregulation</i> Institute of Molecular Biology, NAS RA

## Research Experience and Technical Skills:

Programming skills	Java, R, MATLAB.
Bioinformatics skills	Gene expression, NGS data analysis, Pathway and network analysis, High dimensional data analysis, previous experience in protein structural modeling
Development tools	JetBrains IntelliJ IDEA, NetBeans IDE, Eclipse IDE/ Classic, MS Visual Studio, MS SQL Server, Enterprise Architect
Wet lab experience	DNA Isolation, PCR-SSP, qrt-PCR, ELISA, Flow cytometry.
Languages	Armenian (native), English (fluent), Russian (fluent)

## Research fellowships and stays

2016	BMBF MycSys project (short term research stay in the Interdisciplinary Centre for Bioinformatics, University of Leipzig, Leipzig, Germany) <i>Topic: Aberrant pathway function and telomere lengths in Lymphoma</i>
2015	DAAD (91572203) Short Term Research Scholarship for a 4 months research stay in the Interdisciplinary Centre for Bioinformatics, University of Leipzig, Leipzig, Germany <i>Topic: Bioinformatics pathway activity analysis of epigenetic regulation of gene expression in cancer and pulmonary diseases</i>

## Research grants and awards

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

## Conferences, Workshops and trainings

12-15 Nov, 2016	EMBO Conference “From Functional Genomics to Systems Biology”, Heidelberg, Germany <i>Poster presentation: “A pathway based approach for classification of telomerase positive and ALT cancer cells”</i>
3-7 Sept, 2016	European Conference on Computational Biology (ECCB) 2016, The Hague, Netherlands <i>Poster presentation: “Association of telomere length dynamics with epigenetic regulation of gene expression”</i>
16-24 Aug, 2016	EMBO workshop “Molecular mechanisms of ageing and regeneration: From pluripotency to senescence”, Spetses, Greece
26-30 Sept, 2015	ERS International Congress 2015, Amsterdam, Netherlands <i>Oral presentation: “Telomere-associated gene network in lung adenocarcinoma.”</i>
11-14 July, 2015	14th Annual Conference ISMB/ECCB 2015, Dublin, Ireland <i>Poster presentation: “Association of mean telomere length with biomolecular pathway deregulations in lung adenocarcinoma”</i>
29-10 July, 2015	Second International Conference on Knowledge Engineering in BioMedical Informatics and Digital Health, ITA 2015, Varna, Bulgaria

6-10 Sep, 2014	<p><i>Oral presentation: "Pathway signal flow in looped networks"</i></p> <p>ERS International Congress 2014, Munich, Germany</p> <p><i>Oral presentation: "Methylation associated pathway activity deregulation in lung adenocarcinoma"</i></p>
5-17 May, 2014	EMBO practical course "Bioinformatics and genomes analyses", Athens, Greece
9-10 Oct, 2013	<p>10th Network Biology Symposium and Cytoscape Workshop 2013 in Paris, France</p> <p><i>Oral presentation: "A Cytoscape plugin/app for KEGG pathway map parsing, automatic corrections, and reduction of abstractions"</i></p>
9-13 Sep, 2013	8th Summer School on Biology, Information, and Computation (BCI 2013), Trieste, Italy
3-6 Sep, 2013	International Conference «Young Scientists– Uniting Force of World Science and Culture», 4-6 September 2013, Ashkhabad
3-8 Sep, 2012	<p>FEBS 2012 Practical Course "Bioinformatics for the Bench Biologist", Dubrovnik, Croatia.</p> <p><i>Poster presentation: "In silico molecular modeling of pyrin – the protein of Familial Mediterranean fever"</i></p>
24-27 Apr, 2012	<p>Practical workshop entitled "Formal Approaches to Modelling Bio-molecular Networks" organized by the Centre for Synthetic and Systems Biology (formal CSBE), The University of Edinburgh, UK.</p> <p><i>Poster presentation: "Molecular modeling and docking of pyrin – the protein of Familial Mediterranean fever"</i></p>
26-28 Feb, 2012	4th International Conference on Bioinformatics and Biomedical Technology, 2012, Singapore, Singapore.
14-17 Nov, 2011	2 <sup>nd</sup> International Conference "Postgenomic methods of analyses in biology, laboratory and clinical medicine: genomics, proteomics, bioinformatics", Novosibirsk, Russia.
3-7 Oct, 2011	Workshop on Molecular and immunological bases of host-microbe interactions, Yerevan, Armenia.
26-30 Sep, 2011	8 <sup>th</sup> International Conference on Computer Science and Information Technologies, Yerevan, Armenia.
10-12 Nov, 2010	International young scientists' conference "Perspectives for development of molecular and cellular biology II", Yerevan, Armenia
13-14 Apr, 2010	International Congress of Young Scientists, Yerevan, Armenia.
15-17 Oct, 2009	International Conference "Biotechnology and health-3", Yerevan, Armenia.

### Travel Awards

2016	EMBL travel award to participate in EMBO conference "From Functional Genomics to Systems Biology"
2016	ECCB Travel Fellowship 2016

- 2016 EMBO travel award to participate in Spetses Summer School “Molecular mechanisms of ageing and regeneration: From pluripotency to senescence”
- 2015 ERS Gold Sponsorship to attend the ERS 2015 Congress
- 2014 ERS Gold Sponsorship to attend the ERS 2014 Congress in Munich, Germany.
- 2014 EMBO travel grant to attend the *EMBO Bioinformatics and Genomes Analyses* course in Athens, Greece, 2014.

## Membership in associations and societies

- 2013-present European Respiratory Society (ERS)
- 2012-present Association for Computing Machinery (ACM).
- 2012-present The International Society for Computational Biology (ISCB).
- 2011-present Armenian association for molecular and cellular biology and immunology.

## List of 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.

### *Journals*

1. Nersisyan L. Integration of Telomere Length Dynamics into Systems Biology Framework: A Review. *Gene Regul Syst Bio*. 2016, 10:35-42.
2. Arakelyan A, Nersisyan L, Petrek M, Löffler-Wirth H, Binder H. Cartography of pathway signal perturbations identifies distinct molecular pathomechanisms in malignant and chronic lung diseases. *Front Genet*. 2016, 7:79.
3. Nersisyan L, Löffler-Wirth H, Arakelyan A, Binder H. Gene Set- and Pathway- Centered Knowledge Discovery Assigns Transcriptional Activation Patterns in Brain, Blood, and Colon Cancer: A Bioinformatics Perspective. *International Journal of Knowledge Discovery in Bioinformatics (IJKDB)* 2016, 4(2):46-49.
4. 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.
5. Hopp L., Nersisyan L., Löffler-Wirth H. *et al.* Epigenetic heterogeneity of B-cell lymphoma: Chromatin modifiers. *Genes* 2015, 6(4):1076-1112.
6. Nersisyan L, Johnson G, Riel-Mehan M *et al.* PSFC: a Pathway Signal Flow Calculator App for Cytoscape [version 1; referees: 1 approved] *F1000Research* 2015, 4:480.
7. Nersisyan L, Arakelyan A. Computel: Computation of Mean Telomere Length from Whole-Genome Next-Generation Sequencing Data. *PLoS One* 2015. 10(4): e0125201.
8. Arakelyan A, Nersisyan L, Gevorgyan A, Boyajyan A. Geometric Approach for Gaussian-Kernel Bolstered Error Estimation for Linear Classification in Computational Biology. *International Journal of Information theories & Applications* 2014, 21: 170-182.
9. 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.
10. Nersisyan L, Arakelyan A. MEFV expression during macrophage activation. *National Electronic Journal of Natural Sciences*, 2(21): 77-81, 2013.

11. Arakelyan A, Nersisyan L. KEGGParser: parsing and editing KEGG pathway maps in Matlab. *Bioinformatics* 2013, 29(4): 518-9.
12. Boyajyan A, Arakelyan A, Nersisyan L, Avetisyan N, Martirosyan G. Evidence-Based Validation of Pyrin Structural Models. *Protein Science* 2012, 21 Special Issue, Suppl. 1: 196-196.
13. Nersisyan L, Arakelyan A. In silico structure characterization of Familial Mediterranean fever gene product (pyrin). *IPCBEE* 2012; 29: 40-44.
14. Karapetyan D, Arakelyan A, Nersisyan L, Aslanyan L, Boyajyan A. GOMESH: A tool for analyzing gene ontology data. *Biological Journal of Armenia* 2010, Suppl. 1(62): 41-43.
15. Poghosyan D, Tadevosyan G, Nersisyan L, Arakelyan A. CD4 expression on activated human monocytes after different ways of stimulation. *The New Armenian Medical Journal* 2010, 4(1): 111-112.

### *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. *2<sup>nd</sup> International Conference "Postgenomic methods of analyses in biology, laboratory and clinical medicine: genomics, proteomics, bioinformatics"* 2011 (p. 112), Novosibirsk, Russia.
9. Arakelyan A, Boyajian A, Aslanyan L, Nersisyan L, Sahakyan H. Growing Support Sets For Pathway Specific Microarray Gene Expression Analysis. *"8<sup>th</sup> International Conference on Computer Science and Information Technologies"* 2011 (p.207-210), Yerevan, Armenia.
10. Poghosyan D, Tadevosyan G, Nersisyan L, Arakelyan A. The effect of Id 1F7+ Antibodies on LPS-induced Cytokine Secretion by Monocytes. *Biological Journal of Armenia* 2010, Suppl. 1(62): 83-87.
11. Arakelyan A, Boyajyan A, Aslanyan L, Muradyan D, Chavushyan A, Hovsepyan T, Nersisyan L. Functional gene sets in posttraumatic stress disorder: analysis of disease related gene expression. *International Conference "Biotechnology and health-3"* 2009 (p. 57-60), Yerevan, Armenia.