Ludmila Danilova, Ph.D.

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EDUCATION

April 2004	**Ph.D., Physics & Math,** Institute for Information Transmission Problems Russian Academy of Sciences Thesis title: "Computing search of interacting with regulatory proteins DNA sites in bacteria genomes and its applications"
May 1999	**M.S., Applied Mathematics** Qualification: "mathematician". Diploma with honors Department of Mathematics and Informatics of Maimonides's State Academy, Russia

ADDITIONAL EDUCATION

June 2011	Summer Institute of Epidemiology and Biostatistics at the Johns Hopkins University: - Biostatistics in Medical Product Regulation - Design and Conduct of Clinical Trials
July 2012	Bayesian Adaptive Trials Course in Summer Institute of Epidemiology and Biostatistics at the Johns Hopkins University

WORK EXPERIENCE

2012-present	**Research Associate**, Division of Biostatistics and Bioinformatics, Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins School of Medicine, Baltimore, MD, USA

2010-2012	**Postdoctoral fellow**, Division of Biostatistics and Bioinformatics, Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins School of Medicine, Baltimore, MD, USA
	 Postdoctoral Mentor: Stephen Baylin and Leslie Cope
	 - Analysis of DNA methylation data of the following diseases:
	   o Solid tumors, such as lung squamous cell carcinoma, lung adenocarcinoma, head and neck squamous cell carcinoma, melanoma (cutaneous and uveal), from the Cancer Genome Atlas (TCGA)
	   o Myelodysplastic syndrome from the Stand Up To Cancer program.

2008-2010	**Postdoctoral fellow**, Division of Biostatistics and Bioinformatics, Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins School of Medicine, Baltimore, MD, USA Postdoctoral Mentor: Michael Ochs - Developing model of transcription and translation processes in C.elegans vulval development. - Developing JTopper software for gene set analysis in Java. - Analysis of gene expression and metabolomics data
2007-2008	**Patent writer**, ABBYY Software (www.abbyy.com)

Preparation of patent applications and patent search in the USPTO

2004-2007 **Technical writer**, ABBYY Software (www.abbyy.com)
Development of help documentation for software

2000-2004 **Engineer of advertising department**, Central Geophysical Expedition (CGE) JSC

1999-2003 **Post-graduate Fellow,** Institute for Information Transmission Problems Russian Academy of Sciences
Supervisor: Lyubetsky VA
Development of new algorithms that solve research and applied tasks in bioinformatics; testing these algorithms on model and real data:
- Modeling of RNA secondary structure kinetics by Monte-Carlo method
- Identification of regulatory signals in unaligned DNA sequences

1999-2001 **Trainee,** Department of Mathematics and Informatics of Maimonides's State Academy
Conduction of seminars in Differential Equations and Mathematical Analysis

Citizenship

Russian and US Citizen

Skills:

Languages: Russian (native) and English

Programming Languages: JAVA; Matlab; Object Pascal
Software: Matlab; R
Version Control: CVS, SVN, git

Selected Publications

Complete List of Publications can be found in MyBibliography:

https://www.ncbi.nlm.nih.gov/myncbi/ludmila.danilova.1/bibliography/public/

1. Immuno-oncology. Understanding tumor microenvironment and immune response to cancer immunotherapy, research for prognostic and predictive biomarkers of the response are very important areas of research in era of immune therapy of cancer. Bioinformatic algorithms are critical in helping investigator to dig into immune-related data and integrate different data modalities. I provide my collaborators with support in data analysis in variety cancer types.

   a. Giraldo NA, Berry S, Becht E, Ates D, Schenk KM, Engle EL, Green B, Nguyen P, Soni A, Stein JE, Succaria F, Ogurtsova A, Xu H, Gottardo R, Anders RA, Lipson EJ, **Danilova L**, Baras AS, Taube JM. Spatial UMAP and image-cytometry for topographic immuno-oncology biomarker discovery. Cancer Immunol Res. 2021 Aug 25;. doi: 10.1158/2326-6066.CIR-21-0015. PubMed PMID: 34433588.

b. Berry S, Giraldo NA, Green BF, Cottrell TR, Stein JE, Engle EL, Xu H, Ogurtsova A, Roberts C, Wang D, Nguyen P, Zhu Q, Soto-Diaz S, Loyola J, Sander IB, Wong PF, Jessel S, Doyle J, Signer D, Wilton R, Roskes JS, Eminizer M, Park S, Sunshine JC, Jaffee EM, Baras A, De Marzo AM, Topalian SL, Kluger H, Cope L, Lipson EJ, **Danilova L**, Anders RA, Rimm DL, Pardoll DM, Szalay AS, Taube JM. Analysis of multispectral imaging with the AstroPath platform informs efficacy of PD-1 blockade. Science. 2021 Jun 11;372(6547):eaba2609. doi: 10.1126/science.aba2609. PMID: 34112666.

c. Ho WJ, Erbe R, **Danilova L**, Phyo Z, Bigelow E, Stein-O'Brien G, Thomas DL 2nd, Charmsaz S, Gross N, Woolman S, Cruz K, Munday RM, Zaidi N, Armstrong TD, Sztein MB, Yarchoan M, Thompson ED, Jaffee EM, Fertig EJ. Multi-omic profiling of lung and liver tumor microenvironments of metastatic pancreatic cancer reveals site-specific immune regulatory pathways. Genome Biol. 2021 May 13;22(1):154. doi: 10.1186/s13059-021-02363-6. PubMed PMID: 33985562. PMCID: PMC8118107

d. Lu S, Stein JE, Rimm DL, Wang DW, Bell JM, Johnson DB, Sosman JA, Schalper KA, Anders RA, Wang H, Hoyt C, Pardoll DM, **Danilova L**, Taube JM. Comparison of Biomarker Modalities for Predicting Response to PD-1/PD-L1 Checkpoint Blockade: A Systematic Review and Meta-analysis. JAMA Oncol. 2019 Jul 18. PMID: 31318407

e. **Danilova L**, Anagnostou V, Caushi JX, Sidhom JW, Guo H, Chan HY, Suri P, Tam A, Zhang J, Asmar ME, Marrone KA, Naidoo J, Brahmer JR, Forde PM, Baras AS, Cope L, Velculescu VE, Pardoll DM, Housseau F, Smith KN. The Mutation-Associated Neoantigen Functional Expansion of Specific T Cells (MANAFEST) Assay: A Sensitive Platform for Monitoring Antitumor Immunity. Cancer Immunol Res. 2018 Aug;6(8):888-899. doi: 10.1158/2326-6066.CIR-18-0129. Epub 2018 Jun 12. PubMed PMID: 29895573; PubMed Central PMCID: PMC6072595.

f. **Danilova L**, Wang H, Sunshine J, Kaunitz GJ, Cottrell TR, Xu H, Esandrio J, Anders RA, Cope L, Pardoll DM, Drake CG, Taube JM. Association of PD-1/PD-L axis expression with cytolytic activity, mutational load, and prognosis in melanoma and other solid tumors. Proc Natl Acad Sci U S A. 2016 Nov 29;113(48):E7769-E7777. doi: 10.1073/pnas.1607836113. Epub 2016 Nov 11. PubMed PMID: 27837027; PubMed Central PMCID: PMC5137776.

2. <u>DNA methylation in cancer</u>. As a participant of the Cancer Genome Atlas (TCGA), I have analyzed DNA methylation data of various types of cancer. During these projects, a number of bioinformatics algorithms were developed and applied to genomic data to derive CpG island methylator phenotype and epigenetically silenced genes. This effort also allowed us to look at pan-cancer methylation profiles and looked for tumor type specific methylation that can be used for characterization of human cancer and biomarker development.

a. **Danilova L**, Wrangle J, Herman JG, Cope L.DNA-methylation for the detection and distinction of 19 human malignancies. Epigenetics. 2021 Mar 5:1-11. doi: 10.1080/15592294.2021.1890885. PMID: 33666134

b. Hoadley KA, Yau C, Wolf DM, Cherniack AD, Tamborero D, Ng S, Leiserson MD, Niu B, McLellan MD, Uzunangelov V, Zhang J, Kandoth C, Akbani R, Shen H, Omberg L, Chu A, Margolin AA, Van't Veer LJ, Lopez-Bigas N, Laird PW, Raphael BJ, Ding L, Robertson AG, Byers LA, Mills GB, Weinstein JN, Van Waes C, Chen Z, Collisson EA; **Cancer Genome Atlas Research Network**, Benz CC, Perou CM, Stuart JM. Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. Cell. 2014 Aug 14;158(4):929-44. PMCID: PMC4152462

c. Wrangle J, Machida EO, **Danilova L**, Hulbert A, Franco N, Zhang W, Glöckner SC, Tessema M, Van Neste L, Easwaran H, Schuebel KE, Licchesi J, Hooker CM, Ahuja N, Amano J, Belinsky SA, Baylin SB, Herman JG, Brock MV. Functional identification of cancer-specific methylation of CDO1, HOXA9, and TAC1 for the diagnosis of lung cancer. Clin Cancer Res. 2014 Apr 1;20(7):1856-64. doi: 10.1158/1078-0432.CCR-13-2109. Epub 2014 Jan 31. PubMed PMID: 24486589; PubMed Central PMCID: PMC4019442.

d. **The Cancer Genome Atlas Research Network**. Comprehensive Genomic Characterization of Squamous Cell Lung Cancers. Nature. 2012. 489(7417):519-525. PMCID: PMC3466113

3. <u>Head and neck cancer genomics.</u> I am also involved in analysis and integration of different types of genomic data of head and neck squamous cell carcinoma with the aim to explain cancer development. The main focus of these studies is how epigenetic structure regulates gene expression and alternative splicing. In addition, these studies aim to characterize genomic aberration due to integration of human papilloma virus (HPV), the main risk factor of HPV-related head and neck tumors.

a. Lopatina T, Favaro E, **Danilova L**, Fertig EJ, Favorov AV, Kagohara LT, Martone T, Bussolati B, Romagnoli R, Albera R, Pecorari G, Brizzi MF, Camussi G, Gaykalova DA. Extracellular Vesicles Released by Tumor Endothelial Cells Spread Immunosuppressive and Transforming Signals Through Various Recipient Cells. Front Cell Dev Biol. 2020;8:698. doi: 10.3389/fcell.2020.00698. eCollection 2020. PubMed PMID: 33015029; PMCID: PMC7509153

b. Guo T, Zambo KDA, Zamuner FT, Ou T, Hopkins C, Kelley DZ, Wulf HA, Winkler E, Erbe R, **Danilova L**, Considine M, Sidransky D, Favorov A, Florea L, Fertig EJ, Gaykalova DA. Chromatin structure regulates cancer-specific alternative splicing events in primary HPV-related oropharyngeal squamous cell carcinoma. Epigenetics. 2020 Sep;15(9):959-971. doi: 10.1080/15592294.2020.1741757. Epub 2020 Mar 22. PubMed PMID: 32164487; PubMed Central PMCID: PMC7518675.

c. Kelley DZ, Flam EL, Guo T, **Danilova LV**, Zamuner FT, Bohrson C, Considine M, Windsor EJ, Bishop JA, Zhang C, Koch WM, Sidransky D, Westra WH, Chung CH, Califano JA, Wheelan S, Favorov AV, Florea L, Fertig EJ, Gaykalova DA. Functional characterization of alternatively spliced GSN in head and neck squamous cell carcinoma. Transl Res. 2018 Jul 26. pii: S1931-5244(18)30108-7. doi: 10.1016/j.trsl.2018.07.007. PMID: 30118659; PMCID: PMC6218276

d. Parfenov M, Pedamallu CS, Gehlenborg N, Freeman SS, **Danilova L**, Bristow CA, Lee S, Hadjipanayis AG, Ivanova EV, Wilkerson MD, Protopopov A, Yang L, Seth S, Song X, Tang J, Ren X, Zhang J, Pantazi A, Santoso N, Xu AW, Mahadeshwar H, Wheeler DA, Haddad RI, Jung J, Ojesina AI, Issaeva N, Yarbrough WG, Hayes DN, Grandis JR, El-Naggar AK, Meyerson M, Park PJ, Chin L, Seidman JG, Hammerman PS, Kucherlapati R; Cancer Genome Atlas Network. Characterization of HPV and host genome interactions in primary head and neck cancers. Proc Natl Acad Sci U S A. 2014 Oct 28;111(43):15544-9. PMCID: PMC4217452

4. <u>Mathematical models of dynamics of molecular biology processes.</u> In addition to working with molecular data, I have developed two mathematical models. The one model allows you to predict secondary structure of RNA during the elongation process. The other one is stochastically models signal propagation and feedback in cellular signaling pathways.

a. *Fertig EJ, **Danilova LV**, Favorov AV and Ochs MF. Hybrid modeling of cell signaling and transcriptional reprogramming and its application in C elegans development. Frontiers in Bioinformatics and Computational Biology. 2011: 2:77. PMCID: PMC3268630

b. **Danilova LV**, Pervouchine DD, Favorov AV and Mironov A.A. RNAKinetics: a web server that models secondary structure kinetics of an elongating RNA. J Bioinform Comput Biol. 2006:4(2):589-596. (http://www.worldscinet.com/jbcb/04/0402/S0219720006001904.html)

* Joint first author

Book chapters

1. Fertig, E.J, **Danilova**, **L.V.**, and Ochs, M.F. (2011) Cancer Systems Biology, in Handbook of Computational Biostatistics, edited by Lu H.H-S., Schölkopf, S., and Zhao, H., Springer-Verlag, pp. 533-565.

2. **L. Danilova** and MF Ochs, (2011) Biomarkers of System Response to Therapeutic Intervention, in Handbook of Systems Toxicology, edited by Daniel A. Casciano and Saura C. Sahu. Chichester, UK: John Wiley &Sons, Ltd, pp 669-682