BIOGRAPHICAL SKETCH

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NAME: TROYANSKAYA, OLGA

eRA COMMONS USER NAME (credential, e.g., agency login): troyanskaya

POSITION TITLE: Professor, Lewis-Sigler Institute for Integrative Genomics and Dept. of Computer Science

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
University of Richmond, Richmond, VA	BS	06/1999	Biology and Computer Science
Stanford University, Stanford, CA	PHD	06/2003	Biomedical Informatics

A. Personal Statement

My group's focus is development and implementation of robust computational methods and systems for analysis, integration, modeling and visualization of heterogeneous biological data, tightly integrating these technologies with biological experiments and clinical information, and using them to study processes underlying human biology, disease, drug action, and functional evolution, including in the context of specific tissues and cell lineages. Leveraging machine learning, computer science, and informatics techniques, we develop methods that lead to discovery of novel biology; the integrative data analysis approaches we have developed have demonstrated accuracy through competitions and systematic computational and experimental evaluations. This proposal will build on our prior work developing computational approaches to predict cell-lineage-specific expression and cell-lineage-tissue-specific networks and using these networks for prediction of disease- and drug-associated biomarkers and drivers and disease sub-classification. We will also rely on our extensive background in multi-modal data integration and development and application of predictive methods, including in immune context. This proposal will also leverage my and my group's background in machine learning, computer science, functional genomics, modeling, and data analysis, and our experience of successful and productive collaborations with experimental and clinical researchers, including long-standing collaborations with several PIs on this proposal.

Ongoing and recently completed projects that I would like to highlight include:

R01GM071966 Troyanskaya (PI) 04/2019-03/2023 Integration and Visualization of Diverse Biological Data

FA8650-19-C-7944 Broderick (PI) 09/2019-03/2023 Peerless Operator Biologic Aptitude (Peerless)

U54CA244438 Lim (PI) 09/2019-08/2024 UCSF Center for Synthetic Immunology: Tools to Reprogram the Immune System to Combat Cancer

N6600119C4022 Sealfon (PI) 04/2019-03/2023 WMD ECHO Detector

UG3DK114907 Kretzler (PI) 09/2017-06/2022 Precision Medicine through IntErrogation of Rna in the Kidney (Premiere)

1. Meyer M, Wang Y, Edwards D, Smith GR, Rubenstein AB, Ramanathan P, Mire CE, Pietzsch C, Chen X, Ge Y, Cheng WS, Henry C, Woods A, Ma L, Stewart-Jones GB, Bock KW, Minai M, Nagata BM, Periasamy S, Shi PY, Graham BS, Moore IN, Ramos I, Troyanskaya OG, Zaslavsky E, Carfi A, Sealfon SC, Bukreyev A. Attenuated activation of pulmonary immune cells in mRNA-1273-vaccinated hamsters after SARS-CoV-2 infection. J Clin Invest. 2021 Oct 15;131(20) PubMed Central PMCID: PMC8516449.
2. Chen X, Zhou J, Zhang R, Wong AK, Park CY, Theesfeld CL, Troyanskaya OG. Tissue-specific enhancer functional networks for associating distal regulatory regions to disease. Cell Syst. 2021 Apr 21;12(4):353-362.e6. PubMed PMID: 33689683.

3. Menon R, Otto EA, Sealfon R, Nair V, Wong AK, Theesfeld CL, Chen X, Wang Y, Boppana AS, Luo J, Yang Y, Kasson PM, Schaub JA, Berthier CC, Eddy S, Lienczewski CC, Godfrey B, Dagenais SL, Sohaney R, Hartman J, Fermin D, Subramanian L, Looker HC, Harder JL, Mariani LH, Hodgin JB, Sexton JZ, Wobus CE, Naik AS, Nelson RG, Troyanskaya OG, Kretzler M. SARS-CoV-2 receptor networks in diabetic and COVID-19-associated kidney disease. Kidney Int. 2020 Dec;98(6):1502-1518. PubMed Central PMCID: PMC7543950.
4. Zhou J, Park CY, Theesfeld CL, Wong AK, Yuan Y, Scheckel C, Fak JJ, Funk J, Yao K, Tajima Y, Packer A, Darnell RB, Troyanskaya OG. Whole-genome deep-learning analysis identifies contribution of noncoding mutations to autism risk. Nat Genet. 2019 Jun;51(6):973-980. PubMed Central PMCID: PMC6758908.

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2020 -	Member/Adviser, National Advisory Council for Human Genome Research
2019 -	Scientific Advisory Board, Caris Life Sciences
2018 -	Scientific Advisory Board, Jackson Laboratory
2014 -	Deputy Director of Genomics, Simons Center for Data Analysis, Simons Foundation, NYC
2013 -	Professor, Lewis-Sigler Institute for Integrative Genomics and Dept. of Computer Science, Princeton University
2009 - 2013	Associate Professor, Lewis-Sigler Institute for Integrative Genomics and Dept. of Computer Science, Princeton University
2003 - 2009	Assistant Professor, Lewis-Sigler Institute for Integrative Genomics and Dept. of Computer Science, Princeton University
2002 - 2002	Instructor, Advanced Bioinformatics, California State University, Hayward, CA
1999 - 2003	Doctoral Student, Biomedical Informatics and Genetics, Stanford University, CA
1999 - 1999	Summer Research Fellow, Genome Diversity Center, University of Haifa, Israel
1998 - 1998	Summer Fellow, The Institute for Genomic Research, MD

Honors

2020	Fellow, Association for Computing Machinery
2017	Fellow, International Society for Computational Biology
2014	Ira Herskowitz Award, The Genetics Society of America
2011	Blavatnik Award, Finalist, NYAS
2011	Overton Prize, International Society for Computational Biology
2009	Fellow, Canadian Institute for Advanced Research
2006	NSF Career Award, National Science Foundation
2006	Howard Wentz Faculty Award, Princeton University
2004	TR35 Innovators Award, MIT Technology Review

C. Contribution to Science

1. The goal of my research is to bring the capabilities of computer science and statistics to the study of gene function and regulation in the biological networks and pathways through integrated analysis of biological data from diverse data sources--both existing and yet to come. My group has designed systematic, accurate computational and statistical algorithms for biological signal detection in high-throughput data sets to uncover hidden information within these data to enable novel biological insights about human health and disease.

   Integration of heterogeneous genomics data to predict gene function: As a graduate student in the Altman and Botstein labs, I published the first study that applied a Bayesian approach to combine disparate data to make predictions of gene function for uncharacterized genes in yeast:

a. Troyanskaya OG, Dolinski K, Owen AB, Altman RB, Botstein D. A Bayesian framework for combining heterogeneous data sources for gene function prediction (in Saccharomyces cerevisiae). Proc Natl Acad Sci U S A. 2003 Jul 8;100(14):8348-53. PubMed Central PMCID: PMC166232.

2. Gene function and network comparisons across species: My lab has developed algorithms that go beyond sequence similarity methods to leverage genomics data for the accurate determination of functionally equivalent genes across species and to compare networks across organisms. This work created the foundation for mapping information across species in a data-driven manner. For the most recent example, see:

    a. Wong AK, Krishnan A, Yao V, Tadych A, Troyanskaya OG. IMP 2.0: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. Nucleic Acids Res. 2015 Jul 1;43(W1):W128-33. PubMed Central PMCID: PMC4489318.

3. How networks function and change in a tissue-specific manner: we developed a computational method that generated functional molecular maps specific to 144 different human tissues to enable the better understanding of the functions and complex interrelationships of genes and proteins in specific cellular contexts, see:

    a. Greene CS, Krishnan A, Wong AK, Ricciotti E, Zelaya RA, Himmelstein DS, Zhang R, Hartmann BM, Zaslavsky E, Sealfon SC, Chasman DI, FitzGerald GA, Dolinski K, Grosser T, Troyanskaya OG. Understanding multicellular function and disease with human tissue-specific networks. Nat Genet. 2015 Jun;47(6):569-76. PubMed Central PMCID: PMC4828725.

4. Computationally defining cell-type specificity in human disease: my group developed a novel technique to computationally determine cell lineage-specific gene expression based on expression compendia. In collaboration with the Kretzler lab, we created a proof-of-concept system that virtually dissects a kidney using expression data to separate cells that cannot be separated by physical dissection. We were then able to identify genes that are turned on in very specific kidney cell types, which is key information necessary for the molecular characterization of kidney disease that was up to now not tractable.

    a. Ju W, Greene CS, Eichinger F, Nair V, Hodgin JB, Bitzer M, Lee YS, Zhu Q, Kehata M, Li M, Jiang S, Rastaldi MP, Cohen CD, Troyanskaya OG, Kretzler M. Defining cell-type specificity at the transcriptional level in human disease. Genome Res. 2013 Nov;23(11):1862-73. PubMed Central PMCID: PMC3814886.

5. Development of research resources: in addition to the development of computational algorithms as described above, I take the additional step to turn them into research resources by making them accessible to the biomedical research at large. My group has released over 20 research resources, comprising of web sites, code libraries, and other software tools to allow biologists to explore and visualize our results, or implement our code, in a wide variety of ways.

Complete List of Published Work in My Bibliography:
https://www.ncbi.nlm.nih.gov/myncbi/olga.troyanskaya.1/bibliography/public/