Dr. Mikhail G. Dozmorov

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PROFESSIONAL SUMMARY

Bioinformatics, Biostatistics, Cancer genomics, Single cell technologies, AI/Machine Learning

EMPLOYMENT

Associate professor, with tenure, Department of Biostatistics
July 2020 - present, Virginia Commonwealth University

Affiliated faculty, Department of Pathology
September 2019 – present, Virginia Commonwealth University

Assistant professor, tenure-track, Department of Biostatistics
August 2014 - June 2020, Virginia Commonwealth University

Research assistant member (research assistant professor equivalent), Arthritis and Clinical Immunology program
July 2012 – July 2014, Oklahoma Medical Research Foundation

Senior research scientist, Arthritis and Clinical Immunology program
May 2010 – June 2012, Oklahoma Medical Research Foundation

Postdoc in Cancer Research and Bioinformatics, Department of Urology
June 2005 – April 2010, Oklahoma University Health Science Center

EDUCATION

The Carpentries instructor – a certification program developing foundational coding and data science teaching skills for the global community of instructors, mentors, workshop organizers, etc. January 2022

Preparing Future Faculty - A two-semester program (4 credit hours) designed for trainees interested in acquiring the basic theory and skills necessary to be an effective communicator and educator leader. September 2009 – April 2010, Oklahoma University Health Science Center

Ph.D., Medical Biophysics
March 2005, Gothenburg University, Gothenburg, Sweden
Ph.D. Thesis: Activity-dependent changes of synaptic transmission in a long-term perspective, and processes involved. Advisor: Dr. Holger Wigström

M.S., Computer Sciences and Microelectronics
July 1997, Moscow Institute of Electronic Technology (Technical University), Moscow, Russia
M.S. Thesis: Development of electronic thermometer circuits

B.S., Physics and Chemistry
July 1995, Moscow Institute of Electronic Technology (Technical University), Moscow, Russia

OTHER EXPERIENCE

Industry consultant, Bioinformatics
2014, SensiQ Technologies Inc.

Instructor, Bioinformatics and computer sciences
September 1997 – April 1999, Zelenograd Community College, Russia

HONORS

Blick scholar, supported by the George and Lavinia Blick Research Fund, VCU	2019-2023
Young investigator award, National IDeA Symposium of Biomedical Research Excellence	2014
Outstanding research assistant member, inaugural William G. Thurman award, OMRF	2014
Best paper, 1st place (as first and corresponding author), MCBIOS 2013 conference	2013
Best oral presentation, 1st place award, MCBIOS 2012 conference	2012
Federation of American Societies For Experimental Biology (FASEB) MARC Travel Award	2012
Best oral presentation, 1st place travel award, OMRF	2011
Ingenuity Systems Certified Analyst	2009

RESEARCH SUPPORT

PI and co-PI-level, current

4VA (PI: Enke (JMU), **Dozmorov** (VCU)) $5,000 07/01/24 – 06/30/25
Characterizing novel transcript accumulation and functional relevance across the vertebrate retina
Role: subaward PI (0% efforts)

PI and co-PI-level, completed

PhRMA Foundation (**PI: Dozmorov**) $100,000 01/01/19 – 12/31/21
Druggable 3D genomics of metastasis
Role: PI (10% effort)

VCU Accelerate Fund (**PI: Green, Spiegel, Dozmorov**) $100,000 05/01/22 – 04/30/23
Sphingosine Kinase 2 in Sexual Dimorphism of Hepatocellular Carcinoma
Role: co-PI (1% effort)

VCU Massey Cancer Center (PI: Faber, **co-PI: Dozmorov**) $50,000 07/15/20 – 07/14/21
Exploring race specific therapeutic targets in TNBC
Role: co-PI (1% efforts)

VCU Presidential Research Quest Fund (**PI: Dozmorov**) $50,000 06/01/15 – 12/31/16
Diagnostic and therapeutic strategies of triple-negative breast cancer guided by the patient-specific 'omics' data
Role: PI (20% efforts)

ACS IRG 14-192-40 (**PI: Dozmorov**) $29,046 01/01/17 – 12/31/17
Development of a joint normalization method to compare cancer and normal 3D genomic structures
Role: PI (0% efforts)

VCU Massey Cancer Center (PI: Harrell, **co-PI: Dozmorov**) $50,000 12/01/16 – 11/30/17
Development and RNA Sequencing Analysis of Patient Derived Xenograft Breast Cancer Brain Metastasis Models
Role: co-PI (0% efforts)

NIH/NIGMS 8 P30 GM103510 (PI: James) $49,000   12/01/12 – 07/31/13
PU.1 transcription factor as a master regulator of SLE-specific genes
Role: **subaward PI** (10% efforts)

NIH/NIAMS 2 P30 AR053483-06 (PI: James) $30,000   12/01/12 – 08/31/13
H3K4me1/2 histone methylation marks differences in Systemic Lupus Erythematosus
Role: **subaward PI** (0% efforts)

NIH/NCRR-COBRE 8 P20 GM103456-10 (PI: Gaffney) $20,000   12/01/11 – 09/30/12
GenomeRunner: automating functional genomics
Role: **subaward PI** (0% efforts)

4VA (PI: Sheffield (Uva), **Dozmorov** (VCU)) $5,000   05/15/18 – 07/14/19
A Standardized Database Format for Genomic Locus Enrichment Analysis
Role: Co-PI (0% effort)

4VA (PI: Sheffield (Uva), **Dozmorov** (VCU)) $5,000   05/15/18 – 06/30/19
A linked-data framework for integrative analysis of genomic locus collections
Role: Co-PI (0% effort)

Burroughs Wellcome Fund Travel Grant (**PI: Dozmorov**) $3,908   06/01/17 – 12/31/18
Epigenomic similarity as the unifying engine of disease genotypes and phenotypes
Role: PI (0% efforts)

Collaborative, current
NIH P50AA022537 (PI: Miles) $7,769,279   04/01/20 – 03/31/25
Cross-species investigation of gene networks for ethanol-related behaviors
Role: Co-I, Bioinformatics core co-director (12% efforts)

NCI/NIH (PI: Faber) $2,928,124   10/01/23 – 09/30/28
Platelet-sparing BCL-xL/BCL-2 co-inhibition for SCLC subsets
Role: Co-I (5% efforts)

NCI/NIH 1P01CA275740-01A1 (PI: Sarkar) $2,678,459   08/08/24 – 07/31/29
ExpLoiting thErapeutic VulnerAbilities in hepaTocEllular carcinoma (ELEVATE)
Role: Co-I (3% efforts)

NIH R01CA251405 (PI: Atfi) $2,600,584   07/01/20 – 06/30/25
Targeting Transglutaminase 2 in cancer cachexia
Role: Co-I (1% efforts)

NCI/NIH/DHHS 1R37CA269249 (PI: Bos) $2,102,008   04/01/22 – 03/31/27
Regulatory T cell modulation of reactive astrogliosis in brain metastasis
Role: Co-I (5% effort)

NIH R01CA24004 (PI: Sarkar) $2,435,498   06/01/19 – 05/31/24
A novel role of IGFBP7 in the microenvironment of hepatocellular carcinoma
Role: Co-I (4% efforts)

NIH R01DK107451 (PI: Sarkar) $2,428,156   04/01/22 – 03/31/27
The role of AEG-1 in NASH and NASH-HCC

Role: Co-I (4% efforts). [News](#)

NIH R01CA230561 (PI: Sarkar) $2,392,641   04/01/19 – 03/31/24
Targeting oncogenes for hepatocellular carcinoma
Role: Co-I (4% efforts)

NCI FP00019758 (PI: Faber) $2,264,908   04/01/24 – 03/31/29
ABT-199 based therapies to treat neuroblastoma
Role: Co-I (5% efforts)

NIH R01CA266124 (PI: Green) $1,950,865   09/01/22 – 08/31/27
Sphingosine kinase 2 in sexual dimorphism of hepatocellular carcinoma
Role: Co-I (5% efforts)

NIH R01AI097134 (PI: Sawalha, Univ. of Pittsburgh) $1,895,067   08/12/20 – 07/31/24
Role of DNA methylation in lupus
Role: Co-I, subaward PI (10% efforts)

DOD PC240509 (PI: Fisher) $1,836,611   10/01/24 – 09/30/27
Therapy of advanced prostate cancer with a novel cell therapy
Role: Co-I (3% effort)

NIH R01CA246182 (PI: Harrell) $1,733,955   07/01/20 – 06/30/25
Circumventing acquired carboplatin resistance in triple-negative breast cancers
Role: Co-I (3% efforts)

NCI 1R01CA272710 (PI: Faber) $1,613,654   04/01/23 – 03/31/28
SUMOylation disruption is toxic for SS18-SSX-driven synovial sarcoma
Role: Co-I (3% efforts)

NIH 1 R01 HD111943-01 (PI: Jackson-Cook) $ 1,475,266   05/01/23 - 04/30/26
A mosaic Down syndrome model system comparing isogenic trisomic/disomic cells to unmask trisomy 21 related genomic, epigenomic, and senescence changes acquired across the lifespan
Role: Co-I (10% efforts)

NIH R01CA249219 (PI: Faber) $1,413,434   06/01/20 – 05/31/24
Neuroblastoma reliance on DNMT1 through amplified MYCN
Role: Co-I (5% efforts)

NCI 1U54CA283762-01 (PI: Trevino) $1,030,960   07/19/23 - 06/30/28
United for Health Equity - Living PDX Program (U4HELPP)
Role: (Co-I, Bioinformatics core co-leader, 8%)

NIH/K25AA030072 (PI: Nguyen)   927,980   04/01/22 – 03/31/27
Understanding the genomic basis of problematic alcohol use through integrative analysis of multi-omics data
Role: Co-I (0% efforts)

ACS 5560271FN (PI: Bos) $792,000   01/01/22 – 12/31/25
Regulation of breast cancer progression by Treg cells
Role: Co-I (5% efforts)

NIA 1R01AG082811 (PI: Jackson-Cook) $595,117   09/15/23 – 05/31/28
Cytosolic DNA, Telomeres/Subtelomeres, and Epigenetics: A Longitudinal Twin Study to Assess the Role of Genetics and Environment on their Frequency and Inter-relationships
Role: Co-I (10% efforts)

NCI 1R01CA276207 (PI: Faber) $541,440   09/01/23 – 08/31/28
MYCN drives a ferroptotic vulnerability in neuroblastoma
Role: Co-I (5% effort)

NCI R21CA273779 (PI: Harrell) $399,186   08/01/22 – 07/31/24
Characterization of metastasis models derived from breast cancer patients of African descent
Role: Co-I (3% efforts), News

NCI R21CA277518 (PI: Litovchick) $390,114   02/03/23 – 01/31/25
Role of the DREAM complex in the lung tumor suppression
Role: Co-I (2% efforts)

DOD HT94252311017 (PI: Faber) $350,000   07/01/23 – 06/30/26
Sabasumstat as a sensitizer to radiation therapy in synovial sarcoma
Role: Co-I (3% effort)

Children's Cancer Research Fund (PI: Faber) $250,000   02/01/22 – 01/31/24
MYCN drives a druggable SUMOylation program in neuroblastoma
Role: Co-I (2% efforts)

VA Medical Center (PI: Neuwelt) $100,000   10/01/21 – 09/30/26
High dose acetaminophen with n-acetylcysteine rescue as a novel STAT3 inhibitor with anti-cancer stem cell properties
Role: Biostatistician, Subaward PI (5% efforts)

DOD HT94252311017 (PI: Faber)   09/15/23 – 09/14/26
Sabasumstat as a sensitizer to radiation therapy in synovial sarcoma
Role: Co-I (3% efforts)

NCI R61CA278445 (PI: Dhakal)   04/01/23 – 03/31/26
Single-Molecule High-Confidence Detection of miRNA Cancer Biomarkers
Role: Biostatistician

Collaborative, completed
NIH, U01HD087198 (PI: Walsh) $4,516,149   09/17/15 – 08/31/19
The utilization of photonics technology to rapidly detect bioactive lipids associated with preeclampsia development
Role: Biostatistician (3% effort)

NIH R01DK115563 (PI: Ginder) $3,296,408   07/01/18 – 06/30/23
The role of the MBD2-NuRD complex in y-globin gene silencing
Role: Co-I (4% efforts)

NICHD R01HD088386 (PI: Walsh) $1,906,250   07/01/17 – 06/30/22
Pregnancy specific protease activation of PAR-1 and TET2 in preeclampsia - Implications for therapy
Role: Co-I (2% efforts)

NIH R01CA215610 (PI: Faber) $1,586,225   04/01/17 – 03/31/22
ABT-199 based therapies to treat neuroblastoma
Role: Co-I (8% efforts)

DOD W81XWH-18-1-0561 (PI: Faber) $774,996   09/30/18 – 09/29/21
Noxa loss as a major mechanism of intrinsic resistance to targeted therapies in breast cancer
Role: Biostatistician (5% efforts)

NIH K01AA024152 (PI: Salvatore) $770,662   04/01/16 – 03/31/21
Genetics, Romantic Relationships, and Alcohol Misuse in Emerging Adulthood
Role: Co-mentor

NIH R01MH118239 (PI: Vladimirov) $685,522   04/16/20 – 01/31/22
Assessing miRNA expression in the Corticolimbic System of Major Depressive Disorder
Role: Co-I (4.5% efforts)

Templeton Foundation GF13361-152627 (PI: Kendler) $600,000   09/01/16 – 10/31/19
The Nature of Molecular Risk Variants for Psychiatric and Psychological Phenotypes: Coherence,
Emergence and Levels of Explanation
Role: Co-I (20% effort)

DOD W81XWH1810143 (PI: Sarkar) $563,948   09/01/18 – 08/31/20
TAF2: A potential oncogene for hepatocellular carcinoma (HCC)
Role: Co-I (5% efforts)

NIH/NIA R15AG061649 (PI: McClay) $453,417   07/01/19 – 06/30/22
Effects of aging on epigenetic regulation of drug metabolism
Role: Co-I (10% efforts)

Komen Foundation CCR19608826 (PI: Harrell) $450,000   08/01/19 – 07/31/22
Targeting pathways activated in metastatic breast cancer
Role: Co-mentor (0% efforts)

Komen Foundation CCR18548205 (PI: Bos) $450,000   07/26/18 – 07/25/21
Harnessing regulatory T cell-dependent mechanisms for brain metastasis therapy
Role: Biostatistician (3% efforts)

NIH 1R21NS118359 (PI: Kordula) $427,000   04/01/21 – 03/31/23
Establishment of immunocompetent spontaneous glioma model to study glioma-associated astrocytes
Role: Co-I (3% effort)

NCI R21DE029927 (PI: Litovchik) $426,938   07/01/20 – 06/30/22
Role of the DREAM Complex in Head and Neck Preneoplasia
Role: Co-I (1% efforts)

Duke University subcontract (PI: Fuemmeler) $358,052   06/01/16 – 05/31/20
Maternal Obesity, Child Executive Functions and Child Weight Gain
Role: Co-I (5% effort)

NIH R25CA236630 (PI: Sarkar/Lloyd) $323,951   06/01/20 – 05/31/22
Preparing cancer researchers with a 21st century skill set

Role: Co-I (10% efforts)

236-03-18 Commonwealth Health Research Board (PI: Clevenger) $200,000 07/01/18 – 06/30/21
HDAC6 as a therapeutic target in breast cancer
Role: Other Significant Contributor (1% efforts)

NCI R21CA277518A (PI: Litovchick) $275,000   09/01/22 – 08/31/24
Role of the DREAM complex in the lung tumor suppression
Role: Co-I (2% efforts)

ACS 5100951FN (PI: Faber) $240,000   01/01/21 – 12/31/22
Amplified MYCN drives a ferroptotic vulnerability in neuroblastoma
Role: Co-I (2% efforts)

NIH R01CA210911 (PI: Atfi) $230,000   04/15/17 – 06/30/22
Targeting the TGIF/Twist1 network in osteosarcoma
Role: Co-I (0% efforts)

METAvivor (PI: Clevenger) $200,000   01/28/19 – 01/27/22
Inhibition of breast cancer metastatic outgrowth with non-immunosuppressive cyclosporines
Role: Co-I (1% efforts)

NIH R21AA022749-001 (PI: Vladimirov) $193,750   09/25/15 – 08/31/17
Integrating miRNAs and mRNA with alcohol eQTLs in two postmortem brain regions
Role: Co-I (5% effort)

Duke University subcontract (PI Fuemmeler) $177,717   06/01/16 – 05/31/18
Neurodevelopment and Improving Children's Health following Ets exposure (NICHES)
Role: Co-I (5% effort)

NIH R01CA188571 (PI: Litovchick) $173,809   07/01/18 – 06/30/20
Supplement: DYRK1A signaling in control of cell growth, proliferation and DNA damage repair
Role: Co-I (5% efforts)

VETAR (PI: Harrell) $134,563   07/15/19 – 01/14/21
Single-cell RNA sequencing for selection of therapeutic targets for triple negative breast cancers
Role: Co-I (3% efforts)

Alex's Lemonade Stand Foundation (PI: Faber) $125,000   07/01/15 – 06/30/17
Pharmacogenomics and drug screening lead to a novel targeted therapy with potent and specific activity
against MYCN amplified neuroblastoma
Role: Co-I (10% effort)

VCU Massey Cancer Center (PI: Faber, Hartman) $100,000   04/01/21 - 04/01/22
Development of a peptide therapeutic that directly targets n-Myc for treatment of neuroblastoma
Role: Co-I (0% efforts)

IDP Pharma SL (PI: Faber) $100,000   08/01/20 – 10/01/21
Testing ASCL-1 inhibitors in pre-clinical models of solid tumors
Role: Biostatistician (1% effort)

Rally Foundation (PI: Faber) $100,000   07/01/19 – 06/30/21

SHP2 inhibition for neuroblastoma
Role: Co-I (2% efforts)

American Diabetes Association (PI: Elliott) $100,000   01/01/13 –12/31/14
Quantitative Proteomic Mapping of Diabetic Vasculature
Role: Collaborator (2% efforts)

American Lung Association (PI: Faber) $100,000   05/01/15 – 06/30/17
EMT-mediated resistance to EGFR inhibitors via BIM suppression
Role: Co-I (5% effort)

VCU Massey Cancer Center (PI: Sheppard) $100,000   07/01/19 – 06/30/20
Exploring Bio-behavioral Components of Racial Disparities in Medication Symptoms and Adherence to
Adjuvant Endocrine Therapy
Role: Co-I (0% efforts)

IDP Pharma, SL (PI: Faber) $84,254   11/01/17 – 10/31/18
Investigation of ASCL1-targeting compounds in diverse SCLC models
Role: Biostatistician (1% effort)

NIH, P01ES022831 (PI: Faber) $50,872   11/01/17 – 10/31/18
ASCL1 Children's Health following Ets exposure
Role: Co-I (1% effort)

VCU Massey Cancer Center (PI: Harrell, co-I: Dozmorov) $50,000   7/15/20 – 07/14/21
Assessment of sigma receptors as therapeutic targets on racially diverse sets of triple-negative breast
cancers
Role: Co-I (0% efforts)

VETAR (PI: Koblinski) $50,000   06/01/19 – 11/30/20
Precision medicine for anticancer platinums
Role: Collaborator (0% effort)

VCU Presidential Research Quest Fund (PI: Mohanraj) $50,000   06/01/18 – 12/31/19
Accelerated Epigenetic Age and Frailty: Predictors of Hematopoietic Stem Cell Transplant Outcomes
Role: Co-I (0% effort)

NIH P01ES022831 (PI: Murphy) $33,359   06/01/17 – 05/31/19
Neurodevelopment and Improving Children's Health following Ets exposure
Role: Co-I (10% effort)

VCU Massey Cancer Center (PI: Swift-Scanlan PI) $24,980   01/01/19 – 12/31/19
Ancestry Markers as Predictors of Clinical Outcomes in Triple Negative Breast Cancer
Role: Co-I (0% effort)

PUBLICATIONS

Complete List of Published Work (over 160 original and review papers) in MyBibliography:
https://www.ncbi.nlm.nih.gov/myncbi/mikhail.dozmorov.1/bibliography/public/. H-index (January 2025): 45

Lead/senior author publications

1. Nguyen M, Wall BPG, Harrell JC, Dozmorov MG. **scHiCcompare: an R package for differential analysis of single-cell Hi-C data.** *bioRxiv*. 2024. DOI: 10.1101/2024.11.06.622369

2. Wall BPG, Nguyen M, Harrell JC, Dozmorov MG. **Machine and deep learning methods for predicting 3D genome organization.** *Methods Mol Biol.* 2025. PMID: 39283464

3. Ogata JD, Mu W, Davis ES, Xue B, Harrell JC, Sheffield NC, Phanstiel DH, Love MI, Dozmorov MG. **excluderanges: exclusion sets for T2T-CHM13, GRCm39, and other genome assemblies.** *Bioinformatics*. 2023 Apr 3. PMID: 37067481

4. Dozmorov MG, Marshall MA, Rashid NS, Grible JM, Valentine A, Olex AL, Murthy K, Chakraborty A, Reyna J, Figueroa DS, Hinojosa-Gonzalez L, Da-Inn Lee E, Baur BA, Roy S, Ay F, Harrell JC. **Rewiring of the 3D genome during acquisition of carboplatin resistance in a triple-negative breast cancer patient-derived xenograft.** *Sci Rep.* 2023 Apr 3, PMID: 37012431

5. Dozmorov MG, Mu W, Davis ES, Lee S, Triche TJ Jr, Phanstiel DH, Love MI. **CTCF: an R/bioconductor data package of human and mouse CTCF binding sites**. *Bioinform Adv*. 2022 Dec 16, PMID: 36699364

6. Stilianoudakis SC, Marshall MA, Dozmorov MG*. **preciseTAD: A transfer learning framework for 3D domain boundary prediction at base-pair resolution**. *Bioinformatics*. 2021 Nov 6. PMID: 34741515

7. Dong X, Liu C, Dozmorov M*. **Review of multi-omics data resources and integrative analysis for human brain disorders**. *Brief Funct Genomics*. 2021 May 8. PMID: 33969380

8. Dozmorov MG*, Tyc KM, Sheffield NC, Boyd DC, Olex AL, Reed J, Harrell JC. **Chromatin conformation capture (Hi-C) sequencing of patient-derived xenografts: analysis guidelines**. *Gigascience*. 2021 Apr 21. PMID: 33880552. *-co-senior author

   - Supporting data for "**Chromatin conformation capture (Hi-C) sequencing of patient-derived xenografts: analysis guidelines**", *Gigascience*, March 05, 2021, http://dx.doi.org/10.5524/100870

9. Dozmorov MG*, Cresswell KG, Bacanu SA, Craver C, Reimers M, Kendler KS. **A method for estimating coherence of molecular mechanisms in major human disease and traits.** *BMC Bioinformatics*. 2020 Oct 21. PMID: 33087046

10. Cresswell KG, Stansfield JC, Dozmorov MG*. **SpectralTAD: an R package for defining a hierarchy of topologically associated domains using spectral clustering**. *BMC Bioinformatics*. 2020 Jul 20. PMID: 32689928

11. Cresswell KG, Dozmorov MG*. **TADCompare: An R Package for Differential and Temporal Analysis of Topologically Associated Domains**. *Front Genet*. 2020 Mar 10. PMID: 32211023

12. Stansfield JC, Tran D, Nguyen T, Dozmorov MG*. **R Tutorial: Detection of Differentially Interacting Chromatin Regions From Multiple Hi-C Datasets.** *Curr Protoc Bioinformatics*. 2019 May 24. PMID: 31125519

13. Stansfield JC, Cresswell KG, Dozmorov MG*. **multiHiCcompare: joint normalization and comparative analysis of complex Hi-C experiments.** *Bioinformatics*. 2019 Jan 22. PMID: 30668639

14. <u>Dozmorov MG</u>*. **GitHub Statistics as a Measure of the Impact of Open-Source Bioinformatics Software.** *Front Bioeng Biotechnol*. 2018 Dec 12. PMID: 30619845

15. <u>Dozmorov MG</u>*. **Reforming disease classification system-are we there yet?** *Ann Transl Med*. 2018 Nov 6. PMID: 30613605

16. Stansfield JC, Cresswell KG, Vladimirov VI, <u>Dozmorov MG</u>*. **HiCcompare: an R-package for joint normalization and comparison of HI-C datasets.** *BMC Bioinformatics*. 2018 Jul 31. PMID: 30064362

17. <u>Dozmorov MG</u>*. **Disease classification: from phenotypic similarity to integrative genomics and beyond.** *Brief Bioinform*. 2018 Jun 22. PMID: 29939197

18. <u>Dozmorov MG</u>*. **Epigenomic annotation-based interpretation of genomic data: from enrichment analysis to machine learning.** *Bioinformatics*. 2017 Oct 15. PMID: 29028263

19. Glass ER, <u>Dozmorov MG</u>*. **Improving sensitivity of linear regression-based cell type-specific differential expression deconvolution with per-gene vs. global significance threshold.** *BMC Bioinformatics* 2016 Oct 6. PMID: 27766949

20. <u>Dozmorov MG</u>*, Cara LR, Giles CB, Wren JD. **GenomeRunner web server: Regulatory similarity and differences define the functional impact of SNP sets.** *Bioinformatics* 2016 Apr 1. PMID: 27153607

21. <u>Dozmorov MG</u>*, Dominguez N, Bean K, Macwana S, Roberts V, Glass E, James JA, Guthridge JM. **B cell and monocyte contribution to systemic lupus erythematosus identified by cell-type-specific differential expression analysis in RNA-seq data.** *Bioinformatics and Biology Insights.* 2015 Oct 8. PMID: 26512198

22. <u>Dozmorov MG</u>*, Adrianto I, Giles CB, Glass E, Glenn SB, Montgomery C, Sivils KL, Olson LE, Iwayama T, Freeman WM, Lessard CJ, Wren JD*. **Detrimental effects of duplicate reads and low complexity regions on RNA- and ChIP-seq data.** *BMC Bioinformatics*. 2015 Sep 25. PMID: 26423047

23. <u>Dozmorov MG</u>*. **Polycomb Repressive Complex 2 epigenomic signature defines age-associated hypermethylation and gene expression changes.** *Epigenetics*. 2015 Apr 16. PMID: 25880792

24. <u>Dozmorov MG</u>, Yang Q, Wu W, Wren J, Suhail MM, Woolley CL, Young DG, Fung KM, Lin HK. **Differential effects of selective frankincense (Ru Xiang) essential oil versus non-selective sandalwood (Tan Xiang) essential oil on cultured bladder cancer cells: a microarray and bioinformatics study.** *Chin Med*. 2014 Jul 2. PMID: 25006348

25. <u>Dozmorov MG</u>*, Cara LR, Giles CB, Wren JD. **GenomeRunner: automating genome exploration.** *Bioinformatics*. 2012 Feb 1. PMID: 22155868. News

26. <u>Dozmorov MG</u>*, Wren JD, Alarcón-Riquelme ME. **Epigenomic elements enriched in the promoters of autoimmunity susceptibility genes.** *Epigenetics*. 2013 Nov 8. PMID: 24213554

27. <u>Dozmorov MG</u>*, Giles CB, Koelsch KA, Wren JD. **Systematic classification of non-coding RNAs by epigenomic similarity.** *BMC Bioinformatics.* 2013, Oct 9. PMID: 24267974. Best paper of the MCBIOS X conference

28. <u>Dozmorov MG</u>, Wren JD. **High-throughput processing and normalization of one-color microarrays for transcriptional meta-analyses.** *BMC Bioinformatics*. 2011 Oct 18. PMID: 22166002

29. <u>Dozmorov MG</u>, Giles CB, Wren JD. **Predicting gene ontology from a global meta-analysis of 1-color microarray experiments.** *BMC Bioinformatics*. 2011 Oct 18. PMID: 22166114

30. <u>Dozmorov M</u>, Stone R 2nd, Clifford JL, Sabichi AL, Engles CD, Hauser PJ, Culkin DJ, Hurst RE. **System level changes in gene expression in maturing bladder mucosa.** *J Urol*. 2011. PMID: 21421225

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Book chapters
     Green CD, <u>Dozmorov MG</u>, Spiegel S. **Analysis of Liver Responses to Non-alcoholic Steatohepatitis by mRNA-Sequencing**. *Methods Mol Biol*. 01 January 2022. PMID: 35212994

Dozmorov MG, Hurst RE. **Systems Biology for Signaling Networks**, Chapter 4, From Microarray to Biology, Springer Science+Business Media, LLC 2010

Preprints
 https://www.biorxiv.org/search/author1%3ADozmorov%2BMikhail

PATENTS

| May, 2018 | Oh Y, Dozmorov M, Cai Q **TREATMENT OF DISEASES RELATED TO IGFBP3 AND ITS RECEPTOR** | WO2018/085252 |
| April, 2018 | Faber A, Dozmorov M, Lochmann T. **LONRF2 expression as biomarker and determinant of neuroblastoma prognosis** | Invention disclosure submitted |

INVITED TALKS[1]

International
 Dozmorov M. "The Cancer Genomics Atlas (TCGA) and other cancer genomics resources", Presentation for the Academic skills workshop for the "Sharpening Aptitude for Hepatology" research program at the West Bengal Liver Institute in Kolkata, India. (April 2024)

 Dozmorov M. "preciseTAD: A transfer learning framework for 3D domain boundary prediction at base-pair resolution", MCCMB 2021 (July 2021)

 Stilianoudakis S., **Dozmorov M.** "preciseTAD: A machine learning framework for precise 3D domain boundary prediction at base-level resolution", EuroBioC 2020, virtual conference, (December 2020)

National[2]

 Dozmorov M., keynote, "3D genomics of drug resistance in breast cancer", MCBIOS 2023 conference, University of Dallas, TX (March 2023)

 Dozmorov M., "preciseTAD: A transfer learning framework for 3D domain boundary prediction at base-pair resolution", Bioconductor 2022 conference, Seattle Children's Hospital, WA (July 2022)

 Dozmorov M., Marshall M., Chen S. "preciseTAD: A transfer learning framework for 3D domain boundary prediction at base-pair resolution", American Statistical Association, Old Dominion University (October 2021)

 Dozmorov M. "The genome in action: Detecting changes in 3D genome interactions", Statistical Genetics Seminar, University of North Carolina, (January 2021)

 Dozmorov M. "Detection of Differentially Interacting Chromatin Regions From Multiple Hi-C Datasets", Bioconductor 2020, virtual conference, (July 2020)

 Dozmorov M., *Stansfield J.*, *Cresswell K.* "SpectralTAD: defining hierarchy of Topologically Associated Domains using graph theoretical clustering", JSM (Joint Statistical Meeting), Denver, CO (July 2019)

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[1] Posters are not shown due to page limit consideration

[2] Names of students I directly supervised are ***bold italics***

Dozmorov M., Reimers M., *Cresswell K.*, *Stilianoudakis S.*, Bacanu S., Craver C., Kendler K. "A method for comparing molecular coherence of gene networks", Genetics and Human Agency Annual Meeting, Wintergreen Resort, VA (May 2019)

Dozmorov M., *Stilianoudakis S.*, *Cresswell K.* "Computational Prediction of Boundaries of 3D Genomic Domains in Class Imbalance Settings", Department of Mathematics, Research Seminar, Michigan State University, East Lansing, MI (April 2019)

Dozmorov M. "Bioinformatics approaches in epigenetic studies," ACR (American College of Rheumatology) conference, Chicago, IL (October, 2018)

Cresswell K., **Dozmorov M.** "SpectralTAD: identification of topologically associated domains (TADs) using spectral clustering," Intelligent Systems Molecular Biology Conference, Chicago, IL (July 2018).

Dozmorov M. "3D genomics and epigenomics to better understand complex diseases," University of Virginia, Charlottesville, Center for Public Health Genomics, Research Seminar, VA (October 2017)

Dozmorov M., *Stansfield J.* "A method for comparing 3D structures of normal and cancer genomes," Commonwealth of Virginia Cancer Research Conference, Charlottesville, VA (September 2017)

Dozmorov M. "Effective use of epigenomic data to better understand complex diseases," University of Chicago, Research Seminar, Chicago, IL (August 2017)

Dozmorov M., Reimers M., Bacanu S., Craver C., Kendler K. "Network Biology and disease coherence," Genetics and Human Agency Annual Meeting, University of Virginia, Charlottesville, VA (May 2017)

Dozmorov M. "Reproducible research in data science", Center for Clinical and Translational Research, Research Seminar, Virginia Commonwealth University, Richmond, VA (March, 2017)

Stansfield J., **Dozmorov M.** "Hi-C Loess: A Method for Normalization and Comparison of Multiple Hi-C Datasets," Midsouth Computational Biology & Bioinformatics Society conference, Little Rock, AR (March 2017)

Dozmorov M. "Effective use of epigenomic data to better understand complex diseases," Georgetown University, Innovation Center for Biomedical Informatics, Research Seminar, Washington, DC (January 2017)

Dozmorov M. "Reproducible research in data science," Computer Science Department, Research Seminar, VCU, Richmond, VA (September, 2016)

Dozmorov M. "Reproducibility in Cancer Research," Massey Cancer Center, Richmond, VA (April, 2016)

Dozmorov M., *Cara L.*, Giles C., Wren J. "Genomerunner web server: regulatory similarity and differences define the functional impact of SNP sets," Midsouth Computational Biology & Bioinformatics Society conference, Memphis, TN, Featured Speaker (March 2016)

Dozmorov M. "Epigenomic enrichment and similarity of disease-associated SNPs," MidSouth Conference on Computational Biology and Bioinformatics, Little Rock, AR, Featured Speaker (March 2015)

Dozmorov M. "Connecting genomics, epigenomics, and phenotype," Center for Studying Biological Complexity, Annual Retreat, Virginia Commonwealth University, Richmond, VA (December 2014)

Dozmorov M. "Unlocking the epigenomics of aging," Department of Pathology, Research Seminar, VCU, Richmond, VA (November 2014)

Dozmorov M. "Connecting genomics, epigenomics, and phenotype," Virginia Institute for Psychiatric and Behavioral Genetics, Research Seminar, Richmond, VA (October 2014)

Dozmorov M. "Connecting Genomics and Epigenomics: the rare variants case," Midsouth Computational Biology & Bioinformatics Society conference, Stillwater, OK (March 2014)

Dozmorov M. "Systematic classification of common disease-associated SNPs by their epigenomic relationship," Advances in Genome Biology and Technology (AGBT) conference, Marco Island, FL, Software Demo (February 2014)

Dozmorov M. "GenomeRunner: A Global Positioning System within Genome." BioConferenceLive online two-day conference. http://www.bioconferencelive.org (July 2013).
Dozmorov M. "Systematic classification of disease-associated genomic elements by their epigenomic associations," Midsouth Computational Biology & Bioinformatics Society conference, Columbia, MO (March 2013)

Dozmorov M. "GenomeRunner: Automating genome exploration and our data within it," Midsouth Computational Biology & Bioinformatics Society conference, Oxford, MS (March 2012)

Dozmorov M. "Galaxy tools for next-generation sequencing analysis applied to the analysis of ChIP-seq data." Research Computing & Bioinformatics Seminar, OMRF, Oklahoma City, OK (October 2012)

Dozmorov M. "GenomeRunner: A Global Positioning System within Genome." Research Computing & Bioinformatics Seminar, OMRF, Oklahoma City, OK (December 2011)

Dozmorov M. "MECP2 role in SLE: variants that make the difference". Research Computing & Bioinformatics Seminar, OMRF, Oklahoma City, OK (November 2011)

Dozmorov M. "GenomeRunner: Automating genomic exploration". Oklahoma Medical Research Foundation retreat, Norman, OK (October 2011)

Dozmorov M. "Systems biology approach to understanding the extracellular matrix modulation of phenotype," Midsouth Computational Biology & Bioinformatics Society conference 2008, Oklahoma City, OK. (March, 2008)

Dozmorov M. "Integrating Bioinformatics Tools with Deep Biological Knowledge." OKBIOS 2005 meeting, Oklahoma City, OK. (November 2005)

Internal

Dozmorov M., "3D genomics of drug resistance in breast cancer", Physiology Department, invited talk (October 2024)

Dozmorov M., "Transcriptomics methods", Biology Department, Guest lecture (April 2024)

Dozmorov M., "Transcriptomics methods in molecular psychiatry", Molecular Psychiatry PHIS 691-801, Guest lecture, (February 2024)

Dozmorov M., "RNA-seq technology and analysis, Introduction to the theory and practice of RNA sequencing (RNA-seq) analysis", Human and Molecular Genetics HGEN 603, Guest lecture, (November 2023)

Dozmorov M., "3D genomics of drug resistance in breast cancer", One VCU Research Optimizing Health: Impacts from VCU Researchers Panel, (April 2023)

Dozmorov M. "3D genomics of drug resistance in breast cancer", Research in progress seminar, Department of Pathology, Virginia Commonwealth University, Richmond, VA (May 2022)

Dozmorov M. "Integrative 3D genomics analysis", Virginia Institute for Psychiatric and Behavioral Genetics (VIPBG) seminar, Richmond, VA (May 2022)

Dozmorov M. "Detecting and interpreting changes in the 3D genome organization", First talk in the Human & Molecular Genetics' series of Faculty Introductions (September 2021)

Faber A, Hartman M, Dozmorov M. "Development of a peptide therapeutic that directly targets n-Myc for treatment of neuroblastoma", Molecules to Medicines (M2M) meeting (July 2021)

Dozmorov M. "The genome in action: Detecting and interpreting changes in the 3D genome organization", Virginia Institute for Psychiatric and Behavioral Genetics (VIPBG) seminar, Richmond, VA (April 2021)

Dozmorov M. "[Bioinformatics approaches for cancer genomics](#)", Children's Hospital of Richmond Institute, Richmond, VA (February 2021)

Dozmorov M. "Genomics technologies", Pathology Science Club, Department of Pathology, Virginia Commonwealth University, Richmond, VA (May 2019)

Stansfield J., **Dozmorov M.** "Analytical approaches using the Bland-Altman plot," Department of Biostatistics, Grand Rounds, Virginia Commonwealth University, Richmond, VA (January 2019)

Stansfield, *Cresswell K.*, **Dozmorov M.** "multiHiCcompare: Joint Normalization and Comparative Analysis of Complex Hi-C Experiments," Virginia Chapter of the American Statistical Association Annual Meeting, Richmond, VA (October 2018)

Cresswell K., **Dozmorov M.** "SpectralTAD: identification of topologically associated domains (TADs) using spectral clustering," Virginia Chapter of the American Statistical Association Annual Meeting, Richmond, VA (October 2018)

Stilianoudakis S., **Dozmorov M.** "Predictive Modeling Using Genomic Annotations," Virginia Chapter of the American Statistical Association Annual Meeting, Richmond, VA (October 2018)

Stilianoudakis S., **Dozmorov M.** "Predictive modeling using genomic annotations: pitfalls and recommendations," Biostatistics Student Research Symposium, Virginia Commonwealth University, Richmond, VA (September 2018)

Cresswell K., **Dozmorov M.** "SpectralTAD: identification of topologically associated domains (TADs) using spectral clustering," Biostatistics Student Research Symposium, Richmond, VA (September 2018)

Stilianoudakis S., **Dozmorov M.** "Developing a methylation-based survival analysis for patients with glioblastoma," Biostatistics Student Research Symposium, Virginia Commonwealth University, Richmond, VA (September 2017)

Stansfield J., **Dozmorov M.** "HiCcompare: An R-Package for Joint normalization of Hi-C Datasets and Differential Chromatin Interaction Detection," Biostatistics Student Research Symposium, Richmond, VA (September 2017)

Dozmorov M. "Reproducible research in data science", Department of Biostatistics, Research Seminar, Virginia Commonwealth University, Richmond, VA (January, 2016)

Stansfield J., **Dozmorov M.** "Modeling Proximal Relationships Among Genomic Elements", Biostatistics Student Research Symposium, Virginia Commonwealth University, Richmond, VA (September, 2016)

Dozmorov M. "Effective use of genome annotation data to better understand complex diseases," Department of Biostatistics, Research Seminar, Virginia Commonwealth University, Richmond, VA (January 2017)

TEACHING[34]

BIOS524	Biostatistical Computing in R	2020-24	Course director/Instructor

This 10-lecture course is a part of the 3-credit hour course introducing students to practical aspects of programming in SAS, R, and Python. Course website: https://bios524-biostatistical-computing-r.netlify.app/, https://bios524-r-2021.netlify.app/, https://bios524-r-2022.netlify.app/, https://bios524-r-2023.netlify.app/, developed an MS online program-specific version (2024)

BIOS691	Deep learning with R	2020-25	Course director/Instructor

This 1-credit hour course presents main theoretical concepts and practical implementations of various deep neural network architectures using Keras with TensorFlow backend. Lectures include slide presentations and live coding sessions. Course website: https://bios691-deep-learning-r.netlify.app/, https://bios691-deep-learning-r-2025.netlify.app/

BIOS567/ BIOS668	Statistical Methods for High-throughput Genomic Data I, II	Fall/Spring 2016-18	Course director/Instructor

These two-parts 3-credit hour courses explain basic concepts of statistical genomics, from microarray- and sequencing technologies through statistical methods for high-dimensional data analysis. Topics include R/Bioconductor programming, QC, normalization, differential expression analysis, dimensionality reduction, clustering, genomic alignment, variant calling, microRNA-seq, bulk and single-cell RNA-seq, ChIP-seq, methylation, microbial genomics, chromatin conformation capture data analysis. Course website: https://mdozmorov.github.io/BIOS668.2018/, https://mdozmorov.github.io/BIOS668.2018/

BIOS691	Cancer Bioinformatics	Spring 2021	Course director/Instructor

This 3-credit hour course provides an introduction to genomics, sequencing technologies, data analysis. Course website: https://bios691-cancer-bioinformatics.netlify.app/

BIOS691	Reproducible research tools	Summer 2016-18	Course director/Instructor

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[3] All courses are graduate, Ph.D.-level courses (500-600-level)
[4] Guest lectures (2-4 per year) are standard and not included

This 1-credit hour course introduces the fundamental concepts in computational reproducible research. Through lectures and hands-on exercises students learn best practices of statistical data analysis and programming. Course website: https://mdozmorov.github.io/BIOS691.2018/

PSYCH691	**Molecular Biology Genetics and Epigenetics in Psychiatry**	**2017-2024**	**Guest lecturer**

RNA-seq technology, data analysis and interpretation

HGEN502	**Advanced Human Genetics**	**2017-2024**	**Guest lecturer**

RNA-seq technology, data analysis and interpretation

preciseTAD Workshop	**Precise prediction of TAD/loop boundaries**	**Fall 2020**	**Supervisor**

This workshop introduces methods for transforming the identification of boundaries that demarcate Topologically Associating Domains (TADs)-- referred to as TAD-calling--into a supervised machine learning framework. Course material https://github.com/dozmorovlab/preciseTADworkshop

HiCcompare Workshop	**Detection of Differentially Interacting Chromatin Regions**	**Summer 2020**	**Course director/Instructor**

This workshop introduces methods for the differential analysis of the three-dimensional (3D) structure of the genome using data generated by high-throughput chromatin conformation capture (Hi-C) technologies. Course material https://mdozmorov.github.io/HiCcompareWorkshop/

Workshop	**Microarray data analysis using R/Bioconductor**	**Winter 2013**	**Instructor**

This 4-day workshop provided in-depth hands-on learning of practical aspects of microarray data analysis and interpretation using R/Bioconductor. Place: Trivandrum, India. Course material: https://github.com/mdozmorov/ci-workshop

Seminar series	**Bioinformatics 101**	**Fall 2015-18**	**Instructor**

This series of 10 lectures include introductory topics on bioinformatics. Topics taught include statistics of enrichment analysis, RNA- and ChIP-seq, methylation technology and analysis, reproducible research

Other	**Advanced Topics in Pharmaceutical Sciences**	**Fall semester 2010**	**Guest lecturer**

Molecular and Cellular Biology lectures

SOFTWARE[5]

scHiCcompare	Differential interaction detection in single-cell Hi-C data	https://github.com/dozmorovlab/scHiCcompare
excluderanges	Data package with exclusion (aka, blacklisted) regions	https://bioconductor.org/packages/excluderanges/
nullranges	An R package for generating sets of genomic regions representing the null	https://bioconductor.org/packages/nullranges/ (contributor)

hypothesis

CTCF	Data package with CTCF binding motifs, including motif orientation	https://bioconductor.org/packages/CTCF/
preciseTADhub	Pre-trained random forest models obtained using preciseTAD	https://bioconductor.org/packages/preciseTADhub/
preciseTAD	An R package implementing an optimized machine learning framework for precise detection of 3D genomic domains using genome annotation data	https://bioconductor.org/packages/preciseTAD/
TADcompare	An R package for differential analysis and characterization of Topologically Associated Domains	https://bioconductor.org/packages/TADCompare/
SpectralTAD	An R package for calling Topologically Associated Domains (TADs) using spectral clustering	https://bioconductor.org/packages/SpectralTAD/
multiHiCcompare	An R package for the joint normalization of multiple Hi-C datasets and comparative analysis of complex Hi-C experiments	https://bioconductor.org/packages/multiHiCcompare/
HiCcompare	An R package for joint normalization and differential analysis of chromatin interactions obtained from Hi-C sequencing	https://bioconductor.org/packages/HiCcompare/
HMP2data	An R package for data access from the integrative Human Microbiome data portal	https://bioconductor.org/packages/HMP2Data/
lrcde	An R package for cell type-specific deconvolution and differential gene expression analysis	https://github.com/mdozmorov/lrcde.dev
GenomeRunner	A web server and a standalone tool for enrichment analysis of genomic regions in epigenomic annotations	http://integrativegenomics.org/

TRAINING AND MENTORING

Current trainees

Brydon Wall, M.S. Bioinformatics student   2023-present
My Nguyen, Ph.D candidate. Biostatistics   2023-present
Andreas Voyages, B.S. Biology student   2024-present

Past trainees

Jonathan Ogata, M.S. intern	2022-2023
Alex Lupton, M.S. Bioinformatics student	2022-2023
Maggie Marshall, M.S. student, Senior Research Assistant	2021-2022
Pratiik Kaushik, B.S., Research Assistant	2021
Spiro Stilianoudakis, Ph.D. (currently, Procter&Gamble, OH)	2018-2021
Tyler Steele, Ph.D. (postdoctoral fellow)	2020-2021
Katarzyna Tyc, Ph.D. (postdoctoral fellow, currently assistant professor at VCU)	2019-2020
Kellen G. Cresswell, Ph.D. (currently, Procter&Gamble, OH)	2017-2019
John C. Stansfield, Ph.D. (currently, Pfizer, Cambridge, MA)	2016-2019
Edmund R. Glass, Ph.D. (currently, PharPoint Inc., Durham, NC)	2014-2016

Other training/mentoring

Mentor 2 students from the UOregon "Bioinformatics and Genomics" program	2020-2021
Directed research, supervising 1-3 students over research projects	2014-present
Summer Student Training Project, supervising 1-2 students over summer research	2015-present

GRADUATE COMMITTEE SERVICE

Chair

Walker Rogers, Ph.D. (Quantitative Human Genetics program)	2022
Brian A. Ruiz, MS (Pathology and Biophysics Department, VCU)	2018
Danielle K. Seibert, MS (Department of Human and Molecular Genetics, VCU)	2017
Ahmed H. Alquthami, Ph.D. (Department of Health Care Policy and Research, VCU)	2016

Member

Araba Abaidoo-Myles, Ph.D. candidate (Microbiology and Immunology)	2024-present
Annalise Hassan, Ph.D. candidate (Pharmacology and Toxicology)	2024-present
Bria Pierre, MS candidate (Biochemistry)	2024-present
Carson Walker, Ph.D. candidate (Human and Molecular Genetics)	2024-present
Dalia Al Saeedy, Ph.D. candidate (Pharmaceutical Sciences)	2024-present
Dustin Zeliff, M.S. candidate (Life Sciences)	2023-present
Emily Zboril, Ph.D. candidate (Dept. of Biochemistry)	2023-present
Julia Altman, Ph.D. candidate (Dept. of Pathology)	2022-present
Walker Rogers, Ph.D. candidate (Quantitative Human Genetics program)	2022-present
Tyler Wagner, PharmD candidate (Pharmacoeconomics and Health Outcomes)	2021-present
Marc Kealhofer, MD/Ph.D. candidate (Dept. of Psychiatry)	2020-present
Sara Abudahab, Ph.D. candidate (Dept. of Pharmacotherapy and Outcomes Science)	2020-present
Huseyin Gedik, Ph.D. candidate (VCU Integrative Life Sciences Program)	2019-present
Mohammad Ahangari, Ph.D. candidate (VCU Integrative Life Sciences Program)	2019-present
Shravani Malay, MS (Pharmacotherapy and Outcomes Science)	2023-2024
David Boyd, Ph.D. (VCU Integrative Life Sciences Program)	2020-2023
Saranya Chidambaranathan, Ph.D. (Clinical and Translational Research)	2018-2022
Zachary Sergi, M.S. (Bioinformatics program)	2021-2022
Patrick Coit, Ph.D. (Autoimmunity and epigenetics, University of Pittsburgh)	2019-2022
Borwyn Ann Wang, Ph.D. (CTSA, VCU)	2018-2022
Mohammad Al-Zubi, Ph.D. (VCU Integrative Life Sciences Program)	2017-2020
Han Zhang, Ph.D. (Computer Sciences, VCU)	2019-2020
Alexander Azzo, MD/Ph.D. (CCTR/CMM program, VCU)	2019-2020
Tia Turner, MD/Ph.D. (Pathology Department, VCU)	2017-2020
John Drake, MS in Bioinformatics (VCU Integrative Life Sciences Program)	2018-2019
Mohamad Kronfol, Ph.D. (Dept. of Pharmacotherapy and Outcomes Science, VCU)	2018-2019

James Thomas DeLigio, Ph.D. (Dept. of Biochemistry & Molecular Biology, VCU)	2017-2018
Chelsea Sawyers, Ph.D. (Virginia Institute for Psychiatric and Behavioral Genetics)	2015-2018
Robin F. Chan, Ph.D. (Center for Biomarker Research and Precision Medicine, VCU)	2015-2017

PROFESSIONAL ACTIVITIES/SERVICE

Job search committee, member	2024-present
Promotion & Tenure Appeal committee	2024-present
Admission committee, chair	2023-present
Job search committee, chair	2022-2023
Promotion & Tenure committee, member (X2)	2020-2023
Genomics Task Force advisory panel, member	2019
Admission committee, member	2019-2023
Data Science committee, chair	2018-2023

Member of professional/scientific societies

ASA, The American Statistical Association	2019-2020
ISCB, The International Society for Computational Biology	2010-present
ASHG, American Society of Human Genetics	2010-2017
AACR, American Association for Cancer Research	2007-present
AAAS, American Association for the Advancement of Sciences	2006-2021
MCBIOS, The Oklahoma Bioinformatics Society	2005-2018
OCN, Oklahoma Center for Neuroscience	2005-2014
SFN, Society For Neuroscience	2002-2005
SLS, Svenska Läkaresällskapet	1999-2005

Study section/panel reviewer

NIH/NCI Special Emphasis Panel (HTAN)	2024
NSF CAREER panel (Smart and Connected Health)	2024
VCU Leila Y. Mathers Charitable Foundation	2024
VCU Breakthrough Fund	2023
NIEHS/NTP Special Emphasis Panel	2023
NIH Small Business ETTN (13) Study Section	2021
NWO, the Dutch Research Council, Veni grant in the Talent Scheme	2020
VCU Massey Cancer Center Pilot Proposal Study Section	2018
NIH BST-80 AREA (R15) Bioengineering Study Section	2018
NIEHS2015048 Special Emphasis Panel	2016

Editorial board

Editor, Bioinformatics and Biology Insights supplement	2015
Editor, MCBIOS conference proceedings, BMC Bioinformatics	2011-2017
Statistical Advisor, PLoS ONE, http://www.plosone.org/static/statistical_advisors	2013-2022

Referee for journals[6]

Nature Methods (IF=28)
Nucleic Acid Research (IF=11)
Genome Research (IF=9.94)
Briefings in Bioinformatics (IF=6)
Frontiers in Immunology (IF=6)
Bioinformatics (IF=5)
Computational and Structural Biotechnology Journal (IF=5)

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[6] Complete list of reviewing and editorial work: https://publons.com/a/1496860/

Frontiers in Genetics (IF=4)
BMC Bioinformatics (IF=2.2)
JOSS (Journal of Statistical Software)
F1000Research

Conference service

Bioconductor, Organizer, website developer (BioC2020, BioC2021, BioC2022, EuroBioC2022), BioC2023), reviewer, session chair 2019-present
ASA (American Statistical Association) VA chapter, Organizer, judge 2019-2023
ISCB (International Society for Computational Biology), Judge 2016-2017
MCBIOS (MidSouth Computational Biology and Bioinformatics Society), Board member, secretary, session chair, judge 2014-2023
Organizer and host of keynote/seminar speakers 2010-present

Other service

Book reviewer: Gene Expression Data Analysis, Guest Editor Shikha Garg, CRC Press, Taylor and Francis Group 2019
Web developer for the Virginia Chapter of American Statistical Association 2018-2022
Judge of the Summer Student Training Program (SSTP), Dept. of Biostatistics, VCU 2017-2018