Ryan Mills

Associate Professor
University of Michigan Medical School, Computational Medicine and Bioinformatics, 100 Washtenaw Ave, Room 2055B, Ann Arbor, MI, 48019, United States
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Education and Training

Education

08/1996-05/2000	AB, Wabash College, Crawfordsville, United States
08/2000-08/2003	MS, Georgia Institute of Technology, Atlanta, United States
09/2003-05/2006	PhD, Georgia Institute of Technology, Atlanta, United States

Postdoctoral Training

01/2006-10/2008	Postdoctoral Fellow, Genetics/Genomics, Emory University, Biochemistry, Atlanta, GA, Dr. Scott Devine

Work Experience

Academic Appointment

01/2012-09/2018	Assistant Professor, Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI
01/2012-09/2018	Assistant Professor, Human Genetics, University of Michigan, Ann Arbor, MI
09/2018-Present	Associate Professor, Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI, (Tenured)
09/2018-Present	Associate Professor, Human Genetics, University of Michigan, Ann Arbor, MI

Administrative Appointment

01/2009-12/2011	Team Leader, Bioinformatics and Medical Diagnostics Team, Molecular Genetic Research Unit, Brigham and Women's Hospital, Boston, MA
04/2022-Present	Program Director of DCMB Computing Infrastructure, Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI

Research Position

11/2008-12/2011	Research Associate, Pathology, Brigham & Women's Hospital, Harvard Medical School, Boston, MA

Research Interests

- The primary purpose of sequencing genomes is to identify the underlying genetic variation between individuals and to explore what role those changes have on human phenotypes. Our research laboratory develops and implements methods to precisely identify and resolve different types of genomic variation. Our goal is to integrate this information with other forms of biologically and medically relevant data to improve our overall understanding of human health and disease.

Grants

Current Grants

Improving Bioinformatics Methods for Analysis of Virus-Associated Cancers:
Co-I (Principal Investigator:Chad Brenner)

Innovation in Cancer Informatics (ICI)
08/2022 - 08/2024
$224,000

N/A:*Repetitive elements in human health and disease:*
MPI
Ryan Mills(MPI)
Taubman Institute Innovation Program (TIIP)
07/2022 - 06/2024
$659,764

U01HG011952:*Predicting the Impact of Genomic Variation on Cellular States:*
Co-I (Principal Investigator:Alan Boyle)
National Institutes of Health
08/2021 - 05/2026
$3,179,945

F31DE030000:*Analysis of the E7-Mediated Mechanism of MHC Class I Repression in HNSCC:*
Co-I (Principal Investigator:Chad Brenner)
National Institutes of Health
07/2020 - 06/2023
$114,167

U24HG007497:*Identifying and Characterizing the Full Spectrum of Haplotype-resolved Structural Variation in Human Genome:*
PI
National Institutes of Health-Subcontracts sourced funding through The Jackson Laboratory
08/2019 - 05/2023
$597,831

Past Grants

R21HG011493:*New technologies for accurate capture and sequencing of repeat-associated regions:*
PI
National Institutes of Health
12/2020 - 11/2022
$643,024

F31HG010569:*Discovering Novel Structural Genomic Rearrangements Using Deep Neural Networks:*
PI
National Institutes of Health
04/2019 - 03/2022
$112,983

U41HG007497:*An Integrative Analysis of Structural Variation for the 1000 Genomes Project:*
PI
National Institutes of Health-Subcontracts sourced funding through The Jackson Laboratory
09/2017 - 08/2018
$84,451

R01AI118886:*Fidelity, robustness, and diversity in RNA virus evolution and pathogenesis:*
Co-I (Principal Investigator:Adam Lauring)
National Institutes of Health
01/2016 - 12/2021
$2,023,562

U01MH106892:*2/3 Schizophrenia Genetics and Brain Somatic Mosaicism:*
Co-I (Principal Investigator:John Moran)
National Institutes of Health
05/2015 - 01/2022
$4,706,350

F31NS090883:*Upstream open reading frames in neuronal function: a singular and genome-wide approach:*
Co-I (Principal Investigator:Peter Todd)
National Institutes of Health
03/2015 - 02/2018
$102,399

U41HG007497:*An Integrative Analysis of Structural Variation for the 1000 Genomes Project:*
PI
National Institutes of Health-Subcontracts sourced funding through The Jackson Laboratory
09/2013 - 08/2018
$355,492

R01HG007068:*Discovery and Analysis of Structural Variation in Whole Genome Sequences:*
PI
National Institutes of Health
09/2013 - 07/2018
$1,509,405

R01GM103961:*Comprehensive Characterization of Canine Genomic Structural Diversity:*
Co-I (Principal Investigator:Jeffrey Kidd)
National Institutes of Health
09/2013 - 04/2017
$985,991

F32HG004207:*Improving INDEL Identification in Genomic Sequences:*
Funded by
National Human Genome Research Institute
09/2006 - 10/2008
$99,022

Honors and Awards

National

2006 - 2008	Ruth L. Kirschstein National Research Service Award (NRSA) Individual Postdoctoral Fellowship, Emory University
2012	Sixth Annual Young Investigators, GenomeWeb
2015	Highlighted in "Copy Number Analysis Starts to Add Up, Genetic Engineering & Biotechnology News
2015	Profiled, Journal of Young Investigators
2018	Profiled, Georgia Tech, College of Sciences

Institutional

2014	Endowment for the Basic Sciences Teaching Award, Medical School
2020	Accelerator Award from the Endowment of Basic Sciences, Medical School
2021	Leadership Academy, Medical School, Office of Faculty Affairs & Faculty Development

Study Sections, Editorial Boards, Journal & Abstract Review

Study Sections

National

2014	NIH Study Section - Interpreting Variation in Human Non-Coding Genomic Regions Using Computational Approaches and Experimental Assessment, NIH, (Ad Hoc)
2015	NIH Study Section – Interpreting Variation in Human Non-Coding Genomic Regions Using Computational Approaches and Experimental Assessment, NIH, (Ad Hoc)
2015	NIH Study Section – Genomics, Computational Biology and Technology, NIH, (Ad Hoc)
2016	NIH Study Section – Maximizing Investigators' Research Award for New and Early Stage Investigators, NIH, (Ad Hoc)
2018	NIH Special Emphasis Panel - Rare Genetic Disorders as a Window into the Genetic Architecture of Mental Disorders (Co-Chair), NIH, (Ad Hoc)
2019	NIH Study Section – Genomics, Computational Biology and Technology (February), NIH, (Ad Hoc)
2019	NIH Study Section – Genomics, Computational Biology and Technology (October), NIH, (Ad Hoc)
2022	NIH Study Section - Bioengineering, Biodata, and Biomodeling Technologies, NIH, (Ad Hoc)
2022	Special Emphasis Panel - Expert-Driven Small Projects to Strengthen Gabriella Miller Kids First Discovery, NIH, (Ad Hoc)

Institutional

2018	University of Michigan Precision Health Investigators Awards - Reviewer, Medical School, (Ad Hoc)
2022	PRR Trainee Committee - Application Review, University of Michigan, (Ad Hoc)

Editorial Boards / Journal & Abstract Reviews

Editorial Boards

2015 - 2019	Editorial Board Member, Scientific Reports
2017 - 2020	Editorial Board Member, PeerJ

Journal Review

2012 - present	Bioinformatics (Ad Hoc)
2012 - present	BMC Bioinformatics (Ad Hoc)
2012 - present	Genome Biology (Ad Hoc)
2012 - present	Genome Research (Ad Hoc)
2012 - present	American Journal of Human Genetics (Ad Hoc)
2012 - present	Nature Genetics (Ad Hoc)
2013 - present	Nature Communications (Ad Hoc)
2013 - present	Nature Protocols (Ad Hoc)
2014 - present	Human Genetics (Ad Hoc)
2015 - present	PLoS Computational Biology (Ad Hoc)
2016 - present	Methods (Ad Hoc)
2018 - present	European Journal of Human Genetics (Ad Hoc)

2020 - present	Genetics (Ad Hoc)
2021 - present	Nature (Ad Hoc)

Teaching

Mentorship

Faculty Member

01/2020-Present	Weichen Zhou, University of Michigan, Computational Medicine and Bioinformatics, Research Investigator

Postdoctoral Fellow

01/2012-01/2016	Gargi Dayama, University of Michigan, Computational Medicine and Bioinformatics, Postdoctoral Fellow
01/2015-01/2020	Weichen Zhou, University of Michigan, Computational Medicine and Bioinformatics, Postdoctoral Fellow
01/2019-01/2020	Yifan Wang, University of Michigan, Computational Medicine and Bioinformatics, Postdoctoral Fellow

Graduate Student

01/2013-01/2017	Xuefang Zhao, University of Michigan, Computational Medicine and Bioinformatics, PhD Degree
01/2013-01/2018	Sang Chun, University of Michigan, Computational Medicine and Bioinformatics, PhD Degree
01/2014-01/2014	Fan Zhang, University of Michigan, Computational Medicine and Bioinformatics, PhD Rotation Student
01/2014-01/2018	Akima George, University of Michigan, Computational Medicine and Bioinformatics, MS Degree
01/2014-01/2019	Yifan Wang, University of Michigan, Human Genetics, PhD Degree
01/2015-01/2022	Marcus Sherman, University of Michigan, Computational Medicine and Bioinformatics, PhD Degree
01/2016-01/2017	Nan Lin, University of Michigan, Computational Medicine and Bioinformatics, MS Degree
01/2016-01/2022	Alexandra Weber, University of Michigan, Computational Medicine and Bioinformatics, PhD Degree
01/2017-Present	Chen Sun, University of Michigan, Computational Medicine and Bioinformatics, PhD Student
01/2017-01/2017	Catherine Barnier, University of Michigan, Computational Medicine and Bioinformatics, PhD Rotation Student
01/2017-05/2018	Zhenning Zhang, University of Michigan, Computational Medicine and Bioinformatics, MS Degree
01/2019-Present	Steve Ho, University of Michigan, Human Genetics, PhD Student
01/2021-01/2021	Kai Li, University of Michigan, Computational Medicine and Bioinformatics, PhD Rotation Student
01/2022-Present	Shaomiao Xia, University of Michigan, Computational Medicine and Bioinformatics, MS Student
01/2022-Present	Jinhao Wang, University of Michigan, Biostatistics, MS Student
01/2022-01/2022	Maya Bose, University of Michigan, Computational Medicine and Bioinformatics, PhD Rotation Student
08/2022-10/2022	Brandt Bessell, University of Michigan, Computational Medicine and Bioinformatics, PhD Rotation Student

Undergraduate Student

01/2018-01/2019	Byungjun Kim, Cornell University, Summer Research
01/2019-01/2019	Samantha Rondeau, University of Michigan, Research Experience
01/2020-01/2021	Priya Ghandi, University of Michigan, Research Experience
01/2021-01/2022	Yanming Gan, University of Michigan, Research Experience
01/2022-01/2022	Thomas Chang, University of Michigan, Summer Research
08/2022-Present	Sophia Marcotte, University of Michigan, Research Experience

Teaching Activity

National

06/2014-06/2019	Lecturer, Mathematical and Theoretical Biology Institute, Arizona State University

Institutional

01/2012-Present	Doctoral Preliminary Exams (n=37), University of Michigan
09/2012-09/2012	Lecturer, HG 632 – Experimental Genetics Systems, University of Michigan
09/2012-12/2018	Coursemaster/Lecturer, BIOL 527 – Introduction to Bioinformatics, University of Michigan
01/2014-01/2014	Lecturer, UM NIEHS P30 Center and UM BRCF Bioinformatics Core Workshop – Introduction to Genome Variation, University of Michigan
09/2014-09/2014	Lecturer, Coursera (online) – Introduction to Bioinformatics, University of Michigan
01/2015-05/2019	Lecturer, BIOINF 525 - Foundations in Bioinformatics and Systems Biology, University of Michigan
08/2015-08/2019	Coursemaster/Lecturer, BIOINF/HUMGEN/BIOSTATS 606 – Introduction to Biocomputing, University of Michigan
03/2016-Present	HUMGEN 803 – Current Methods, University of Michigan, Human Genetics, Lecturer
03/2016-Present	Lecturer, HUMGEN 551 – Computational Genomics, University of Michigan
01/2019-Present	Coursemaster/Lecturer, BIOINF 529 - Bioinformatics Concepts and Algorithms, University of Michigan
01/2021-Present	Session Leader, PIBS 503 - Responsible Conduct in Research, University of Michigan

Dissertation Committees

05/2013-04/2017	Xuefang Zhao, Understanding the complexity of human structural genomic variation through multiple whole genome sequencing platforms, University of Michigan, Computational Medicine and Bioinformatics, Chair
05/2013-11/2017	Sang Chun, Development and Application of Next-Generation Sequencing Methods to Profile Cellular Translational Dynamics, University of Michigan, Computational Medicine and Bioinformatics, Chair
09/2013-09/2016	Brendan Veeneman, Development and application of methods to discover cancer-associated transcript variants, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
05/2014-05/2019	Yifan Wang, Detection of Rare Events in Complex Sequencing Data, University of Michigan, Human Genetics, Chair
07/2014-03/2016	Kärt Tomberg, Identification of Thrombosis Modifier Genes Using ENU Mutagenesis in the Mouse, University of Michigan, Human Genetics, Committee Member

08/2014-04/2016	Killeen Kirkconnell, Capturing transcriptional dynamics using nascent RNA sequencing, University of Michigan, Human Genetics, Committee Member
09/2014-03/2018	Caitlin Rodriguez, The role of upstream open reading frames in regulating neuronal protein synthesis, University of Michigan, Neuroscience, Committee Member
09/2014-09/2017	Diane Flasch, LINE-1 Integration Preferences in Human Somatic Cells, University of Michigan, Human Genetics, Committee Member
04/2015-04/2017	Andy Kong, Computational strategies for proteogenomic analyses, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
10/2015-09/2017	Daniel H. Hovelson, Precision oncology opportunities and disease insights from next-generation sequencing profiling of routine clinical biospecimens, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
01/2016-07/2022	Marcus Sherman, Cultivation of enhanced bioinformatic-specific pedagogical manipulatives, interventions, and professional development, University of Michigan, Computational Medicine and Bioinformatics, Chair
06/2016-04/2019	Fan Zhang, , Leveraging Genetic Variants for Rapid, Robust, and Scalable Analysis of Massive Sequence Datasets, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
08/2016-09/2020	Sierra Nishizaki, Decoding the Non-coding Genome: Novel Technologies for the Characterization of Non-coding Elements and Variation, University of Michigan, Human Genetics, Committee Member
09/2016-05/2022	Alexandra Weber, Integrating Diverse Technologies for Genomic Variant Discovery, University of Michigan, Computational Medicine and Bioinformatics, Chair
10/2016-05/2021	Nguyen Vo, The Genetic Heterogeneity and Drug Resistance Mechanisms in Relapse Refractory Multiple Myeloma, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
10/2016-04/2018	Adrian Tan, Statistical and Computational Methods for the Unified Analysis of Short Genetic Variants, University of Michigan, Biostatistics, Committee Member
04/2017-03/2021	Shengcheng Dong, Computational methods to identify regulatory variants in the non-coding regions of the human genome, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
05/2017-Present	Hillary Miller, University of Michigan, Cellular and Molecular Biology, Committee Member
01/2018-Present	Chris Castro, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
03/2018-06/2019	Scott Ronquist, Methods for Analyzing the 4D Nucleome, with Application to Cellular Reprogramming, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
03/2018-Present	Chen Sun, University of Michigan, Computational Medicine and Bioinformatics, Chair
04/2018-01/2022	Ningxin Ouyang, Deciphering Transcriptional Regulatory Circuits: Transcription Factor Binding and Regulatory Variants Identification, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
12/2018-05/2021	Siyu Liu, Epigenetic effects in head and neck cancer and di-2-ethylhexyl phthalate (DEHP) exposure, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
01/2019-Present	Steve Ho, University of Michigan, Human Genetics, Chair
01/2019-Present	Wenjin Gu, University of Michigan, Computational Medicine and Bioinformatics, Chair
01/2019-07/2020	James Delorme, Linking intracellular events to network reorganization in sleep-

	dependent memory consolidation, University of Michigan, Neuroscience, Committee Member
05/2019-Present	Kevin Hu, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
08/2019-Present	Elizabeth Gensterblum-Miller, University of Michigan, Cellular and Molecular Biology, Committee Member
03/2020-07/2022	Daniel Geislzer, Computational Methods for Characterizing Post-translational and Chemical Modifications Found in Open Searches, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
11/2020-Present	Camille Mumm, University of Michigan, Human Genetics, Committee Member
09/2021-Present	Samantha Grudzien, University of Michigan, Neuroscience, Committee Member
02/2022-Present	D. Ford Hannum, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
03/2022-Present	Shiting Li, University of Michigan, Computational Medicine and Bioinformatics, Committee Member
04/2022-Present	Anthony Nguyen, University of Michigan, Human Genetics, Committee Member
05/2022-Present	Itzaira Mercado-Hernandez, University of Michigan, Human Genetics, Committee Member
06/2022-Present	Noshad Hosseini, University of Michigan, Computational Medicine and Bioinformatics, Committee Member

Memberships in Professional Societies

2009 - Present	American Society of Human Genetics
2011 - Present	International Society for Computational Biology

Committee/Service

National

2011	Program Committee, First RECOMB Satellite Workshop on Massively Parallel Sequencing, Member
2015 - present	Program Committee, Great Lakes Bioinformatics Conference, Member
2015	Program Committee, Fifth RECOMB Satellite Workshop on Massively Parallel Sequencing, Member
2016	Abstract Committee, American Society of Human Genetics, Other, Abstract Reviewer
2018 - present	Program Committee, Intl. Conference on Algorithms for Computational Biology, Member
2018	Abstract Committee, American Society of Human Genetics, Other, Abstract Reviewer
2019 - present	National Association of Wabash Men, Wabash College, Board of Directors

Departmental

2012	Master's Program Admissions Committee, DCM&B, Member
2013 - 2020	Master's Admission Committee, Human Genetics, Member
2014 - 2016	Seminar Series Committee, DCM&B, Co-Chair
2014 - 2017	Picnic Committee, Human Genetics, Chair
2014 - 2021	PhD Admissions Committee, DCM&B, Member
2016 - present	Chair's Advisory Committee, DCM&B, Member

2016 - 2019	Website Committee, DCM&B, Chair
2019 - present	Space Committee, DCM&B, Member
2021 - present	Faculty Search Committee, DCM&B, Member
2021 - present	IT Committee, DCM&B, Chair
2022 - present	PhD Admissions Committee, DCM&B, Co-Chair
2022	Retreat Committee, DCM&B, Chair

Institutional

2015 - 2016	Faculty Leading Change, U-M ADVANCE Program, Other, Participant
2017 - present	Basic Research IT (BRIT) Committee, Medical School, Co-Chair
2018 - 2020	HITS Learning Services Governance Committee, Medical School, Member
2019 - 2020	PIBS Curriculum Committee, Medical School, Member
2020 - 2022	Advisory Committee on Appointments, Promotions, and Tenure (ACAPT), Medical School, Member
2020 - 2022	Pedagogy of Interdisciplinary Science Education (POISE) Training Program, University of Michigan, Advisory Board
2022 - present	Advisory Committee on Appointments, Promotions, and Tenure (ACAPT), Medical School, Chair
2022	Grievance Hearing Board, University of Michigan, Member

Scholarly Activities

Presentations

Extramural Invited Presentation

Speaker

1. Improving gene annotation of cytomegalovirus genomes by statistical and comparative genomics as verified by a proteomics-based analysis of isolated MCMV virions, 9th International Cytomegalovirus Workshop, 05/2003, Maastricht, Netherlands

2. Designing Custom CGH Arrays: Considerations for CNV Discovery and Genotyping, Agilent Technologies Workshop, American Society of Human Genetics, 10/2009, Honolulu, HI

3. Capturing Structural Variation from Whole Genome Population-Scale Sequencing: Perspectives from the 1000 Genomes Project, Cambridge Healthtech Institute, X-GEN Congress and Expo, 03/2011, San Diego, CA

4. Challenges in Mapping Copy Number Variation from Population-scale Genome Sequence Data, Open Science Grid, 2011 All Hands Meeting, 03/2011, Boston, MA

5. Structural Variation in the 1000 Genomes Project, Genomic Disorders 2012, Wellcome Trust Sanger Institute, 03/2012, Hinxton, UK

6. Discovery and functional impact of structural variation across 1000 genomes, Cambridge Healthtech Institute, NGx: Applying Next Generation Sequencing, 08/2012, Providence, RI

7. Discovery and Analysis of Structural Genomic Variation in Human Populations, School of Biology Seminar, Wabash College, 10/2012, Crawfordsville, IN

8. 1000 Genomes Project Data Tutorial, International Congress of Human Genetics, 11/2012, Montreal, Canada

9. 1000 Genomes Project Data Tutorial, American Society of Human Genetics Annual Meeting, 11/2012, San Francisco, CA

10. Mapping structural variation by population-scale genome sequencing, Radiation Effects Research Foundation, 03/2013, Hiroshima, Japan

11. Exploring Complex Structural Genomic Variation using Next-Gen Sequencing, BioConference Live,

Genetics and Genomics, 08/2014, Online (Live Virtual Presentation)

12. Genomic landscape of polymorphic nuclear mitochondrial insertions in humans and other primates, American Society of Human Genetics Annual Meeting, 10/2014, San Diego, CA

13. Exploring the Hidden Genome: Deciphering Cryptic and Complex Structural Variation, Ewha Womans University, 07/2016, Seoul, South Korea

14. Excavating the Deep Genome: Deciphering Structural Variation in Complex and Repetitive Regions, Oakland University, 04/2019, Rochester, MI

15. Identification and Characterization of Cryptic Structural Variation in Human Genomes, Association for Molecular Pathology Annual Meeting & Expo, 11/2019, Baltimore, MD

16. Identification and Characterization of Cryptic Genomic Repetitive Elements, Stanford University, 05/2020, Stanford, CA (Live Virtual Presentation)

17. Identification and Characterization of Structural Variation in Human Genomes, Future Biotech Winter Retreat, 11/2020, Novosibirsk, Russia

18. New Technologies for Identifying and Characterizing Genomic Repetitive Elements, Department of Biomedical Informatics Colloquium, University of Pittsburgh, 02/2021, Pittsburgh, PA (Live Virtual Presentation)

19. New Technologies for Identifying and Characterizing Genomic Repetitive Elements, SV Working Group, Broad Institute, 02/2022, Boston, MA (Live Virtual Presentation)

Moderator

1. Platform Moderator, American Society of Human Genetics Annual Meeting, 11/2012, San Francisco, CA

2. Invited Session Moderator, American Society of Human Genetics Annual Meeting, 10/2014, San Diego, CA

Panel

1. Panel Discussion: Copy Number Variants, 3rd Annual PQG Conference, Harvard School of Public Health, 11/2009, Boston, MA

Intramural Invited Presentation

Speaker

1. Analysis of Structural Variationin the 1000 Genomes Project Pilot:New Methods, New Insights (co-speaker), Medical and Population Genetics Seminar, Broad Institute, 09/2010, Boston, MA

2. Natural Structural Variation in the Human Genome, Interdisciplinary Group Seminar (IGS), Rackham Graduate School, University of Michigan, 04/2012, Ann Arbor, MI

3. Navigating Genomic Complexity: Discovery and Analysis of Structural Variation, NCIBI Tools and Technology Series, University of Michigan, 05/2012, Ann Arbor, MI

Publications/Scholarship

(First Author *; Corresponding author **, Last author ***)

Peer-Reviewed

Journal Article

1. Borodovsky M, **Mills R**, Besemer J, Lomsadze A: Prokaryotic gene prediction using GeneMark and GeneMark.hmm., *Curr Protoc Bioinformatics*.Chapter 4: Unit4.5, 05/2003. PM18428700

2. Borodovsky M, Lomsadze A, Ivanov N, **Mills R**: Eukaryotic gene prediction using GeneMark.hmm., *Curr Protoc Bioinformatics*.Chapter 4: Unit4.6, 05/2003. PM18428701

3. Perelygina L, Zhu L, Zurkuhlen H, **Mills R**, Borodovsky M, Hilliard JK: Complete sequence and comparative analysis of the genome of herpes B virus (Cercopithecine herpesvirus 1) from a rhesus monkey, *Journal of Virology*.77(11): 6167-6177, 06/2003. PM12743273

4. **Mills R**, Rozanov M, Lomsadze A, Tatusova T, Borodovsky M: Improving gene annotation of complete viral genomes., *Nucleic Acids Res*.31(23): 7041-7055, 12/2003. PM14627837

5. Kattenhorn LM, **Mills R**, Wagner M, Lomsadze A, Makeev V, Borodovsky M, Ploegh HL, Kessler BM: Identification of proteins associated with murine cytomegalovirus virions., *J Virol*.78(20): 11187-11197, 10/2004. PM15452238

6. **Mills RE**, Bennett EA, Iskow RC, Luttig CT, Tsui C, Pittard WS, Devine SE: Recently mobilized transposons in the human and chimpanzee genomes., *Am J Hum Genet*.78(4): 671-679, 04/2006. PM16532396

7. **Mills RE**, Luttig CT, Larkins CE, Beauchamp A, Tsui C, Pittard WS, Devine SE: An initial map of insertion and deletion (INDEL) variation in the human genome., *Genome Res*.16(9): 1182-1190, 09/2006. PM16902084

8. Lange A, **Mills RE**, Lange CJ, Stewart M, Devine SE, Corbett AH: Classical nuclear localization signals: definition, function, and interaction with importin alpha., *J Biol Chem*.282(8): 5101-5105, 02/2007. PM17170104

9. **Mills RE**, Bennett EA, Iskow RC, Devine SE: Which transposable elements are active in the human genome?, *Trends Genet*.23(4): 183-191, 04/2007. PM17331616

10. Lange A, **Mills RE**, Devine SE, Corbett AH: A PY-NLS nuclear targeting signal is required for nuclear localization and function of the Saccharomyces cerevisiae mRNA-binding protein Hrp1., *J Biol Chem*.283(19): 12926-12934, 05/2008. PM18343812

11. Bennett EA, Keller H, **Mills RE**, Schmidt S, Moran JV, Weichenrieder O, Devine SE: Active Alu retrotransposons in the human genome., *Genome Res*.18(12): 1875-1883, 12/2008. PM18836035

12. Kim J-I, Ju YS, Park H, Kim S, Lee S, Yi J-H, Mudge J, Miller NA, Hong D, Bell CJ, Kim H-S, Chung I-S, Lee W-C, Lee J-S, Seo S-H, Yun J-Y, Woo HN, Lee H, Suh D, Lee S, Kim H-J, Yavartanoo M, Kwak M, Zheng Y, Lee MK, Park H, Kim JY, Gokcumen O, **Mills RE**, Zaranek AW, Thakuria J, Wu X, Kim RW, Huntley JJ, Luo S, Schroth GP, Wu TD, Kim H, Yang K-S, Park W-Y, Kim H, Church GM, Lee C, Kingsmore SF, Seo J-S: A highly annotated whole-genome sequence of a Korean individual., *Nature*.460(7258): 1011-1015, 08/2009. PM19587683

13. Lange A, McLane LM, **Mills RE**, Devine SE, Corbett AH: Expanding the definition of the classical bipartite nuclear localization signal., *Traffic*.11(3): 311-323, 03/2010. PM20028483

14. Park H, Kim J-I, Ju YS, Gokcumen O, **Mills RE**, Kim S, Lee S, Suh D, Hong D, Kang HP, Yoo YJ, Shin J-Y, Kim H-J, Yavartanoo M, Chang YW, Ha J-S, Chong W, Hwang G-R, Darvishi K, Kim H, Yang SJ, Yang K-S, Kim H, Hurles ME, Scherer SW, Carter NP, Tyler-Smith C, Lee C, Seo J-S: Discovery of common Asian copy number variants using integrated high-resolution array CGH and massively parallel DNA sequencing., *Nat Genet*.42(5): 400-405, 05/2010. PM20364138

15. Iskow RC, McCabe MT, **Mills RE**, Torene S, Pittard WS, Neuwald AF, Van Meir EG, Vertino PM, Devine SE: Natural mutagenesis of human genomes by endogenous retrotransposons., *Cell*.141(7): 1253-1261, 06/2010. PM20603005

16. Mullaney JM, **Mills RE**, Pittard WS, Devine SE: Small insertions and deletions (INDELs) in human genomes., *Hum Mol Genet*.19(R2): R131-R136, 10/2010. PM20858594

17. 1000 Genomes Project Consortium, Abecasis GR, Altshuler D, Auton A, Brooks LD, Durbin RM, Gibbs RA, Hurles ME, McVean GA: A map of human genome variation from population-scale sequencing., *Nature*.467(7319): 1061-1073, 10/2010. PM20981092

18. Sudmant PH, Kitzman JO, Antonacci F, Alkan C, Malig M, Tsalenko A, Sampas N, Bruhn L, Shendure J, 1000 Genomes Project, Eichler EE: Diversity of human copy number variation and multicopy genes., *Science*.330(6004): 641-646, 10/2010. PM21030649

19. Gokcumen O, Babb PL, Iskow RC, Zhu Q, Shi X, **Mills RE**, Ionita-Laza I, Vallender EJ, Clark AG, Johnson WE, Lee C: Refinement of primate copy number variation hotspots identifies candidate genomic regions evolving under positive selection., *Genome Biol*.12(5): R52, 01/2011. PM21627829

20. **Mills RE**, Pittard WS, Mullaney JM, Farooq U, Creasy TH, Mahurkar AA, Kemeza DM, Strassler DS, Ponting CP, Webber C, Devine SE: Natural genetic variation caused by small insertions and deletions in the human genome., *Genome Res*.21(6): 830-839, 06/2011. PM21460062

21. Pinto D, Darvishi K, Shi X, Rajan D, Rigler D, Fitzgerald T, Lionel AC, Thiruvahindrapuram B, MacDonald JR, **Mills R**, Prasad A, Noonan K, Gribble S, Prigmore E, Donahoe PK, Smith RS, Park JH, Hurles ME, Carter NP, Lee C, Scherer SW, Feuk L: Comprehensive assessment of array-based platforms and calling algorithms for detection of copy number variants, *Nature Biotechnology*.29(6): 512-520,

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Non-Peer Reviewed

Published Erratum

1. Zook JM, Hansen NF, Olson ND, Chapman L, Mullikin JC, Xiao C, Sherry S, Koren S, Phillippy AM, Boutros PC, Sahraeian SM E, Huang V, Rouette A, Alexander N, Mason CE, Hajirasouliha I, Ricketts C, Lee J, Tearle R, Fiddes IT, Barrio AM, Wala J, Carroll A, Ghaffari N, Rodriguez OL, Bashir A, Jackman S, Farrell JJ, Wenger AM, Alkan C, Soylev A, Schatz MC, Garg S, Church G, Marschall T, Chen K, Fan X, English AC, Rosenfeld JA, Zhou W, **Mills RE**, Sage JM, Davis JR, Kaiser MD, Oliver JS, Catalano AP, Chaisson MJ P, Spies N, Sedlazeck FJ, Salit M: Author Correction: A robust benchmark for detection of germline large deletions and insertions., *Nat Biotechnol*.38(11): 1357, 11/2020. PM32699374

2. Rodin RE, Dou Y, Kwon M, Sherman MA, D'Gama AM, Doan RN, Rento LM, Girskis KM, Bohrson CL, Kim SN, Nadig A, Luquette LJ, Gulhan DC, Brain Somatic Mosaicism Network, Park PJ, Walsh CA: Author Correction: The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing., *Nat Neurosci*.24(4): 611, 04/2021. PM33753946