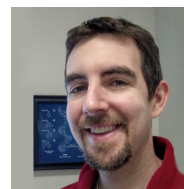


# Christopher A. Miller, Ph.D.

Curriculum Vitae

Updated: Dec 22, 2020



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**Citizenship:** United States of America

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**Present Position:**

Assistant Professor  
Division of Oncology  
McDonnell Genome Institute  
Washington University School of Medicine

**Education:**

May 2005 B.S. Biology and Computer Science  
Truman State University, Kirksville, MO

May 2011 Ph.D. Structural and Computational Biology and Molecular  
Biophysics Program  
Baylor College of Medicine, Houston, TX  
Thesis topic: Computational Cancer Genomics

**Academic Positions:**

2011-2013 Staff Scientist - Medical Genomics  
The Genome Institute  
Washington University in St Louis

2013-2017	Cancer Analysis Group Leader The Genome Institute Washington University in St Louis
2015-2016	Instructor in Medicine Division of Genomics and Bioinformatics Washington University School of Medicine
2016-Present	Assistant Professor in Medicine Division of Oncology Washington University School of Medicine

**Editorial/Review Responsibilities:**

Ad-hoc reviewer for *Bioinformatics*, *Cancer Cell*, *Genome Biology*, *PLoS Computational Biology*, *Nucleic Acids Research*, *Nature Communications*, *Genome Research*.

Grant reviewer for Dutch Cancer Society (KWF Kankerbestrijding)

**Professional Societies:**

American Association for Cancer Research  
International Society for Computational Biology

**Oral Presentations (conference - title):**

2012	TCGA Symposium - Assessing Tumor Heterogeneity and Tracking Clonal Evolution Using Whole Genome or Exome Sequencing
2013	TCGA Steering Committee Meeting - Automatic inference of therapeutically relevant subclones in heterogeneous tumors
2013	Precision Medicine: Personal Genomes and Pharmacogenomics – SciClone: Inferring clonal architecture and tracking the spatial and temporal patterns of tumor evolution and therapy resistance
2014	TCGA Symposium - Ultra-deep whole-genome sequencing reveals clinically relevant low-frequency subclones in an acute myeloid leukemia
2015	Genome Informatics - Assessing tumor heterogeneity and tracking clonal clearance in response to therapy
2016	Festival of Genomics - Genomic insights into tumor evolution and therapy response

2016                      Genome Informatics - Characterizing genomic responses to cancer immunotherapy

### **Research Support**

1 R50 CA211782 (PI)

NIH-NCI

09/01/2017-08/31/2022

Title: Comprehensive informatic analyses of AML genomes and epigenomes

1 PO1 CA101937 (Core C Director)

NIH-NCI

09/19/03-03/31/2023

Title: Genomics of Acute Myeloid Leukemia (PPG)

### **Teaching Title and Responsibilities**

2005                      Teaching Assistant - Advanced Topics: Quantitative Biology (2005)  
2007-2008              Teaching Assistant - Computer Aided Discovery Methods  
2008                      Teaching Assistant - Computational Mathematics for Biomedical Scientists  
2015-2017              Lecturer - Investigating Eukaryotic Genomes  
2015-2019              Lecturer - Molecular Basis of Heredity  
2017-2018              Lecturer - Computational Statistical Genetics  
2018                      Lecturer - Research Explorations in Genomics  
2019                      Lecturer - Human Genetics  
2018-                      Co-organizer – MGI Bioinformatics Workshops

### **Trainees (date and current position):**

Mentor to undergraduate research students

Yang Li	2013	Working in industry
Callie Federer	2014	PhD, now scientist at RadiaSoft
Jonas Neichen	2017	Medical Student at Rush Medical College
Megan Neveau	2017	Graduate Student at Iowa State University
Zhaohe Zhao	2020	Student at WUSTL

Training and Supervision of WUSTL computational staff, including

Dr. Gue Su Chang	2013-	Cancer Analysis Group, TGI
Dr. Tiandao Li	2013-	Cancer Analysis Group, TGI
Dr. Allegra Petti	2013-16	Cancer Analysis Group, TGI
Dr. Yevgeniy Gindin	2014-15	Cancer Analysis Group, TGI
Dr. Charles Lu	2013-15	Cancer Analysis Group, TGI

## Training of external collaborators:

Dr. Corrine Segal	2013	ICR, London UK
Dr. Alice Gao,	2013	ICR, London UK

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(\* indicates co-first authorship)

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3. Coarfa C, Yu F, **Miller CA**, Chen Z, Harris RA, Milosavljevic A. Pash 3.0: A versatile software package for read mapping and integrative analysis of genomic and epigenomic variation using massively parallel DNA sequencing. *BMC Bioinformatics*. 2010. doi:10.1186/1471-2105-11-572
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Magrini V, Demeter RT, Larson DE, Kulkarni S, Ozenberger BA, Welch JS, Walter MJ, Graubert TA, Westervelt P, Radich JP, Link DC, Mardis ER, DiPersio JF, Wilson RK, Ley TJ. Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. *Jama*. 2015. doi:10.1001/jama.2015.9643

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