

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors in the order listed on Form Page 2.

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NAME Tang, Ming	POSITION TITLE Postdoctoral Fellow MD Anderson Cancer Center
eRA COMMONS USER NAME (agency login) MINGTANG	

EDUCATION/TRAINING

(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)

INSTITUTION AND LOCATION	DEGREE (if applicable)	MM/YYYY	FIELD OF STUDY
Shanghai Jiao Tong University, Shanghai	BS	06/2008	Biotechnology
University of Florida, Gainesville, FL	PHD	08/2014	Cancer Genetics and Genomics
MD Anderson Cancer Center, Houston, TX	Postdoctoral Fellow	09/2016	Functional Genomics for Brain Tumor
MD Anderson Cancer Center, Houston, TX	Postdoctoral Fellow	Current	Intra-tumor heterogeneity of lung cancer and Epigenomics for Melanoma

A. PERSONAL STATEMENT

I have more than six years' experience in analyzing sequencing related data. During my postdoctoral training in MD Anderson Cancer Center with Dr. Roel Verhaak, I have gained extensive experience in handling large-scale genomic data sets and pipelining workflows. I primarily use Unix, python and R for my daily data analysis and am familiar with high performance computing clusters. To accommodate our computational need for large-scale ChIP-seq, ATAC-seq, RNA-seq and DNA-seq data analysis, I built pipelines for each using snakemake, a workflow management system extended from python. With the pipeline set up, one can submit thousands of jobs to the computing cluster simultaneously and wait for the results next day. The pipelines can be found in my gitlab <https://gitlab.com/tangming2005> or github <https://github.com/crazyhottommy> page. I have analyzed other types of data including GRO-seq, ChIA-PET, single cell RRBS, 450K DNA methylation array and mRNA microarray. I also gained intimate familiarities with public data sets such as TCGA. I once processed over 1000 TCGA whole-genome sequencing samples (~300G in size each sample) to identify structural variations and resulted a co-authored paper in *Nature Genetics*.

I am familiar with commonly used tools in the bioinformatics field such as samtools, bedtools, bwa-mem, bowtie, STAR, GATK, freebayes, GSEA, MACS1/2, DESeq2 bioconductor packages and many others. I share my experience with the tools and data analysis using R on my blog <http://crazyhottommy.blogspot.com/>. Now it attracts more than 6,000 views per month. I also have more than 900 followers on twitter @tangming2005 who frequently share my idea and tips on bioinformatics. Following ~200 leaders in the bioinformatics field on twitter makes me stay on the current of bioinformatics. I learned quite a bit on epigenomic data analysis with self - bioinformatics training during my PhD. My github repo on ChIP-seq and RNA-seq analysis are starred by more than 190 people. I was invited to write a ChIP-seq book chapter for biostar handbook <https://read.biostarhandbook.com/>. Because of the github pages, blog posts and the

book, I frequently receive emails all over the world asking for help on sequencing related data analysis.

I have gained machine-learning experience during the course of my postdoc training as well. I am experienced with principle component analysis (PCA), MDS, unsupervised-clustering (hierarchical clustering, NMF clustering, k-means clustering etc). I have put some notes on Rpub <https://rpubs.com/crazyhottommy/>. I also started using random forest based machine learning techniques for feature selection in epigenomic data sets https://github.com/crazyhottommy/pyflow-chromForest/tree/vsurf_dynamic . I have experience using common parametric and non-parametric statistical tests in R as well.

Being trained in a molecular biology lab during my PhD has established my solid understanding and skills in experimental cancer biology, which is evident by my two first author publications in *PNAS* and *JBC*. I am a certified instructor for software carpentry <https://software-carpentry.org/> and data carpentry <http://www.datacarpentry.org/>. I once served as an instructor for the software Carpentry workshop held in the University of Miami to teach biologists Unix and R for data analysis. <http://xuf12.github.io/2015-04-02-umiami/>. I am also a member of the Genomics Curriculum Committee for data carpentry, which is headed by Tracy Teal and a maintainer of the wrangling genomic course material <https://github.com/datacarpentry/wrangling-genomics> .My previous training has enabled me to understand the biological questions I ask, to carefully interpret the data and to effectively present the results. Through my teaching experience, I have gained communication skills, which is critical as a scientist to communicate our research. I have put my other training experience/ over 30 certificates on my linkedin page <https://www.linkedin.com/in/ming-tang-40650014/>.

After Join Dr.Jianjun Zhang and Dr.Andrew Futreal's lab, I applied my bioinformatics skills to study intra-tumor heterogeneity in lung cancer by analyzing next-generation sequencing data. I have learned a lot on lung cancer biology and familiarized myself on the data analysis in this area. At the same time, I am jointly supervised by Dr.Kunal Rai in analyzing a large scale in-house generated ChIP-seq data set from melanoma.

B. POSITIONS AND HONORS

Positions and Employment

2015 - Postdoctoral Fellow, MD Anderson Cancer Center, Houston, TX
2008 - 2014 Research Assistant, University of Florida, Gainesville, FL

Other Experience and Professional Memberships

- Certified Instructor, Software Carpentry, Data Carpentry, USA
- Member of the Genomics Curriculum Committee, Data Carpentry, USA
- Trusted member, BioStar online bioinformatics forum
- Member of Society of Neuro-Oncology (SNO)
- Member of American Society of Clinical Oncology (ASCO)

Honors

- 2018 Data Science RoAD-Trip fellow supported by USC BD2K Training Coordinating Center. Stayed in Pacific Northwest National Lab(PNNL) for 2 weeks developing machine learning algorithms for chromatin state data.
- 2017 One out of 23 trainees from all over the world for software carpentry instructor training in Data Intensive Biology Summer Research Institute, University of California, Davis
- 2017 American Society of Clinical Oncology (ASCO) annual meeting, Chicago. Histology determination of lung cancers: A report on genomic profiling of lung cancer of mixing histology. Poster presentation. (Only 30% of more than 6000 abstracts accepted)
- 2016 Data Manipulation in R with dplyr certificate. Data Camp.
- 2015 Johns Hopkins University online Data science specification certificate, Coursera
- 2015 2015 Summer Institutes in Statistics for Big Data Scholarship, University of Washington
- 2015 Instructor of Shell and R at the 2-day software carpentry workshop held in the University of Miami, Software Carpentry, USA
- 2015 MIT Introduction to Computer Science and Programming Using Python online course certificate, edX
- 2015 Harvard PH525X Data Analysis for Genomics edX online course Bioconductor & ChIP-seq certificate, edX
- 2014 Michigan State University Next Generation Sequencing course certificate, Michigan State University, USA
- 2014 Teaching Assistant at Data Carpentry 2-day workshop held by iDigBio, Software Carpentry, USA
- 2014 Invited lecture on ChIP-seq GSM6232 Advanced Application of Bioinformatics, University of Florida, USA
- 2013 Genetics & Genomics program Travel Grant, University of Florida, USA
- 2013 Keystone Symposia: Epigenetic Marks and Cancer Drugs. Santa Fe, New Mexico, USA. Poster presentation: The MBT domain protein SFMBT1 is an integral chromatin reader component of the LSD1 demethylase complex for epithelial-to-mesenchymal transition.
- 2012 Outstanding International Student, University of Florida, USA
- 2012 4th SOUTHEAST STEM CELL CONSORTIUM WORKSHOP. Turnbull Conference Center. Florida State University, Tallahassee, Florida, USA. Poster presentation: Requirement of SFMBT1 to repress E-cadherin expression by Snai1.
- 2010 Proficient English speaking certificate from International Friendship, International Friendship, USA
- 2007 National Scholarship for Academic Excellence, Shanghai Jiao Tong University, China
- 2007 National Stipend for Academic Excellence, Shanghai Jiao Tong University, China
- 2006 People's Scholarship, Shanghai Jiao Tong University, China

C. SELECTED PEER-REVIEWED PUBLICATIONS

- **Tang M**, Chen B, Lin T, Li Z, Pardo C, et al. Restraint of angiogenesis by zinc finger transcription factor CTCF-dependent chromatin insulation. *Proc Natl Acad Sci U S A*. 2011 Sep 13;108(37):15231-6. PubMed PMID: 21896759; PubMed Central PMCID: PMC3174592.
- Lu J and **Tang M**. CTCF-dependent chromatin insulator as a built-in attenuator of angiogenesis. *Transcription*. 2012 Mar-Apr;3(2):73-7. PubMed PMID: 22414750; PubMed Central PMCID: PMC3337828.
- **Tang M**, Shen H, Jin Y, Lin T, Cai Q, et al. The malignant brain tumor (MBT) domain protein SFMBT1 is an integral histone reader subunit of the LSD1 demethylase complex for chromatin association and epithelial-to-mesenchymal transition. *J Biol Chem*. 2013 Sep 20;288(38):27680-91. PubMed PMID: 23928305; PubMed Central PMCID: PMC3779763.
- Ai L, Kim WJ, Alpay M, **Tang M**, Pardo CE, et al. TRIM29 suppresses TWIST1 and invasive breast cancer behavior. *Cancer Res*. 2014 Sep 1;74(17):4875-87. PubMed PMID: 24950909.
- Fan AX, Papadopoulos GL, Hossain MA, Lin IJ, Hu J, **Tang M**, et al. Genomic and proteomic analysis of transcription factor TFII-I reveals insight into the response to cellular stress. *Nucleic Acids Res*. 2014;42(12):7625-41. PubMed PMID: 24875474; PubMed Central PMCID: PMC4081084.
- Luo HC, Shenoy AK, Li X, Jin Y, Jin L, Cai Q, **Tang M**, Liu Y, Chen H et al. MOF Acetylates the Histone Demethylase LSD1 to Suppress Epithelial-to-Mesenchymal transition. *Cell Reports*. 2016. PMID: 27292636
- **Tang M** and Verhaak R. A Molecular Take on Malignant Rhabdoid Tumors. *Trends in Cancer*. 2016. May;2(5):217-218
- **Tang M**, Deng C, Patel B, Jin Y, Huang S, Lu J. Genomic study of HIF1 binding sites reveals pre-looping status of distal enhancers. (Under preparation)
- Wang X, Schoenhals JE, Li A, Valdecanas DR, Ye H, Zhang F, Tang C, **Tang M**, Liu CG, Liu X, Krishnan S, Allison JP, Sharma P, Hwu P, Komaki R, Overwijk WW, Gomez DR, Chang JY, Hahn SM, Cortez Mam Welsh JW. Suppression of type I IFN signaling in tumors mediates resistance to anti-PD-1 treatment that can be overcome by radiotherapy. *Cancer Res*. 2016. Nov 7. pii: canres.3142.2015.
- Shenoy AK, Jin Y, Luo H, **Tang M**, Pampo C, Shao R, Siemann DW, Wu L, Heldermon C, Law BK, Chang LJ, Lu J. Epithelial-to-mesenchymal transition confers pericyte properties on cancer cells. *Journal of Clinical Investigation*. 2016. Nov 1;126(11):4174-4186. doi: 10.1172/JCI86623
- Barthel FP, Wei W, **Tang M**, Martinez-Ledesma E, Hu X, Amin S, Seth S, Song X, Lichtenberg T, Hu J, Zhang J, Zheng S, Verhaak R. Systematic Analysis of Telomere Length, Telomerase and Telomere Maintenance across 31 cancer types. 2017. *Nature Genetics*. 2017. doi:10.1038/ng.3781
- Zhao D, Lu X, Wang G, Lan Z, Liao W, Li J, Liang X, Chen J, Shah S, Shang X, **Tang M**, Deng P, Dey P, Chakravarti D, Chen P, Spring D, Navone N, Troncoso P, Zhang j, Wang YA, DePinho RA. Synthetic essentiality of chromatin remodeling factor CHD1 in PTEN-deficient cancer. *Nature*. 2017. doi:10.1038/nature21357.
- Robertson AG, Shih J, Yau C, Gibb EA, Mungall KL, Hess JM, Uzunangelov V, Walter V, Danilova L, Lichtenberg TM, Kucherlapati M, Kimes PK, **Tang M**, Penson A, Babur O, Bristow CA, Hoadley KA, Iype L, Chang MT, Oba J, The Cancer Genome Atlas (TCGA)

- Network, Cherniack AD, Benz C, Verhaak R, Griewank KG, Felau I, Zenklusen JC, Gershenwald JE, Schoenfeld L, Lazar AJ, Abdel-Rahman M, Roman-Roman S, Stern, MH, Cebulla CM, Williams MD, Jager MJ, Coupland S, Esmaeli B, Kandath C, Woodman SE. Integrative Analysis identifies Four Molecular and Clinical Subsets in Uveal Melanoma. **Cancer Cell**. 2017.32:2:p204-220.e15. (I did RNA-seq fusion and mutual exclusive mutation analysis).
- Fan A, Aryan M, Shen Y, Hossain M, **Tang M**, Lu J, Strouboulis J, Bungert J. TFII-I interacts with E2F transcription factors and regulates their association with the co-occupied ATF3 gene locus. **Journal of Cellular Biochemistry**. 2017. Doi:10.1002/jcb.26235
 - **Tang M**. 2017. Pyflow-ChIPseq: a snakemake based ChIP-seq pipeline. Zenodo. <http://doi.org/10.5281/zenodo.819971>
 - Hu X, Wang Q, **Tang M**, Barthel FP, Amin S, Yoshihara K, Lang FM, Lee SH, Zheng S, Verhaak R. TumorFusions: an integrative resource for reporting cancer-associated transcript fusion in 33 tumor types. **Nucleic Acids Research**. 2017. Doi:10.1093/nar/gkx1018/4584571.
 - Terranova C, **Tang M**, Orouji E, Maitituoheti M, Raman A, Amin S, Liu Z, Rai K. An Integrated Platform for Genome-wide Mapping of Chromatin States Using High-throughput ChIP-sequencing in Tumor Tissues. **J Vis Exp**. 2018;In press

D. BOOK CHAPTERS

- **Tang M**, Luo HC and Lu J. **Book Chapter** Genetically altered cancer epigenome. **Epigenetic Gene Expression and Regulation**. 2016. Elsevier, Inc. Edited by Suming Huang, Michael Litt, and Cynthia Ann Blakey. <http://store.elsevier.com/Epigenetic-Gene-Expression-and-Regulation/isbn-9780127999586/>
- Sebastian A, Albert R, Leipzig J, Kelkar H, **Tang M**, Shen W, Coster WD. **The biostar Handbook: A Beginner's Guide to Bioinformatics**. <https://read.biostarhandbook.com/> 2017. Edited by Istvan Albert.
- Rai K, **Tang M**. **Book Chapter**: Computational analysis of epigenetic modifications in melanoma cancer. **Computational Epigenetics and Diseases**. 2017. Elsevier, Inc.

E. RESEARCH SUPPORT

Ongoing Research Support

2018/03/01-current

National Cancer Institute.

Kunal Rai (PI)

Epigenomic profiling (ChIP-seq) of melanoma by six histone marks in 50 tumor samples.

The goal of this study is to study epigenomic alterations in melanoma and correlate with RNA-seq data, copy-number data and mutation data.

Role: Postdoctoral Fellow

Completed Research Support

2016/10/01-2018/03/01

Andrew Futreal, Jianjun Zhang (PI)
Cancer Prevention Research Institute of Texas (CPRIT)
Intra-tumor heterogeneity in lung cancer.
The goal of this study is to infer the molecular mutation timing of primary lung cancer and recurrent diseases by analyzing multi-region whole-exome sequencing data and DNA methylation array data.
Role: Postdoctoral Fellow

2015/03/01-2016/10/01
National Cancer Institute.
Roel Verhaak (PI)
Enhancer malfunction in gliomas.
The goal of this study is to identify genomic alterations (mutations and structural variations) targeting non-coding regulatory genomic regions (enhancers) in the glioma samples. ChIP-seq was performed in 20 tumor samples and 10 glioma sphere forming cell lines to identify glioma-specific enhancers. malfunctional enhancers in gliomas were identified by integrating whole genome and RNA-seq data.
Role: Postdoctoral Fellow

2009/08/01-2015/05/31
R01CA137021, National Cancer Institute
Lu , Jianrong (PI)
Genomic study of HIF1 binding sites reveals pre-looping status of distal enhancers
The goal of this study is to investigate the function of Hypoxia-inducible transcription factor (HIF) dependent enhancers in a genome-wide scale.
Role: Graduate Research Assistant

2009/08/01-2015/05/31
R01CA137021, National Cancer Institute
Lu , Jianrong (PI)
Restraint of angiogenesis by zinc finger transcription factor CTCF-dependent chromatin insulation
The goal of this study is to investigate how the angiogenic factor VEGFA is controlled by transcription factor CTCF by its enhancer blocking activity in breast cancer.
Role: Graduate Research Assistant

2011/08/01-2013/05/31
09BN-12-23092, Florida Bankhead-Coley Cancer Research Program
Lu , Jianrong (PI)
The malignant brain tumor (MBT) domain protein SFMBT1 is an integral histone reader subunit of the LSD1 demethylase complex for chromatin association and epithelial-to-mesenchymal transition
The goal of this study is to investigate the functions of MBT domain-containing protein SFMBT1, a novel chromatin reader of H3K4me2 and H3K4me3 in the LSD1 complex associated with Snai1, during epithelial-to-mesenchymal transition (EMT)-a critical step during tumor metastasis.

Role: Graduate Research Assistant