MING (Tommy) TANG

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EDUCATION and TRAINING

2018.10-present	Bioinformatics Scientist III, FAS informatics, Harvard University. USA
2018.3-2018.10	Research Scientist, MD Anderson Cancer Center. USA
2015.4-2018.2	Postdoctoral fellow. MD Anderson Cancer Center. USA
2008.7-2014.8	Ph.D. Genetics & Genomics, University of Florida. USA
2004.8-2008.6	Bachelor. Biotechnology, Shanghai JiaoTong University. China.

HONORS

2018	Instructor, ANGUS Next-Gen Sequence Analysis Workshop, UC Davis, USA
2018	USC BD2K Data Science Road-Trip fellow. USC, USA
2017	Genomics Advisory committee member for Data Carpentry. Data Carpentry, USA
2017	Certified instructor for Data Carpentry. Data Intensive Biology Summer Research Institute, University of California, Davis
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. Univ. 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

2012	Outstanding International Student, University of Florida, USA
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
2005	National Environmental Protection Conference Excellent Volunteer Award, National environmental protection administration, China

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
- Wang X, Schoenhals JE, Li A, Valdecanas DR, Ye H, Zhang F, Tang C, **Tang M**, Liu CG, LiuX, Krishnan S, Allison JP, Sharma P, Hwu P, Komaki R, Overwikjk 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, Schoenfield L, Lazar AJ, Abdel-Rahman M, Roman-Roman S, Stern, MH, Cebulla CM, Williams MD, Jager MJ, Coupland S, Esmaeli B, Kandoth C, Woodman SE. Integrative Analysis identifies Four Molecular and Clinical Subsets in Uveal Melanoma. ***Cancer Cell.*** 2017.32:2:p204-220.e15.
- 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. ***Jounral 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. ***Journal of Visualized Experiments***. 2018.(134),e56972,doi:10.3791/56972.
- Menghi F, Barthel FP, Yadav V, **Tang M**, Ji B, Tang Z, Cater GW, Ruan Y, Scully R, Verhaak R, Jonkers J, Liu E. The Tandem Duplicator Phenotype Is a Prevalent Genome-Wide Cancer Configuration Driven by Distinct Gene Mutations. ***Cancer Cell***. 2018. 13;34(2)197-210.e5 doi:10.1016/j.ccell.2018.06.008.
- Ghosh K, **Tang M**, Kumari N, Nandy A, Basu S, Mall DP, Rai K, Biswas D. Positive Regulation of Transcription by Human ZMYND8 through Its Association with P-TEFb Complex. ***Cell Reports***. 2018. Aug21;24(8):21441-2154.e6 doi:10.1016/j.celrep.2018.07.064.

- Yan B, Chen Q, Shimada K, **Tang M,** Li H, Gurumurthy A, Khoury JD, Xu B, Huang S, Qiu Y. Histone deacetylase inhibitor targets CD123/CD47-positive cells and reverse chemoresistance phenotype in acute myeloid leukemia. ***Leukemia***. 2018. Doi:1038/s41375-018-0279-6.
- Alam H*, **Tang M*,** Maitituoheti M, Dhar SS, Amin S, Gu B, Chen T, Lin Y, Chen J, Muller F, DeMayo FJ, Baseler L, Rai K, Lee M. Super-enhancer impairment is a link between MLL4 inactivated lung tumors and their vulnerability to glycolysis pathway inhibition. ***BioRxiv.*** 2018. https://doi.org/10.1101/507202
- Matituoheti M, Keung E, **Tang M**, Yan L, Alam H, Han G, Raman A, …, Wang L, Ying H, Rai K. Enhancer Reprogramming Confers Dependence on Glycolysis and IGF signaling in KMT2D mutant Melanoma. ***BioRxiv***. 2018. https://doi.org/10.110/507327.

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.*

SKILLS

Wet lab skills

- shRNA mediated gene knock-down, RT-qPCR, gel-electrophoresis, DNA cloning, Northern blotting, Western blotting, tissue culture, luciferase reporter assay, GST pull-down assay, chromatin immuoprecipitation (ChIP) assay, immunostaining, co-immunoprecipitation, Chromatin Confromation Capture (3C) assay, FACS etc.

Bioinformatics skills

- Python programming, R/Bioconductor programming and bash scripting. Differential gene expression analysis for microarray data, RNA-seq data. Familiar with Next Generation Sequencing (NGS) data analysis, especially for ChIP-seq (I developed a pipeline using python https://github.com/crazyhottommy/pyflow-ChIPseq) and RNA-seq (https://gitlab.com/tangming2005/STAR_htseq_RNAseq_pipeline), whole-exome sequencing, whole-genome sequencing (https://gitlab.com/tangming2005/snakemake_DNAseq_pipeline/tree/lancet), RRBS-seq and ATAC-seq (https://github.com/crazyhottommy/pyflow-ATACseq) etc. I can handle from initial data quality control, reads mapping to downstream analysis.

  - NGS files (fastq, bam, sam, bed, VCF, GFF etc) manipulation: FASTX, FASTQC, seqtk, bioawk, gffutils, HTSeq, bedtools, pybedtools, samtools, bamtools, Picard, VCFtools, tabix, SRA-tool kits etc.
  - Mapping NGS fastq file to reference genome with bowtie2 and bwa in a remote computing cluster.
  - Familiar with UCSC, IGV, IGB, SeqMonk and Mochview etc Genome browsers.
  - Analysis software: Homer for ChIP-seq, MACS peak calling for ChIP-seq, repdiffs for differential ChIP-seq peaks identification, python packages(bio-python, cruzdb, pygr, pycogent, HTSeq, pybedtools, bx-python) for sequence manipulation, database accession and Genomic Interval algebra etc, bioconductor packages (limma for microarray and RNA-seq, ShortRead, IRanges, DESeq1/2 for ChIP-seq and RNA-seq)
  - Reference mapping free RNA-seq quantification with Salmon/Kallisto.
  - Motif and pathway analysis: Homer software, MEME suites, GREAT tool, GSEA, DAVID and GAGE bioconductor package etc.
  - GATK variant calling pipeline, mutect and SNPEFF and GEMINI to explore functional SNVs.
  - Graphing skills: box-plot, bar plot, line plot, scatter plot, heatmap, PCA analysis with ggplot2.
  - Git version control.
  - Mysql database
- Familiar with Linux command line. Good at sed and awk for text reformatting. Good at data wrangling. Know how to interact with remote computing clusters by ssh and screen command.
- Familiar with web based GUI tools like Galaxy (cistrome from Shirely Liu’s lab), GenomeSpace etc.

To have a better idea of what I am capable of doing, you may want to visit a blog I’ve been maintaining: http://crazyhottommy.blogspot.com/
my github page: https://github.com/crazyhottommy
my Gitlab page: https://gitlab.com/users/tangming2005/projects
and my personal website: https://divingintogeneticsandgenomics.rbind.io

RESEARCH EXPERIENCE

Ongoing Research Support

2018/10/01-present

2016/10/01-2018/03/01
Tim Sackton (bioinformatics core director)
Harvard University, FAS informatics
Work closely with Catherine Dulac's lab to catalog and understand the diversity and function of cell types in the mouse brain using single-cell RNA-seq and other cutting-edge techniques.

Role: Bioinformatics Scientist III https://informatics.fas.harvard.edu/

Completed Research Support

2016/10/01-2018/03/01
Andrew Futreal, Jianjun Zhang (PI)
University of Texas MD Anderson Cancer Center
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 muti-region whole-exome sequencing data and DNA methylation array data.
Role: Postdoctoral Fellow

2016/10/01-2018/10/01
University of Texas MD Anderson Cancer Center
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/Research Scientist

2015/03/01-2016/10/01
University of Texas MD Anderson Cancer Center
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
University of Florida
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

University of Florida
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
University of Florida
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

POSTERS & PRESENTATIONS

- **Tang M**, Histology determination of lung cancers: A report on genomic profiling of lung cancer of mixing histology (2017). American Society of Clinical Oncology (ASCO) annual meeting, Chicago.
- **Tang M.** Shen H, Lin T, Tran Q, Jin Y, Cai Q, Lu J (2013) The MBT domain protein SFMBT1 is an integral chromatin reader component of the LSD1 demethylase complex for epithelial-to-mesenchymal transition**.** Keystone Symposia: Epigenetic Marks and Cancer Drugs. Santa Fe, New Mexcio, USA.
- **Tang M,** Shen H, Lin T, Tran Q, Jin Y, Cai Q, Lin S, Wu L, Lu J (2012). Requirement of SFMBT1 to repress E-cadherin expression by Snai1. 4th SOUTHEAST STEM CELL CONSORTIUM WORKSHOP. Turnbull Conference Center. Florida State University, Tallahasee, FL.
- **Tang M,** Chen B, Li T, Pampo C, Siemann D, Cepko C, Lu J (2012). The chromatin insulator CTCF regulates VEGF expression and angiogenesis. Celebration of Research. College of Medicine, UF.
- **Tang M**, Chen B, Lin T, Li Z, Pardo C, Pampo C, Chen J, Lien C-L, Wu L, Ai L, Wang H, Yao K, Oh SP, Seto E, Smith LEH, Siemann DW, Kladde MP, Cepko CL, Lu J (2011). Zinc finger protein CTCF in regulation of VEGF expression and angiogenesis. The Seventh Annual Symposium of the UF Genetics Institute (UFGI).
- **Tang M** (2012). Chromatin insulator CTCT regulates VEGF expression and angiogenesis. UFGI Scientific Advisory Board Meeting. Invited Presenter.