

Dechao Tian

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<https://tian-dechao.github.io>

An enthusiast of statistics and data science, hold a doctor's degree in statistics, have rich experience of developing and applying various statistical models and machine learning algorithms.

PROFESSIONAL EXPERIENCE

CENTERS FOR DISEASE CONTROL AND PREVENTION , USA

ORISE Fellow, April 2019 - Present

- Develop advanced machine learning algorithms to identify anomaly clusters from high-dimensional character Whole-genome sequencing data and linked epidemiological data.
- Teach R software.

CARNEGIE MELLON UNIVERSITY, USA

Postdoctoral Research Associate, April 2015 - March 2019

- Develop high-dimensional machine learning algorithms based on graphical model and graph theory for genomics.
- Build a novel hypothesis test model based on random matrix theory to identify significant spatial patterns.
- Analyze genomic data by applying multiple statistical models and machine learning algorithms.
- Write up sample size calculation and power analysis for grant application.

NATIONAL UNIVERSITY OF SINGAPORE, SINGAPORE

Research Assistant, September 2014 - April 2015

- Build a novel classification model to identify marker genes from biological networks.

SINGAPORE EYE RESEARCH INSTITUTE (SERI), SINGAPORE

Part-Time Statistician, February 2011 - April 2015

- Analyze multiple clinical data by applying various statistical models.

EDUCATION

NATIONAL UNIVERSITY OF SINGAPORE, SINGAPORE

Ph.D. in Statistics and Applied Probability, June 2015

NORTHEAST NORMAL UNIVERSITY, CHINA

M.S. in Probability and Mathematical Statistics, June 2011

NORTHEAST NORMAL UNIVERSITY, CHINA

B.S. in Mathematics and Applied Mathematics, June 2009

SKILLS

- Programming (Most used first): Python, Bash, Matlab.
- Data analysis: R, Python scikit-learn, SAS.
- Biological database: 4D Nucleome Data, UCSC Genome Browser, ENCODE, TCGA.
- Language: English (using it as daily and working language for 8 years), Chinese (native).

CERTIFICATE

- Base Programmer for SAS 9.

PUBLICATIONS

12. MOCHI enables discovery of heterogeneous interactome modules in 3D nucleome. bioRxiv, doi: <https://doi.org/10.1101/542092>. First round revision for Genome Research.
11. Diffdomains: model-based identification of significantly reshaped chromatin domains from Hi-C contact matrices between normal and disease conditions. In Preparation.
10. Exploiting the interplay between chromatin interactome and transcriptional regulatory network. In Preparation.
9. Identifying gene regulatory network rewiring using latent differential graphical models. Nucleic Acids Research.
8. Retinal vein occlusion in a multi-ethnic asian population: the singapore epidemiology of eye disease study. Ophthalmic Epidemiology.
7. Plasma metabonomic profiling of diabetic retinopathy. Diabetes.
6. Ex vivo propagation of human corneal stromal “activated keratocytes” for tissue engineering. Cell Transplantation.
5. Global metabonomic and proteomic analysis of human conjunctival epithelial cells (IOBA-NHC) in response to hyperosmotic stress. Journal of Proteome Research.
4. Quantitation of 47 human tear proteins using high resolution multiple reaction monitoring (HR-MRM) based-mass spectrometry. Journal of Proteomics.
3. Profiling human cell-type specific transcription factor regulatory networks. Nucleic Acids Research.
2. Involvement of GABA transporters in atropine-treated myopic retina as revealed by iTRAQ quantitative proteomics. Journal of Proteome Research.
1. Sharp bounds and normalization of wiener-type indices. PLOS ONE.