

**BIOGRAPHICAL SKETCH**

Provide the following information for the Senior/key personnel and other significant contributors.  
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Zhiyu Zhao, Ph.D.

eRA COMMONS USER NAME (credential, e.g., agency login): zhiyuzhao

POSITION TITLE: Assistant Professor, Research

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

| INSTITUTION AND LOCATION                                | DEGREE<br>(if<br>applicable) | Completion<br>Date<br>MM/YYYY | FIELD OF STUDY                    |
|---|------------------------------|-------------------------------|-----------------------------------|
| Huazhong University of Science and Technology,<br>China | B.E.                         | 06/1997                       | Computer Engineering              |
| Huazhong University of Science and Technology,<br>China | M.E.                         | 06/2000                       | Computer Engineering              |
| University of New Orleans, USA                          | M.S.                         | 12/2006                       | Computer Science                  |
| University of New Orleans, USA                          | Ph.D.                        | 08/2008                       | Engineering & Applied<br>Sciences |

**A. Personal Statement**

I am a bioinformaticist and biostatistician with broad knowledge and experience in computational algorithms design, software development, workflow development of bioinformatics and biostatistical methods, and data analysis. I have been supporting the bioinformatic and biostatistical needs of my institution for over five years. I have extensive experience in processing and analyzing data from next-generation sequencing data, including RNA-seq, ChIP-seq, whole-genome sequencing, whole-exome sequencing, mitochondrial genome sequencing, and targeted DNA sequencing. Additionally I have experience in the analysis of microarray data, proteomics data, and biomedical imaging data. I frequently work with datasets that require various types of statistical analyses including parametric and non-parametric tests, linear/non-linear regression models and/or machine-learning approaches. Many of the experiments and datasets include complex setups and variables. I am familiar with the processing of big data using high-performance computing resources and parallel storage systems in the cloud/cluster environment. I am also an experienced software architect in the design and development of automated bioinformatic/biostatistical workflows, pipelines, and scientific computation programs in such environments. I believe my knowledge and skills are necessary and sufficient for supporting the proposed research project.

**B. Positions and Honors****Positions and Employment**

|                |  |
|----------------|--|
| 1997 – 2004    | Lecturer/Instructor, Department of Computer Engineering, Huazhong University of Science and Technology, China                                  |
| 1997 – 2004    | Software Engineer/Project Manager, Wuhan Wearnes Technology Co. Ltd., China  |
| 2004 – 2005    | Visiting Scholar, Politecnico di Milano University, Italy  |
| 2005 – 2008    | Research Assistant / Teaching Assistant, University of New Orleans, LA   |
| 2008 – 2012    | Computational Scientist, LONI (Louisiana Optical Network Initiative) Institute & Department of Computer Science, University of New Orleans, LA |
| 2012 – present | Assistant Professor, Research, Children's Research Institute, University of Texas Southwestern Medical Center, TX                              |

**Other Experience and Professional Memberships**

|      |   |
|------|---|
| 2000 | Solutions Expert of Planning, Implementing and Supporting the IBM Net. Commerce Version 3 Product |
|------|---|

|             |  |
|-------------|--|
| 2001 – 2002 | Vice Chairwoman, Central China Microsoft Technology Club (CCMTC) |
| 2003        | Member, System Group of MPEG-China                               |
| 2009 – 2012 | Member, IEEE & IEEE Women in Engineering (WIE)                   |

## Honors

|             |   |
|-------------|---|
| 1997        | Recommended to the Graduate Study Program at Huazhong University of Science and Technology with an exemption of the Graduate Entrance Examinations of China |
| 2003        | Excellent Graduate Research Paper Award, Graduate Study Program at Huazhong University of Science and Technology, China                                     |
| 2004 – 2005 | Governmental Scholarship, Visiting Scholar Exchange Program, China & Italy  |
| 2008        | Received compliment letter from University of New Orleans for maintaining a GPA of 4.0 by the time of PhD graduation  |
| 2011        | Granted permanent residence in USA under the Outstanding Professors and Researchers category of first preference EB-1                                       |

## **C. Contribution to Science**

1. Publications about bioinformatic algorithms in protein 3-D structure alignment and structural similarity search: My contribution in these publications involved computational algorithms design and software development.
  - a. Zhao Z., B. Fu, F.J. Alanis, and C.M. Summa. 2008. Feedback Algorithm and Web-Server for Protein Structure Alignment. **Journal of Computational Biology** 15:505 – 524. PMID 18549304.
  - b. Zaixin L., Z. Zhao, S. Garcia, K. Krishnaswamy, and B. Fu. 2009. Search Similar Protein Structures with Classification, Sequence and 3-D Alignments. **Journal of Bioinformatics and Computational Biology** 7:755 – 771. PMID: 19785044.
  - c. Zaixin L., Z. Zhao and B. Fu. 2010. Efficient Protein Alignment Algorithm for Protein Search. **BMC Bioinformatics** 2010 11:S34. PMC3009506.
2. Selected publications about other bioinformatic algorithms and software tools: My contribution was computational algorithms design and software development.
  - a. Diego L., S. Bittanti, S. Garatti, Z. Zhao and M. Pappalettera. 2005. Classification of Leukemia Patients via Micro-array Data Analysis. **Proceedings of the National Conference on Biomedical Engineering Systems** (BIOSYS 2005, June 2005, Italy).
  - b. Deng N., A. Puetter, K. Zhang, K. Johnson, Z. Zhao, C. Taylor, E. Flemington and D. Zhu. 2011. Isoform-level microRNA-155 Target Prediction using RNA-seq. **Nuc. Acid Res.** 39:e61. PMC3089486.
  - c. Zhao Z., T.C. Nguyen, N. Deng, K.M. Johnson, Z. Dongxiao. 2011. SPATA: A seeding and patching algorithm for de novo transcriptome assembly. **Bioinformatics and Biomedicine Workshops**. IEEE International Conference pp. 26-33.
  - d. Zhao Z., D. Worthylake, L. LeCour Jr, G.A. Maresh, and S.H. Pincus. 2012. Crystal Structure and Computational Modeling of the Fab Fragment from a Protective Anti-Ricin Monoclonal Antibody. **PLoS ONE** 7:e52613. PMC3526572.
3. Publications in melanoma and leukemia studies: My contribution was computational algorithms design and software development, bioinformatic/biostatistical methods, workflows development, and data analysis.
  - a. Piskounova E., M. Agathocleous, M.M. Murphy, Z. Hu, S.E. Huddlestun, Z. Zhao, A.M. Leitch, T.M. Johnson, R.J. DeBerardinis, and S.J. Morrison. 2015. Oxidative stress inhibits distant metastasis by human melanoma cells. **Nature** 527:186-91. PMC4644103
  - b. Eskiocak U., V. Ramesh, Z. Zhao, S. Yuan, J. Gill, M. Wang, T. Vandergriff, M. Shackleton, E. Quintana, T. Johnson, R. DeBerardinis and S.J. Morrison. 2016. Synergistic effects of ion transporter and MAP kinase pathway inhibitors in melanoma. **Nature Communications** 7:13080. PMID27681157
  - c. Agathocleous M., C.E. Meacham, R.J. Burgess, E. Piskounova, Z. Zhao, G.M. Crane, B.L. Cowin, E. Bruner, M.M. Murphy, W. Chen, G.J. Spangrude, Z. Hu, R.J. DeBerardinis, S.J. Morrison. 2017. Ascorbate regulates haematopoietic stem cell function and suppresses leukaemogenesis. **Nature** In Press. PMID 28825709
4. Selected publications in stem cell studies: My contribution was computational algorithms design and software development, bioinformatic / biostatistical methods, workflows development, and data analysis.

- a. Acar M., K.S. Kocherlakota, M.M. Murphy, J.G. Peyer, H. Oguro, C.N. Inra, C.J. Jaiyeola, Z. Zhao, K. Luby-Phelps and S.J. Morrison. 2015. Deep imaging of bone marrow shows non-dividing stem cells are mainly perisinusoidal. **Nature** 526:126-130. PMID26416744
- b. Yue R., B.O. Zhou, I.S. Shimada, Z. Zhao and S.J. Morrison. 2016. Leptin receptor promotes adipogenesis and reduces osteogenesis by regulating mesenchymal stromal cells in adult bone marrow. **Cell Stem Cell** 18:782-796. PMC4127103
- c. Zhou B.O., H. Yu, R. Yue, Z. Zhao, J. Rios, O. Naveiras, and S.J. Morrison. 2017. Bone marrow adipocytes promote the regeneration of stem cells and hematopoiesis by secreting SCF. **Nature Cell Biology** 19: 891-903. PMID: 28714970
- d. Shimada I.S., M. Acar, R.J. Burgess, Z. Zhao, S.J. Morrison. 2017. Prdm16 is required for the maintenance of neural stem cells in the postnatal forebrain and their differentiation into ependymal cells. **Genes & Development** 31: 1134-1146. PMID 28698301

All of our papers can be found at the following URL:  
<https://www.ncbi.nlm.nih.gov/pubmed/?term=zhao+z>

#### D. Additional Information: Research Support and/or Scholastic Performance

##### Ongoing Research Support

2 R37 AG024945 (PI, Sean Morrison) 8/1/14 – 7/31/19  
 NIH/NIA (MERIT Award)  
 “The Regulation of Stem Cell Aging”

To test whether the Bmi-1 polycomb protein is required to maintain adult neural stem cells and neurogenesis by opposing the age-related increase in p16<sup>Ink4a</sup>/p19<sup>Arf</sup> expression such that Bmi-1 deficiency leads to stem cell depletion and behavioral deficits that worsen with age.

Role: Faculty

Responsibilities: computational algorithms design and software development, bioinformatic / biostatistical methods / workflows development and data analysis.

RP170114 (PI, Sean Morrison) 12/1/16 - 11/30/19  
 Cancer Prevention and Research Institute of Texas  
 “Mechanisms of melanoma metastasis”

To test whether metastasizing melanoma cells exhibit increased dependence on pentose phosphate and malic enzyme pathways relative to primary cutaneous melanoma cells and whether RUNX3 promotes melanoma metastasis by transcriptionally regulating metabolic changes required for oxidative stress resistance.

Role: Faculty

Responsibilities: computational algorithms design and software development, bioinformatic / biostatistical methods / workflows development and data analysis.

##### Completed Research Support

RP1109 (PI, Sean Morrison) 9/1/11-8/31/16  
 Cancer Prevention and Research Institute of Texas  
 “Stem Cells and Cancer”

The goal of this project is to study the extent to which the mechanisms used by normal stem cells to self-renew and migrate are hijacked by cancer cells to undergo neoplastic proliferation and metastasis.

Role: Faculty

Responsibilities: computational algorithms design and software development, bioinformatic / biostatistical methods / workflows development and data analysis