Nan Xiao

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Education

2015 -	Ph.D. student (Human Genetics), University of Chicago.	Chicago, IL, U.S.
2012 - 2015	Master student (Statistics), Central South University.	Changsha, China
2008 - 2012	Bachelor of Science (Statistics), Central South University.	Changsha, China

Publications

Journal articles

- Nan Xiao and Q.-S. Xu (2015). "Multi-step adaptive elastic-net: reducing false positives in high-dimensional variable selection". *Journal of Statistical Computation and Simulation*. doi: 10.1080/00949655.2015.1016944.
- Nan Xiao, D.-S. Cao, M.-F. Zhu, and Q.-S. Xu (2015). "protr/ProtrWeb: R package and web server for generating various numerical representation schemes of protein sequence". *Bioinformatics*. doi: 10.1093/bioinformatics/btv042.
- D.-S. Cao*, <u>Nan Xiao*</u>, Q.-S. Xu and A. F. Chen (2014). "Rcpi: R/Bioconductor package to generate various descriptors of proteins, compounds, and their interactions", *Bioinformatics*. *Joint first authors. doi: 10.1093/bioinformatics/btu624.
- D.-S. Cao, <u>Nan Xiao</u>, Y.-J. Li, W.-B. Zeng, Y.-Z. Liang, A.-P. Lu, Q.-S. Xu, A. F. Chen (2015). "Integrating multiple evidence sources to predict adverse drug reactions based on systems pharmacology model". *CPT: Pharmacometrics & Systems Pharmacology*. doi: 10.1002/psp4.12002.
- J.-B. Wang, D.-S. Cao, M.-F. Zhu, Y.-H. Yun, Nan Xiao, Y.-Z. Liang (2015). "In silico evaluation of $\log D_{7.4}$ and comparison with other prediction methods". Journal of Chemometrics. doi: 10.1002/cem.2718.
- L. Shen, D.-S. Cao, Q.-S. Xu, X. Huang, Nan Xiao, Y.-Z. Liang (2015). "A novel local manifold-ranking based k-NN for modeling the regression between bioactivity and molecular descriptors". Chemometrics and Intelligent Laboratory Systems. doi: 10.1016/j.chemolab.2015.12.005.

Book translations

Max Kuhn and Kjell Johnson (2015). *Applied Predictive Modeling*. (Hui Lin, Yi-Xuan Qiu, En-Chi Ma, <u>Nan Xiao</u>, & Vivian Zhang, Trans.). China Machine Press (Original work published in 2013). ISBN: 978-7-1115-3342-9.

- Winston Chang (2014). *R Graphics Cookbook*. (Nan Xiao, Yi-Shuo Deng, Tai-Yun Wei, & Yi-Xuan Qiu, Trans.). Posts and Telecom Press (Original work published in 2013). ISBN: 978-7-115-34227-0.
- Hadley Wickham (2013). *ggplot2: Elegant Graphics for Data Analysis*. (Tai-Yun Wei, Yi-Xuan Qiu, <u>Nan Xiao</u>, Tao Gao, & Wei-Cheng Zhu, Trans.). Xi'an Jiaotong University Press (Original work published in 2010). ISBN: 978-7-5605-4969-9.
- Robert Kabacoff (2013). *R in Action: Data Analysis and Graphics with R*. (Tao Gao, Nan Xiao, & Gang Chen, Trans.). Posts and Telecom Press (Original work published in 2011). ISBN: 978-7-115-29990-1. [Sold **27,500** copies by December 2014.]

Conference presentations & posters

- hdnom.io: High-Dimensional Survival Modeling with Shiny.

 Lightning talk. Shiny Developer Conference, Stanford University. January 30, 2016.
- Introduction to Reproducible Research in Bioinformatics.
 Invited talk. 2015 Bioinformatics Workshop, Center for Research Informatics, University of Chicago. December 3, 2015.
- liftr & sbgr kickstart (Workshop with Dan Tenenbaum and Tengfei Yin). BioC 2015, Fred Hutchinson Cancer Research Center, Seattle, WA. July 2015.
- Integrated Pipeline for Systems Pharmacology in R/Bioconductor
 The 7th China R Conference, Renmin University of China, Beijing, China. May 2014.
- Web Scraping with R
 The 6th China R Conference, Renmin University of China, Beijing, China. May 2013.
- Security Issues and Vulnerabilities of the R Environment
 The 2nd China R Conference, Renmin University of China, Beijing & East China Normal University, Shanghai. December 2009.

Software and web applications

R/Bioconductor packages

grex

R package for mapping Ensembl gene IDs in Genotype-Tissue Expression (GTEx) data to Entrez IDs, HGNC symbols, and UniProt IDs. Project website: http://nanx.me/grex/. Available from CRAN: https://cran.r-project.org/package=grex.

ggsci

R package offering a collection of ggplot2 color palettes inspired by scientific journals and science fiction TV shows. Project website: http://ggsci.net.

Available from CRAN: https://cran.r-project.org/package=ggsci.

hdnom

R package building nomograms for high-dimensional survival data, with support for model validation, calibration, and comparison. Project website: http://hdnom.org.

Available from CRAN: https://cran.r-project.org/package=hdnom.

liftr

R package for dockerizing R Markdown documents with support for Rabix in reproducible research. Project website: http://liftr.me.

Available from CRAN: https://cran.r-project.org/package=liftr.

sbgr

R Client for Seven Bridges Genomics API.

Available from Bioconductor: https://bioconductor.org/packages/sbgr and
GitHub: https://github.com/road2stat/sbgr.

Rcpi

2013 - 2014 R/Bioconductor package as a comprehensive molecular informatics platform for systems pharmacology and drug discovery. [Downloaded **over 10,000 times** by December 2015.] Available from Bioconductor: https://bioconductor.org/packages/Rcpi.

protr

R package generating various numerical representation schemes of protein sequence for bioinformatics and proteochemometrics research.

Available from CRAN: https://cran.r-project.org/package=protr.

enpls

R package for ensemble partial least squares regression, a unified framework for feature selection, outlier detection, and ensemble learning. Project website: http://enpls.org.

Available from CRAN: https://cran.r-project.org/package=enpls.

RECA

R package for relevant component analysis (RCA) in supervised distance metric learning and supervised dimensionality reduction.

Available from CRAN: https://cran.r-project.org/package=RECA.

Web applications

hdnom.io

Web application for building penalized Cox models for high-dimensional data with survival outcomes. The web app streamlined the process of nomogram building, model validation, calibration, comparison, and reproducible report generation.

Available at: http://hdnom.io. Included by RStudio Shiny User Showcase:

https://www.rstudio.com/products/shiny/shiny-user-showcase/

Signify

Web application for making your (>0.05) *p*-values sound significant. Available at https://nanx.shinyapps.io/signify.

ProtrWeb

Web application for computing 20 types of protein sequence-derived structural and physic-ochemical features in bioinformatics. [Over 2,000 users from 40 countries.]

Available at http://protr.org.

ImgSVD

Web application for image compression via singular value decomposition. Collaborated with *Yihui Xie* (RStudio Inc.), *Yixuan Qiu* (Purdue University), and *Tong He* (Simon Fraser University). Available at https://yihui.shinyapps.io/imgsvd.

Honors and awards

- National scholarship for graduate students (5%).
 - Highest award the government established for graduate students in China.
- Outstanding graduate student award (5%). Central South University, Changsha, China.
- ²⁰¹¹ 1st Prize (top 5%) in Hunan Contest District in China Undergraduate Mathematical Contest in Modeling (CUMCM). With *Guan-Chun Liu* and *Tian-Yu Zhao*.
- Meritorious award (2nd in 1,000+) of Central China Undergraduate Mathematical Contest in Modeling (CCUMCM). With *Tao Gao* and *Chen-Xi Guo*.

Professional services

- 2015 Reviewer. *Journal of Statistical Computation and Simulation*
- 2014 Contributing Editor. ICSA (International Chinese Statistical Association) Bulletin
- Organizing Committee Member. The 7th China R Conference (Beijing). http://china-r.org
- 2013 **Co-Organizer.** *The* 6th *China R Conference (Beijing)*
- 2010 Editor. Capital of Statistics, http://cos.name. Largest online community on statistics in China.
- Volunteer. The 2nd China R Conference (Beijing, Shanghai)

Membership

- 2016 American Statistical Association (ASA)
- 2015 International Chinese Statistical Association (ICSA)
- 2015 American Society of Clinical Oncology (ASCO)

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