

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

Work experience

2015	Intern. Seven Bridges Genomics, Inc. Advisor: Dr. Tengfei Yin. <i>Cambridge, MA, U.S.</i> <ul style="list-style-type: none">• Developed R/Bioconductor package <i>sbgr</i>: R client for SBG Platform / NCI Cancer Genomics Cloud Platform API; the first shipped official language binding for SBG API.• Developed R package <i>liftr</i>: dockerizing R Markdown documents with support for Rabix. First enabled OS-level reproducibility for bioinformatics & statistical data analysis.• Presented the packages at the BioC 2015 conference (workshop session and poster session), Fred Hutchinson Cancer Research Center, Seattle, WA.
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Publications

Journal articles

2015	Nan Xiao and Q.-S. Xu (2015). “Multi-step adaptive elastic-net: reducing false positives in high-dimensional variable selection”. <i>Journal of Statistical Computation and Simulation</i> . doi: 10.1080/00949655.2015.1016944 .
2015	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”. <i>Bioinformatics</i> . doi: 10.1093/bioinformatics/btv042 .
2014	D.-S. Cao*, Nan Xiao *, Q.-S. Xu and A. F. Chen (2014). “Rcpi: R/Bioconductor package to generate various descriptors of proteins, compounds, and their interactions”, <i>Bioinformatics</i> . * Joint first authors . doi: 10.1093/bioinformatics/btu624 .
2015	D.-S. Cao, Nan Xiao , 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”. <i>CPT: Pharmacometrics & Systems Pharmacology</i> . doi: 10.1002/psp4.12002 .
2015	J.-B. Wang, D.-S. Cao, M.-F. Zhu, Y.-H. Yun, Nan Xiao , Y.-Z. Liang (2015). “In silico evaluation of logD _{7.4} and comparison with other prediction methods”. <i>Journal of Chemometrics</i> . doi: 10.1002/cem.2718 .

- 2015 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](https://doi.org/10.1016/j.chemolab.2015.12.005).

Book translations

- 2016 Max Kuhn and Kjell Johnson (2015). *Applied Predictive Modeling*. (Hui Lin, Yi-Xuan Qiu, En-Chi Ma, Nan Xiao, & Vivian Zhang, Trans.). China Machine Press (Original work published in 2013). ISBN: [978-7-1115-3342-9](https://www.isbn-international.org/product/978-7-1115-3342-9).
- 2014 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](https://www.isbn-international.org/product/978-7-115-34227-0).
- 2013 Hadley Wickham (2013). *ggplot2: Elegant Graphics for Data Analysis*. (Tai-Yun Wei, Yi-Xuan Qiu, Nan Xiao, Tao Gao, & Wei-Cheng Zhu, Trans.). Xi'an Jiaotong University Press (Original work published in 2010). ISBN: [978-7-5605-4969-9](https://www.isbn-international.org/product/978-7-5605-4969-9).
- 2013 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](https://www.isbn-international.org/product/978-7-115-29990-1). [Sold 27,500 copies by December 2014.]

Conference presentations & posters

- 2016 **hdnom.io: High-Dimensional Survival Modeling with Shiny**.
Lightning talk. Shiny Developer Conference, Stanford University. January 30, 2016.
- 2015 **Introduction to Reproducible Research in Bioinformatics**.
Invited talk. 2015 Bioinformatics Workshop, Center for Research Informatics, University of Chicago. December 3, 2015.
- 2015 Nan Xiao and Tengfei Yin. **liftr: Reproducible Bioinformatics and Statistical Data Analysis with Docker, Rabix, and knitr** (Poster).
BioC 2015, Fred Hutchinson Cancer Research Center, Seattle, WA. July 2015.
- 2015 **liftr & sbgr kickstart** (Workshop with Dan Tenenbaum and Tengfei Yin).
BioC 2015, Fred Hutchinson Cancer Research Center, Seattle, WA. July 2015.
- 2014 **Integrated Pipeline for Systems Pharmacology in R/Bioconductor**
The 7th China R Conference, Renmin University of China, Beijing, China. May 2014.
- 2013 **Web Scraping with R**
The 6th China R Conference, Renmin University of China, Beijing, China. May 2013.
- 2009 **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

2016 – 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

2016 – 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

2015 – 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

2015 – 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

2015 – 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

2012 – 2014 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

2014 – 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

2012 – 2014 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

- 2015 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

- 2015 Web application for making your (>0.05) p -values sound significant. Available at <https://nanx.shinyapps.io/signify>.

ProtrWeb

- 2013 – 2014 Web application for computing 20 types of protein sequence-derived structural and physicochemical features in bioinformatics. [Over 2,000 users from 40 countries.] Available at <http://protr.org>.

ImgSVD

- 2014 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>.

TargetNet

- 2014 Web application for predicting the binding of 623 drug targets for given molecules. Driven by large-scale machine learning modeling of chemogenomics data. Available at: <http://targetnet.scbdd.com>.

Honors and awards

- 2014 Best poster award. *Genes and associated environmental factors affecting skin aging in different ethnic groups*. CAS-MPG Partner Institute for Computational Biology Scientific Exchange Meeting, Shanghai. With *Miaozhu Li*.
- 2013 National scholarship for graduate students (5%). Highest award the government established for graduate students in China.
- 2013 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*.
- 2010 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*

2014 – **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.
2009 – **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)

Programming skills

- R/Bioconductor package development (6 years)
- Complex web application development with R/Shiny (4 years)
- Biological data visualization with lattice, ggplot2, Circos, and D3.js (4 years)
- Good knowledge of Docker, PostgreSQL, Git, T_EX and shell programming (4 years)
- Experience of Linux server setup, management and application deployment (4 years)

Research interests

My research interests are in the area of statistical machine learning, primarily method development for real-world predictive modeling tasks:

- High-dimensional linear models and feature selection
- High-dimensional data fusion and network inference
- Deep learning and population-scale genomics

Last revision: April, 2016