

Nan Xiao

Genomic Data Scientist
Seven Bridges Genomics

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Work Experience

- 2016 – Now Genomic Data Scientist. Seven Bridges Genomics, Inc. Cambridge, MA
- Program Analyst Team Lead. Seven Bridges R API client package author and maintainer.
 - Deep collaboration with Program, Product, Project, Strategy, BD, and Marketing team.
 - Delivered Shiny apps for analyzing platform usage data to drive business decisions.

R Packages

- sevenbridges-r**
- 2016 – - Seven Bridges API client, CWL schema, metadata schema, and SDK helper in R.
- <https://bioconductor.org/packages/sevenbridges/>
- msaenet**
- 2016 – - Multi-step adaptive elastic-net algorithm for high-dimensional feature selection.
- <https://msaenet.com> | <https://cran.r-project.org/package=msaenet>
- Integrated by the *caret* package for streamlined machine learning modeling.
- ggsci**
- 2016 – - Scientific journal and sci-fi themed color palettes for ggplot2.
- <https://ggsci.net> | <https://cran.r-project.org/package=ggsci>
- Downloaded 12k/month. Top 2% of 11,000+ R packages on CRAN.
- liftr**
- 2015 – - Containerize R Markdown documents with Docker.
- <https://liftr.me> | <https://cran.r-project.org/package=liftr>
- OHPL**
- 2017 – - Ordered homogeneity pursuit lasso algorithm for group feature selection.
- <https://OHPL.io> | <https://cran.r-project.org/package=OHPL>
- enpls**
- 2014 – - Ensemble partial least squares algorithm for feature screening and outlier detection.
- <https://enpls.org> | <https://cran.r-project.org/package=enpls>
- hdnom**
- 2015 – - Benchmarking and visualization toolkit for high-dimensional survival modeling.
- <https://hdnom.org> | <https://cran.r-project.org/package=hdnom>
- protr**
- 2012 – - Efficient protein sequence feature extraction for machine learning modeling.
- <https://nanx.me/protr/> | <https://cran.r-project.org/package=protr>

Rcpi

- 2013 - Integrative molecular feature extraction for computational drug discovery.
- <https://nanx.me/Rcpi/> | <https://bioconductor.org/packages/Rcpi/>

RECA

- 2012 - Relevant component analysis algorithm for supervised distance metric learning.
- <https://nanx.me/RECA/> | <https://cran.r-project.org/package=RECA>

grex

- 2016 - Gene ID mapping for Genotype-Tissue Expression (GTEx) data.
- <https://nanx.me/grex/> | <https://cran.r-project.org/package=grex>

mxnet-r

- 2015 - Contributor of the R binding for the deep learning framework MXNet.

Web Applications

dockflow.org

- 2017 - Bioconductor workflow containerization and orchestration using Docker and liftr.
- <https://dockflow.org>

hdnom.io

- 2015 - Shiny application for benchmarking and visualizing high-dimensional survival models.
- <http://hdnom.io>

targetnet.org

- 2014 - Shiny application for drug target identification with large-scale binding affinities data.
- <http://targetnet.org>

protr.org

- 2013 - Shiny application for protein sequence feature extraction.
- <http://protr.org>

ImgSVD

- 2014 - Shiny application for image compression via singular value decomposition.
- Joint work with Yihui Xie, Yixuan Qiu, and Tong He.
- <https://nanx.shinyapps.io/imgsvd/>

Signify

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

Publications

Preprints

- 2016 **Nan Xiao**, Q.-S. Xu, and M.-Z. Li (2016). hdnom: Building nomograms for penalized Cox models with high-dimensional survival data. *bioRxiv*. doi: [10.1101/065524](https://doi.org/10.1101/065524).

Journal articles

- 2015 **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](https://doi.org/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. *Bioinformatics*. doi: [10.1093/bioinformatics/btv042](https://doi.org/10.1093/bioinformatics/btv042).
- 2015 D.-S. Cao*, **Nan Xiao***, Q.-S. Xu and A. F. Chen (2015). Rcpir: R/Bioconductor package to generate various descriptors of proteins, compounds, and their interactions, *Bioinformatics*. *Joint first authors. doi: [10.1093/bioinformatics/btu624](https://doi.org/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. *CPT: Pharmacometrics & Systems Pharmacology*. doi: [10.1002/psp4.12002](https://doi.org/10.1002/psp4.12002).
- 2017 Y.-W. Lin, **Nan Xiao**, L.-L. Wang, C.-Q. Li, Q.-S. Xu (2017). Ordered homogeneity pursuit lasso for group variable selection with applications to spectroscopic data. *Chemometrics and Intelligent Laboratory Systems*. doi: [10.1016/j.chemolab.2017.07.004](https://doi.org/10.1016/j.chemolab.2017.07.004).
- 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. *Journal of Chemometrics*. doi: [10.1002/cem.2718](https://doi.org/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 (2016). *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://doi.org/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://doi.org/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://doi.org/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://doi.org/978-7-115-29990-1).

Conference Presentations

- 2017 *DockFlow: Bioconductor Workflow Containerization and Orchestration with liftr*
Poster. **Nan Xiao**, Tengfei Yin, and Miao Zhu Li.
BioC 2017, Dana-Farber Cancer Institute, Boston, MA. July 2017.
- 2017 *The Deep Connection between Drugs and Side Effects*
Poster. **Nan Xiao**.
ISCB Art in Science Competition. ISMB/ECCB 2017, Prague, Czech Republic. July 2017.
- 2017 *Persistent Reproducible Reporting with Docker and R*
Invited talk. The 10th China R Conference, Tsinghua University, China. May 2017.
- 2017 *Reproducible Dynamic Report Generation with Docker and R*
Invited talk. DockerCon 2017, Austin, TX. April 2017.
- 2016 *hdnom.io: High-Dimensional Survival Modeling with Shiny*
Invited lightning talk. Shiny Developer Conference, Stanford University. January 2016.
- 2015 *Introduction to Reproducible Research in Bioinformatics*
Invited talk. CRI Bioinformatics Workshop, Center for Research Informatics,
The University of Chicago. December 2015.
- 2015 *liftr: Reproducible Bioinformatics and Statistical Data Analysis with Docker, Rabix, and knitr*.
Poster. **Nan Xiao**, Tengfei Yin, and Miao Zhu Li.
BioC 2015, Fred Hutchinson Cancer Research Center, Seattle, WA. July 2015.

Academic Degrees

- 2008 – 2012 Bachelor of Science (Statistics). Central South University. Changsha, China

Studies

- 2015 – 2016 Ph.D. Student (Human Genetics). The University of Chicago. Chicago, IL
2012 – Now Ph.D. Student (Statistics). Central South University. Changsha, China

Services

- 2017 – Reviewer. *Chemometrics and Intelligent Laboratory Systems*
2017 – Reviewer. *Genetic Epidemiology*
2016 – Reviewer. *The R Journal*
2015 – Reviewer. *Journal of Statistical Computation and Simulation*

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