Nan Xiao

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Work experience

2016 - Now Genomic Data Scientist. Seven Bridges Genomics, Inc.

Cambridge, MA, U.S.

- Seven Bridges R API client package author & maintainer.
- Analyst team lead. Analyze usage metric data to support product & business decisions.

Software and web applications

R/Bioconductor packages

liftr

- Containerize R Markdown documents with Docker.
 - https://liftr.me
 - https://cran.r-project.org/package=liftr

sevenbridges-r

- Seven Bridges API client, CWL schema, meta schema, and SDK helper in R.
 - https://sbg.github.io/sevenbridges-r/
 - https://bioconductor.org/packages/sevenbridges/

msaenet

- 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.

enpls

- 2014 Ensemble partial least squares regression for feature selection and outlier detection.
 - https://enpls.org
 - https://cran.r-project.org/package=enpls
 - Integrated by the caret package.

OHPL

- 2017 Ordered homogeneity pursuit lasso algorithm for group variable selection.
 - https://OHPL.io
 - https://cran.r-project.org/package=OHPL

hdnom

- 2015 Benchmarking and visualization toolkit for high-dimensional survival modeling.
 - https://hdnom.org
 - https://cran.r-project.org/package=hdnom

protr

- Protein sequence feature extraction for machine learning research.
 - 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/

ggsci

- Scientific journal and sci-fi themed color palettes for ggplot2.
 - https://ggsci.net
 - https://cran.r-project.org/package=ggsci

RECA

- Relevant component analysis (RCA) for supervised distance metric learning.
 - https://nanx.me/RECA/
 - https://cran.r-project.org/package=RECA

grex

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

sbgr

- Seven Bridges Genomics API (v1) client in R.
 - https://nanx.me/sbgr/
 - https://github.com/road2stat/sbgr/

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

- 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 web 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

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.

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 (2015). "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.
- Y.-W. Lin, <u>Nan Xiao</u>, 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.
- J.-B. Wang, D.-S. Cao, M.-F. Zhu, Y.-H. Yun, <u>Nan Xiao</u>, 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, <u>Nan Xiao</u>, 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 (2016). *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, Nan Xiao, 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.

Conference presentations & posters

- DockFlow: Bioconductor Workflow Containerization and Orchestration with liftr Poster. Nan Xiao, Tengfei Yin, and Miaozhu Li.
 BioC 2017, Dana-Farber Cancer Institute, Boston, MA. July 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.
- hdnom.io: High-Dimensional Survival Modeling with Shiny
 Invited lightning talk. Shiny Developer Conference, Stanford University. January 2016.
- Introduction to Reproducible Research in Bioinformatics
 Invited talk. CRI Bioinformatics Workshop, Center for Research Informatics,
 The University of Chicago. December 3, 2015.
- liftr: Reproducible Bioinformatics and Statistical Data Analysis with Docker, Rabix, and knitr. Poster. Nan Xiao, Tengfei Yin, and Miaozhu Li.
 BioC 2015, Fred Hutchinson Cancer Research Center, Seattle, WA. July 2015.
- liftr & sbgr kickstart
 Workshop. Joint with Dan Tenenbaum and Tengfei Yin.
 BioC 2015, Fred Hutchinson Cancer Research Center, Seattle, WA. July 2015.
- Web Scraping with R
 Invited talk. The 6th China R Conference, Renmin University of China. May 2013.

Academic degrees

2013

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, U.S. Ph.D. Student (Statistics). Central South University. Changsha, China 2012 - Now **Academic services** 2017 -Reviewer. Chemometrics and Intelligent Laboratory Systems **Reviewer.** *Genetic Epidemiology* 2017 -**Reviewer.** The R Journal 2016 -Reviewer. Journal of Statistical Computation and Simulation 2015 -**Session Chair on Software Tools.** *The* 10th *China R Conference (Beijing)* 2017 **Organizing Committee Member.** *The* 7^{th} *China R Conference (Beijing)* 2014

Co-Organizer. The 6th China R Conference (Beijing)

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