

# Nan Xiao

---

Genomic Data Scientist  
Seven Bridges Genomics  
Cambridge, Massachusetts

[me@nanx.me](mailto:me@nanx.me)  
<https://nanx.me>  
[GitHub](#) | [LinkedIn](#)

## Qualifications

- Machine learning researcher with 5 years' experience and published learning methods for high-dimensional data analysis, data fusion, and translational bioinformatics.
- R developer with 8 years' of R engineering experience. Author and contributor of 20+ open source R packages and Shiny applications. Journal referee for *The R Journal*.
- Data science practitioner with experience building and leading data science teams; managing and guiding complex data analysis projects; coordinating data sharing and collaborations across engineering and product teams to serve the executive team.

## Work Experience

- 2016 – Now    Genomic Data Scientist. [Seven Bridges Genomics, Inc.](#)    Cambridge, MA  
Program Analyst Team Lead. Led a data science team to:
- Apply intensive quantitative and analytical skills to internal/external data to design a new pricing model that can reduce customers' AWS instance costs significantly.
  - Provide direct decision support to the Chief Strategy Officer, Business Development, Product, and Marketing teams to help shape optimized data-driven company strategy.
  - Deliver Shiny web applications for internal data visualization, reporting, and consulting.
  - Develop the R API client package and related software for accessing, analyzing, and democratizing petabyte-scale genomic data on cloud-based Seven Bridges Platform.

## R Packages Authored

My R packages for machine learning, data visualization, and dynamic reporting.

- [sevenbridges-r](#)  
2016 – Seven Bridges API client, CWL schema, metadata schema, and SDK helper in R.
- [msaenet](#)  
2016 – Multi-step adaptive elastic-net algorithm for high-dimensional feature selection. Integrated by Max Kuhn's *caret* package for streamlined machine learning modeling.
- [ggsci](#)  
2016 – Scientific journal and sci-fi themed color palettes for ggplot2. Downloaded 12k/month. Top 2% of 11,000+ R packages on CRAN.
- [liftr](#)  
2015 – Containerize R Markdown documents with Docker. DockerCon 2017 [talk invited](#) by Docker, Inc.
- [enpls](#)  
2014 – Ensemble partial least squares algorithm for feature screening and outlier detection. Integrated by Max Kuhn's *caret* package for streamlined machine learning modeling.

## **OHPL**

2017 – Ordered homogeneity pursuit lasso algorithm for group feature selection.

## **hdnom**

2015 – Benchmarking and visualization toolkit for high-dimensional survival modeling.

## **protr**

2012 – Efficient protein sequence feature extraction for machine learning modeling.

## **Rcpi**

2013 – Integrative molecular feature extraction for computational drug discovery.

## **RECA**

2012 – Relevant component analysis algorithm for supervised distance metric learning.

## **grex**

2016 – Gene ID mapping for Genotype-Tissue Expression (GTEx) data.

## **R Packages Contributed**

### **mxnet-r**

2015 – [Contributor](#) of the R binding for Amazon-backed deep learning framework [MXNet](#).

## **Web Applications Authored**

2013 – 6 Shiny web applications for biological, pharmaceutical, and image data analysis.

- [hdnom.io](#) (selected as [Shiny User Showcase](#) by RStudio, Inc.)
- [dockflow.org](#) | [imgsvd.com](#) | [targetnet.org](#) | [protr.org](#) | [p-values.org](#)

## **Publications**

- 2013 –
- 8 journal papers on statistical machine learning methodology, high-dimensional sparse regression, feature selection, and recommender systems. [[Google Scholar](#)]
  - 4 translated books on predictive modeling, data visualization, and R programming.

## **Education**

2015 – 2016	Ph.D. Student (Human Genetics). The University of Chicago.	Chicago, IL
2012 – 2018	Ph.D. Candidate (Statistics). Central South University.	Changsha, China
2008 – 2012	Bachelor of Science (Statistics). Central South University.	Changsha, China

## **Skills**

Substantial research and engineering expertise in: R, Shiny, Docker, Redis, AWS, Google Cloud Platform, statistical machine learning, deep learning, predictive modeling, large-scale linear models, recommender system, data fusion, data visualization, cancer genomics, computational systems pharmacology.

Last revision: October 2017.