

# Yunlong Jiao

Chinese nationality, born 1989  
Tel: +44 (0)1865 281243 (office)  
E-mail: [yunlong.jiao@stats.ox.ac.uk](mailto:yunlong.jiao@stats.ox.ac.uk)  
Homepage: <https://YunlongJiao.github.io/>

Address:  
Department of Statistics  
24-29 St Giles'  
Oxford OX1 3LB, United Kingdom

## Education

PhD in Bioinformatics, [Center for Computational Biology](#), [MINES ParisTech](#), [PSL Research University](#), Paris, France, supervised by Prof. [Jean-Philippe Vert](#), obtained September 2017  
**Thesis title:** "Rank-based Molecular Prognosis and Network-guided Biomarker Discovery for Breast Cancer"

MSc with highest mention in Mathematics for Life Sciences, [Department of Mathematics](#), [Université Paris-Sud \(Paris XI\)](#), Orsay, France, supervised by Prof. [Christophe Giraud](#), obtained July 2013

BSc with Honors in Mathematics and Applied Mathematics, [Department of Special Class for the Gifted Young](#), [University of Science and Technology of China \(USTC\)](#), Hefei, China, obtained July 2012

## Professional Experience

Nov 2017 – Present	Postdoctoral research scientist at <a href="#">Wellcome Centre for Human Genetics</a> and <a href="#">Department of Statistics</a> , <a href="#">University of Oxford</a> , Oxford, UK, working with Prof. <a href="#">Mark McCarthy</a> and Prof. <a href="#">Chris Holmes</a>
Mar 2016 – Jun 2016	Research intern at <a href="#">Department of Computational Genomics</a> , <a href="#">Centro de investigación Príncipe Felipe (CIPF)</a> , Valencia, Spain, advised by Prof. <a href="#">Joaquín Dopazo</a> <b>Title:</b> "Signaling Pathway Activities Improve Prognosis for Breast Cancer"
Apr 2015 – Jun 2015	Data analyst intern at Department of System Integration and Product Care, <a href="#">Roche Diagnostics GmbH</a> , Penzberg, Germany, working with Dr. <a href="#">Stefan Kobel</a> <b>Title:</b> "Failure State Prediction for Automated Analyzers for Analyzing a Biological Sample"
Apr 2013 – Jul 2013	Research intern at <a href="#">Center for Computational Biology</a> , <a href="#">MINES ParisTech</a> / <a href="#">Institut Curie</a> / <a href="#">INSERM, U900</a> , Paris, France, advised by Prof. <a href="#">Jean-Philippe Vert</a> <b>Title:</b> "Post-hoc Analysis on Competition-based Breast Cancer Prognosis Modeling"
Dec 2011 – Jun 2012	Undergraduate Scientific Research Practice intern at <a href="#">Academy of Mathematics and Systems Science (AMSS)</a> , <a href="#">Chinese Academy of Sciences</a> , Beijing, China, supervised by Prof. <a href="#">Min Chen</a> <b>Title:</b> "Credit Rating Migration: Models and Analysis"

## Awards & Distinctions

Sep 2013 – Sep 2016	Early Stage Researcher Fellowship in <a href="#">Machine Learning for Personalized Medicine</a> , a Marie Curie Initial Training Network, funded by the European Union within the 7th Framework Programme
Nov 2013	2nd place in <a href="#">DREAM 8 NIEHS-NCATS-UNC Toxicogenetics Challenge</a> , an international bioinformatics competition, with E. Bernard, E. Scornet, V. Stoven, T. Walter and J.-P. Vert
Sep 2012 – Aug 2013	Master scholarship from <a href="#">Fondation Mathématique Jacques Hadamard (FMJH)</a> , Orsay, France
Dec 2011 – May 2012	Undergraduate Scientific Research Practice Funding from <a href="#">Chinese Academy of Sciences</a> , Beijing, China (total of 1000 winners nationwide)
Aug 2011	Honorable Mention of 2nd <a href="#">S.-T. YAU College Student Mathematics Contest</a> in Probability and Statistics (top 15 nationwide)
Dec 2010 – Jul 2012	Selected into "Hua Loo-Keng" Elite Program in Mathematics, a <a href="#">USTC-AMSS</a> joint training program

## Skills

Programming: skilled with R, C/C++, Bash, adequate with Python, MATLAB

Language: Chinese (native), English (fully proficient with IELTS/CEFR level C2), French (conversational), Spanish (learning)

## Research

### Working Papers and Preprints

**Jiao, Y.** and Vert, J.-P. (2017). Network-based wavelet smoothing for analysis of genomic data.

**Jiao, Y.**, Hidalgo, M. R., Çubuk, C., Amadoz, A., Carbonell-Caballero, J., Vert, J.-P., and Dopazo, J. (2017). Signaling pathway activities improve prognosis for breast cancer. *bioRxiv preprint bioRxiv-132357*.

### Published Papers

**Jiao, Y.** and Vert, J.-P. (2018b). The weighted Kendall and high-order kernels for permutations. In *Proc. Int. Conf. Mach. Learn. (ICML)*, volume 80 of *Proc. Mach. Learn. Res. (PMLR)*, pages 2319–2327.

**Jiao, Y.** and Vert, J.-P. (2018a). The Kendall and Mallows kernels for permutations. *IEEE Trans. Pattern Anal. Mach. Intell. (TPAMI)*, 40(7):1755–1769.

Bernard, E., **Jiao, Y.**, Scornet, E., Stoven, V., Walter, T., and Vert, J.-P. (2017). Kernel multitask regression for toxicogenetics. *Mol. Inform.*, 36(10):1700053.

**Jiao, Y.**, Korba, A., and Sibony, E. (2016a). Controlling the distance to a Kemeny consensus without computing it. In *Proc. Int. Conf. Mach. Learn. (ICML)*, volume 48 of *Proc. Mach. Learn. Res. (PMLR)*, pages 2971–2980.

Eduati, F., Mangravite, L. M., Wang, T., Tang, H., Bare, J. C., Huang, R., Norman, T., Kellen, M., Menden, M. P., Yang, J., Zhan, X., Zhong, R., Xiao, G., Xia, M., Abdo, N., Kosyk, O., **The NIEHS-NCATS-UNC DREAM Toxicogenetics Collaboration**, Friend, S., Dearry, A., Simeonov, A., Tice, R. R., Rusyn, I., Wright, F. A., Stolovitzky, G., Xie, Y., and Saez-Rodriguez, J. (2015). Prediction of human population responses to toxic compounds by a collaborative competition. *Nat. Biotechnol.*, 33(9):933–940.

**Jiao, Y.** and Vert, J.-P. (2015). The Kendall and Mallows kernels for permutations. In *Proc. Int. Conf. Mach. Learn. (ICML)*, volume 37 of *Proc. Mach. Learn. Res. (PMLR)*, pages 1935–1944.

### Patents and Patent Applications

**Jiao, Y.**, Vert, J.-P., Heinemann, F., Dahlmanns, S., and Kobel, S. (2016b). Failure state prediction for automated analyzers for analyzing a biological sample. Pending European patent filed by Roche Diagnostics GmbH, F. Hoffmann–La Roche AG, December 2016.

### Software

**kernrank** — R package implementing kernel functions and kernel methods for analyzing rank data, publicly available on GitHub, **author and maintainer**.

**kmr** — R implementation of a kernel multitask regression algorithm to solve simultaneously several regression problems, publicly available on GitHub, **co-author** with J.-P. Vert.