



Bohdan Bohdanovich Khomtchouk

Postdoctoral Research Fellow, Biology

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BIO

Bohdan Khomtchouk, Ph.D. is a data science postdoctoral fellow working in the field of computational epigenetics in the Gozani Lab at Stanford University in Stanford, CA USA. Bohdan's research involves understanding the data science behind aging-related diseases as well as creating artificial intelligence and machine learning software to organize the world's biological information at a massive scale -- working at the interdisciplinary interface of big data, integrative bioinformatics, multi-omics, natural language processing, and statistical learning. Bohdan serves as the chief bioinformatician and computational biologist for the Gozani Lab, working across a broad array of next-generation sequencing data, including RNA-seq, small RNA-seq, methyl-seq, ATAC-seq, mass spectrometry, and ChIP-seq. Bohdan is also the founder and organizer of the open-source Biolisp organization, Stanford Biolisp Meetup, pyStanford (Stanford Python Meetup), and StanfordR (Stanford R Meetup).

HONORS AND AWARDS

- NIH/NIA Stanford Training Program in Aging Research (T32 AG0047126), National Institute on Aging of the National Institutes of Health (2017-2018)
- National Defense Science & Engineering (NDSEG) Graduate Fellowship (32 CFR 168a), Department of Defense, Army Research Office (Biosciences Division) (2014-2017)
- UM Graduate Fellowship, University of Miami (2013-2014)

PROFESSIONAL EDUCATION

- Doctor of Philosophy, University of Miami Miller School of Medicine , Computational Human Genetics & Genomics (2017)
- Bachelor of Science, Benedictine University , Molecular Biology & Biochemistry (summa cum laude) (2013)
- Bachelor of Science, Benedictine University , Physics (summa cum laude) (2013)
- Bachelor of Science, Benedictine University , Mathematics (summa cum laude) (2013)

LINKS

- Personal Homepage: <https://about.me/bohdankhomtchouk>

Publications

PUBLICATIONS

- **shinyheatmap: Ultra fast low memory heatmap web interface for big data genomics.** *PloS one*
Khomtchouk, B. B., Hennessy, J. R., Wahlestedt, C.
2017; 12 (5)
- **How the strengths of Lisp-family languages facilitate building complex and flexible bioinformatics applications.** *Briefings in bioinformatics*
Khomtchouk, B. B., Weitz, E., Karp, P. D., Wahlestedt, C.

2016

- **Ischemic Preconditioning Confers Epigenetic Repression of Mtor and Induction of Autophagy Through G9a-Dependent H3K9 Dimethylation** *JOURNAL OF THE AMERICAN HEART ASSOCIATION*
Gidlof, O., Johnstone, A. L., Bader, K., Khomtchouk, B. B., O'Reilly, J. J., Celik, S., Van Booven, D. J., Wahlestedt, C., Metzler, B., Erlinge, D.
2016; 5 (12)
- **MicroScope: ChIP-seq and RNA-seq software analysis suite for gene expression heatmaps** *BMC BIOINFORMATICS*
Khomtchouk, B. B., Hennessy, J. R., Wahlestedt, C.
2016; 17
- **Dependence-induced increase of alcohol self-administration and compulsive drinking mediated by the histone methyltransferase PRDM2.** *Molecular psychiatry*
Barbier, E., Johnstone, A. L., Khomtchouk, B. B., Tapocik, J. D., Pitcairn, C., Rehman, F., AUGIER, E., Borich, A., Schank, J. R., Rienas, C. A., van Booven, D. J., Sun, H., Nätt, et al
2016
- **Survival Guide to Organic Chemistry: Bridging the Gap from General Chemistry**
McMahon, P. E., Khomtchouk, B. B., Wahlestedt, C.
CRC Press (Taylor & Francis).2016
- **HeatmapGenerator: high performance RNAseq and microarray visualization software suite to examine differential gene expression levels using an R and C++ hybrid computational pipeline.** *Source code for biology and medicine*
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2014; 9 (1): 30-?