Curriculum Vitae
Paul Sheridan

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Date of Birth: 1979 (Halifax, Canada)
Date of CV: November 2018

Education/Employment

2018 –		Chief Science Officer, Tupac Bio, Inc. (CEO: Eli T. Lyons)
2016 – 2018		Assistant Professor, Hirosaki University, Social Medicine (lab head: Shigeyuki Nakaji)
2011 – 2016		Systems Cancer Postdoc, The University of Tokyo, Cancer Bioinformatics and Topics in Complex Networks (lab head: Satoru Miyano)
2011	Ph.D.	Tokyo Institute of Technology, Data Science (advisor: Hidetoshi Shimodaira)
2006 – 2007		MEXT Scholar, Tokyo Institute of Technology
2006	M.Sc.	Dalhousie University, Probability and Statistics (advisor: Edward Susko)
2003	B.Sc.	Dalhousie University, Mathematics with Honours (advisor: Keith Johnson)
2002 – 2002		NSERC Scholar, Dalhousie University, Elliptic Curves (advisor: Keith Johnson)
2001 – 2001		NSERC Scholar, Dalhousie University, Topics in Cryptography (advisor: Karl Dilcher)
2000 – 2000		NSERC Scholar, Dalhousie University, Bernoulli Numbers (advisor: Karl Dilcher)

Teaching

2015 – 2016	Tutor, KAIS International School
2009 – 2014	ESL Teacher, Marshall English School
2007 – 2011	Global COE Scholar (Teaching Assistant), Tokyo Institute of Technology
2004 – 2006	Teaching Assistant, Dalhousie University
2002 – 2003	Teaching Assistant, Dalhousie University

Research interests

I'm presently working as CSO at the biotech startup Tupac Bio, of which I am a co-founder. My research interests range from topics in bioinformatics, complex networks, and even the digital humanities.

References

Upon request.

Publications

Peer-reviewed articles

2018 17. (with M. Onsjö, S. Jimenez, G. Dueñas) *A Knowledge-based Filtering Story Recommender System for Theme Lovers with an Application to the Star Trek Television Franchise*, Under review. https://arxiv.org/abs/1808.00103

16. (with M. Onsjö) *Theme Enrichment Analysis: A Statistical Test for Identifying Significantly Enriched Themes in a List of Stories with an Application to the Star Trek Television Franchise*, Under review. https://arxiv.org/abs/1707.06227

15. (with Pham Thong, and Hidetoshi Shimodaira) *PAFit: An R Package for Modeling and Estimating Preferential Attachment and Node Fitness in Temporal Complex Networks*, Conditionally accepted to Journal of Statistical Software. https://arxiv.org/abs/1704.06017

14. (with D. Inoue, T. Fujino, Paul Sheridan, Y. Zhang, R. Nagase, S. Horikawa, Z. Li, H. Matsui, A. Kanai, M. Saika, R. Yamaguchi, H. Kozuka-Hata, K. Kawabata, A. Yokoyama, S. Goyama, T. Inaba, S. Imoto, S. Miyano, M. Xu, F. Yang, M. Oyama, T. Kitamura) *A Novel ASXL1-OGT Axis Plays Roles in H3K4 Methylation and Tumor Suppression in Myeloid Malignancies*, Leukemia. doi:10.1038/s41375-018-0083-3

13. (with Taku Onodera) *A Preferential Attachment Paradox: How Preferential Attachment Combines with Growth to Produce Networks with Log-normal In-degree Distributions*, Scientific Reports. doi:10.1038/s41598-018-21133-2

2017 12. (with Eli Lyons, Georg Tremmel, Satoru Miyano, and Sumio Sugano) *Large-scale DNA Barcode Library Generation for Biomolecule Identification in High-throughput Screens*, Scientific Reports. doi:10.1038/s41598-017-12825-2

2016 11. (with Pham Thong, and Hidetoshi Shimodaira) *Joint Estimation of Preferential Attachment and Node Fitness in Growing Complex Networks*, Scientific Reports. doi:10.1038/srep32558

10. (with Hideto Koso, Hungtsung Yi, Satoru Miyano, Yasushi Ino, Tomoki Todo, and Sumiko Watanabe) *Identification of RNA-Binding Protein LARP4B as a Tumor Suppressor in Glioma*, Cancer Research. doi: 10.1158/0008-5472.CAN-15-2308

2015 9. (with Pham Thong, and Hidetoshi Shimodaira) *PAFit: A Statistical Method for Measuring Preferential Attachment in Temporal Complex Networks*, PLoS ONE. doi.org/10.1371/journal.pone.0137796

8. (with Pham Thong, and Hidetoshi Shimodaira) *Nonparametric estimation of the preferential attachment function in complex networks: evidence of deviations from log linearity*, Proceedings of ECCS'14: European Conference on Complex Systems.

7. (with Y. Takahashi, A. Niida, G. Sawada, R. Uchi, H. Mizuno, J. Kurashige, K. Sugimachi, S. Sasaki, Y. Shimada, K. Hase, M. Kusunoki, S. Kudo, M. Watanabe, K. Yamada, K. Sugihara, H. Yamamoto, A. Suzuki, Y. Doki, S. Miyano, M. Mori, and K. Mimori) *The AURKA/TPX2 axis drives colon tumorigenesis cooperatively with MYC*, Annals of Oncology. doi:10.1093/annonc/mdv034

2014 6. (with Taku Onodera) *Maximum likelihood estimation of preferential attachment in growing networks*, Topologica.

5. (with E.O. Balogun, J.B. Balogun, S. Yusuf, H.M. Inuwa, I.S. Ndams, Paul Sheridan, D.K. Inaoka, T. Shiba, S. Harada, K. Kita, K.A.N. Esievo, and A.J. Nok) *Anemia Amelioration by Lactose Infusion During Trypanosomosis Could be Associated with Erythrocytes Membrane De-galactosylation*, Veterinary Parasitology. doi:10.1016/j.vetpar.2013.10.013

2012 4. (with Yuichi Yagahara, and Hidetoshi Shimodaira) *Measuring preferential attachment in growing networks with missing-timeline using Markov chain Monte Carlo*, Physica A. doi:10.1016/j.physa.2012.05.041

2010 3. (with Takeshi Kamimura, and Hidetoshi Shimodaira) *A scale-free structure prior for graphical models with applications in functional genomics*, PLoS ONE. doi:10.1371/journal.pone.0013580

2009 2. (with Takeshi Kamimura, and Hidetoshi Shimodaira) *On scale-free priors and their applicability in large-scale network inference with graphical models*, Complex Sciences: Lecture Notes of the Institute of Computer Sciences, Social Informatics and Telecommunications Engineering Volume 4. doi:10.1007/978-3-642-02466-5-9

2008 1. (with Yuichi Yagahara, and Hidetoshi Shimodaira) *A preferential attachment model with Poisson growth for scale-free networks*, Annals of the Institute of Statistical Mathematics. doi:10.1007/s10463-008-0181-5

Posters

2015 4. (with Georg Tremmel, Atsushi Niida, Rui Yamaguchi, Seiya Imoto, and Satoru Miyano) *Headache-free geneset analysis for the working molecular biologist*, 42nd IMSUT Founding Commemorative Symposium.
http://paulsheridan.net/files/IMSUT_symposium_2015_poster.pdf

2013 3. (with Y. Takahashi, A. Niida, G. Sawada, R. Uchi, H. Mizuno, J. Kurashige, K. Sugimachi, S. Sasaki, Y. Shimada, K. Hase, M. Kusunoki, S. Kudo, M. Watanabe, K. Yamada, K. Sugihara, H. Yamamoto, A. Suzuki, Y. Doki, S. Miyano, M. Mori, and K. Mimori) *Genomic co-amplification of TPX2 and AURKA with MYC cooperatively promote MYC-driven carcinogenesis*, Systems Cancer Project Workshop.
http://paulsheridan.net/files/Systems_Cancer_2013_poster.pdf

2. (with Taku Onodera) *The Resolution of a Minor Preferential Attachment Paradox Makes Major Confusions Plain*, International Workshop on Phase Transition, Critical Phenomena and Related Topics in Complex Networks.
http://paulsheridan.net/files/Hokudai2013_poster.pdf

2007 1. (with Takeshi Kamimura, and Hidetoshi Shimodaira) *Comparing Scale-free Priors over Graph Structures for Bayesian Inference of Gene Networks*, Pacific Symposium on Biocomputing (PSB) 2007.
http://paulsheridan.net/files/PSB2007_poster.pdf

Software

2017 3. (with Mikael Onsjö) *stoRy R package*,
https://cran.r-project.org/web/packages/stoRy/index.html.

2014 2. (with Pham Thong, and Hidetoshi Shimodaira) *PAFit R package*,
https://cran.r-project.org/web/packages/PAFit/index.html.

2010 1. (with Takeshi Kamimura, and Hidetoshi Shimodaira) *Gene network estimation with scale-free structure prior software.*
http://paulsheridan.net/files/MH-sampler_code.zip

Referee and review activities

Journals refereed

International Journal of Molecular Sciences
Journal of Bioinformatics and Computational Biology
IEEE Transactions on Computational Biology and Bioinformatics
Microarrays
PLoS Computational Biology

Conferences refereed

24rd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2016)
20th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2016)
The Fourteenth Asia Pacific Bioinformatics Conference (APBC 2016)
The 2015 IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2015)
23rd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2015)
19th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2015)
The Thirteenth Asia Pacific Bioinformatics Conference (APBC 2015)
1st International Conference on Algorithms for Computational Biology (AlCoB 2014)
18th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2014)
The Twelfth Asia Pacific Bioinformatics Conference (APBC 2014)
The 2013 IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2013)
Sixth Annual RECOMB/ISCB conference on Regulatory and Systems Genomics,
with DREAM Challenges (RECOMB DREAM 2013)
17th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2012)
1st International Conference on the Theory and Practice of Natural Computing (TPNC 2012)

Workshops refereed

15th Workshop on Algorithms in Bioinformatics (WABI 2015)
14th Workshop on Algorithms in Bioinformatics (WABI 2014)
13th Workshop on Algorithms in Bioinformatics (WABI 2013)

Computing

Familiarity with Unix
Fluent in the statistical programming language R
Programming languages: Python, R, C, HTML, Java, Unix shell scripting
Human Genome Center (HGC) supercomputer certification license
Computer algebra systems: Mathematica, Matlab, Maple

Languages

English
French
Conversational Japanese