

SON PHAM

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PARTICULARS

CURRENT POSITION

Research associate in Professor Fred Gage's lab, at Salk Institute For Biological Studies, San Diego, California.

EDUCATION

University of California, San Diego
Ph.D in Computer Science

San Diego, CA
December 2013

University of California, San Diego
M. S. in Computer Science

San Diego, CA
June 2010

Saint Petersburg State University
B. Tech. in Computer Science and Engineering

Saint Petersburg, Russia
July 2007

RESEARCH INTERESTS

I have a special interest in bioinformatics, where solutions of computational problems often contribute to new biological discoveries. My current research topics include the molecular mechanisms of neurological diseases and algorithms for genome assembly, genome comparison, graph theory.

DISSERTATION

Title: "De Bruijn Graphs in Genome Assembly and Genome Comparison"
Advisor: Prof. Pavel Pevzner

PUBLICATIONS

Journal Papers

1. Jerome Mertens, Qiu-Wen Wang, Yongsung Kim, Diana X. Yu, **Son Pham**, Bo Yang, Yi Zheng, Kenneth E Diffenderfer, Jian Zhang, Sheila Soltani, Tameji Eames, Simon T Schafer, Leah Boyer, Maria C Marchetto, John I Nurnberger, Joseph R Calabrese, Ketil J degaard, Michael J McCarthy, Peter P Zandi, Martin Alba, Caroline M Nievergelt, Shuangli Mi, Kristen J Brennan, John R Kelsoe, Fred H Gage and Jun Yao. "Differential responses to lithium in hyperexcitable neurons from patients with bipolar disorder". *Nature* 2015, pp. 95-102.
2. Suguna Rani Krishnaswami, Rashel V. Grindberg, Mark Novotny, Pratap Venepally, Benjamin Lacar, Kunal Bhutani, Sara B. Linker, **Son Pham**, Jennifer A. Erwin, Jeremy A. Miller, Rebecca Hodge, James K. McCarthy, Martijn Kelder, Jamison McCarrison, Jun Lee, Ed S. Lein, Nicholas Schork, Michael J. McConnell, Fred H. Gage, Roger S. Lasken. "RNA-Seq from single nuclei: capturing the transcriptome of postmortem neurons". Accepted to *Nature Protocols* 2015.
3. Mikhail Kolmogorov, Brian Raney, Benedict Paten, and **Son Pham**. "Ragout a reference-assisted assembly tool for bacterial genomes". *Bioinformatics* 2014 pp. 302-309 (Corresponding author).
4. Ilya Minkin, Hoa Pham, Ekaterina Starostina, Nikolay Vyahhi, **Son Pham**: "C-Sibelia: an easy-to-use and highly accurate tool for bacterial genome comparison". F1000 research (Corresponding author).
5. **Son Pham***, Dmitry Antipov*, Alexander Sirotkin, Glenn Tesler, Pavel Pevzner, and Max Alekseyev, "Pathset Graphs: A Novel Approach for Comprehensive Utilization of Mate-Pairs in Genome Assembly". *Journal of Computational Biology* 2012, pp. 359-371. (Co-first author).

6. Anton Bankevich, Sergey Nurk, Dmitry Antipov, Alexey Gurevich, Mikhail Dvorkin, Alexander Kulikov, Valery Lesin, Sergey Nikolenko, **Son Pham**, Andrey Prjibelski, Alexey Pyshkin, Alexander Sirotkin, Nikolay Vyahhi, Glenn Tesler, Max Alekseyev, and Pavel Pevzner, “SPAdes: a New Genome Assembly Algorithm and its Applications to Single-Cell Sequencing”. *Journal of Computational Biology*, 2012, pp. 455-477.
7. Paul Medvedev*, **Son Pham***, Mark Chaisson, Glenn Tesler and Pavel Pevzner, “Paired de Bruijn graphs: a novel approach for incorporating mate pair information into genome assemblers”. *Journal of Computational Biology* 2011, pp. 1625-1634. (Co-first author).
8. **Son Pham** and Pavel Pevzner, DRIMM-Synteny, “Decomposing Genomes into Evolutionary Conserved Segments”. *Bioinformatics* 2010, pp. 2509-2516 (Corresponding author).
9. Konstantin Avrachenkov, Nelly Litvak, **Son Pham**, “A Singular Perturbation Approach for Choosing the PageRank Damping Factor”. *Internet Mathematics* 2009, pp. 47-69.
10. Konstantin Avrachenkov, Danil Nemirovsky, **Son Pham**, Roberto Cascella, Roberto Battiti, Mauro Brunato, “Eigenvector based reputation measures”. *Paradigms for Biologically-Inspired Autonomic Networks and Services* 2008, pp. 260-278.

Conference Papers

11. Mikhail Kolmogorov, Brian Raney, Benedict Paten, and **Son Pham**. “Ragout a reference-assisted assembly tool for bacterial genomes”. ISMB2014 (Accepted from the first round review, with acceptance rate 13%, corresponding author).
12. Andrey Prjibelski, Irina Vasilinets, Anton Bankevich, Alexey Gurevich, Tatiana Krivosheeva, Sergey Nurk, **Son Pham** et al, “ExpPander: a universal repeat resolver for DNA fragment assembly”. ISMB2014 (Best Student Paper Award).
13. Ilya Minkin, Anand Patel, Mikhail Kolmogorov, Nikolay Vyahhi, and **Son Pham**, “Sibelia: A scalable and comprehensive synteny block generation tool for closely related microbial genomes”. WABI 2013. (Corresponding author).
14. Viraj Deshpande, Eric Fung, **Son Pham** and Vineet Bafna, “Cerulean: A hybrid assembly using high throughput short and long reads”. WABI 2013.
15. Nikolay Vyahhi, Alex Pyshkin, **Son Pham** and Pavel Pevzner, “From de Bruijn Graphs to Rectangle Graphs for Genome Assembly”. WABI 2012 (Corresponding author).
16. **Son Pham** and Paul Medvedev, “Mate-pair Consistency and Generating Problems”. RECOMB-AB 2012.
17. **Son Pham***, Dmitry Antipov*, Alexander Sirotkin, Glenn Tesler, Pavel Pevzner, and Max Alekseyev, “Pathset Graphs: A Novel Approach for Comprehensive Utilization of Mate-Pairs in Genome Assembly”. RECOMB 2012 (Acceptance rate 17%, co-first author).
18. Paul Medvedev*, **Son Pham***, Mark Chaisson, Glenn Tesler and Pavel Pevzner, “Paired de Bruijn graphs: a novel approach for incorporating mate pair information into genome assemblers”. RECOMB 2011 (Acceptance rate 17%, co-first author).
19. Konstantin Avrachenkov, Vladimir Dobrynin, Danil Nemirovsky, **Son Pham** and Elena Smirnova, “PageRank Based Clustering of Hypertext Document Collections”. *Proceedings of ACM SIGIR* 2008, pp. 873-874.
20. Konstantin Avrachenkov, Nelly Litvak, and **Son Pham**, “Distribution of PageRank Mass Among Principle Components of the Web”. *Proceedings of the 5th Workshop on Algorithms and Models for the Web-Graph*, WAW2007, pp. 16-28.
21. Konstantin Avrachenkov, Danil Nemirovsky and **Son Pham**, “A survey on distributed approaches to graph based reputation measures”. *Proceedings of International Workshop on Tools for Solving Structured Markov Chains: SMCTools* 2007, p. 82.
22. Vladimir Dobrynin, **Son Pham**, David Patterson, Niall Rooney, Mykola Galushka, “SOPHIA in Enterprise Track”. *The Fifteenth Text REtrieval Conference Proceedings* 2006 (TREC2006).

Papers Under Review

23. Ilya Minkin, **Son Pham**, Paul Medvedev, “An efficient algorithm to build the compacted de Bruijn graph from many complete genomes”.
24. Ketil J. Oedegaard, Martin Alda, Yokesh Balaraman, Wade H. Berrettini, Abesh Bhattacharjee; Kristen J. Brennan, Katherine E. Burdick, Joseph R. Calabrese, Cynthia V. Calkin, William H. Coryell, David Craig, Anna DeModena, Mark Frye, Fred H. Gage, Julie Garnham, Elliot Gershon, Michael J. McCarthy, Melvin

G. McInnis, Adam X. Meihof, Jerome Mertens, Caroline M Nievergelt, John Nurnberger, **Son Pham**, Tatyana Shekhtman, Paul D. Shilling, Szabolcs Szelinger, Bruce Tarwater, Jun Yao, Peter P. Zandi, John R. Kelsoe. “The Pharmacogenomics of Bipolar Disorder study (PGBD): identification of genes for lithium response in a prospective sample”. (In submission to BMC Psychiatry).

25. Mikhail Kolmogorov, Brian Raney, Duncan Odom, Paul Flicek, David Thybert, Benedict Paten, and **Son Pham***, “Ragout2: a reference-assisted rearrangement-based tool for mammalian genome assembly”, (Corresponding author).

Posters

26. Ilya Minkin, Nikolay Vyahhi and **Son Pham**, “Sibelia: A Synteny Blocks Generation and Genome Comparison Tool”. WABI 2012.
27. Andrey D. Prjibelski, Tatiana Krivosheyeva, Anton Bankevich, Sergey Nurk, **Son Pham** and Pavel A. Pevzner, “Path-Extend: A New Approach for Repeat Resolution in Genome Assembly”. WABI 2012.

TALKS

CONFERENCE TALKS

1. “Paired de Bruijn Graphs in Genome Assembly”, *Genome 10K Meeting 2011, Santa Cruz*.
2. “Paired de Bruijn graphs: a novel approach for incorporating mate pair information into genome assemblers”, *Acceptance rate 17%, RECOMB 2011, Vancouver*.
3. “Pathset graphs: a novel approach for comprehensive utilization of paired reads in genome assembly”, *Acceptance rate 17%, RECOMB 2012, Barcelona*.
4. “Mate-pair consistency and Generating Problems”, *RECOMB-AB 2012: Open Problems in Algorithmic Biology, Saint Petersburg*.

SOFTWARE DEVELOPED

1. Ragout/Ragout2 for reference assisted assembly for both mammalian and bacterial genomes: <https://github.com/fenderglas>
2. Sibelia (Synteny Blocks Exploration Tool): github.com/bioinf/Sibelia
3. Sibelia’s webservice: etool.me/software/sibelia
4. INIGO: Retrotransposon Insertion Identification.
5. C-Sibelia’s webservice: etool.me/software/csibelia
6. DRIMM-Synteny: bix.ucsd.edu/projects/drimm/
7. Rectangles graphs: <http://bioinf.spbau.ru/rectangles>
8. SPAdes: <http://bioinf.spbau.ru/spades>
9. Bioturing (A cloud platform for RNA-seq analysis using natural language): bioturing.com

TEACHING EXPERIENCE

- **Coursera: Bioinformatics Algorithms** Joint lecture with Pavel Pevzner and Phillip Compeau in Bioinformatics Algorithms on Coursera, 2013, with 40000 students registered.
- **Teaching Assistant.** CSE/BIMM/BENG 181: Molecular Sequence Analysis (Undergraduate Course).
- **Teaching Assistant.** CSE/BIMM/BENG 282: Introduction to Bioinformatics Algorithms (Graduate Course).

Students Supervised

- Ilya Minkin: MS from Academic University, Saint Petersburg, Russia. Currently Ph.D student at PennState University, USA.
- Mikhail Kolmogorov: MS from Academic University, Saint Petersburg, Russia. Currently Ph.D student at UCSD, USA.

SERVICE

- Reviewer (Journals) - *Bioinformatics*, *BMC Bioinformatics*, *Nucleic Acids Research*, *Frontiers in Bioinformatics and Computational Biology*, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, *sub-reviewer for Nature*, *Nature Communication*, *Cell*.
- Reviewer (Conferences) - *RECOMB 2012*, *2013*, *RECOMB'seq-2013*, *ISMB 2015*.
- Organizing Committee Member: RECOMB Satellite Conference on Bioinformatics Education (RECOMB-BE 2009), Mar. 2009.
- Organizing Committee Chair: RECOMB Satellite Conference on Bioinformatics Education (RECOMB-BE 2009), Mar. 2010.
- Chair and co-organizer for Genomic Medicine 2015: <http://genomicmedicine2015.hcmiu.edu.vn/>.

LANGUAGES

Proficient in English, Russian and Vietnamese.

REFERENCES

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