

Aleksander Jankowski

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Education

University of Warsaw, Faculty of Mathematics, Informatics and Mechanics

Ph.D. in computer science

May 2015

Thesis: *Modeling transcription factor complex binding to eukaryotic genomes*

Supervisors: Jerzy Tiurnyn (University of Warsaw) and Shyam Prabhakar (Genome Institute of Singapore)

Ph.D. studies in computer science

Oct 2009 – Sep 2014

University of Warsaw, Faculty of Mathematics, Informatics and Mechanics

Master's degree in mathematics, summa cum laude

Sep 2009

Thesis: *Predicting nucleosome binding sites in yeast genome*

Supervisor: Jerzy Tiurnyn (University of Warsaw)

M.Sc. studies in mathematics

Oct 2007 – Sep 2009

University of Warsaw, Faculty of Mathematics, Informatics and Mechanics

Bachelor's degree in computer science

Sep 2008

Bachelor's degree in mathematics

Sep 2007

Double Degree Program in Computer Science and Mathematics

Oct 2004 – Sep 2007

Employment

University of Warsaw, Faculty of Mathematics, Informatics and Mechanics

Assistant professor

Mar 2020 – present

- Developing new algorithms to interpret three-dimensional organization of the genome, as measured by Hi-C and Capture-C experiments.
- Integrating multiple types of single-cell genomics data, in particular single cell RNA-seq, ATAC-seq and Hi-C data.

European Molecular Biology Laboratory, Heidelberg, Germany

Postdoctoral fellow, Eileen Furlong's group

Oct 2014 – Sep 2019

- Studying the role and mechanisms underlying enhancer-promoter interactions in *Drosophila melanogaster* by analyzing chromosome conformation data from Hi-C and Capture-C experiments.
- Developing a computational pipeline for allele-, time- and tissue-specific Hi-C and Capture-C data.
- Designing the targeted regions for Capture-C experiments.
- Integrating chromatin conformation capture data with other functional genomics datasets.

University of Warsaw, Faculty of Mathematics, Informatics and Mechanics and Genome Institute of Singapore, Computational and Systems Biology

Ph.D. student, Jerzy Tiurnyn's group and Shyam Prabhakar's group

Sep 2009 – Oct 2014

Joint Ph.D. student, working for two years with Shyam Prabhakar's group in Singapore, and the remaining time with Jerzy Tiuryn's group in Warsaw.

- Developed an algorithm (TACO) for predicting cell-type-specific transcription factor dimers from genome-wide data, such as DNase-seq or ChIP-seq.
- Analyzed structural properties of transcription factor complexes and their chromatin openness profiles derived from DNase-seq data.
- Developed a computational method (Romulus) for identifying individual transcription factor binding sites from genome information and cell-type-specific experimental data, such as DNase-seq.

University of Warsaw, Interdisciplinary Centre for Mathematical and Computational Modelling

Summer intern, Witold Rudnicki's group

Jul 2008 – Sep 2008

- Work on Boruta, a random-forest-based algorithm for feature selection in information systems.

University of Warsaw, Interdisciplinary Centre for Mathematical and Computational Modelling

Summer intern, Witold Rudnicki's group

Jul 2007 – Sep 2007

- Implementation of Smith-Waterman algorithm for local DNA sequence alignment on Cell Broadband Engine Architecture.
- Developing a proof-of-concept application of NVIDIA graphics cards for hardware acceleration of large database querying. Project commissioned by Prokom Software S.A.

Publications

1. Yad Ghavi-Helm*, Aleksander Jankowski*, Sascha Meiers*, Rebecca R. Viales, Jan O. Korbel, and Eileen E. M. Furlong. Highly rearranged chromosomes reveal uncoupling between genome topology and gene expression. *Nature Genetics*, 51(8):1272–82, August 2019.

* – equal contribution

<https://www.nature.com/articles/s41588-019-0462-3>

2. Xuecong Wang, Yogesh Srivastava, Aleksander Jankowski, Vikas Malik, Yuanjie Wei, Ricardo C. H. del Rosario, Vlad Cojocaru, Shyam Prabhakar, and Ralf Jauch. DNA-mediated dimerization on a compact sequence signature controls enhancer engagement and regulation by FOXA1. *Nucleic Acids Research*, 46(11):5470–5486, June 2018.

<https://academic.oup.com/nar/article/46/11/5470/4970502>

3. Aleksander Jankowski, Jerzy Tiuryn, and Shyam Prabhakar. Romulus: robust multi-state identification of transcription factor binding sites from DNase-seq data. *Bioinformatics*, 32(16):2419–2426, August 2016.

<https://academic.oup.com/bioinformatics/article/32/16/2419/2288439>

4. Aleksander Jankowski, Paulina Obara, Utsav Mathur, and Jerzy Tiuryn. Enhanceosome transcription factors preferentially dimerize with high mobility group proteins. *BMC Systems Biology*, 10(1):14, February 2016.

<https://bmcsystbiol.biomedcentral.com/articles/10.1186/s12918-016-0258-3>

5. Yong-Heng Huang, Aleksander Jankowski, Kathryn S. E. Cheah, Shyam Prabhakar, and Ralf Jauch. SOXE transcription factors form selective dimers on non-compact DNA motifs through multifaceted interactions between dimerization and high-mobility group domains. *Scientific Reports*, 5:10398, May 2015.

<https://www.nature.com/articles/srep10398>

6. Aleksander Jankowski, Shyam Prabhakar, and Jerzy Tiuryn. TACO: a general-purpose tool for predicting cell-type-specific transcription factor dimers. *BMC Genomics*, 15(1):208, March 2014.
<https://bmcgenomics.biomedcentral.com/articles/10.1186/1471-2164-15-208>
7. Aleksander Jankowski, Ewa Szczurek, Ralf Jauch, Jerzy Tiuryn, and Shyam Prabhakar. Comprehensive prediction in 78 human cell lines reveals rigidity and compactness of transcription factor dimers. *Genome Research*, 23(8):1307–1318, August 2013.
<https://genome.cshlp.org/content/23/8/1307.short>
8. Miron B. Kursa, Aleksander Jankowski, and Witold R. Rudnicki. Boruta – A System for Feature Selection. *Fundamenta Informaticae*, 101(4):271–285, 2010.
<https://content.iospress.com/articles/fundamenta-informaticae/fi101-4-02>
9. Witold R. Rudnicki, Aleksander Jankowski, Aleksander Modzelewski, Aleksander Piotrowski, and Adam Zadrozny. The new SIMD Implementation of the Smith-Waterman Algorithm on Cell Microprocessor. *Fundamenta Informaticae*, 96(1-2):181–194, 2009.
<https://content.iospress.com/articles/fundamenta-informaticae/fi96-1-2-10>

Conference presentations

1. Aleksander Jankowski, Ewa Szczurek, Jerzy Tiuryn and Shyam Prabhakar. Comprehensive prediction of cooperative regulatory elements in multiple human cell types. *Symposium of the Polish Bioinformatics Society*, May 26, 2012, Gdańsk, Poland.
2. Aleksander Jankowski, Jerzy Tiuryn and Shyam Prabhakar. Predicting cell type-specific transcription factor cooperative binding. *RECOMB Regulatory Genomics*, October 19, 2011, Barcelona, Spain.
3. Aleksander Jankowski, Jerzy Tiuryn and Shyam Prabhakar. Predicting cell type-specific transcription factor cooperative binding. *Symposium of the Polish Bioinformatics Society*, October 1, 2011, Kraków, Poland.
4. Aleksander Jankowski, Shyam Prabhakar and Jerzy Tiuryn. Predicting nucleosome binding sites in yeast genome. *Symposium of the Polish Bioinformatics Society*, October 3, 2009, Będlewo, Poland.

Research projects

Polish Returns

Polish National Agency for Academic Exchange

Mar 2020 – Feb 2024

Principal Investigator of the project *Algorithms for inferring multi-contact interactions from chromosome conformation capture data* in the program aimed at encouraging the return of Polish scientists from abroad (4 years, 1,672,220 PLN, project number PPN/PPO/2019/1/00042).

Marie Skłodowska-Curie Individual Fellowship

Horizon 2020

Jan 2017 – Dec 2018

Principal Investigator (Marie Skłodowska-Curie Fellow) of the project *4DGenomeReg: Predictive modelling of 3D genome topology during progressive stages of embryonic development* funded by the European Commission (2 years, 171,461 EUR, project number 708111).

Individual pre-doctoral grant (PRELUDIUM)

National Science Centre, Poland

Sep 2012 – Sep 2014

Principal Investigator of the project *Comprehensive prediction of cooperative regulatory elements in eukaryotic genomes* (2 years, 79,100 PLN, project number 2011/03/N/NZ2/03177).

Professional memberships

Polish Bioinformatics Society: Member since 2008

Teaching experience

University of Warsaw, Faculty of Mathematics, Informatics and Mechanics

Over 180 hours of undergraduate and graduate level teaching, including the following courses:

- WWW Applications (laboratory classes, Spring 2009, Spring 2010 and Spring 2012)
- Operating Systems (classroom and laboratory classes, Autumn 2011)
- Introduction to Computational Biology (laboratory classes, Spring 2010).

Certified **Software Carpentry** and **Data Carpentry** instructor. The Carpentries teach introductory coding and data science skills to researchers who have little to no prior computational experience.

Academic service

Reviewer for conferences:

European Conference on Computational Biology (ECCB, 2014 and 2016)

Research in Computational Molecular Biology (RECOMB, 2017)

International Workshop on Algorithms in Bioinformatics (WABI, 2012)

Reviewer for journals:

Bioinformatics (2016, 2017 and 2019)

Briefings in Bioinformatics (2020)

Journal of Open Source Software (2018)

PLOS Computational Biology (2020)

Conference organization:

Member of RECOMB 2015 conference organizing committee (April 12–15, 2015, Warsaw, Poland)

Mentorship

European Molecular Biology Laboratory, Heidelberg

Piotr Śliwa, a B.Sc. student of bioinformatics at the University of Warsaw Jul 2017 – Aug 2018

His work focused on comparisons of TAD structures and significant Hi-C contacts between replicates and timepoints, as well as correlating changes in chromatin structure to changes in gene expression level across embryonic development.

University of Warsaw, Faculty of Mathematics, Informatics and Mechanics

Utsav Mathur, a B.Tech. student of chemical engineering

at the Indian Institute of Technology, Delhi

May–Jul 2014

His project focused on the interferon-beta enhanceosome, an enhancer bound by transcription factor complex of extremely rigid structure. He explored how the fragments of the enhanceosome are re-used in other human and mouse enhancers.

Outreach activities

Gifted high school students (aged 15-19): Short course (3 days, 3 hours each) entitled “Genomika dla informatyków” (“Genomics for computer scientists”, 17-19 Aug 2017). The course was part of the 13. Wakacyjne Warsztaty Wielodyscyplinarne (13th Summer Scientific School).

General audience: Popular science talk “What can we learn about genome organization from fruit flies?” during the European Researchers’ Night taking place in Heidelberg (28 Sep 2018).