

# Aleksander Jankowski

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## Education

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### 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)

### 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)

### University of Warsaw, Faculty of Mathematics, Informatics and Mechanics

*Bachelor's degree in computer science*

Sep 2008

*Bachelor's degree in mathematics*

Sep 2007

## Employment

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### University of Warsaw, Faculty of Mathematics, Informatics and Mechanics

*Assistant Professor*

Mar 2020 – present

- Developing methods to interpret three-dimensional organization of the genome, as measured by Hi-C and Capture-C experiments, considering in particular multi-way and transhomologous contacts.
- Integrating single-cell genomics data (scRNA-seq and scATAC-seq) with chromosome conformation information to infer mechanisms of long-range gene regulation.

### 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 by analyzing chromosome conformation data from haplotype-, time- and tissue-specific Hi-C and 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 Tiurnyn'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.
- Proposed 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

- o 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

- o Implementation of Smith-Waterman algorithm for local DNA sequence alignment on Cell Broadband Engine Architecture.
- o Developing a proof-of-concept application of NVIDIA graphics cards for hardware acceleration of large database querying.

## Publications

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1. Giriram Mohana, Julien Dorier, Xiao Li, H el ena Malek, Marion Leleu, Daniel Rodriguez, Patrycja Rosa, Marion Mougnot, Pascal Cousin, Christian Iseli, Simon Restrepo, Nicolas Guex, Aleksander Jankowski, Michael S. Levine, and Maria Cristina Gambetta. Chromosome-level organization of the regulatory genome in the *Drosophila* nervous system. *Cell*, 186(18):3826–3844.e26, August 2023.  
<https://doi.org/10.1016/j.cell.2023.07.008>
2. Tim Pollex, Adam Rabinowitz, Maria Cristina Gambetta, Raquel Marco-Ferrerres, Rebecca R. Viales, Aleksander Jankowski, Christoph Schaub, Eileen E. M. Furlong. New enhancer-promoter interactions are gained during tissue differentiation and reflect changes in E/P activity. *bioRxiv preprint*.  
<https://doi.org/10.1101/2022.12.07.519443>
3. Jacob W. P. Potuijt, Anna Sowinska-Seidler, Ewelina Bukowska-Olech, Picard Nguyen, Aleksander Jankowski, Frank Magielsen, Karolina Matuszewska, Christianne A. van Nieuwenhoven, Robert-Jan H. Galjaard, Annelies de Klein, and Aleksander Jamsheer. The pZRS non-coding regulatory mutation resulting in triphalangeal thumb–polysyndactyly syndrome changes the pattern of local interactions. *Molecular Genetics and Genomics*, 297(5):1343–1352, July 2022.  
<https://link.springer.com/article/10.1007/s00438-022-01921-2>
4. Yad Ghavi-Helm\*, Aleksander Jankowski\*, Sascha Meiers\*, Rebecca R. Viales, Jan O. Korb el, and Eileen E. M. Furlong. Highly rearranged chromosomes reveal uncoupling between genome topology and gene expression. *Nature Genetics*, 51(8):1272–1282, August 2019.  
\* – equal contribution  
<https://www.nature.com/articles/s41588-019-0462-3>
5. Xuecong Wang, Yogesh Srivastava, Aleksander Jankowski, Vikas Malik, Yuanjie Wei, Ricardo C. H. del Rosario, Vlad Cojocar, 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>
6. 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>
7. 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>

8. 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>
9. 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://bmcbgenomics.biomedcentral.com/articles/10.1186/1471-2164-15-208>
10. 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>
11. 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>
12. 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

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1. Aleksander Jankowski. Variation in gene expression at single-cell level. *Summer School of Single Cell*, September 7, 2022, Pilsen, Czech Republic.
2. 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.
3. Aleksander Jankowski, Jerzy Tiuryn and Shyam Prabhakar. Predicting cell type-specific transcription factor cooperative binding. *RECOMB Regulatory Genomics*, October 19, 2011, Barcelona, Spain.
4. 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.
5. 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

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### SONATA grant

National Science Centre, Poland

Oct 2021 – Sep 2024

Principal Investigator of the project *Integrative analysis of single-cell genomics data* (3 years, 350,140 PLN, project number 2020/39/D/NZ2/03461).

### Polish Returns grant

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

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**Polish Bioinformatics Society:** Member since 2008

## Teaching experience

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Undergraduate and graduate level teaching at the **University of Warsaw, Faculty of Mathematics, Informatics and Mechanics**, including the following courses:

- *WWW Applications*, laboratory classes, Spring 2009, 2010 and 2012
- *Operating Systems*, classroom and laboratory classes, Autumn 2011
- *Introduction to Computational Biology*, laboratory classes, Spring 2010
- *Introduction to Computer Science*, laboratory classes, Autumn 2020, 2021 and 2022
- *Genome-scale technologies 2*, lectures and laboratory classes, Autumn 2022.

**Lecturer** at summer/autumn schools:

- *Summer School of Single Cell*, teaching R programming and single cell data analysis, Pilsen, Czech Republic, Sep 2022
- *Cajal Neuroepigenetics: writing, reading and erasing the epigenome*, instructor of the bioinformatics unit, Bordeaux, France, Nov–Dec 2022

Certified **Software Carpentry** and **Data Carpentry** instructor, teaching introductory coding and data science skills to researchers. Co-taught the following short courses (usually 16 hours each):

- *Data Carpentry Genomics*, Rutgers University, online, Jan 2020
- *Exploratory Analysis of Biological Data*, Max Delbrück Center for Molecular Medicine, online, Feb 2020
- *Data Analysis and Visualization in R*, University of Warsaw, online, Jun 2021
- *Data Analysis and Visualization in R*, University of Warsaw, Apr 2022
- *Data Analysis and Visualization in Python*, University of Warsaw, May 2023

## Academic service

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### Reviewer for conferences:

- *Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB)*, 2023
- *European Conference on Computational Biology (ECCB)*, 2014 and 2016
- *Research in Computational Molecular Biology (RECOMB)*, 2017 and 2021
- *International Workshop on Algorithms in Bioinformatics (WABI)*, 2012

### Reviewer for journals:

- *Bioinformatics*, 2016, 2017 and 2019
- *Briefings in Bioinformatics*, 2020, 2021 and 2022
- *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2022
- *Journal of Open Source Software*, 2018
- *PLOS Computational Biology*, 2020

### Conference organization:

- Member of RECOMB 2015 organizing committee, Warsaw, Poland, Apr 2015
- Member of the Autumn Conference of the Polish Bioinformatics Society program and organizing committee, online, Sep 2021

### Seminar organization:

- Co-organizer (with Anna Gambin and Bartek Wilczyński) of the working seminar *Computational Biology and Bioinformatics*, Oct 2021 – present

## Mentorship

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### Supervision of Ph.D. students:

- Patrycja Rosa, jointly supervised with Bożena Kamińska-Kaczmarek, 2021 – present

### Supervision of M.Sc. students:

- Paulina Duda, graduated 2023
- Damian Kokot, 2021 – present
- Michał Maruchin, 2021 – present
- Aleksandra Cupriak, 2022 – present
- Weronika Trawińska, 2023 – present

### Supervision of interns:

- Utsav Mathur, at the University of Warsaw, May–Jul 2014
- Piotr Śliwa, at EMBL Heidelberg, Jul 2017 – Aug 2018
- Andrii Nyporko, at the University of Warsaw, Sep 2020 – Jun 2021

### Supervision of student activities:

- Mentor of a bioinformatics student interest group *Koło Naukowe Bioinformatyki*, Mar 2023 – present

## Outreach activities

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### General audience:

- Popular science talk *What can we learn about genome organization from fruit flies?*, European Researchers' Night, Heidelberg, Sep 2018
- Popular science talk *The power of genetics, and the power of fruit flies*, European Researchers' Night, Heidelberg, Sep 2019

### Gifted high school students:

- Short course (3 days, 3 hours each) *Genomika dla informatyków (Genomics for computer scientists)*, 13. Wakacyjne Warsztaty Wielodyscyplinarne (13th Summer Scientific School), Wierchomla Wielka, Aug 2017