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 Tiuryn (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 Tiuryn (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

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 Tiuryn'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.
- 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*
○ 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.

Publications

1. Tim Pollex, Raquel Marco-Ferreres, Lucia Ciglar, Yad Ghavi-Helm, Adam Rabinowitz, Rebecca Rodriguez Viales, Christoph Schaub, Aleksander Jankowski, Charles Girardot, and Eileen E. M. Furlong. Chromatin gene-gene loops support the cross-regulation of genes with related function. *Molecular Cell*, 2023.

   `https://doi.org/10.1016/j.molcel.2023.12.023`

2. Giriram Mohana, Julien Dorier, Xiao Li, Héléna Malek, Marion Leleu, Daniel Rodriguez, Patrycja Rosa, Marion Mouginot, 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`

3. Tim Pollex, Adam Rabinowitz, Maria Cristina Gambetta, Raquel Marco-Ferreres, Rebecca R. Viales, Aleksander Jankowski, Christoph Schaub, and 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`

4. 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`

5. 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):1272–1282, August 2019.
   * – equal contribution
   `https://www.nature.com/articles/s41588-019-0462-3`

6. 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`

7. 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`

8. 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`

9. 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`

10. 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`

11. 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`

12. 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`

13. Witold R. Rudnicki, Aleksander Jankowski, Aleksander Modzelewski, Aleksander Piotrowski, and Adam Zadrożny. 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. 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

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

Polish Bioinformatics Society: Member since 2008

Teaching experience

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

- *Algorithms for genomic data analysis*, lecture and lab, winter 2023/24
- *Introduction to computer science*, lab, winter 2020/21, 2021/22, 2022/23 and 2023/24
- *Genome-scale technologies 2*, lecture and lab, winter 2022/23
- *Web applications*, lab, summer 2008/09, 2009/10 and 2011/12
- *Operating systems*, classes and lab, winter 2011/12
- *Introduction to computational biology*, lab, summer 2009/10

Lecturer at summer/autumn schools:

- *Cajal Neuroepigenetics: writing, reading and erasing the epigenome*, instructor of the bioinformatics unit, Bordeaux, France, Nov–Dec 2022
- *Summer School of Single Cell*, teaching R programming and single cell data analysis, Pilsen, Czech Republic, Sep 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 Analysis and Visualization in Python*, University of Warsaw, May 2023
- *Data Analysis and Visualization in R*, University of Warsaw, Apr 2022
- *Programming with R*, Max Delbrück Center for Molecular Medicine, online, Oct 2021
- *Data Analysis and Visualization in R*, University of Warsaw, online, Jun 2021
- *Exploratory Analysis of Biological Data*, Max Delbrück Center for Molecular Medicine, online, Feb 2021
- *Data Carpentry Genomics*, Rutgers University, online, Jan 2021

Academic service

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

Reviewer for journals:
- *Bioinformatics*, 2016, 2017 and 2019
- *Briefings in Bioinformatics*, 2020, 2021, 2022 and 2023
- *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2022
- *Journal of Open Source Software*, 2018
- *PLOS Computational Biology*, 2020

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

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

Mentorship

Supervision of Ph.D. students:
- Patrycja Rosa, jointly supervised with Bożena Kamińska-Kaczmarek, 2021 – present

Supervision of M.Sc. students:
- Weronika Trawińska, 2023 – present
- Damian Kokot, graduated 2024
- Michał Maruchin, graduated 2023
- Aleksandra Cupriak, graduated 2023
- Paulina Duda, graduated 2023

Supervision of B.Sc. students:
- Joanna Dąbrowska, 2023 – present

Supervision of interns:
- Julia Bartczak and Tomasz Kostrzewa, at the University of Warsaw, Nov 2023 – Jul 2024

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

Supervision of student activities:

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

Outreach activities

General audience:

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

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