

JOB OFFER: data science and computational modelling in Human genomics (PhD student)

Position in the project:	PhD student , data-driven computational modelling of Human genome at the population scale using 3D genomics experimental techniques (chromatin conformation capture) as input
Scientific discipline:	bioinformatics, computational genomics, data science, polymer modelling, biophysics. The role of 3D chromatin structure in storing, processing and evolving biological information; Human evolution; Spatiotemporal 4D Human genome organization; transcription regulation in human population
Job type (employment contract/stipend):	PhD stipend
Number of job offers:	1
Remuneration/stipend amount/month	5,000 PLN (first two years), 6,000 PLN (last two years)
Position starts on:	1st October 2020
Maximum period of contract/stipend agreement:	48 months
Institution:	<i>Laboratory of Bioinformatics and Computational Genomics</i> , Faculty of Mathematics and Information Science, Warsaw University of Technology, Warsaw, Poland
Project leader:	Dariusz Plewczynski, PhD
Project title:	<i>Spatial network model of sequence and structure diversity of Human genome at a population scale</i> Project is carried out within the PRELUDIUM-BIS programme of the National Science Centre
Project description:	The aim of the research project is to explore the relationship between the sequence, three-dimensional structure and gene expression for various mammalian cell types using spatial network model of Human genome. The project will exploit the whole genome sequencing data from 1000 Genomes project together with the three dimensional genomic public datasets from 4DNucleome consortium and proprietary ones from our collaborators. We will develop computational algorithms for the design of spatial network model using experimental interaction data and polymer simulations. The project will result in establishing the software platform that will be able first to identify single nucleotide polymorphisms (SNPs) and sequence rearrangements (i.e. structural variants SV, such as deletions, duplications, inversions, insertions, translocations) using the Illumina next generation sequencing data. Secondly, it will be able to predict the three-dimensional structure of a genome for a given cell type using its individual 1D sequence together with the reference 3D conformation for the cell type of interest. Thirdly, it will allow for probabilistic estimation of expression profile for genes at the whole genome scale. Finally, we will perform functional study focused on the genomic regions related to cancer oncogenesis according to large scale Genome-Wide Association Studies (GWAS) and various molecular data collected in TCGA database.
Key responsibilities include:	<ol style="list-style-type: none"> 1. Three-dimensional computational modeling using ChIA-PET, Hi-C and HiChIP experimental data 2. Statistical analysis of epigenomic data, ATAC-seq, ChIP-seq, RNAseq experimental data 3. Analyzing the simulations results, formulating biophysical hypothesis

	4. Publications preparation
Profile of candidates/requirements:	<ol style="list-style-type: none"> 1. MSc in computer science, biophysics, biochemistry, bioinformatics or related discipline 2. Documented experience with genomics data 3. Preferred experience in population genomics, DNA sequencing data, epigenomics, RNA-seq, ATAC-seq data analysis 4. Priority will be given to candidates with expertise relevant to the PRELUDIUM-BIS project and in agreement with the general profile of the laboratory. Preliminary work done by applicant in the context of 3DGenomics will be treated as the strong asset. 5. Essential requirements cover the ability to work in collaboration with others, within a large research team, performing several parallel scientific tasks, independent thinking and finally the ability to deliver publishable results. 6. Needed the highly motivated individuals willing to work in an interdisciplinary environment under stress and with strict deadlines. 7. Excellence in English language, 8. Proficiency in bioinformatics methods, data science, programming and computational genomics techniques
Required documents:	<ol style="list-style-type: none"> 1. CV 2. Motivation letter (<i>why I would like to join 3DGenomics field?</i>) 3. Letter of support 4. MSc certificate 5. Short (up to 2 pages) written document about recent advances in 3D genomics
We offer:	<ul style="list-style-type: none"> • PhD fellowship 5000-6000 PLN/month • Appointment starting 1st October 2020, funding guaranteed for 48 months. • PRELUDIUM-BIS project provides unique opportunities for interdisciplinary work between bioinformatics, biology, physics, and computer sciences, as well as well established and long-lasting international collaborations with recognized academic institutes and universities in US, China and EU. • We plan close collaboration with industry as well. • We provide also the access to modern 1D and 3D genomics equipment and support from other experienced researchers. • International partner (Prof. Yijun Ruan) will be co-supervising your work at the laboratory. • Access to the latest NVIDIA HPC infrastructure (A100, SuperPOD)
Please submit the following documents to:	<p>dr hab. Dariusz Plewczynski, PhD, prof. PW; e-mail: dariuszplewczynski@gmail.com, or darman@mini.pw.edu.pl tel.: +48 22 234 7219;</p> <p><i>Laboratory of Bioinformatics and Computational Genomics, Faculty of Mathematics and Information Science Warsaw University of Technology www: http://4dnucleome.mini.pw.edu.pl</i></p>

Application deadline:	1 August 2020
For more details about the position please visit (website/webpage address):	http://4dnucleome.mini.pw.edu.pl and https://www4.mini.pw.edu.pl
Euraxess job/stipend offer (in case of PhD and postdoc positions):	

To allow us to process your data, please include the following statement in your application:

“I hereby consent to have my personal data processed by the Faculty of Mathematics and Information Science, Warsaw University of Technology with its registered office at ul. Koszykowa 75, 00-662 Warsaw, Poland for the purpose of carrying out a recruitment process and selecting an employee and concluding a contract for employment at the Warsaw University of Technology. I have been informed of my rights and duties. I understand that provision of my personal data is voluntary.”

In accordance with Article 13 of REGULATION (EU) 2016/679 OF THE EUROPEAN PARLIAMENT AND OF THE COUNCIL of 27 April 2016 on the protection of natural persons with regard to the processing of personal data and on the free movement of such data – general regulation on data protection (Official Journal of the EU L 119/1 of 4 May 2016) the Warsaw University of Technology informs that:

1. The Controller of your personal data is the Faculty of Mathematics and Information Science, Warsaw University of Technology with its registered office at ul. Koszykowa 75, 00-662 Warsaw, Poland ;
2. The Controller has designated the Data Protection Officer who supervises the processing of personal data, and who can be contacted via the following e-mail address: darman@mini.pw.edu.pl;
3. Your personal data will be processed for the purpose of carrying out a recruitment process and selecting an employee and concluding a contract for employment at the Warsaw University of Technology;
4. The provided data will be processed pursuant to Article 221 § 1 of the Act of 26 June 1974 Labour Code (uniformed text: Dz.U. of 2018, item 917) and your consent for processing of personal data;
5. Provision of data in the scope stipulated in the Labour Code is mandatory, and the remaining data are processed according to your consent for processing of personal data;
6. The data will not be shared with any external entities;
7. The data will be stored until you withdraw your consent for processing of personal data;
8. You have the right to access your personal data, to rectify, erase them, restrict their processing, object to processing, and to withdraw the consent at any time;
9. You have the right to lodge a complaint to the President of the Office for the Protection of Personal Data.”

Researcher profile:	First Stage (R1) Researcher
Type of Contract:	Temporary
Form of Employment:	Scholarship
Job Status:	Full time
Research Field:	Computational genomics (bioinformatics)
Keywords:	bioinformatics; structural variants; chromatin loops; mammalian 3D genome; Topologically Associating Domains; deep learning; spatial network model; Biophysical Modelling; Cell differentiation; Hematopoietic development; oncogenesis; immortalization; 1000 Genomes project; 4DNucleome; ENCODE; genome structure; higher order chromatin organisation; ChIA-PET; Hi-C; genome architecture; bioinformatics; structural variants; copy number variants; autoimmune diseases; cancer