COMPUTATIONAL BIOLOGY/BIOINFORMATICS/ DATA ANALYSIS

Moscow Institute of Physics and Technology (National Research University)

Degree or qualification is awarded: **PhD (Candidate of Science)**

Language of study: **English**
Mode of study: **full-time**
Duration: **4 years**
Availability of free education: **yes**
Price: **375 000 RUB**

Programme curator: **Denis Ustyuzhaninov**
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Research supervisor:
Yulia Medvedeva
PhD

Supervisor's research interests:
Development of bioinformatics tools and resources for regulatory genomics, cell fate engineering and drug repurposing. Computational investigation of regulatory transcriptomics and epigenomics in application to normal and pathological processes.

Research highlights:
The scope of our group's research includes studies of the fundamental mechanisms of genome regulation that can be applied to solving practical tasks, such as cell conversion and drug repositioning. Our projects require usage and development of modern bioinformatics tools and machine learning techniques to process chemical, biological and biomedical data. Our group is a member of international consortia, such as FANTOM, GREEKS, Human Cell Atlas. The candidate is expected to get involved in collaborations with computational and experimental groups both internationally and locally. Our research is supported by different Foundations, after a trial period the committed candidate can be supported financially. The results of the projects are intended to be published in high impact journals.

Supervisor's specific requirements:

- Degree in Bioinformatics, Computer Science or related quantitative field; degree in Biology can be considered if accompanied with strong programming skills.
- Programming skills in Python/R and Unix shell scripting.
- Understanding general concepts of Molecular Biology.
- Profound writing and communication skills.

Main publications:

- Bonetti A, Agostini F, Suzuki AM, Hashimoto K, Pascarella G, Gimenez J, et al. RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. Nature Communications 2020;11:1018. https://doi.org/10.1038/s41467-020-14337-6
- Lioznova AV, Khamis AM, Artemov AV, Besedina E, Ramensky V, Bajic VB, et al. CpG traffic lights are markers of regulatory regions in human genome. BMC Genomics 2019;20:102. https://doi.org/10.1186/s12864-018-5387-1
- Hon C-C, Ramilowski JA, Harshbarger J, Bertin N, Rackham OJL, Gough J, et al. An atlas of human long non-coding RNAs with accurate 5' ends. Nature 2017;543:199-204. https://doi.org/10.1038/nature21374

Specializations within this programme