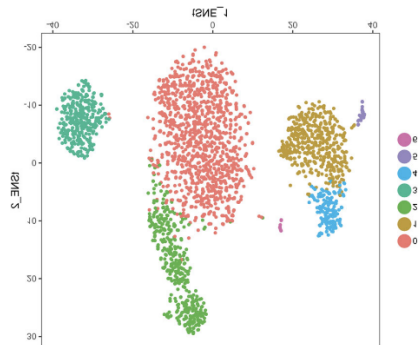
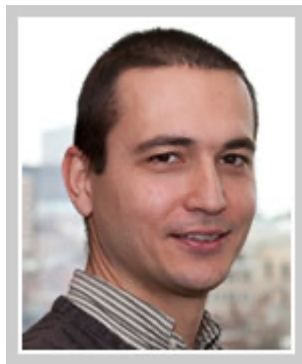


The Technology Seminar Series Presents:

**“Next-Generation sequencing platforms
for epigenomics and single-cell profiling”**

Ruslan Sadreyev
Director of Bioinformatics,
Director of MGH Next-Generation Sequencing Core
Assistant Professor
Department of Molecular Biology, MGH
Department of Pathology, MGH, HMS



Thursday, December 15th, 2022
12:00 – 1:00 pm
MEE 243 Charles Street Boston, MA, The Meltzer
Auditorium (3rd Floor) and Zoom

<https://masseyeandear.zoom.us/j/583662273?pwd=TWJTUEV6ZTFUTzUzaWx5dXFmR2puQT09>

Meeting ID: 583 662 273

Passcode: 248969

Summary of talk:

Next-generation sequencing (NGS) platforms provide the opportunity interrogate various genomic functions in unprecedented comprehensive detail. This presentation will overview experimental, technical, and computational aspects of NGS platforms in two specific areas, epigenomics (ATAC-seq, ChIP-seq, CUT&RUN etc) and single-cell analyses (scRNA-seq, scATAC-seq etc). MGH NGS core (nextgen.mgh.harvard.edu/Pricing.html) has been assisting its customers in applying these and many other platforms in the context of their specific biomedical projects.

About Dr. Sadreyev:

Dr. Sadreyev is Director of Bioinformatics and Director of Next-Generation Sequencing Core at Massachusetts General Hospital (MGH) and Assistant Professor at Harvard Medical School. He received his Ph.D. from the Department of Physics, Moscow State University, Russia, did his postdoc at the University of Florida, and worked as a Bioinformatics research scientist at Howard Hughes Medical Institute (UTSW Medical Center and MGH/ Harvard Medical School). The Sadreyev lab is focused on computational analyses of large-scale biomedical data with the aim to better understand molecular mechanisms of genome regulation and pathophysiology of disease. Dr Sadreyev is particularly interested in the role of chromatin in the regulation of gene activity and other genomic functions. The lab combines large-scale approaches of quantitative epigenomics with more focused approaches of biochemistry and genetics to test computational hypotheses. When necessary, the lab develops new computational methods to advance these analyses.

