No. 2021-22

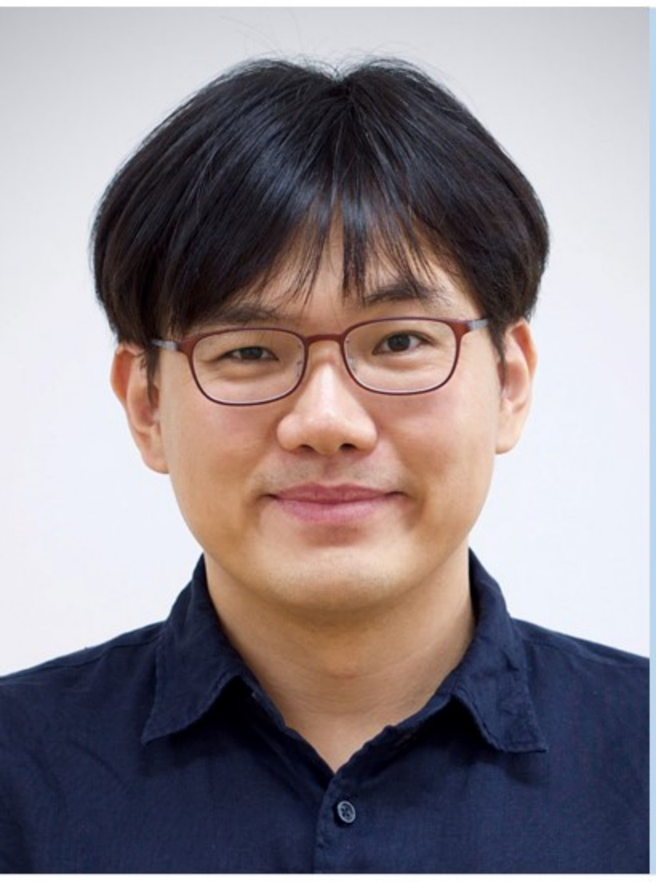
School of Life Sciences
Seminar Series

Thursday
4:00 PM

25 November

Online seminar

Zoom ID 315 451 8934 (Password: Life2021Fa)



Single-molecule RNA Analysis Using Nanopore Sequencing

연사 장혜식 교수

소속 서울대학교

Host 이선재 교수

언어: 한국어

학력

2009-2014 Ph.D., in Biological Sciences, Seoul National University

2007-2009 M.S.E., in Bio and Brain Engineering, KAIST

1998-2007 B.S.E., in Information and Industrial Engineering, Yonsei University

경력

2019 - Now Assistant Professor, School of Biological Sciences, Seoul National University

2014 - Now Research Fellow, Center for RNA Research, Institute for Basic Science

2014 - 2019 Research Assistant Professor, Seoul National University

2001 - 2005 Software Developer, Solution Development Team, LinuxKorea, Inc.

Abstract

RNA is a complex molecule that holds more than just A, C, G, and U. It contains a 5' cap and a poly(A) tail on the ends. Chemical modifications also diversify the composition of a single RNA species. Protein bindings and subcellular localization modify the status of an RNA in the cells. All these play some roles in the middle of the RNA regulatory mechanisms. Since the introduction of RNA-Seq to the field, newly developed high-throughput techniques have driven the massive transcriptome-wide discovery of novel RNA regulatory elements. However, two common drawbacks in the second-generation sequencers have prohibited analyzing the status of regulatory sites in the broader context of the transcripts. The first problem comes from the indispensable reverse-transcription, and another is from the short-read lengths. Nanopore sequencing is an entirely different approach that is free from those limitations. It reads the nucleic acid sequences by measuring ionic current changes during their migrations through a tiny hole in the middle of a transmembrane protein. This alternative strategy makes it possible to directly monitor the chemical details of the bases throughout the full lengths of RNA molecules one by one. We are carrying out examinations on how nanopore direct RNA sequencing adds new dimensions of the understanding across the life cycle of RNA. In this talk, I will briefly discuss the preliminary results from our first trials. They include poly(A) tail length measurement, transcriptome timestamping, multiplexed sequencing, targeted sequencing, secondary structure probing, and base modification detection.