## 강의개요

# Big data for RNA informatics

최근 생성되는 전사체 데이터셋들은 다양한 open repository 데이터베이스들을 통하여 scientific community와 공유되어지고 있는 실정임에도 불구하고 제한된 patient cohort 크기와 QC-passed 된 세포의 수, 임상 정보와 cell metadata 정보의 부재 등으로 인하여 새로운 결과를 도출해 내기에 현실적으로 많은 한계들이 있다. 이를 극복하기 위하여 하나의 큰 big data, 즉 통합된 데이터를 생성하여 uniform 한 파이프라인을 적용하여 효율적이고 효과적인 분석을 할 수 있는 핵심 역량을 갖추는 것을 목표로 한다.

강의는 다음의 내용을 포함한다:

- Bulk RNA-Seq 개요
- Single-Cell RNA-Seq 개요
- Data Integration for RNA Informatics
- Deep Learning for scRNA-seq
- Spatial RNA informatics

*참고강의교재:
없음

*교육생준비물:
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* 강의 난이도: 초급

* 강의: 임수빈 교수 (아주대학교 의과대학)

# Curriculum Vitae

**Speaker Name: Su Bin Lim, Ph.D.**

**▶Personal Info**

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| Name | Su Bin Lim |
| Title | Assistant Professor |
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**Research interest :** RNA informatics, computational genomics, systems biology, single-cell analysis

**Educational Experience**

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|---|---|
| 2015 | B.S. in Biomedical Engineering, National University of Singapore, Singapore |
| 2019 | Ph.D. in Integrative Sciences and Engineering, National University of Singapore, Singapore |

**Professional Experience**

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|---|---|
| 2020-2021 | Postdoctoral Fellow, Johns Hopkins University School of Medicine, USA |
| 2021- | Assistant Professor, Ajou University School of Medicine, South Korea |
| 2022- | Nature Scientific Data, Editorial Board Member |
| 2023- | Frontiers in Cell and Developmental Biology, Editorial Board Member |

**Selected Publications (5 maximum)**

1. SB Lim et al. An extracellular matrix-related prognostic and predictive indicator for early-stage non-small cell lung cancer. Nature Communications 8, 1736, 2017.
2. SB Lim et al. Addressing cellular heterogeneity in tumor and circulation for refined prognostication. PNAS 116(36), 2019.
3. KY Goh et al. Matrisomal genes in squamous cell carcinoma of head and neck influence tumor cell motility and response to cetuximab treatment. Cancer Communications 42(4), 355-359, 2022.
4. SB Lim et al. Macrophage-derived TNF-enriched tumor microenvironment shapes pancreatic ductal adenocarcinoma into the basal-like molecular phenotype through upregulating TAp63. Clinical and Translational Medicine 13, 12, 2023
5. Hong J et al. SRSF7 downregulation induces cellular senescence through generation of MDM2 variants. Aging 15, 14591-14606, 2023.