INDRAPRASTHA INSTITUTE *of* INFORMATION TECHNOLOGY **DELHI**

10 YEARS *of* EXCELLENCE

Invitation to M.Tech. Thesis Defense of Princey Yadav: July 17, 2020 (Friday): 10.45-11.30 IST

In Partial Fulfillment of the Requirements for the Degree of

M.Tech. CB

Princey Yadav (MT18246)

Will defend her thesis

Title: "**Tracking age-related changes in mRNA homeostasis at single cell resolution**"

IIIT-D Faculty and Students are invited

Date: July 17, 2020 (Friday)
Time: 10.45-11.30 IST
Place: Online (Google Meet)

Examiner:	**Internal:**	**Gaurav Ahuja & GPS Raghava**
	External/Internal:	**Malay Bhattacharya, ISI Kolkata**
	Advisor:	**Debarka Sengupta**

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Abstract

Aging is the time-dependent functional decline of biological systems due to the accumulating cellular damage. Diabetes, cardiovascular diseases, cancer, neurodegenerative diseases like Alzheimer's, Parkinson's disease are all a result of aging. Aging which is a gradual and slow process affects the body's ability to maintain regulation and homeostasis. Therefore, we attempt to understand the age-related changes in mRNA homeostasis at single cell resolution.

We elaborate on how RNA velocity can be used as a method to quantify the mRNA homeostasis divergence at single cell resolution. The method is validated on the aging human pancreas dataset. We proposed a method to identify genes that suffer homeostasis breakdown with aging. We identified 171 such genes. Not only that, we saw that homeostasis breakdown is not the only phenomenon that happens with aging. We also observed homeostasis restoration in 40 genes, which could be body's way to cope with the dysregulations and loss of mRNA homeostasis due to aging.

We then explore whether mRNA homeostasis imbalance can be used to predict cellular age. Since previous studies suggest increased transcriptional noise in old organisms, we compared the performance of our method with the very known aging hallmark transcriptional noise as a feature to predict the cellular age. We find that mRNA homeostasis imbalance as a feature outperforms transcriptional noise in all kinds of prediction settings.