INDRAPRASTHA INSTITUTE of INFORMATION TECHNOLOGY DELHI

Invitation to MTech Thesis Defense of **Gauri Mittal**: October 17(Wednesday): 10.00 – 11.30 IST

In Partial Fulfillment of the Requirements for the Degree of
M.Tech CB

Gauri Mittal (MT16126)

Will defend her thesis

Title: "Design Computational annotation of mutation-specificity of therapies from genome scale data-sets"

IIIT-D Faculty and Students are invited

Date: October 17(Wednesday)
Time: 10:00 - 11:**30 IST**
Place: A320, Meeting Room 3rd Floor(NAB)

Examiner: **Internal:** **GANESH BAGLER**
External/Internal: **DEBASIS DASH (CSIR IGIB)**
Advisor: **VINOD SCARIA (CSIR IGIB)**

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Abstract
Background: Diverse genomic and epigenomic alterations results in unwanted cellular growth which ultimately leads to cancer development in humans. Technological advancement in data storing, data sharing and data analysis has transformed cancer research into a data-intensive field. With the increasing amount of data on cancer drugs and genomic variants, it is essential to carefully annotate them and perform various statistical analysis. This study determines the association between specific oncogenic mutations and tumor characteristics of patients with a specific type of cancer. Methods: Data of mutation specific therapies for cancer was curated from the published literatures. Retrospective clinical and pathologic TCGA data were collected for patients with advanced melanoma, colorectal, lung and breast cancer. The demographics, tumor characteristics, and clinical outcomes of the patients were compared to identify significant mutation-specific associations using Fisher's exact t-test. Results: Prevalence of BRAF V600E mutation is associated with the older age of melanoma patient. Similar results were obtained for colorectal patients with BRAF V600E, KRAS G12X and KRAS A146T mutations. EGFR exon 19 deletion mutation, EGFR substitution mutation and BRAF V600E mutation were highly correlated to the gender and ethnicity of colorectal cancer patient. Whereas, no significant association was found between BRCA1/2 mutation and clinical characteristics of breast cancer patients. Conclusion: Association of presence of different mutation with patient demographics, tumor characteristics, and prognosis differ significantly with cancer type and this information is an important measure to design clinical trials in future.