## International Conference on COMPUTATIONAL BIOLOGY AND BIOINFORMATICS September 05-06, 2018 Tokyo, Japan

Multi-loci association test in genetic association study using similarity between individuals

Indranil Mukhopadhyay Indian Statistical Institute, India

The common paradigm in Genome Wide Association Studies (GWAS) is to test for association using only one SNP at a time that gives rise to multiple comparison problems ignoring their genomic and environmental context. Gene-based association tests are gaining importance for the analysis of genome-wide association studies because it reduces multiple testing burdens and provides directions for future functional studies. Moreover, with whole-genome sequencing on the horizon, there is increasing recognition that agnostic biostatistical approaches will get us no far, development of comprehensive and fully informative analyses of GWAS using newer approaches is required that combine information from multiple markers at a time. So, within a gene or any genomic region of interest, testing for joint association of genetic variants would be desirable to determine their synergistic effects. Based on this idea we have proposed Kernel Based Association Test (KBAT) for binary trait as well as for Quantitative Phenotype (QT-KBAT) including information for both common and rare variants. These tests are shown to be powerful to detect such association. We have evaluated the power of the proposed test statistics for case-control samples and quantitative traits using the extensive simulated data sets. We have also extended our multi-loci approach to family data and to study gene-gene interaction. In each case, we have developed asymptotic distribution of the test statistic under null hypothesis of no association. This enables us to calculate p-value vary fast without using any time-consuming computational procedure.

## **Biography**

Indranil Mukhopadhyay has completed his PhD in Time Series Analysis from Calcutta University, India and Postdoctoral Fellowship from University of Pittsburgh, USA. He is currently an Associate Professor at Indian Statistical Institute, Kolkata, India. He has published more than 40 research papers. His current research includes genomic data integration, single cell data analysis, mathematical modeling of disease dynamics, cluster analysis and statistical inference.

indranilm100@gmail.com

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