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Citation (summary) on the outstanding research work signed by the nominator.

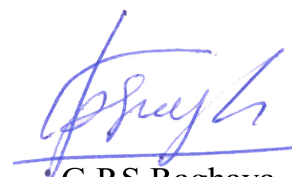
Prof. Bandyopadhyay is being nominated for her outstanding contributions in developing artificial intelligence and machine learning based algorithms for analysing biological data, specifically for novel algorithms for analysis of single cell RNA-seq (scRNA-seq) data, innovative methods of mapping single molecule real-time data (SMRT) reads to the reference genome, providing molecular insights into HIV pathogenesis through analysis of exosomal microRNAs and making her techniques freely available to the scientific community through web servers and tools.

While scRNA-seq data captures cellular heterogeneity, particularly in cancerous tumors, the data is large in both the number of samples and number of features, and has high dropouts. Prof. Bandyopadhyay provided robust algorithms that scale with the number of dimensions for tasks like clustering, identifying differentially expressed genes and measuring differential co-expression.

The usual methods of mapping the SMRT reads to the reference genome do not work well because of the high level of noise in them. Prof. Bandyopadhyay developed novel alignment-based and alignment-free methods of SMRT read mapping that outperformed the state-of-the-art.

Another important contribution of Prof. Bandyopadhyay was analysing the microRNA load in the exosomes of cells infected with HIV-1 expressing the Nef viral protein in particular. The analysis revealed that an overwhelming majority of the microRNAs selectively secreted into Nef exosomes had targets within the HIV genome. Hence the purpose of secreting these seems to be a viral strategy for enhancing pathogenicity.

Almost all methods developed by Prof. Bandyopadhyay are free for use of the scientific community.



G.P.S Raghava