Debarka Sengutpta, Ph.D.

DEBARKA SENGUPTA
Assoc. Professor, IIIT-Delhi

A306, R&D block
IIIT-Delhi
Okhla Phase 3
Delhi 110020
Emails: debarka@iiitd.ac.in;

T: +91 11 2690 7446

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Declaration

Here I declare that the two main works the award is being claimed for **have not been awarded previously**. Below I cite the works and our contribution.

1. Poonia S, Goel A, Chawla S, Bhattacharya N, Rai P, Lee YF, Yap YS, West J, Bhagat AA, Tayal J, Mehta A, Ahuja G, Majumdar A*, Ramalingam N*, **Sengupta D***. Marker-free characterization of full-length transcriptomes of single live circulating tumor cells. **Genome Res.** 2023 Jan;33(1):80-95. Doi: 10.1101/gr.276600.122. Epub 2022 Nov 22. PMID: 36414416; PMCID: PMC9977151.

   Circulating tumor cells (CTCs) harbor a wealth of molecular information about the tumor of origin. However they are rare in blood (1 or fewer cells in 105 - 106 PBMCs). This makes the detection and characterisation of CTCs challenging. Size an/or marker based CTC enrichment techniques might potentially miss out on CTCs of unusual phenotype or suffer from WBC contamination. We developed unCTC, a tailored computational framework for label free characterisation of single CTC transcriptomes, while avoiding WBC contaminants. As a remarkable achievement, our software could accurately recognise single circulating Triple Negative Breast Cancer cells (TNBCs). I conceived and led the study in consultation with Dr. Naveen Ramalingam (Senior Director, Fluidigm Corp., USA), and Prof. Angshul Majumdar (my colleague at IIIT-D). Dr. Ramalingam produced the CTC transcriptomes, while Prof. Majumdar assisted in the algorithm development. The first author of the study is a Ph.D. student affiliated with our laboratory (soon to join Cleveland Clinic as a postdoc).

   Note: Below is another related publication.

1. Iyer A, Gupta K, Sharma S, Hari K, Lee YF, Ramalingam N, Yap YS, West J, Bhagat AA, Subramani BV, Sabuwala B, Tan TZ, Thiery JP, Jolly MK, Ramalingam N*, **Sengupta D***. Integrative Analysis and Machine Learning based Characterization of Single Circulating Tumor Cells. **J Clin**

Med. 2020 Apr 22;9(4):1206. Doi: 10.3390/jcm9041206. PMID: 32331451; PMCID: PMC7230872.

2. Chawla S, Rockstroh A, Lehman M, Ratther E, Jain A, Anand A, Gupta A, Bhattacharya N, Poonia S, Rai P, Das N, Majumdar A, Jayadeva, Ahuja G, Hollier BG, Nelson CC*, **Sengupta D***. Gene expression based inference of cancer drug sensitivity. **Nat Commun**. 2022 Sep 27;13(1):5680. Doi: 10.1038/s41467-022-33291-z. PMID: 36167836; PMCID: PMC9515171.

   Precision oncology research aims to utilize molecular profiles of cancers for personalized therapeutic choices, with the assistance of AI. To enhance the generalizability of AI approaches to unseen drug compounds, we developed a chemo-transcriptomics approach called Precily. This approach incorporates cancer molecular profiles and drug descriptors as explanatory variables. Precily demonstrated significant improvements compared to existing solutions. We evaluated Precily using cell lines, in-house mouse xenografts (in collaboration with Prof. Colleen Nelson's lab at QUT, Brisbane), and TCGA human cancer data. We also demonstrated how Precily can accurately infer dose response of unseen drugs. Our predictions were supported by in-house experimental data. I conceived the study with Prof. Nelson. The first author of the study is a Ph.D. student affiliated with our laboratory (currently a postdoc at the Harvard Medical School).

Sincerely,
Debarka Sengupta