EDITORIAL

Systems Genomics in the Age of Next Generation Sequencing (Part II)

With systems genomics burgeoning, there is always a need to prioritise candidates post bioinformatics analyses. This is where machine learning approaches have steadfastly been in use. While the articles in part I have seen a seminal research on the applications of the genes, this second part constituting three articles emphasizing the need for machine learning heuristics.
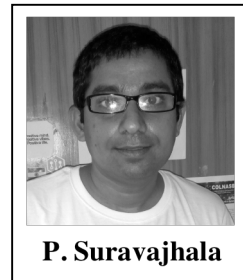
Roy *et al.* in their article entitled, "Deciphering the novel target genes involved in the epigenetics of hepatocellular carcinoma using graph theory approach" [1] applied graph theory approaches for drawing a network of genes in identifying novel targets for hepatocellular carcinoma epigenetic therapy. The candidates they found were statistically coherent for the therapeutic use.

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Natarajan *et al.*, in their article entitled, "*Helicobacter pylori* reactivates Human Immunodeficiency Virus-1 in latently infected monocytes with increased expression of IL-1β and CXCL8" [2] have aptly used HIV infected monocytes for measuring the expression of genes reactivated by H. Pylori.

Parveen *et al.* emphasized a review on "Applications of machine learning in miRNA discovery and target prediction" [3] which brings a subtle understanding of these approaches for miRNA target prediction and early phase discovery.

In conclusion, systems genomics has shaped up from nascent stage to a phase where we set actions to prevent diseases, thanks to machine learning approaches.

"The goal of getting your genome done is not to tell you what you will die from, but it's how to learn how to take action to prevent disease". George M. Church.

REFERENCES

[1]   Roy, N.; Raj, R.; Rai, S.; Varadwaj, P.K. Deciphering the novel target genes involved in the epigenetics of hepatocellular carcinoma using graph theory approach. *Curr. Genomics*, **2019**, *20*(8), 545-555. Doi: 10.2174/1389202921666191227100441.

[2]   Natarajan, V.; Moar P.; Kaur, U.S.; Venkatesh, V.; Kumar, A.; Chaturvedi, R.; Himanshu D, Tandon, R. *Helicobacter pylori* reactivates human immunodeficiency virus-1 in latently infected monocytes with increased expression of IL-1β and CXCL8. *Curr. Genomics*, **2019**, *20*(8), 556-568. Doi: 10.2174/1389202921666191226091138.

[3]   Parveen, A.; Mustafa, S.H.; Yadav, P.; Kumar, A. Applications of machine learning in miRNA discovery and target prediction. *Curr. Genomics*, **2019**, *20*(8), 537-544. Doi: 10.2174/1389202921666200106111813.

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