

# An Improved Integrative Random Forest for Gene Regulatory Network Inference for Breast Cancer

Suntharaamurthi Chandran<sup>1</sup>, Kohbalan Moorthy<sup>1</sup>, Mohd Arfian Ismail<sup>1</sup>, Mohd Zamri Osman<sup>1</sup>, Mohd Azwan Mohamad @ Hamza<sup>1</sup>,  
Ferda Ernawan<sup>1</sup>

<sup>1</sup> Soft Computing & Intelligent System Research Group, Faculty of Computer Systems & Software Engineering,  
Universiti Malaysia Pahang, 26300, Kuantan, Pahang, Malaysia

Corresponding author Email: suntharaam@gmail.com

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Gene Regulatory Network (GRN) inference aims to capture the regulatory influences between the genes and regulatory events in the GRN. Integrative Random Forest for Gene Regulatory Network Inference (iRafNet) is a RF based algorithm which provides a great result in constructing GRN inference by integrating multiple data types. Most of the approaches did justify their duty but there are some limitations which don't allow it to reach its optimal state and needs a very long computational time to construct a GRN inference. Other than that, they do not provide optimal performance. There are redundant genes in the dataset. GRN inference by existing methods has a lower accuracy on benchmark and real dataset. Furthermore, the computational time to produce the GRN inference is very long in the existing methods. To overcome these issues is proposed improved the existing method by adding a gene selection into it. To perform the improvement the existing methods was studied and analyzed on their performance in constructing GRN inference. Improved iRafNet was designed and developed to reduce the computational time to construct the GRN inference gene from the dataset. Finally, the accuracy and computational time of the proposed method was validated and verified with the benchmark and real dataset. Improved iRafNet has proven its performance by having a higher AUC and lower computational time.

**Keywords:** Random Forest, Gene Regulatory Network Inference, Microarray Data, Computational Intelligence, Breast  
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