

(12) PATENT APPLICATION PUBLICATION

(21) Application No.1014/CHE/2013 A

(19) INDIA

(22) Date of filing of Application :11/03/2013

(43) Publication Date : 23/01/2015

(54) Title of the invention : RANK NORMALIZATION FOR DIFFERENTIAL EXPRESSION ANALYSIS OF TRANSCRIPTOME SEQUENCING DATA

(51) International classification	:G06F19/00	(71) <b>Name of Applicant :</b>
(31) Priority Document No	:13/459529	<b>1)INTERNATIONAL BUSINESS MACHINES</b>
(32) Priority Date	:30/04/2012	<b>CORPORATION</b>
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Filing Date	:NA	(72) <b>Name of Inventor :</b>
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(61) Patent of Addition to Application Number	:NA	<b>2)LAXMI P. PARIDA</b>
Filing Date	:NA	
(62) Divisional to Application Number	:NA	
Filing Date	:NA	

(57) Abstract :

A computer-implemented method for rank normalization for differential expression analysis of transcriptome sequencing data includes receiving, by a computer, a first dataset comprising transcriptome sequencing data, the first dataset comprising a plurality of genes, and further comprising a respective ranking value associated with each of the plurality of genes; assigning a rank to each of the genes of the plurality of genes based on the ranking value to produce a first rank normalized dataset; determining a change between a first rank of a particular gene in the first rank normalized dataset, and a second rank of the particular gene in a second rank normalized dataset, the second rank normalized dataset being based on a second dataset comprising transcriptome sequencing data; and determining whether the particular gene is differentially expressed between the first dataset and the second dataset based on the determined change in rank.

No. of Pages : 22 No. of Claims : 10