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**Correction**

**Correction: Triclustering method for finding biomarkers in human immunodeficiency virus-1 gene expression data**

**Titin Siswantining\***, Alhadi Bustamam, Devvi Sarwinda, Saskya Mary Soemartojo, Moh. Abdul Latief, Elke Annisa Octaria, Anggrainy Togi Marito Siregar, Oon Septa, Herley Shaori Al-Ash and Noval Saputra

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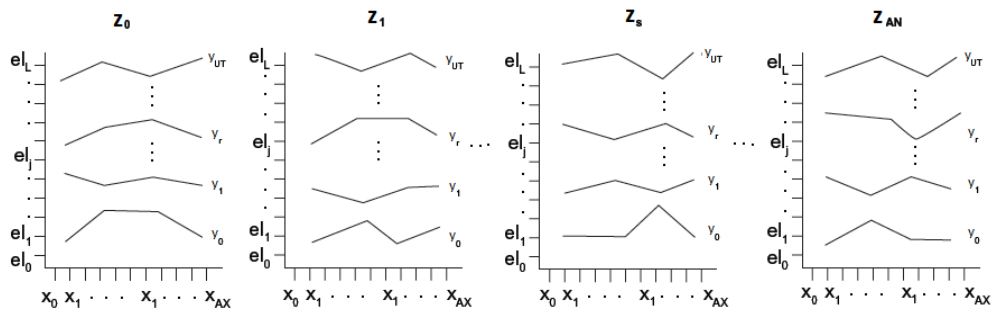
**A correction on**

Triclustering method for finding biomarkers in human immunodeficiency virus-1 gene expression data by Titin Siswantining, Alhadi Bustamam, Devvi Sarwinda, Saskya Mary Soemartojo, Moh. Abdul Latief, Elke Annisa Octaria, Anggrainy Togi Marito Siregar, Oon Septa, Herley Shaori Al-Ash and Noval Saputra. *Mathematical Biosciences and Engineering*, 2022, 19(7):6743-6763. doi: 10.3934/mbe.2022318.

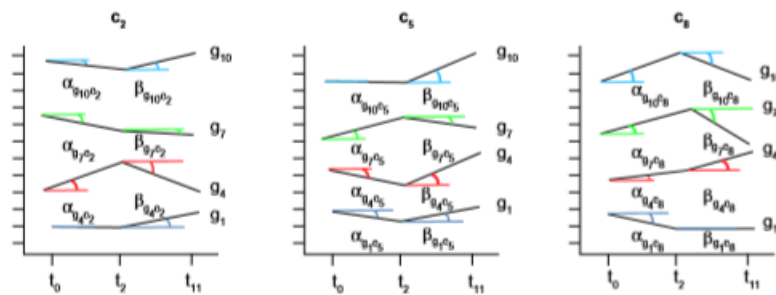
We have updated Subsection 2.2.2 especially about Multi Slope Measure (MSL) in pages 6747–6749. We've added citations for this section [1], rewritten the sentences, and changed some of the equation notation (Eqs (2.9)–(2.12)). Then, we change notation in Figure 2 and added source for Figures 2 and 3.

Understanding MSL requires a graphic representation of tricluster  $TRI_{xyz}$ , where  $x$ ,  $y$ , and  $z$  are one of gene  $G$ , condition  $C$ , and time or depth  $T$  so that element  $x$  on  $TRI_{xyz}$  will be on the  $X$ -axis, and element  $y$  on  $TRI_{xyz}$  will outline the panels that are elements  $z$  on  $TRI_{xyz}$  as shown in Figure 2 [2]. MSL calculates the difference among the angles formed by every series traced on each of three representations, taking into account  $TRI_{gct}$ ,  $TRI_{gtc}$ , and  $TRI_{tgc}$  on Figure 3. MSL accounts for the effect of adjacent points in time.

MSL measures the average difference between the angles formed by the probe ID gene in all rows and columns for each individual or candidate tricluster. To calculate the MSL measure of a tricluster, a multiangular ratio calculation is first performed. Define the  $FG_{multi}$  tricluster  $TRI_{tgc}$  as the average



**Figure 2.** Graphic representation of a tricluster (Source: D. Gutiérrez-Avilés & C. Rubio-Escudero, 2015).



**Figure 3.** Graphic view angle for  $TRI_{tgc}$  (Source: D. Gutiérrez-Avilés & C. Rubio-Escudero, 2015).

difference  $\Delta$  from an angle vector  $av_{yz} \in \text{angset}$  from all of the outlines  $y$ , for each panel  $p$  ( $V_{mc}$ ), and the same for the rest of panels ( $H_{mc}$ ), where  $N_{mc}$  is the number of differences that are formed. All the angular vectors of an outline  $y$  on panel  $z$  are defined as a set of angles formed by outline  $y$ , taking into account each data point on the  $X$ -axis. Each outline will have many (axis mark  $X-1$ ) angles. The difference  $\Delta$  between two vector angles  $av_A$  and  $av_B$  is defined as the average of  $MAX - MIN$  ( $MAX$  is the maximum, and  $MIN$  is the minimum of the two angles  $av_A(i)$  and  $av_B(i)$ ) of any component or angle  $i$  from  $av_A$  and  $av_B$ .

$$FG_{multi}(TRI_{xyz}) = \frac{V_{mc} + H_{mc}}{N_{mc}} \tag{2.9}$$

where:

$$\begin{aligned} \text{angset} &= \{av_{y_1z_1}, av_{y_2z_1}, av_{y_3z_1}, \dots, av_{y_1z_2}, av_{y_1z_3}, \dots, av_{y_{UT}, z_{AN}}\} \\ V_{mc} &= \sum_{\text{angset}} \Delta(av_{yz}, av_{next(y)z}) \\ H_{mc} &= \sum_{\text{angset}} \Delta(av_{yz}, av_{y_{next}(z)}) \\ N_{mc} &= \frac{|y| \times |z| \times (|y| + |z| - 2)}{2} \\ av_y &= \{a_{x_i}\} \text{ where } i = 1, 2, \dots, AX - 1 \end{aligned}$$

$$\Delta(av_A, av_B) = \frac{\sum_{i \in av_A, av_B} MAX(av_A(i), av_B(i)) - MIN(av_A(i), av_B(i))}{|av_{A,B}|}$$

$FG_{multi}$  is based on multiple operations with the  $av_{yz}$  angle vector. These elements are obtained based on the concept of a series, so the series  $S_{yz}$  from the outline  $y$  for each panel  $z$  is the set of value pairs from the  $X$ -axis ( $x_i$ ) and expression level ( $el_j$ ), which forms the outline. For each set  $S_{yz}$ , the angle of alpha  $a_{x_i}$  is the spin arctangent of the slope of the line formed by the points  $(x_i, el_i)$  and  $(x_{next(i)}, el_{next(i)})$ . The spin operation from an angle is the positive equivalent of the angle if it is negative.

$$S_{yz} = \{(x_0, el_0), \dots, (x_{AX}, el_L)\} \quad (2.10)$$

$$a_{x_i} = spin\left(\arctan\left(\frac{x_{next(i)} - x_i}{el_{next(i)} - el_i}\right)\right) \quad (2.11)$$

$$spin(a_{x_i}) = a_{x_i}, \text{ if } a_{x_i} \geq 0 \text{ and } spin(a_{x_i} = a_{x_i} + (2 + \pi) \text{ if } a_{x_i} < 0$$

To conclude, the MSL measure of a TRI tricluster as shown in Eq (2.12) is the mean of the angular comparisons of three graphical representations of a tricluster.

$$MSL(TRI) = \frac{1}{3}[FG_{multi}(TRI_{gct}) + FG_{multi}(TRI_{gtc}) + FG_{multi}(TRI_{tgc})] \quad (2.12)$$

In Section 2.5. Trigen Algorithm, we have rewritten the sentences for first and second paragraph, and changed some of the equations for pages 6753 and 6754. We also added citation for this section in [2].

Trigen algorithm is an algorithm based on the theory of evolution, genetic algorithm [1]. Genetic algorithm is an algorithm that aims to maximize a problem that will produce the best solution. Because in the Trigen algorithm we want to produce  $N$ -set triclusters, we need to do a genetic algorithm that is  $N$ -times.

For the Trigen algorithm, MSL results are added to the genetic algorithm fitness function  $FF(TRI)$  along with the individual size and overlap control [2]. MSL combined with six other factors to be a weighted average. The first three factors is  $1 - \frac{|TRI_G|}{|D_G|}$ ,  $1 - \frac{|TRI_C|}{|D_C|}$ , and  $1 - \frac{|TRI_T|}{|D_T|}$  measure the number of genes, conditions, and time of  $TRI(TRI_{G,C,T})$  compared to the size of the dataset ( $|D_{G,C,T}|$ ). Because MSL minimizes the fitness function, therefore on these three factors are made 1- each proportion to produce a TRI with a larger size when the parameter  $w_g$ ,  $w_c$  or  $w_t$  is increased. The next three factors  $\frac{R_G(TRI, SOL)}{|TRI_G| \times |SOL|}$ ,  $\frac{R_C(TRI, SOL)}{|TRI_C| \times |SOL|}$ , and  $\frac{R_T(TRI, SOL)}{|TRI_T| \times |SOL|}$  measure the number of genes, conditions, and time or depth elements  $TRI$  on the set of solutions that have been found previously  $SOL(|TRI_{G,C,T}| \times |SOL|)$  to produce  $TRI$  with a small overlap as the  $wa_g$ ,  $wa_c$ , or  $wa_t$  value increases. Finally, the main function  $\frac{MSL(TRI)}{2\pi}$  measures the  $MSL(TRI)$  proportional value close to its maximum value of  $2\pi$  to produce  $TRI$  with a small MSL value when the  $w_f$  value is increased. The default total configuration value for  $w_f$ ,  $w_g$ ,  $w_c$ ,  $w_t$ ,  $wa_g$ ,  $wa_c$ ,  $wa_t$  is 1, with fix value for  $w_f$  is 0.8 and the total others variables are 0.2.

$$FF(TRI) = \left( w_f \times \frac{MSL(TRI)}{2\pi} + w_g \left( 1 - \frac{|TRI_G|}{D_G} \right) + w_c \left( 1 - \frac{|TRI_C|}{D_C} \right) + w_t \left( 1 - \frac{|TRI_T|}{D_T} \right) \right. \\ \left. + wa_g \times \frac{R_G(TRI, SOL)}{|TRI_G| \times |SOL|} + wa_c \times \frac{R_C(TRI, SOL)}{|TRI_C| \times |SOL|} + wa_t \times \frac{R_T(TRI, SOL)}{|TRI_T| \times |SOL|} \right) \quad (2.16)$$

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## References

1. D. Gutiérrez-Avilés, C. Rubio-Escudero, F. Martínez-Álvarez, J. C. Riquelme, TriGen: A genetic algorithm to mine triclusters in temporal gene expression data, *Neurocomputing*, **132** (2014), 42–53. <https://doi.org/10.1016/j.neucom.2013.03.061>
2. D. Gutiérrez-Avilés, C. Rubio-Escudero, MSL: a measure to evaluate three-dimensional patterns in gene expression data, *Evol. Bioinf.*, **11** (2015), EBO-S25822. <https://journals.sagepub.com/doi/full/10.4137/EBO.S25822>



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