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CORRECTION

Correction: Tensor decomposition-based unsupervised feature extraction applied to matrix products for multi-view data processing

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The image for Fig 1 is incorrectly duplicated from Fig 4. Please view the correct Fig 1 here.

Citation: Taguchi Y-h. (2018) Correction: Tensor decomposition-based unsupervised feature extraction applied to matrix products for multi-view data processing. PLoS ONE 13(7): e0200451. https://doi.org/10.1371/journal.pone.0200451

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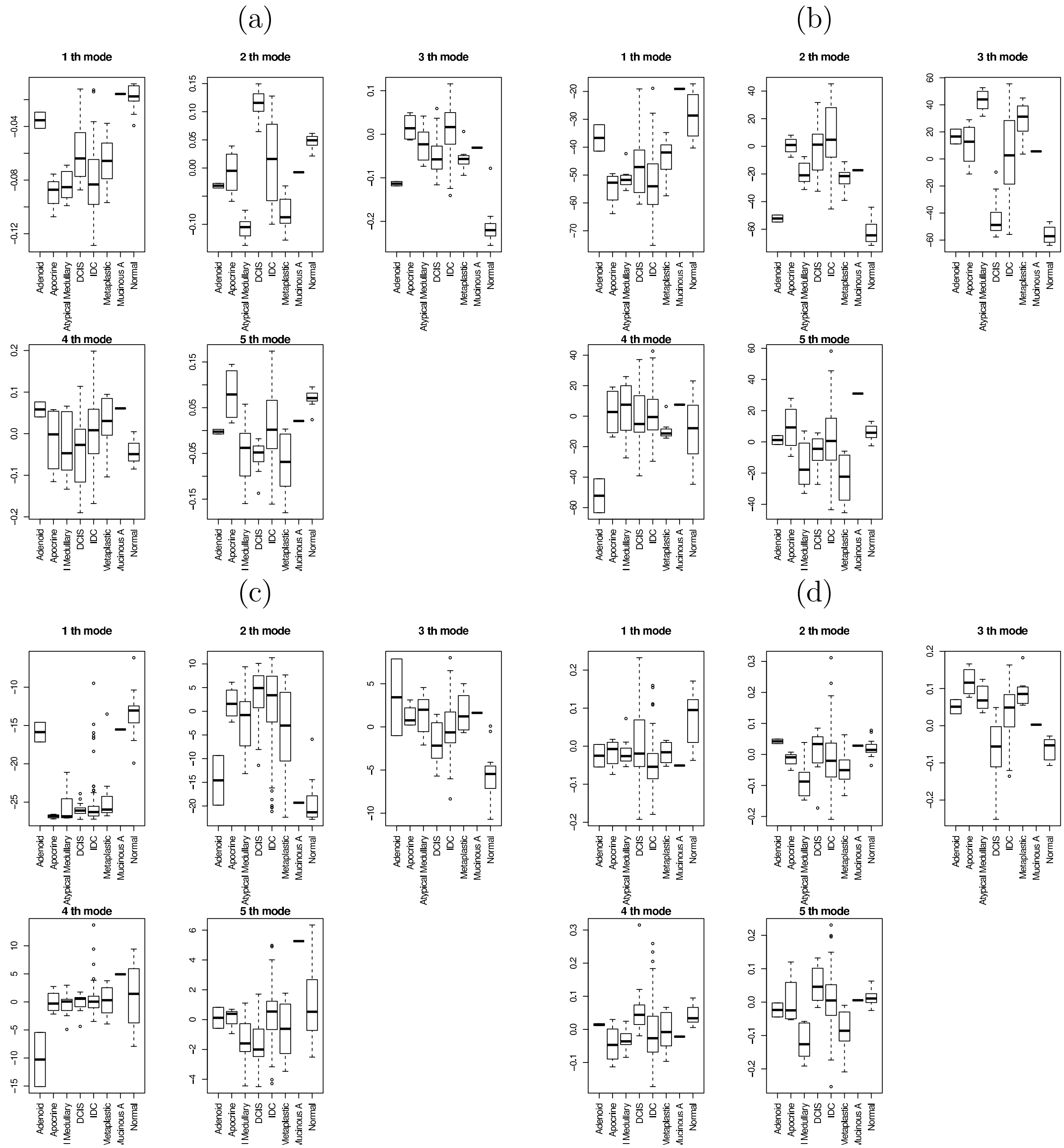

ℓ_3	(a)	(b)	(c)	(d)
1	2.39×10^{-15}	4.07×10^{-11}	3.36×10^{-27}	3.61×10^{-6}
2	5.83×10^{-14}	4.36×10^{-22}	3.91×10^{-13}	7.67×10^{-2}
3	1.36×10^{-24}	2.03×10^{-22}	7.39×10^{-9}	1.99×10^{-13}
4	2.58×10^{-2}	4.14×10^{-4}	9.32×10^{-5}	9.73×10^{-3}
5	2.12×10^{-5}	1.57×10^{-4}	2.82×10^{-5}	1.06×10^{-6}

Fig 1. Boxplots of sample singular value vectors $x_{\ell 3,j}$ (a) when TD was applied to the type I tensor and $\tilde{x}^{mRNA}_{\ell_3,j}$ (b), $\tilde{x}^{miRNA}_{\ell_3,j}$ (c), $1 \leq \ell_3 \leq 5$, when TD was applied to the type II tensor, generated from mRNA and miRNA expression profiles of multi-omics datasets. (d) Sample singular value vectors when HO GSVD was applied to multi-omics datasets. *P*-values computed by categorical regression attributed to (a) to (d) were below the figures.

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There are errors in the second paragraph of the subsection titled, "Definition and terminology of TD" in the Materials and Methods section. All instances of the following, "$G(n_1, n_2, \ldots, n_m)$" should instead read as, $G(\ell_1, \ell_2, \ldots, \ell_m)$. The correct paragraph should be: TD is the expansion of tensor $x_{n_1,n_2,\ldots,n_m}$, $n_k = 1, \ldots, N_k$, $1 \leq k \leq m$ in the form

$$x_{n_1,n_2,\ldots,n_m} = \sum_{\ell_1=1}^{N_1} \cdots \sum_{\ell_m=1}^{N_m} G(\ell_1, \ell_2, \ldots, \ell_m) \prod_{k=1}^{m} x_{n_k,\ell_k}$$

where x_{n_k,ℓ_k}, $1 \leq k \leq m$, are orthogonal matrices. Since $x_{n_1,n_2,\ldots,n_m}$ is as large as $G(\ell_1, \ell_2, \ldots, \ell_m)$, this formula is clearly overcomplete and does not give unique expansion. In this study, in order to decide $G(\ell_1, \ell_2, \ldots, \ell_m)$, x_{n_k,ℓ_k}, $1 \leq k \leq m$ uniquely, I employ the higher order singular value decomposition (HOSVD) algorithm [23], which has successfully used to analyse microarrays [24] previously. $G(\ell_1, \ell_2, \ldots, \ell_m)$ is a core matrix. x_{n_k,ℓ_k}, $1 \leq k \leq m$, are singular value matrices and their column vectors are singular value vectors. $G(\ell_1, \ell_2, \ldots, \ell_m)$, having larger absolute values, has more contribution to $x_{n_1,n_2,\ldots,n_m}$. Since the combination of x_{n_k,ℓ_k}, $1 \leq k \leq m$, associated with $G(\ell_1, \ell_2, \ldots, \ell_m)$ to which larger absolute values were attributed contributes more collectively to $x_{n_1,n_2,\ldots,n_m}$, they are more likely to be associated with one another.

Reference

1. Taguchi Y-h (2017) Tensor decomposition-based unsupervised feature extraction applied to matrix products for multi-view data processing. PLoS ONE 12(8): e0183933. https://doi.org/10.1371/journal.pone.0183933 PMID: 28841719