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OPEN **Erratum:** Predictive analytics of environmental adaptability in multi-omic network models

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This Article contains typographical errors.

In the Results section under subheading ‘METRADE: a novel method to integrate and optimize gene expression and codon usage in FBA’,

“Through the function $h(\cdot)$, the gene expression arrays have a continuous effect on the FBA model, rather than only an on/off effect on reactions as in the Boolean approaches.”

should read:

“Through the function $h(\cdot)$, the gene expression arrays have a continuous effect on the FBA model, rather than only an on/off effect on reactions as in the Boolean approaches.”

In the Results section under subheading ‘Mapping genotype-phenotype associations to multidimensional objective spaces’,

“Then, we solve the bilevel problem (4) replacing the function h with the function $k(y_i) = [1 + |\log(y_i)|]^{\text{sgn}(y_i-1)}$, where σ_i^2 is the variance of the gene set responsible for the i th reaction, and γ is a weight for the variance.”

should read:

“Then, we solve the bilevel problem (4) replacing the function h with the function $k(y_i) = [1 + \frac{\gamma}{\sigma_i^2} |\log(y_i)|]^{\text{sgn}(y_i-1)}$, where σ_i^2 is the variance of the gene set responsible for the i th reaction, and γ is a weight for the variance.”



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