

DEPARTMENT OF INTEGRATIVE BIOLOGY

the University of Texas at Austin

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June 5, 2018

Dear Editor:

We are submitting for your consideration a manuscript titled *“Predicting bacterial growth conditions from mRNA and protein abundances”*. We believe that this study makes an important contribution to our understanding of environmental-specific gene expression regulation and the utility of using microbial gene expression measurements for discriminating between different external conditions. Specifically, we trained machine learning models on a dataset of *E. coli* mRNA and protein abundances measured under various growth conditions and show that the resulting models can accurately discriminate between conditions given molecular abundances. Recent studies have speculated that species composition may serve as an important low-cost biosensor for detecting environmental toxins and contaminants. Our study expands this research to show how gene expression patterns may provide important and orthogonal information about the identity of growth conditions, particularly for generalist species that may be found across many different environments.

We believe that our work makes an essential and unique contribution that is of interest to the broad readership of *PLOS ONE.*

We thank you very much for your time and consideration and look forward to hearing from you.

Sincerely Yours,

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| Claus O. Wilke  Professor and Department Chair, Department of Integrative Biology  The University of Texas at Austin |