Computational Prediction of Gene Expression in New Organisms Based on Measurements from Model Organisms

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Determining protein abundance (PA) levels in organisms is crucial for both answering fundamental questions related to genome evolution and biophysics and for solving various biotechnological problems.

It is challenging, and in some cases impossible, to measure PA in non-model organisms. Thus, while there are hundreds of thousands of sequenced genomes, measurements of protein abundance have been generated only to a few dozen organisms.

In this study, we propose a novel approach to predict PA of non-model organisms based on measurements of PA of model organisms. To this end, we consider the evolutionary distances between the organisms in addition to the experimental PA data. We demonstrate that our approach gives better estimations of PA than approaches that are based only on the genomic information.