Abstract Submitted
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Temperature compensation model for the circadian clock of *Neurospora crassa*[1] XIAOJIA TANG, HEINZ-BERND SCHÜTTLER, Department of Physics and Astronomy, University of Georgia, JONATHAN ARNOLD, Department of Genetics, University of Georgia — In the lowly bread mould, *Neurospora crassa*, biomolecular reactions involving the *white-collar-1* (*wc-1*), *white-colloar-2* (*wc2*), and *frequency* (*frq*) genes and their products constitute building blocks of the biological clock that would response to temperature as well as light. The period of the biological clock remains stable in response to variation in ambient temperature, which is called a compensation phenomenon. Recent experimental results show evidences that the temperature compensation could be explained by the temperature sensitive translational control of production of two isoforms of the main oscillator protein FRQ: a long form FRQ^{1-989} which is more abundantly produced at higher temperature; and a short from $FRQ^{100-989}$, more abundantly produced at lower temperature. With our recently developed method of genetic network identification, we are now simulating the network's temperature response based on published experimental data. These will serve as the starting point for a simulation-prediction-experiment-simulation workflow cycle. In this cycle, the maximally informative next experiment (MINE) technology will be employed to select the best experimental control parameters specifying the temperature response to be used in the next step of the workflow cycle.

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