How periodic signals can tell time

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***Abstract* — The coordination of biological activities in daily cycles provides an important advantage for the fitness of several organisms. The circadian clock in cyanobacteria *S. elongatus* drives daily genome-wide oscillations in mRNA expression levels, controls genome compaction and supercoiling, and modulates cell division. The clock contains a core oscillator consisting of the proteins KaiA, KaiB, and KaiC, which together generate circadian oscillations in the four phosphorylation states of KaiC. This clock controls the circadian expression of the transcriptome via phosphorylation of a single protein, RpaA. In this project we address how reliably temporal information can be transmitted from the clock to downstream genes. We have developed a mathematical model that describes how cells can infer the time from an ensemble of oscillatory genes. Using techniques of Statistical Mechanics and Information theory, we are able to compute how many time-states cells can uniquely distinguish. This enables us to analytically derive the error in measuring the perception of time.**

***Keywords* — Circadian Clocks, Mutual Information, cyanobacteria, noise**

PURPOSE

Circadian clock is one of the main ways to keep track of time for a wide range of biological organisms [1]. Generating rhythms in metabolic and behavioral processes helps cells distinguish between different moments in time [2] and this in turn optimizes the cells' biochemical functionality. Clocks are connected to the genome and drive oscillations in the whole transcriptome [3]. This connection is generally mediated by a single linking protein that oscillates along with the clock and triggers the expression of downstream genes. The purpose of this work was to study the dynamical features of this read out system that lead to an accurate perception of time in cells. To analyze this network we used information theory and statistical analysis [4]. We defined some of the relations occurring between oscillatory genes that maximize the information on time. Moreover, using analytical tools we were able to derive the error relative to the measure of time for each moment of the day [5].

CONCLUSION

In the study of the behaviour of genes that read out the clock we found the optimal region in the parameter space that optimizes the information and minimizes the error on time. It turned out that the key parameter is the phase shift between the oscillatory genes. The insertion of cross correlation among the noises [6] induces changes in the optimal phase shift. Therefore, having cross correlation could help cells infer better information on time. Since oscillations in both time and space are very common in biology, our analysis has a general validity and can be equally applied to all the systems that need to infer information from oscillatory signals.

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