

## Team creates math model for circadian rhythm

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The internal clock in living beings that regulates sleeping and waking patterns -- usually called the circadian clock -- has often befuddled scientists due to its mysterious time delays. Molecular interactions that regulate the circadian clock happen within milliseconds, yet the body clock resets about every 24 hours. What, then, stretches the expression of the clock over such a relatively long period?

Cornell researchers have contributed to the answer, thanks to new mathematical models recently published.

In the August online edition of Public Library of Science (PLOS) *Computational Biology*, Cornell biomolecular engineer Kelvin Lee, in collaboration with graduate student Robert S. Kuczenski, Kevin C. Hong '05 and Jordi Garcia-Ojalvo of Universitat Politecnica de Catalunya, Spain, hypothesize that the accepted model of circadian rhythmicity may be missing a key link, based on a mathematical model of what happens during the sleeping/waking cycle in fruit flies.

"We didn't discover any new proteins or genes," Lee said. "We took all the existing knowledge, and we tried to organize it."

Using mathematical models initially created by Hong, who has since graduated, the team set out to map the molecular interactions of proteins called period and timeless -- widely known to be related to the circadian clock.



The group hypothesized that an extra, unknown protein would need to be inserted into the cycle with period and timeless, a molecule that Kuczenski named the focus-binding mediator, in order for the cycle to stretch to 24 hours.

Lee said many scientists are interested in studying the circadian clock, and not just to understand such concepts as jet lag -- fatigue induced by traveling across time zones. Understanding the body's biological cycle might, for example, lead to better timing of delivering chemotherapy, when the body would be most receptive, Lee said.

Source: Cornell University

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