Mathematical model of the circadian rhythm in a population of hepatocytes

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The circadian clock influences behavioral and physiological processes over a period of around 24 hours. Recent studies such as [2] have shown that some synchronization at the level of an isolated population of cells. Mathematical models of the circadian rhythm have already been developed for the dynamics of the intracellular regulatory network. But it is inadequate for studying the synchronization in an entire population.
To address this gap, an oscillator network model based on the Kuramoto model [1] is constructed to represent cells and their progression through the circadian cycle. Different coupling terms based on biological assumptions are created. Numerical simulations are carried out to explore the dynamics of the model and show either a synchronized or desynchronized asymptotic behavior. In addition to the numerical simulations, analytical results on the synchronization conditions in the model are discussed, highlighting the influence of the form of the coupling term, initial conditions and particular parameters.

Références

[1] Yoshiki KURAMOTO. "Chemical Turbulence". In : *Chemical Oscillations, Waves, and Turbulence*. Berlin, Heidelberg : Springer Berlin Heidelberg, 1984, p. 111-140. ISBN : 978-3-642-69689-3. DOI : 10.1007/978-3-642-69689-3_7. URL : https://doi.org/10.1007/978-3-642-69689-3_7.

[2] Flore SINTUREL et al. "Circadian hepatocyte clocks keep synchrony in the absence of a master pacemaker in the suprachiasmatic nucleus or other extrahepatic clocks". In : *Genes & development* 35.5-6 (2021), p. 329-334.

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