Job description

I am looking for a researcher to assume a 36-month post-doctoral position on the field of computational chronobiology. The position will be hosted by the Institute for Theoretical Biology, HU Berlin / Charité Berlin. The project is a bilateral JST/DFG-funded Japanese-German undertaking in understanding the spatio-temporal structure of the core clock gene expression in the mammalian SCN.

Ideal candidate

An ideal candidate would have a strong background in modeling of biological systems and theory of oscillations combined with a great curiosity for the molecular details of the core clock mechanism in the mammalian SCN. In particular, experience with numerical solutions of ODEs and PDEs would be a great advantage. Understanding the theory of synchronization and its application in chronobiology would be advantageous, too.

Project summary

The outstanding challenge of circadian biology has been and remains the understanding of the mechanisms of behavioural and psychological adaptation to changes in the light-dark cycles. Such changes can be either rather abrupt, as in the case of jet lag phase shift; or they can be seasonal which sometimes causes mood disorders as seasonal affected disorder. In mammals, including humans, the circadian rhythm of the whole body is modulated by a small hypothalamic region called suprachiasmatic nucleus (SCN). Recently, we have found that the SCN features a rich heterogeneity not only in variations in neuropeptide contents but also in distribution of intrinsic circadian periods which are surprisingly well-structured and labile to external input of light duration (Myung et al., 2012). Yet, the strength of coupling among SCN neurons can determine the fate of their overall rhythmicity in response to external driving (Abraham et al., 2010). Both results provide new clues to unravel the mechanism of how light information is coded in the SCN through controlled management of its heterogeneity. However, the sheer number of neurons available for simultaneous recording and the size of parameter set as a result make it impossible to tackle this challenge without computational methods and advanced non-linear mathematical techniques such as bifurcation analysis. We aim to supplement each other with respective specialities in computational and theoretical biology (Germany) and molecular and systems biology (Japan).

Contact

Unofficial requiries should be made to Grigory Bordyugov.

References