Usage Report for Fiscal Year 2017

Project Title:

Non-coding RNA structure

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Description of the project

Most transcripts produced by mammalian genomes, including human, are long non-coding RNAs which do not code for proteins, but instead are thought to have important roles in cellular regulation. For the vast majority of long non-coding RNAs, the biological function and mechanism of action is now unknown. Understanding the function of long non-coding RNAs is the main theme of the sixth edition of the FANTOM (Functional Annotation of the Mammalian Genome) project, currently underway at our laboratory.

The 3D structure of long non-coding RNAs may provide important clues to their function and mode of action. In this project, we evaluate the potential of simulation techniques to investigate the 3D structure of non-coding RNAs, using only the nucleotide sequence of RNAs as input information. For this purpose, we have been using the Amber molecular dynamics simulation software, which is a very mature software package oftentimes used for the simulation of proteins in 3D space.

We are finding that molecular dynamics simulations of RNA remain very challenging, in particular with regards to simulation time and convergence issues. We are considering whether integration of experimental data such as ic-SHAPE [1], which provides information on the secondary structure of RNA, may help to infer the tertiary structure of RNA.

[1] Spitale R.C. *et al.*: Structural imprints in vivo decode RNA regulatory mechanisms. *Nature* **519** (7544): 486-490 (2015).