

Project Title: Predicting 3D structure of the human genome

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In recent years the long noncoding RNA is emerged as an important regulatory element in the cell. The long non-coding RNAs were originally thought to be nonfunctional “junk RNA”, however studies have shown that they play an important role in different biological processes, in particular cellular regulation. However, the understanding about the mechanism behind how the long non-coding RNAs works is still lacking. The three dimensional structure of the genome was predicted in different cell types as part of FANTOM6 project to identify the function of long non-coding RNAs.

The Hi-C data was mapped to the human genome and the mapped reads were processed using different Hi-C related tools for the analysis. Three-dimension structure prediction is a computationally intensive process and the supercomputer facility was used extensively to determine these structures.

Currently, different databases are getting integrated together to determine the potential function of the lncRNAs. The entire analysis will take another few months to be finished as many more cell types are planned to be included in the project. This primary results of the analysis are promising and further exploration of the data will be providing a platform for understating the role of lncRNAs in the cell.

Usage Report for Fiscal Year 2017

Fiscal Year 2017 List of Publications Resulting from the Use of the supercomputer

[Oral presentation at an international symposium]

1. The role of 3D localization of long non-coding RNAs in the nucleus on their function, Consortium of Biological Sciences (ConBio2017), December 2017, Kobe, Japan.