

Project Title: Predicting 3D structure of the human genome

Name:

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| <p>1. Background and purpose of the project, relationship of the project with other projects</p> <p>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. Several studies have used 3D chromosome conformation data to identify the function of specific non-coding regions in the genome. 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.</p> | <p>3. Result/Conclusion</p> <p>Currently, different databases are getting integrated together to determine the potential function of the lncRNAs. Also, many other cell types will be integrated in the future to extend the scope of study.</p> |
| <p>2. Specific usage status of the system and calculation method</p> <p>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.</p> | <p>4. Schedule and prospect for the future</p> <p>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.</p> <p>5. If no job was executed, specify the reason.</p> <p>Not applicable</p> |

Usage Report for Fiscal Year 2018

Fiscal Year 2018 List of Publications Resulting from the Use of the supercomputer

[Paper accepted by a journal]

None

[Conference Proceedings]

None

[Oral presentation]

- “*Association between Three-Dimensional Localization and Function of Long Noncoding RNAs*” at Chromatin Architecture and Chromosome Organization, Keystone meeting, Whistler, British Columbia, Canada, March, 2018.
- “*Identifying long noncoding RNAs partners in human cells*” at Human Genome Meeting, Yokohama, Japan, March 2018.
- “*Identifying long noncoding RNAs partners in human cells*” at RIKEN Trainee session, Human Genome Meeting, March 2018.

[Poster presentation]

- “*Association between Three-Dimensional Localization and Function of Long Noncoding RNAs*” at Chromatin Architecture and Chromosome Organization, Keystone meeting, Whistler, British Columbia, Canada, March, 2018.
- “*Identifying long noncoding RNAs partners in human cells*” at Human Genome Meeting, Yokohama, Japan, March 2018.

[Others (Book, Press release, etc.)]

None