Usage Report for Fiscal Year 2019

Project Title:

Predicting 3D structure of the human genome

Name:
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1. Background and purpose of the project, relationship of the project with other projects

The goal of project is to functionally annotate the long non-coding RNAs in human cells.

The mechanism underlying transcription regulation is still not well understood. In recent years the long noncoding RNA has emerged as an important transcription regulatory element. However, it is still not well established how the long non-coding RNAs (lncRNAs) regulate the process. Several studies have shown 3D location of lncRNAs dictates their function. 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.

2. Specific usage status of the system and calculation method

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. Identifying interacting genomic regions is a computationally intensive process and the supercomputer facility was used extensively to determine these structures.

3. Result

We have obtained interacting genomic regions in multiple cell types. Next we have overlaid the annotations to identify the different gene interacting with lncRNA locus. We have found both cell type specific and common features among cell types.

4. Schedule and prospect for the future

We need few more months to finish the analysis as we are integrating different data sets types to further interpret the results.

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Fiscal Year 2019 List of Publications Resulting from the Use of the supercomputer

[Paper accepted by a journal]

None

[Conference Proceedings]

None

[Oral presentation]

1. Agrawal Saumya, Ramilowski Jordan, Yip Chi Wai , Hon Chung Chau, Yasuzawa Kayoko, Ito Masayoshi, Kasukawa Takeya, Kondo Naoto, Yagi Ken, Suzuki Harukazu, Dostie Josee, Shin Jay W, De Hoon Michiel Jan Laurens, Carninci Piero. Functional annotation of long non-coding RNAs based on their spatial localization, The Biology of Genomes, Cold Spring Harbor Laboratory, New York, United States May 7, (2019)
2. Agrawal Saumya, Ramilowski Jordan, Yip Chi Wai, Hon Chung Chau, Yasuzawa Kayoko, Ito Masayoshi, Kasukawa Takeya , Kondo Naoto, Yagi Ken, Suzuki Harukazu, Dostie Josee, Shin Jae Woo, De Hoon Michiel, Carninci Piero. Functional annotation of long non-coding RNAs based on their interacting partners in three-dimensional space, The 13th International Workshop on Advanced Genomics, Hitotsubashi Hall, Tokyo, Japan June 25, (2019)

[Poster presentation]

1. Agrawal Saumya, Severin Jessica, Yasuzawa Kayoko, Ito Masayoshi, Kasukawa Takeya, Kondo Naoto, Yagi Ken, Suzuki Harukazu, Dostie Josee, Hon Chung Chau, Shin Jay W, Carninci Piero, De Hoon Michiel Jan Laurens. Repressor human lncRNAs, Long Noncoding RNAs: From Molecular Mechanism to Functional Genetics (X2), Whistler Conference Centre , Whistler, British Columbia, Canada February 24, (2019)
2. Agrawal Saumya, Ramilowski Jordan, Yip Chi Wai, Hon Chung Chau, Yasuzawa Kayoko, Ito Masayoshi, Kasukawa Takeya , Kondo Naoto, Yagi Ken, Suzuki Harukazu, Dostie Josee, Shin Jae Woo, De Hoon Michiel, Carninci Piero. Functional annotation of long non-coding RNAs based on their interacting partners in three-dimensional space, The 13th International Workshop on Advanced Genomics, Hitotsubashi Hall, Tokyo, Japan June 25, (2019)

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

None