RICC Usage Report for Fiscal Year 2013

Project Title:

Whole-genome alignment of higher organisms

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Our laboratory is interested in transcriptomics and transcriptional regulation in higher organisms. To analyze gene regulatory networks, we make use of transcription factor binding site predictions based on known binding motifs. The accuracy of transcription factor binding site prediction can be improved significantly by considering the conservation of transcription factor binding sites between organisms. For this purpose, we align the genome sequences of higher organisms against each other. Since the genome sequence of higher organisms is very long (about 3 GB for human), these whole-genome alignments take a considerable amount of time, in particular because the genome each organism needs to be aligned to the genomes of each of the other organisms. Whole-genome alignments are perfectly suited for parallelization, since the alignment of each pair of chromosomes can be run independently. We also predicted transcription factor binding sites for tens of thousands of position-weight matrices, which would be very difficult to accomplish in a reasonable amount of time without the resources of the RICC.

This project was primarily focused on supporting the FANTOM5 project. In the beginning of FY2013, we finished the analysis for FANTOM5, and therefore we will not need to continue to use the RICC resources in FY2014.

Usage statistics for FY2013 are shown in the Table.

	Limit (h)	Used (h)	Used (%)
Total	832200.0	768.4	0.1%
+- mpc		1.8	
+- upc		488.6	
+- ssc		278.1	

Fiscal Year 2013 List of Publications Resulting from the Use of RICC[Publication]

[Proceedings, etc.]

[Oral presentation at an international symposium]

Alistair Forrest: “A promoter level expression atlas”. The 35nd Annual Meeting of the Molecular Biology Society of Japan (MBSJ), Kobe, Japan, 2013.

[Others]