

Project Title: Using a supercomputer system in exploring the variability of individual human genomes

Host Laboratory: Laboratory for Functional Analysis *In Silico*

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Our institute owns a supercomputer system that is primarily used for human genome research. Thus, in this proposal, visitor students will learn the basics of genome sequence data analysis using this facility. This project, of course, greatly depends on the current skills of applicants in using computers. If he or she is a novice in computer programming, it will be a good opportunity to learn a conventional script language, such as Perl, Python, or Ruby, as well as the R language for statistical analyses; if he or she has a little experience in computer programming but has not used a relatively large computer system, maybe he or she wants to experience the RNA-seq data analysis using some real data downloaded from a public database. Finally, if he or she is already a hacker, we will provide him/her with an opportunity in performing his/her own project using our supercomputer system. For example, since we maintain a mirror of the so-called 1000 genome project, it might be interesting to explore the sequence variability between individuals using such data. In our laboratory, there are many international students and then any visitor would not feel isolated during his/her stay.

Publications from our lab:

Please check the web site: http://fais.hgc.jp/paper/publication_en.html