

Position: Bioinformatics Scientist Opportunity at Tohoku University in Japan

Tohoku University School of Medicine launched the large-scale prospective cohort study using high throughput sequencing technology. In this project, as the final goal, whole-genomes of 150,000 people in Tohoku area are planned to be sequenced and other multi-omics data, e.g. epigenomics, transcriptome and metabolome, will be also measured to boost the discovery by combining with the massive core whole-genome dataset.

The laboratory mission of Professor Masao Nagasaki, Ph.D., is to setup the supercomputer environment that fully automates the standard pipeline analysis of these data. Our research group will mainly focus on the downstream analyses on that environment using information science and statistical methods, especially combining other sequencing data, e.g. RNA-Seq, BS-Seq, ChIP-Seq and Exome-Seq, and medical diagnostics data. We already have the experiences to setup standard pipeline analysis on super computer environment and apply analyses to these multi-omics dataset [Nature, Yoshida et al 2011; Nature Genetics, Fujimoto et al 2010]. Recently, our laboratory is also taking the responsibility to reveal the direct-reprogramming mechanism using HiTSeq technology on supercomputer with the collaboration with Dr. Suzuki [Nature; Sekiya et al 2011].

RESPONSIBILITIES:

From the information science and statistical point of view, our research group will tightly collaborate with other medical laboratories including wet-lab experimental design to minimize the steps and maximize productivity of scientific discovery. The candidate must have experience in computer programming and high-throughput analysis of biological data, as the position involves integration of large-scale data sets, design and implementation of data processing pipeline for whole-genome, transcriptome, and/or epigenomic data on supercomputer. The researchers who can develop new algorithm or statistical model to multiomics HiTSeq data are highly welcomed.

REQUIREMENTS:

- Ph. D. degree in bioinformatics, computational biology, computer science, statistics, mathematics, molecular biology, biochemistry, biophysics, or related fields.
- At least two years' experience annotating and analyzing genomic data.
- Advanced skills in two or more of shell script, Perl, Python, C++, Java or Ruby.
- Ability to process a large amount of genomic data efficiently.
- Solid science background.
- Good communication and interpersonal skills.
- Knowledge of bioinformatics concepts, methods, and tools.
- Familiarity with genomic data, tools and databases.
- Strong initiative and ability to take ownership of assigned tasks and projects.
- Demonstrated attention to detail and analytical skills.
- Ability to work effectively in a team environment .

SALARY:

Commensurate with experience. Minimum starting salary is \$45,000/year before tax and health insurance (will vary with the exchange rate between yen and dollar). The contract can be extended every year and up to maximum five years (or nine years, depending on research grant).

POSITION:

Research Associate (Researcher)

HOW TO APPLY:

Applicants should send CV, a brief statement of research interests, up to three reprints/preprints, and arrange for two letters of recommendation. Application material should be sent by email (a single PDF file preferred) to Prof. Masao Nagasaki: ig-nagalab-jimu at ml.megabank.tohoku.ac.jp

REFERENCE:

<http://nagasakilab.csml.org/en/>

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Professor