

Division of Electrical Engineering and Computer Science	Research field	Genome informatics	Lab. ID EC26
Laboratory web site	http://gie.ec.t.kanazawa-u.ac.jp/		
Research subjects			
<p>After completion of the human genome project in 2003, the large-scale research for human genes was started for the purpose of clarification of the biological mechanism and medical development. Therefore, implementation of comprehensive genetic engineering experiments and computer analysis for large experimental data obtained from them are needed. For this reason, we conduct various genetic research by genetic engineering experiments and computer analysis.</p>			
Master/Doctor course: Education policy, curriculum, typical activity in the laboratory			
<p>Students read a text book in a programming language in turn, and answer an end-of-chapter question. Moreover, students read English papers for their research to give an explanation of their contents at laboratory meetings. They also report the progress in their research.</p>			
Daily life in the laboratory, etc.			
<p>Students can choose their own research themes according to their interest. They can also borrow a personal computer and use it freely in our laboratory. Server computers are also in our laboratory, because statistical calculations often require large amounts of memory and a long period of time. There are also laboratory equipments to perform genetic engineering. In addition, various events will be held jointly with other laboratories.</p>			
Message or comments by the laboratory faculty staffs			
<p>The students who go on to the master's program will be assigned to a teaching assistant for undergraduate practice education. While most graduates have an employment in electrical and electronic or IT companies, some graduates find a job in the civil service and banking.</p>			
Recent Master theses in these 3 years (+ more if appropriate)			
year.month	Thesis title (including English translation of Japanese thesis title)		
2017.3	Identification of allele-specific methylation regions from NGS data		
2017.3	Identification of mouse substrain-specific epigenome		
2017.3	Improvement of a gene set analysis method to identify differentially expressed gene sets		
2016.3	Function prediction of transcription factors using histone acetylation patterns		
2015.3	Elucidation of the function of MAP kinase scaffold proteins, JSAP1 and JLP by gene expression analysis		
2014.3	Improvement for an identification method of differentially expressed gene sets and its accuracy verification		
2014.3	Presumption of pleiotropic genes using gene networks		
2013.3	Validation of MIMGO: a method to identify differentially expressed GO terms in a microarray dataset		
Recent Doctoral theses in these 3 years (+ more if appropriate)			
year.month	Thesis title (including English translation of Japanese thesis title)		
Laboratory mail address	Yoichi Yamada <youichi *at* t.kanazawa-u.ac.jp>		