

DATE: Day 30 Month 06 Year 2017

**SUMMARY of
2016 RESEARCH RESULTS REPORT
For International Collaborative Research with IPR, Osaka University**

Research Title		Software tools and method for interpreting mass spectrometry experiments and proteomics data
Applicant	Name	Jorge Fernandez de Cossio
	Affiliation	Center for Genetic Engineering and Biotechnology
	Present Title	Dr. Mathematical Science, Senior Researcher
Research Collaborator (Host PI)		Prof. Toshifumi Takao
<p>Summary</p> <p>We address methods for the join analysis of genome and proteomics data. An algorithm for photpeak detection has been adopted for the accurate positioning of the individual peaks of the isotopic distribution in mass spectra, previous to isotopic distribution fitting. The methods improved the efficiency for the a priori blind detection of low counting mass peaks, and are being implemented in the accurate analysis of MS/MS fragment ions by posteriori isotope peaks fitting. We derive a bias introduced in patient-only data when the analysis is restricted to somatic mutation and germline variant are filtered out. Redesign of models for the analysis of somatic data in cancer patients are required when the proportion of inherited alterations are moderate or large, to avoid the bias.</p>		

***Deadline: July 31, 2016**

***Please submit it to E-mail: tanpakuken-kyoten@office.osaka-u.ac.jp.**

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