DATE: Day 17 Month ____ Year 2018

SUMMARY of
2017 RESEARCH RESULTS REPORT
For International Collaborative Research with IPR, Osaka University

Research Title		
Applicant	**Name**	**Jorge Fernandez de Cossio**
	Affiliation	**Center for Genetic Engineering and Biotechnology**
	Present Title	**Senior Researcher**
Research Collaborator (Host PI)		**Prof. Toshifumi Takao**

Summary

Interaction patterns provide valuable information on the mechanism of action of associated alteration. Various measure of interactions co-exist in the literature, and long-controversy persist on their relative merits. On the other hand, mass spectra data carry most of the information provided in proteomics experiments. Detailed and accurate analysis of peaks is then crucial to capture the maximum information of the mass signals and their concurrency. Particular rearrangements observed in MALDI TOF instrumentation (Takao's lab finding) confer peculiar peak-shape than can provide valuable information on peptides and protein identification.

We develop a customized algorithm for the systematic and exhaustive identification of peaks apex and valleys, and a second pass to positioning the isotopic-average distribution that best correlates with train of consecutive apex. A range of resolution is scanned to discern between particular peak-shapes, like those observed in MALDI TOF.

We also demonstrate that additive, multiplicative, and odd ratio neutral models for interactions, widely advocated, are biased and leads to spurious missing interactions (Fernandez-de-Cossio, Fernandez-de-Cossio Diaz, Takao, & Perera Negrín, 2017).

Interaction subject occupy an inescapable place in big-data analysis, in particular for the analysis of large scale genomics and proteomics experiment. Conceptual and pragmatic advances are central for consistent and optimal inference interaction. We anticipate further fruitful collaboration with IPR in this controversial subject.

***Deadline: May 18, 2018**
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