ERRATA

Computational identification of discriminating features of
pathogenic and symbiotic Type III secreted effector proteins
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It was pointed out that biological interpretation of the above paper was wrong.    In fact, discriminating features reported in this paper should have been interpreted as those of effector proteins in animal and plant bacteria, rather than pathogenic and symbiotic bacteria.    The paper was based on "animal pathogen" and "plant symbiont" dataset of Arnold (2009).    However, the latter was for *Pseudomonas* which can cause diseases in plants, and the authors weren't aware of it.

At the same time, three proteins of non-plant organisms used in the paper (Q84H14, Q6MCQ9, A1WKP8) should be excluded.    The authors have done reanalysis after excluding them.    Overall results are consistent with the previous results, but the authors would like to report two main differences here.    First, four features (isoleucine, acidic amino acids, lysine, and arginine) attained the smallest minimum GBIC.    Second, the region that gave the highest classification by the four discriminating features was N26-68.

A file which corrected the interpretation and all results based on the reanalysis is available at http://yahara.hustle.ne.jp/correction/corrected_doc_TBIO2010.pdf

This ERRTA was submitted to the editor-in-chief on May 22 in 2013, which was then passed to IPSJ (Information Processing Society of Japan).

The authors' primary purpose was to develop a methodological framework in the context of feature selection and classification problems in the presence of correlated relationships among features.    The 1st author has full responsibility for preparing the dataset and writing the paper, would like to sincerely apologize for it, and will be careful in order not to make this kind of error again.

Sincerely,