QBiC CDB JOINT SEMINAR

Yoshihiro Taguchi, Ph.D.

Faculty of Science and Engineering, Chuo University

Date & Location	Thursday, March 12, 2015 16:00 - 17:00 CDB Seminar room A7F (2-2-3 Minatojima-minamimachi, Chuou-ku, Kobe) There will be a video broadcast in OLABB 1F lounge
Title	**How to screen out liars**

Abstract

Suppose that you have ten samples that consist of five controls and five treated samples. Then, you are responsible for identifying "significant" genes among several thousand genes. There can be many seemingly promising candidates. How can you be confident which ones are truly significant? It is something like identifying who tells the truth if thousand suspects were investigated. The detective already had the answer; Ask them one by one and try to find who declared samely. Unfortunately, this "pairwise comparison criteria" does not always work in the case of the gene screening, since pairwise comparison increases the number of tests which may miss many modestly (but in fact truly) significant candidates.

In this talk, I propose the solution that can overcome this difficulty; i.e., Ask them whose opinion is the majority. The reason why it works is simply because many cannot lay simultaneously without mutual negotiations. I demonstrate that this "who is majority" strategy is easily achieved by applying principal component analysis not to samples, but to features (i.e., genes, promoters, proteins, and so on). This strategy works surprisingly well for e.g,, identifications of promoters with aberrant methylation associated with diseases, circulating microRNA that can discriminate patients from healthy controls, genotype specific DNA methylations associated with diseases, simultaneous anomaly of gene expression and promoter methylations also associated with diseases, and differential protein expression during bacterial culture.

Host	Tatsuo Shibata Laboratory for Physical Biology tatsuo.shibata@riken.jp Tel: 078-306-3264