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On bringing genome informatics innovation to life science industry in Odaiba

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Abstract

We are living in biological big data era. In the years ahead, genome information of many individuals will be sequenced. However, their applications to keep our health and avoid side effects of drugs are not straightforward because of the lack of fundamental computational and statistical methods to use them efficiently and accurately. In this talk, as an example to advance the use of genome big data by fundamental computational and statistical innovation, we introduce a new multiple testing correction method called Limitless Arity Multiple-testing Procedure (LAMP), which is a multiple-testing correction method to find statistically significant combinatorial effect, such as complexes of transcriptions and epistatic effects in GWAS data, by combining biological big data. While our initial application results of LAMP to transcription factor data and GWAS data showed the possibility to give us deeper understandings of the cellular mechanisms, further sophisticated algorithm and the biologist-friendly procedure are required in order that LAMP is widely used in life science community. I introduce the current situation and discuss how to bridge new computational methods to life science industry.