Fast-computation of multi-omics interactions effects

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Abstract:

In the context of multi-omics data analysis, the traditional approach only considers the main effects, either by univariate or multivariate analysis, to search for associations between biomarkers such as metabolites, proteins or microbiome, and a given phenotype.

However, it is now generally accepted that taking into account the interactions effects in a model can improve the estimation of phenotypic variance, at the cost of a greater multiple testing burden. Indeed, while classical associations schemes (i.e. hypothesis testing) in a high dimension setting are subject to false positives, and therefore fail to detect small effect, it can only get worse when considering interactions effects.

In this work we tried to face part of the limitations mentioned above by proposing a novel approach for efficiently detecting interactions between complementary datasets in a high-dimensional setting with a reduced computational cost [1]. The method, named SICOMORE, reduces the dimension of the search space by selecting a subset of supervariables in the two complementary datasets. These supervariables are given by a weighted group structure defined on sets of variables at different scales. A Lasso selection is then applied on each type of supervariable to obtain a subset of potential interactions that will be explored via linear model testing.

We compare SICOMORE with other approaches in simulations, with varying sample sizes, noise, and numbers of true interactions. SICOMORE exhibits convincing results in terms of recall, as well as competitive performances with respect to running time.

In the context of an exposome study conducted on 200 Chinese women living in polluted cities, we used the algorithm to detect interaction effects between metabolomic and metagenomic markers related to cosmetic disorder.

Keywords: biomarkers; association; High dimension; lasso; SICOMORE

References:

1. Guinot, Florent et al. "Fast computation of genome-metagenome interaction effects." *Algorithms for molecular biology : AMB* vol. 15 13. 1 Jul. 2020, doi:10.1186/s13015-020-00173-2

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