

COVID-19 GWAB : Functional Analysis of COVID-19 GWAS Data with Network-based Boosting

Seungbyn Baek¹ and Insuk Lee^{1*}

¹ Department of Biotechnology, College of Life Science & Biotechnology, Yonsei University, Seoul 03722, Korea

Abstract

Large scale Genome-wide association studies (GWAS) for COVID-19 have been conducted through various projects and institutions which are largely organized through COVID-19 Host Genetics Initiative (HGI). While such studies can be helpful for identifying disease-related genotypes, it is often difficult to fully understand and interpretate the results for translational research and for connecting to disease-related phenotypes. Furthermore, strict p-value threshold for significance limits number of related genes and genomic elements that can be analyzed for discovery of novel disease-related candidates. To overcome such limitations, it is possible to utilize comprehensive functional human gene networks for boosting GWAS results by identifying various disease-related genes connected on the networks. In 2017, Such algorithm for network-based boosting called Genome-Wide Association Boosting (GWAB) was developed. GWAB has been adapted and optimized for this COVID-19 specific GWAS study. As an upcoming web-based tool, COVID-19 GWAB can provide boosting results of various COVID-19 GWAS datasets and further provides multi-omics gene sets for validation. Through this study, we expect to discover novel candidate genes that are critical in our understandings and treatments of COVID-19.