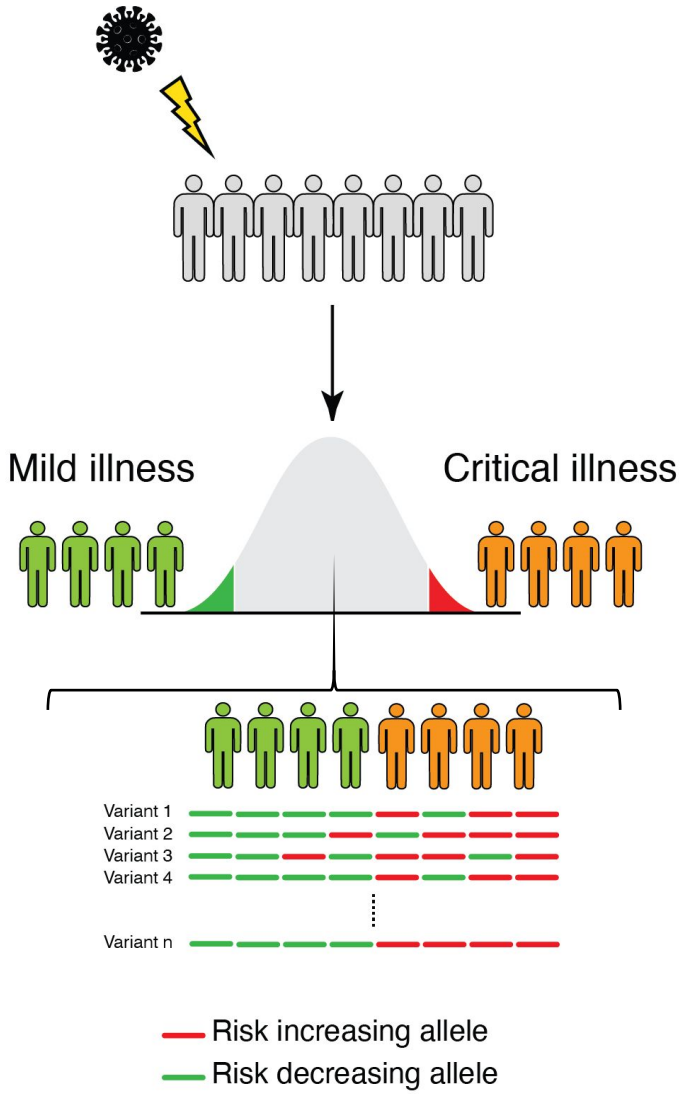
COVID-19 polygenic risk score (PRS)



- **PRS:** a tool for predicting individuals' genetic risk relative to population's average.

$$PRS_i = \sum_{1}^{m} d_{i,v} \,.\, \beta_v$$

d: allele count of variant **v** in individual **i**
***β*:** effect size of variant v
m: total number of variants

- **Challenge:** PRS calculated base don GWAS in one population may be inaccurate in other populations.
- **Goal**: To calculate PRSs for COVID-19 susceptibility & severity, test their performance, & improves their accuracy for trans-ethnic risk prediction.

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PRS calculation

1. Effect size estimation
2. Testing different p-value thresholds for variant selection
3. Selection of independent variants
4. PRS calculation
5. Testing prediction accuracy (stratified by genetic ancestry)
6. Improve trans-ethnic accuracy (fine mapping, functional annotation: *Amariuta & Ishigak et al Nat Gen, 2020*)

PRS application

- Starting from *BioMe*

- Using the selected set of SNPs to generate PRS for other cohorts and testing its predictive power.

- **Next step**: comparing immunophenotypes in individuals that are at high or low risk for COVID-19 susceptibly/severity.