Using machine learning applications to predict patients' risk of developing COPD

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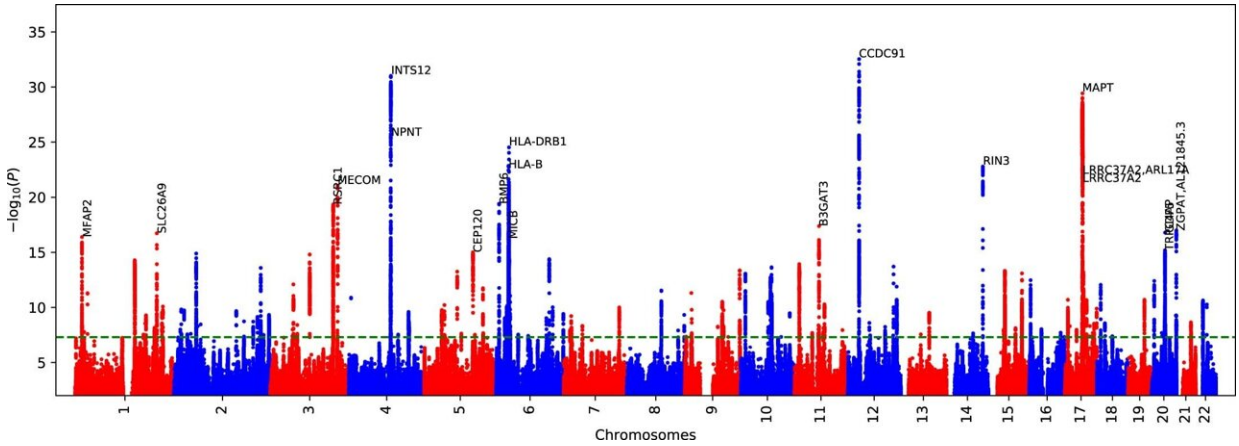

ML-based COPD GWAS Manhattan plot via DeepNull. We performed ML-based COPD GWAS where we used the same set of covariates as the Fig. 4 with one additional covariate provided by DeepNull. DeepNull model predicts the ML-based COPD using age, sex, genotype-array, and FEV_1/FVC as inputs. The additional DeepNull-covariate is the DeepNull model prediction of ML-based COPD. DeepNull learns a function (that is, linear or non-linear) that predicts ML-based COPD via age, sex, genotype-array, and FEV_1/FVC as inputs. Thus, this analysis is similar to the ML-based COPD GWAS conditional on FEV_1/FVC where instead of assuming that FEV_1/FVC has linear relationship with ML-based COPD, DeepNull handles cases where age, sex, and FEV_1/FVC can have non-linear relationship with ML-based COPD. We obtained p-values from BOLT-LMM using a two-sided test. The green dashed line is the genome-wide significant level (P

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