

Numero of scenario	Dataset	Size of training set	Causal SNPs (number and location)	Distribution of effects	Heritability	Simulation model
1	All 22 chromosomes	6000	30 in HLA 30 in all 300 in all 3000 in all	Gaussian Laplace	0.8 0.5	simple fancy
2	Chromosome 6 only	-	-	-	-	simple
3	All 22 chromosomes	1000 2000 3000 4000 5000	300 in all	-	-	-

Table 1: Results for the real Celiac dataset. The results are averaged over 100 runs where the training step is randomly composed of 12,000 individuals. In the parentheses is reported the standard deviation of 10^5 bootstrap samples of the mean of the corresponding variable. Results are reported with 3 significant digits.

Method	AUC	pAUC	# predictors	Execution time (s)
PRS-max	0.824 (0.000704)	0.0286 (0.00016)	9850 (781)	148 (0.414)
logit-simple	0.888 (0.000468)	0.0414 (0.000164)	3220 (62)	83.8 (1.27)