(1) End user loads GWAS files of interest. These can be either in VCF or PLINK format. For end users with raw .CEL files, it is recommended to use the Cloud-based GWAS Analysis Pipeline for Clinical Researchers to obtain VCF files.

(2) Prior to epistatic analysis, of interest to carry out single SNP association analysis. This is performed using the widely used tool PLINK.

(3) Next, epistatic analysis is carried out using an optimised implementation of BOOST that takes advantage of the multi-core environment of modern computers.

(4) The next step is to use the FaST-LMM analysis tools. Prior to using these, the user files are converted to ensure compatibility.

(5) Single SNP association analysis using FaST-LMM, that corrects for population structure.

(6) Finally, epistatic analysis using an optimised multi-core implementation of FaST-LMM.