An integrated system supports genotype calling and haplotype/phenotype translation for PGx implementation

# Main idea

The single base primer extension method (SBE) is an effective and sensitive approach that can cover over 30 loci in a single reaction. As a cost-effective approach, this method has been widely used in many applications such as forensics, disease diagnosis, and pharmacogenetics (PGx).

Several studies confirmed the benefit of panel-based PGx testing in clinical settings and identifying star-alleles (haplotypes) from customed panels plays a role in PGx implementation. Many tools have been developed such as PharmCAT, Stargazer, Astrolabe, and Aldy and all of them mainly focus on analyzing Next-Generation Sequencing data. Moreover, genotyping software does not support matching haplotypes (GeneMapper in our case). Therefore, identifying haplotypes of customed PGx test panels remains challenging.

Conventionally, PGx experts often have two options (Figure 1A): (1) they manually identify the haplotypes from raw intensity data (chromatogram plots); or (2) they identify genotype results using a genotyping software and upload the result to other tools to match haplotypes. Then, they must manually manage the data and analytical results, and history for further steps. This way raises several following risks: firstly, manual processes increase human biases; secondly, it is hard to record and track the history of the whole process; finally, it is difficult to scale to many testing samples because it requires more effort to manage all those data and processes.

In this work, we developed a cloud system that integrates all processes to overcome these challenges (Figure 1B). Once PGx experts upload the raw intensity data to the system, they can do all further steps: identifying genotypes, quality controlling, and matching haplotypes/phenotypes. All activity logs have also been recorded for any further tracking steps. Figure 2 demos how the system implemented on a website application.

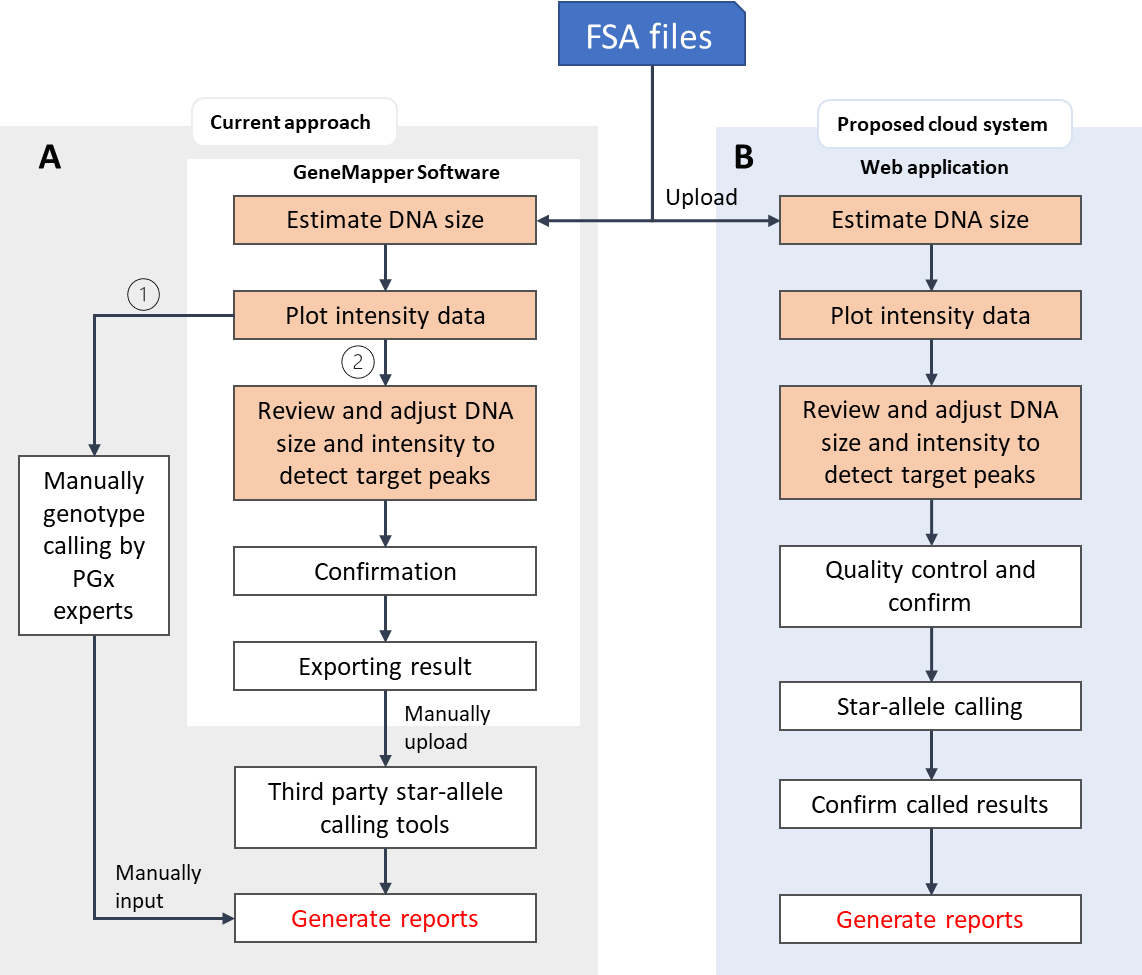


Figure 1. Overview of current approach and purpose system

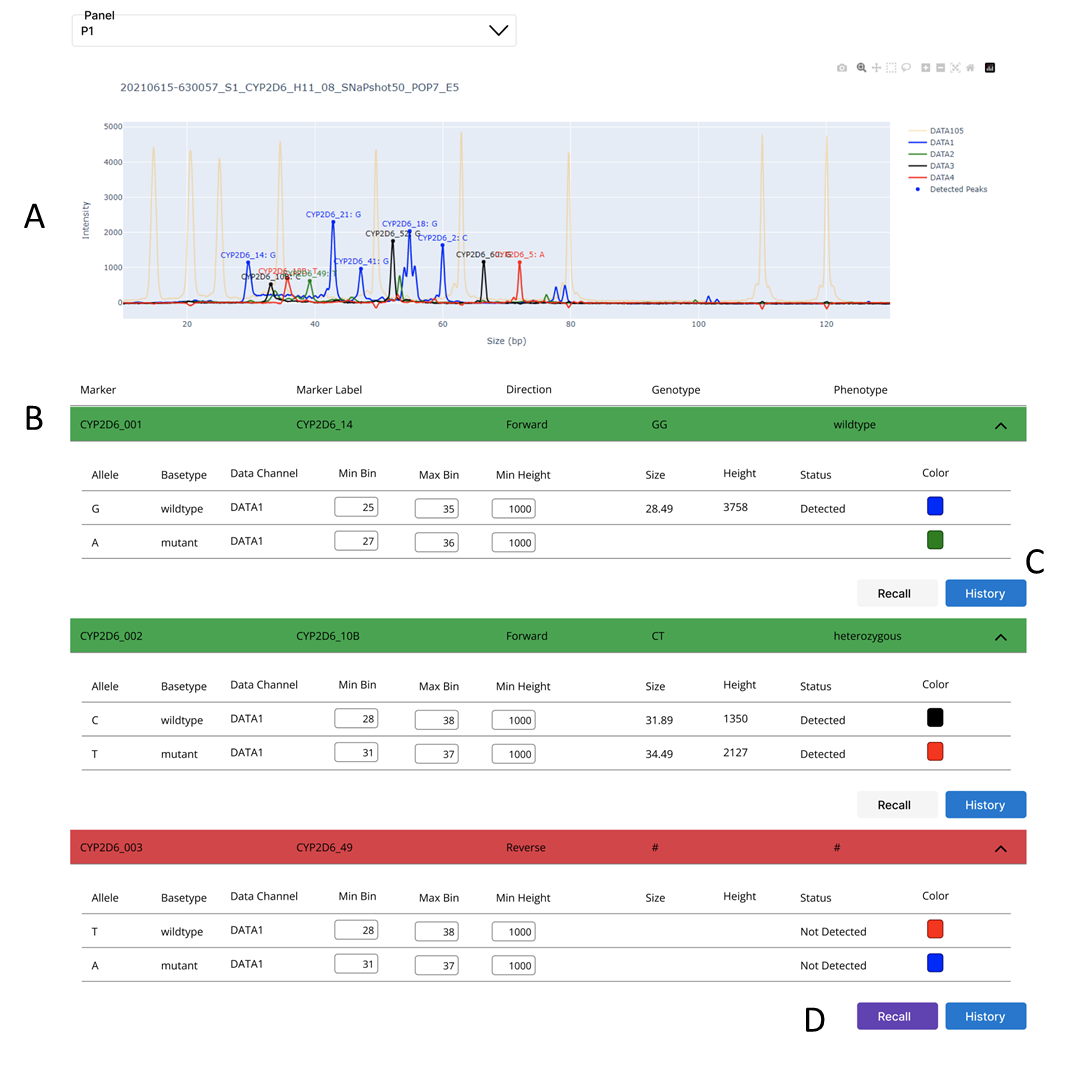


Figure 2. Prototype of the system implemented on web application; (A) raw intensity plot with detected markers; (B) genotype calling results of each marker in a panel; (C) history of each marker; (D) user can adjust data and re-identify genotype for a specific marker.