

A Laboratory Information Management System (LIMS) for a Small-Scale Single Nucleotide Polymorphism Detection**Barenboim, Maxim, Guo, Yongjian, and Jamison, Curtis*****School of Computational Sciences, George Mason University, Manassas, VA, USA**

Diversity within a population is the result of genetic differences. The most common source of genetic differences are single nucleotide polymorphisms, which account for over 90% of all human phenotypic differences. While several massive projects exist to catalog all known SNPs, we are still faced with the task of correlating genotypes to phenotypes. Much of the latter work will be performed in small laboratories focusing upon a limited number of genes. These labs are often ill-equipped to handle the large amount of data generated by SNP detection experiments.

Laboratory information management systems (LIMS) are often used to ease the task of data management. We have created a LIMS system to support small-scale SNP detection experiments. Based upon gene resequencing protocols, the SNP LIMS provides most of the required organizational and analysis tools to perform SNP detection experiments. The SNP LIMS eases the interaction between the bench scientist and the computer, making it easier to integrate the computational tools into the experimental procedure.

The SNP LIMS is a semi-automated system for SNP analysis and storage that consists of a sequencing assay, semi-automated dataflow, and analysis tools which will speed up the workflow and increase the amount of data that can be treated in the laboratory. The analyses tools help, as well, avoid errors that would appear with the handling of increasing amounts of data. The database is being expanded to include clinical and demographic data to allow correlation between SNP frequency and clinical measures (e.g. race or disease progression). The SNP LIMS software is freely available at <http://rna.gmu.edu/software/SNP>.

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