## MISO - Documenting a LIMS for a Sequencing Lab

MISO is a Laboratory Information Management System (LIMS), a piece of software designed to streamline and organize genomic sequencing workflows. When used to its full potential, MISO can simplify the day-to-day work of a sequencing lab by standardizing and automating chemistry procedures, tracking samples across multiple steps, and linking lab instruments to data.

MISO is an open-source LIMS solution suited for small university labs, but it is unintuitive (like most LIMS) and has terse documentation. If the product were made more accessible by improving the documentation, it would provide a viable 3rd option to either an expensive paid product or a product built in-house.

#### Workflow

In very broad terms, a sequencing lab begins with a biological sample collected by medical professionals and ends with a file containing the genome sequence fragments produced by the sequencer. The following explains each step, along with how the LIMS supports the process:

1. **Collecting the Sample**

The process begins by collecting a sample, either urine or blood, from a patient.

The LIMS assigns this original sample or a processed version, such as white blood cell extraction, a unique barcode. This is meant to prevent mix-ups and provide a clear chain of custody by linking the sequence with original clinical details and patient information.

1. **DNA Extraction**

DNA extraction occurs through a chain of standardized operating procedures (SOPs), such as centrifugation, purification, etc. These procedures also involve standardized kits and reagents.

Recording the extraction in the LIMS ensures that the lab technician performs the extraction protocols consistently and tracks the inventory of consumables used.

1. **DNA Fragmentation**

The extracted DNA is usually too long to be directly sequenced by most machines. To prepare it for sequencing, the DNA is fragmented into smaller pieces.

The LIMS can record which fragmentation method is used (e.g., mechanical vs. enzymatic). It also records any parameters like fragment size ranges. By recording these fragmentation settings, the lab can determine which ones lead to the best outcomes and use this information to produce better-quality sequences in the future.

1. **Library Preparation**

In this step, the fragmented DNA is converted into a format the sequencing machine can read, known as a DNA library. It’s created by adding adapters to each fragment for identification during sequencing and extra sample barcodes if multiple samples are sequenced at once (multiplexing).

If library preparation fails (e.g., low yields or poor quality), the LIMS allows lab staff to trace back which lot numbers of reagents were used and which steps might have gone wrong. Recording the multiplex adapter also ensures that the output sequence can be separated from each original sample.

1. **Sequencing**

The DNA library is loaded into the sequencing machine, which reads each fragment at a constant length (called read length).

The LIMS ensures that all instrument-related data is adequately documented. If there are machine errors or poor sequencing quality, it can provide an audit trail to help diagnose issues with the sequencing run. This helps reduce downtime and troubleshooting time.

1. **Data Output**

The sequencing machine outputs a file containing the nucleotide (i.e., A/T/C/G) sequence and a quality score for each nucleotide indicating how sure the machine is that the A/T/C/G is correct.

The LIMS can then trigger other bioinformatics workflows once this raw data file is available.

#### Target User Roles

1. **Lab Technicians**

Lab technicians prepare and process samples, maintain instruments, and record data accurately. They require the LIMS to have a predictable and consistent workflow and the ability to record deviations easily.

1. **Bioinformaticians**

Bioinformaticians analyze the sequencing data generated in the lab, most often for clinical reporting. They QC the final sequence file and need to access the LIMS to cross-reference the initial sample information with their data.

1. **Lab Managers**

Lab managers oversee daily operations, including workflow management, inventory control, and protocol compliance.

#### Existing Resources

1. **MISO Documentation**
2. **Galaxy Project**

A related platform for bioinformatics workflows, often integrated with LIMS systems.

1. **BMC Bioinformatics**

A journal that publishes articles on bioinformatics tools and workflows