# User case studies

Lab technician - Judy Langford

This case study comes from a co-worker who worked at the sequencing lab I used to work at. I’ve anonymized her name, and I got back in touch to ask some follow-up questions about her relationship with the LIMS she uses.

### User story

As a lab technician, I want to perform lab processes consistently and generate reports efficiently so I can focus on delivering accurate sequencing results on time.

### Profile

#### Tasks & knowledge

Judy receives blood samples for sequencing and constructs DNA/RNA libraries for use in sequencing machines. Judy has a B.Sc. in biology and is familiar with downstream bioinformatics software. She relies on the LIMS for these tasks:

* **Sample entry & tracking**: Recording both the sample’s biological information (e.g. patient records, sample type, sample amount) and location in the lab.
* **Protocol tracking**: Following a strict lab protocol to create the correct type of library, based on the type of sequencing to be done. Each step and reagent need to be tracked for transparency, troubleshooting and inventory purposes.
* **Report generation**: Generating reports on QC results to share with lab managers and scientists.

#### Personality

Due to the job requiring her to process many batches of similar samples, she is detail-oriented and has a high tolerance for repetitive tasks. Judy’s primary stress is maintaining an extremely high accuracy standard, which comes second to efficiency.

She is a practical learner, as she works under very tight deadlines. She will explore the software and docs piecemeal, only looking up what is required immediately. She is also slightly resistant to new features and materials since it takes a lot of time and effort to feel like an expert in that new area.

### User scenario

#### Sample Entry

Judy has received a batch of blood samples for a clinical sequencing study. She enters patient information, sample type and freezer location by hand and links it with the barcode.

#### Library Preparation

Judy selects the relevant library preparation protocol, which lists each step of DNA extraction and library preparation. As she completes each step, she records reagent lot numbers, times, and temperatures in the LIMS.

#### QC

If any sample’s concentration falls below the acceptable range, Judy flags the deviation and suggests possible troubleshooting steps based on past data. She also generates a QC summary report for review by the lab manager. This report includes metrics on library concentration, fragment size, and any issues.

#### Sample Tracking

Judy updates the sample status from “in process” to “sequencing,” allowing all stakeholders to view the progress. She adds any relevant notes regarding the sample for downstream bioinformatician use.

Bioinformatician - Sarah Khan

### User Story

As a bioinformatician, I need access to structured and accurate data so that I can deliver comprehensive and timely insights to researchers and clinicians.

### Profile

#### Tasks & Knowledge

Sarah’s primary role is to process and analyze sequencing data, transforming raw information into actionable patient insights. She relies on the LIMS for these tasks:

* **Pipeline management**: Storing and choosing bioinformatics pipelines (variant calling, alignment, annotation) depending on the sample sequenced. As well documenting any deviations or unique parameters for transparency.
* **Viewing QC**: Analyzing the quality of the sequenced library before starting any bioinformatics pipelines.
* **Data extraction**: Programmatically accessing sequencing data, QC metrics, and patient/sample metadata as pipeline input.

Sarah has a Ph.D. in bioinformatics, with expertise in computational biology. Familiar with coding languages such as Python and R, she can adjust analytical pipelines as needed, although she requires the LIMS to facilitate data transfer with her existing tools.

#### Personality

Sarah is analytical and detail-oriented, working mostly on her own. However, she is also highly collaborative and communicative, working closely with lab managers and fellow academics. She values flexibility because of off-standard analyses are required based on the patient’s requirements and fast development of bioinformatics tools.

She approaches new software features with enthusiasm but requires comprehensiveness in their documentation. Sarah is comfortable working independently, preferring to troubleshoot any issues on her own.

### User scenario

#### Accessing Data

Sarah is tasked to generate a variant call analysis from a batch of RNA sequencing data.

She logs into the LIMS and navigates to the project dashboard, where she sees a real-time view of the runs associated with these samples.

#### Data Preparation

Sarah selects the data files and exports them in a format compatible with her external bioinformatics pipeline (e.g., FASTQ and CSV files). She also sets automated flags within the LIMS to alert her if any new data does not meet these QC thresholds.

#### Pipeline Setup in LIMS

Sarah opens the custom analysis pipeline section in the LIMS and configures a series of steps for RNA sequence alignment, differential expression analysis, and annotation.

During the initial run, Sarah receives an alert from the LIMS indicating that certain samples deviate from expected RNA integrity metrics. She reviews any flagged samples and adjusts as necessary.

#### Generating Reports

Once the analysis is complete, Sarah generates a report using an automated template. This report includes high-level summaries for clinicians and in-depth technical details for her team. She customizes the report with visualizations, including gene expression heat maps and variant distribution graphs, using the LIMS’s built-in visualization tools.

# Materials

For text-based documentation, I would argue that the best type for these sorts of users is:

1. Examples of a typical workflow for each user (tutorial)

Using the user scenarios as a rough outline, these are meant for new employees/beginners to get started. It should include screenshots and focus on a typical scenario for each role. Customized changes or deviations should be avoided.

1. Short reference articles for individual actions

This is meant for people well versed in the software but need a reminder. Examples could include:

* How do I print off a QC report?
* How do I set custom parameters for my bioinformatics pipeline?
* How do I view the status of upcoming libraries?

I would expect the tutorials to be a numbered step-by-step guide over multiple pages and use as many screenshots as possible.

Each reference article should be relatively brief. I would expect half a page each, but no more than a page.