



five strategies to improve the efficiency of your lab

According to Merriam-Webster, efficiency is defined as “effective operation as measured by a comparison of production with cost (as in energy, time, and money).” Thus, efficiency gains save time, money, and resources, and are the crux of the adage “work smarter, not harder.” With increases in efficiency, come increases in productivity, leading to more rapid turnaround of actionable scientific results or clinical diagnoses.

An example of a technology-driven efficiency gain in our daily lives is the rise of smartphone technology. Smartphones have created a paradigm shift for the way we manage our lives; we used to have paper lists and postits for reminders, grocery lists, and to-do lists, paper calendars, and day planners. Now we have all of these items in one place on our smartphones.

Just as we have become more efficient in managing our lives, it’s equally important to apply the same principles to become more efficient in managing our labs. While existing laboratory information management systems (LIMS) provide a good start to tackling this problem, there remain inefficiencies prevalent in the laboratory environment, especially as samples move from person to person and through the laboratory process, including steps in the wet lab, in data generation, and in computational/bioinformatics environments.

At L7 Informatics, our core development team has more than 75 years of combined experience in developing and deploying scientific software in complex, high-performance environments, so we are highly familiar with the inefficiencies present in most labs. Based on our experience, this white paper identifies five inefficiencies we’ve commonly seen and explores ways you can make your lab more efficient using a fully customizable workflow engine.



EFFICIENCY GAIN #1: STOP MANAGING YOUR INSTRUMENTS AND SOFTWARE PLATFORMS INDEPENDENTLY

A typical lab is a highly complex environment with a variety of instruments and software systems running simultaneously to perform myriad operations that support multiple ongoing experiments. The addition of data intensive technologies and the subsequent reliance on more advanced bioinformatics further complicate the overall operations of the lab. As labs become increasingly complex, the task of managing data through the multiple systems in place becomes a serious undertaking.

What further exacerbates the already complex environment is the disparate nature of the software that operates these many systems. Often times, the software being used is a mix of commercial systems, open-source tools, and repurposed office tools, all with different interfaces and data formats. Therefore, data cannot be easily converged, and samples cannot seamlessly move from one experiment to another. For example, sample metadata tracked in spreadsheets and paper lab notebooks is difficult to integrate with results generated by analysis software. Therefore, researchers often use manual methods to track and collate data and results from different tools, complicating downstream analysis and reporting.

To resolve this issue, L7's Enterprise Science Platform (ESP) offers the ability to integrate a variety of different laboratory systems into unified workflows, not only in the wet lab, but also from the bioinformatics side.

Using a mix of technologies, including our APIs and pipeline management system, ESP can communicate with and obtain data from a variety of instruments and software tools as the workflows progress. Under the hood, ESP's Resource Manager ties all the data in the workflow back to the samples, resulting in a seamless aggregation of data across the entirety of the experiment. This enables the user to monitor and record all data generated in the lab in one common location, thereby eliminating the inefficiencies caused when these systems operate independently.

EFFICIENCY GAIN #2: STOP USING AD HOC SYSTEMS TO MAINTAIN SAMPLE AND DATA PROVENANCE

As mentioned in the previous topic, scientific labs are resorting to using a variety of manual methods for data management and collation. As a result, labs often experience poor record-keeping regarding the "who, what, when, where, and how" of experiments, effectively making management of data provenance not just inefficient, but a rather difficult, if not impossible, task. The issue becomes even more critical as new data-rich technologies find their way into regulated laboratory environments, with the primary example being the broader use of next-generation sequencing (NGS) in clinical labs.

A review in Lab Manager states the need simply, "Data generated by laboratories are used to make strategic decisions for all types of projects (investigation, remediation,, compliance, etc.). It is important that the data are of the highest quality to avoid costly resampling and budget overruns. A laboratory audit ensures that the laboratory has quality systems in place, follows good laboratory practices, and generates data of integrity and quality."

These rigorous requirements are a challenge to maintain using a collection of ad hoc tools. However, with ESP, everything gets tracked in a single location, including the full provenance of sequencing data, from wet lab to instruments to quality control, as well as mapping pipelines and experiment-specific analyses. Scientists have full access to the provenance chain and all the data associated with each step, enabling complex queries that allow them to fully explore their results with access to deep audit trails that satisfy all regulatory requirements.

EFFICIENCY GAIN #3: MAKE THE TRANSITION FROM THE WET LAB TO ANALYSIS SEAMLESS

Having just read the topic on ad hoc provenance methods, you might be thinking, "I get that, but I have a LIMS that takes care of it all for me." Yes, you might have a LIMS, but can you think of any LIMS tool that manages data through bioinformatics and reporting, while maintaining provenance through the whole process? Labs can configure their LIMS platforms to



communicate with analysis tools, but in every instance, the result is a custom solution that simply “throws it over the fence” and does not track anything beyond the point of “sent to bioinformatics.” Data analysis software then only performs analysis and creates results, but these are not natively tied to any of the sample prep steps. In most cases, what really happens is that a full bioinformatics team, or worse, a single overworked bioinformatician, simply takes the raw data from the analytical system (e.g., sequencer, mass spec, or imaging system) and runs with it, only returning some type of analysis report. This results in a major inefficiency in laboratory data processing: separate and independent wet lab and analysis systems.

As we discussed, maintaining full provenance of sample and experimental data through multiple systems is inefficient enough, so managing two completely different environments, wet lab and analysis, is even more inefficient. The solution to this inefficiency is to have both wet lab and bioinformatics working together on a common platform that enables direct communication between the two sides of the data-intensive laboratory operation. This way, the “who, what, when, where and how” associated with experimental workflows extend to all analytical operations and manipulations of the data, thereby lengthening the provenance chain beyond where traditional LIMS stop.

With L7’s ESP, sample and experiment tracking are designed to provide full transparency into your operations, both in the wet lab and in bioinformatics. This enables you to easily transition between the two sides of the lab while maintaining an uninterrupted provenance trail. As samples move from the lab into analysis, users can see results directly from ESP as they become available, giving all stakeholders a detailed view of a sample’s status in its workflow. This means no more hunting around for spreadsheets, digging through complex file hierarchies, or emailing technicians for status reports.

EFFICIENCY GAIN #4: DELEGATE ROUTINE PROCEDURES TO YOUR LAB TECHNICIANS

The democratization of data-intensive technologies such as NGS, mass spec-driven multi-omics workflows, and

high-resolution imaging systems, is making bioinformatic analysis a required function. In the vast majority of labs, a dedicated staff of highly trained computer scientists handles bioinformatics, given that a biologist or bench scientist typically is not trained on using command line tools, the standard environment for informatics analysis. The complexity of bioinformatics analysis can make data processing difficult for a non-computational researcher or lab technician.

When you require your bioinformatics team, or bioinformatician in a small lab, to perform routine tasks for an experiment, such as running standardized variant calling pipelines in an NGS lab, this causes multiple inefficiencies including the following:

1. Running your experiments can only happen on the timeline and availability of the bioinformatician/bioinformatics team.
2. You are using your highly skilled bioinformatician/bioinformatics team to perform tasks the lab tech could do.

Instead, by using a software platform like ESP that integrates bioinformatic analysis with a system that manages your wet lab operations, you can relinquish control of these simple tasks to the lab technicians. Allowing non-computational techs to fire off routine analyses lets the bioinformatician/bioinformatics team focus on doing what they do best—developing and testing novel analytical methods, which will likely lead to even more efficiencies in your lab in the future.

EFFICIENCY GAIN #5: DON’T LET DATA AND KNOWLEDGE LEAVE THE LAB WHEN EMPLOYEES DO

There is no doubt that well-managed commercial software platforms can be costly from a licensing standpoint; therefore many labs elect to build their own data management and provenance systems.

However, the teams tasked with developing these tools almost never include the head of the laboratory, who is the single constant member of the lab, especially in academic settings. Instead, the job of building infrastructure is tasked primarily to graduate students,



postdoctoral fellows, or staff bioinformaticians. By the nature of their roles, they are transient through the lab, with their stays not lasting more than three to five years until they graduate, find tenure-track positions, or flee the lab for more lucrative positions at biotech and pharmaceutical companies.

When the person who built one of the ad hoc systems leaves, no one else may know how to work the system properly. This means simple things from instrumentation settings for an experiment, or more sensitive information such as data or instructions kept in a notebook, can be lost. Thus, with the loss of expertise comes a significant inefficiency in laboratory operations.

With a comprehensive commercial data management solution like ESP, data and methods are never lost, not even if the lab elects to forgo annual license renewals. In addition, ESP software is deliberately designed to be user-friendly and adaptable to changing laboratory environments, from new lab members to updates in lab protocols and analyses. ESP maintains a registry of all samples, data, and files that pass through the system, and it can retrieve any critical data a laboratory might require, even years after the data was originally generated.

PUTTING IT ALL TOGETHER TO CREATE A MORE EFFICIENT LAB

It is clear that removing inefficiencies from laboratories is critical to improved turnaround times for actionable scientific results and clinical outcomes. The democratization of data-intensive technologies and the hurdles of bioinformatic analysis posed by these technologies are magnifying the effects of inefficient operations. However, becoming a more efficient lab cannot be achieved overnight, but it can be realized by making processes more reliable, repeatable, and reproducible. With traditional LIMS solutions you can make strides towards these efficiency gains in various areas of the lab, but you aren't going to make your whole process more seamless and efficient until you include the computational aspects of modern labs.

Just like smartphones have changed the way we manage and organize our personal lives, L7's ESP provides a platform for streamlining your laboratory operations. ESP is the industry's only data and workflow management system that integrates all of the disparate functions in the lab, including both wet lab operations and bioinformatic analysis. By removing the traditional disconnect between the two sides of modern data-intensive labs, ESP can remove many of the inefficiencies we described in this document. ESP also helps organizations and individual researchers track samples, process data, produce reports, and manage workflows and analysis pipelines—increasing the lab's efficiency and thereby increasing sample throughput and freeing space for new opportunity in the lab.

To learn more about L7 Informatics' synchronized solutions for science + health, please visit the L7 ESP software page at [L7informatics.com](https://www.l7informatics.com) or email us at info@l7informatics.com



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