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CAPACITY ANALYSIS IN A GENETIC SEQUENCING LABORATORY THROUGH DISCRETE EVENT SIMULATION

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ABSTRACT

Discrete-event simulation is widely used in the healthcare field to optimize processes and manage resources. This study presents a DES model developed for a molecular biology laboratory in Colombia, recognized by Oxford Nanopore Technologies and specializing in Sanger and Nanopore sequencing techniques. Using real data, the model analyzes processing times for each sequencing method and estimates the laboratory's maximum capacity under varying technician experience, equipment availability, task durations and number of samples processed. The goal is to provide genomic laboratories and regulatory stakeholders with a flexible tool to evaluate performance, the impact of alternative configurations, and support capacity planning under resource and demand constraints.

1 INTRODUCTION

Genetic sequencing has advanced rapidly since the Human Genome Project, with next-generation technologies reducing time and cost to less than a day and under $1,000 per genome (National Human Genome Research Institute 2024). This expansion has increased laboratory demands, yet their design and optimization remain underexplored. Although discrete-event simulation (DES) is widely applied in healthcare, few studies address laboratory environments (Vázquez-Serrano et al. 2021). Recent work has begun to fill this gap through models of cytology and histopathology labs that improved task allocation and identified workflow inefficiencies (Pongjetanapong et al. 2019; Chan et al. 2024).

Building on this emerging line of research, this work introduces a DES model of a Colombian molecular biology lab specializing in Sanger and Nanopore sequencing. Using real operational data, the model incorporates technician expertise, resource availability, and workload composition to estimate maximum processing capacity and evaluate alternative configurations. Implemented in Python with SimPy, it provides a flexible tool to support capacity planning, resource allocation, and responsiveness under variable demand and limited resources.

2 METHODOLOGY AND MODEL DESIGN

The simulation represents the operations of the GenCore sequencing laboratory from sample reception through Sanger and Nanopore workflows. Technician activities were categorized into administrative (e.g., checking sample integrity, responding to client emails, cleaning equipment, preparing documentation) and operational activities directly linked to sequencing (e.g., pipetting, instrument setup). The proportion of time allocated to each category was modeled as a configurable parameter to assess its impact on processing capacity.

Task durations were modeled as functions of batch size and technician expertise; for instance, pipetting times increased with the number of samples and differed between expert and apprentice technicians. Input data were collected through direct observation and interviews with laboratory staff. Autocorrelation tests

confirmed there were no temporal dependencies in the data. Homogeneity tests showed that in most pipetting activities there were no statistically significant differences in average time per sample across batch sizes, supporting the use of the same fitted distribution across different batch sizes. The model was verified through expert review and sensitivity analysis, and validated by comparing simulated and observed processing times, with deviations consistently kept within a 10% margin.

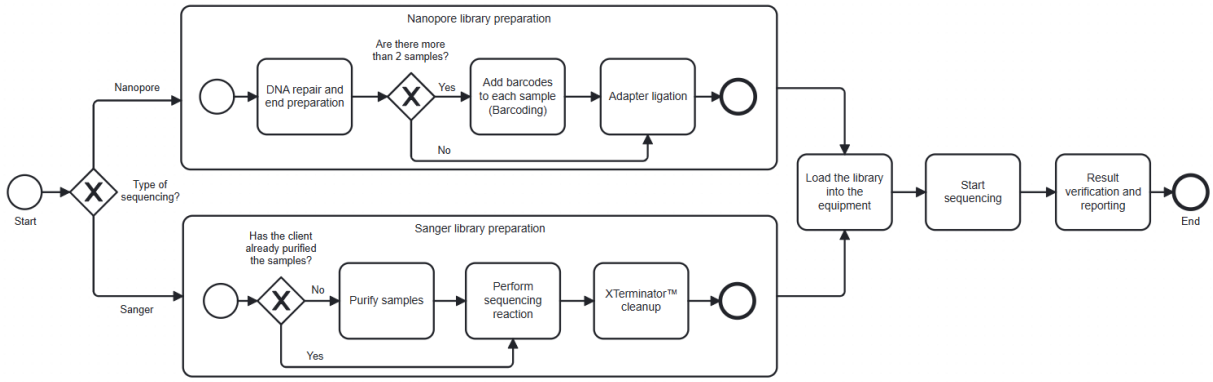

Figure 1: Simulation model diagram showing the main sequencing steps for Sanger and Nanopore workflows.

3 RESULTS

The highest capacity was achieved with two expert technicians dedicating 100% of their time to operational tasks, processing an average of 38 Sanger lots and 22.5 Nanopore lots per month. In contrast, with only one expert at 50% operational time, capacity dropped to 15 Sanger and approximately 6.7 Nanopore lots.

Intermediate scenarios, such as mixed teams or reduced time allocations, showed proportional declines in throughput. For example, a mixed team at full operational time processed 36 Sanger and 19.5 Nanopore lots per month on average. Results are based on 30 simulation replications and reflect how technician availability and time allocation significantly affect monthly processing capacity. These findings underscore the operational trade-offs between staffing levels, expertise, and task prioritization.

4 CONCLUSION AND FUTURE WORKS

The simulation model provides a practical tool for estimating laboratory capacity and evaluating operational performance under different staffing and scheduling conditions. It highlights how technician composition and time allocation directly affect sequencing throughput, offering valuable insights for planning and resource optimization. The model is adaptable to other laboratory environments and can support strategic decision-making in contexts with fluctuating demand. Future extensions could incorporate learning curves to assess how technician experience gained over time influences efficiency and long-term capacity.

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