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Impact of Inaccurate Laboratory Test Result on the Spread of Infectious Disease: Mathematical Modelling Approach

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Abstract
This study examines the impact of diagnostic inaccuracies on the transmission dynamics of infectious diseases using an extended SEIR model. By incorporating compartments for false-positive and false-negative cases, the model simulates the effects of faulty testing, no testing, and varying testing rates on disease progression. Simulations reveal that while no testing results in rapid disease spread, introducing a 10% testing rate significantly reduces infections but generates substantial diagnostic errors—1.8 million false positives and 600,000 false negatives within 40 days. These findings underscore the critical role of accurate testing in mitigating false negatives, reducing undetected transmission, and optimizing public health interventions. The model bridges the gap between theoretical epidemiology and practical disease management, offering actionable insights for enhancing testing strategies to improve epidemic control.

INTRODUCTION
Infectious diseases remain a persistent global health challenge due to their dynamic nature and the complexity of managing outbreaks. Accurate laboratory testing is an essential tool for identifying infected individuals, guiding treatment protocols, and implementing effective public health interventions (Trevethan, 2017). Diagnostic metrics such as sensitivity i.e. the ability to correctly identify true positive cases and specificity i.e. the ability to correctly identify true negative cases are critical in evaluating the effectiveness of laboratory tests (Mouliou & Gourgoulianis, 2021). Despite their importance, inaccuracies in testing, such as false positives and false negatives, can significantly distort disease dynamics and complicate containment strategies. In the context of bio-mathematics, specificity refers to the ability of a test to correctly identify those individuals who do not have a particular disease or condition (Trevethan, 2017). It is the proportion of true negatives among all individuals who do not have the disease. Mathematically, specificity is defined as:

$$Specificity = \frac{True\ Negatives}{(True\ Negatives + False\ Positives)} \quad (1)$$

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False negatives or/and false positives can cause unwarranted reactions, which can hinder attempts to control disease (Sahinoglu and Sahinoglu, 2022).

The use of mathematical models to study infectious disease dynamics has been well-documented in literature. Traditional compartmental models, such as the SEIR (Susceptible, Exposed, Infected, and Recovered) framework, provide a foundational approach to understanding disease progression and the effects of interventions (Li, 2018). However, these models often assume ideal diagnostic conditions, ignoring the potential impact of diagnostic inaccuracies on disease spread. Recent advancements, such as the integration of sensitivity and specificity into epidemic models, addressed this limitation. Sahinoglu and Sahinoglu (2022) emphasize the cascading consequences of diagnostic errors during the COVID-19 pandemic, including the unchecked transmission caused by false negatives and the resource strain associated with false positives.

Despite these contributions, a critical gap persists in existing models: few studies explicitly quantify the dynamic impact of diagnostic inaccuracies over time. This gap limits our understanding of how diagnostic errors influence the effectiveness of public health interventions. To address this, the current study builds on the foundational SEIR framework by introducing additional compartments for false-positive and false-negative individuals. This novel extension allows for a detailed examination of how diagnostic inaccuracies affect disease dynamics and offers actionable insights for optimizing testing strategies.
The objective of this study lies in its ability to dynamically integrate diagnostic metrics into the SEIR framework, providing a comprehensive analysis of testing inaccuracies across different scenarios. By simulating the effects of faulty testing, no testing, and varying testing rates, this study bridges the gap between theoretical modeling and practical disease management, offering a robust tool for improving public health strategies.

MODEL FORMULATION AND METHODS
This study builds upon the classical SEIR model, incorporating additional scenario to account for individuals with false-positive and false-negative test results. This extension allows for a detailed examination of how diagnostic inaccuracies influence disease dynamics. The approach aligns with the framework established by Li (2018) and extends it by integrating diagnostic metrics as dynamic variables. Therefore we assume SEIR with addition of two compartments to account for individuals who were incorrectly diagnosed by the test. Those who are false positives (P) as well as false negatives (N) compartments. The modified model allows us to explore via simulation how erroneous test results affect the overall dynamics of the disease spread, guiding public health interventions and resource allocation.

Hence, we hereby propose a six compartmental model as follows: $S(t)$, susceptible individuals which comprises of persons who are at risk of infection but not yet infected. Then $E(t)$, exposed individuals, referring to those who have been infected but are not yet infectious. The exposed compartment accounts for the incubation period of the disease. Next compartment is $I(t)$, the infectious individuals who are infected and can transmit the disease to susceptible individuals. Then $R(t)$, the recovered individuals who have recovered from the disease and are assumed to be immune.

Moving further, we introduced $P(t)$, false positive to refer to those individuals who do not have the disease but have been incorrectly diagnosed as positive. The rate at which false

positives are generated can be calculated using $(1 - specificity)$. For example, if α is the rate of testing, the rate of generating false positives can be given by:

$$\frac{dP}{dt} = \alpha \times \left(Non-Infected\ Individuals\right) \times \left(1 - specificity\right) \quad (2)$$

And lastly, we added $N(t)$, false negative to account for those individuals who have the disease but have been incorrectly diagnosed as negative. The rate of false negative is computed almost the same way false positives are generated. For instance, if σ is the rate at which exposed individuals become infectious, the rate of generating false negatives can be given by:

$$\frac{dN}{dt} = \sigma \times \left(Exposed\ Individuals\right) \times \left(1 - sensitivity\right) \quad (3)$$

All the state variables change continually with respect to time t. The state variables of the models are presented in table 1.

Table 1: State Variables of the Model

State Variable	Description
$S(t)$	Susceptible Individuals
$E(t)$	Exposed Individuals
$I(t)$	Infected Individuals
$R(t)$	Recovered Individuals
$P(t)$	Individuals diagnosed false positives
$N(t)$	Individuals diagnosed false negatives
$T(t)$	Total Individuals

Beside the introduction of two new state variables, we assume a constant recruitment rate Λ into the susceptible compartment. The disease is being transmitted by a parameter β as a result of effective interaction between the inflected and susceptible individuals by means of frequency-dependent transmission term $\frac{\beta SI}{T}$. The movement from exposed compartment to infected compartment is represented by parameter σ as the rate at which exposed individuals become infectious (inverse of the incubation period). We assume a constant recovery rate γ (inverse of the infectious period). The disease induced death rate is d while the deaths due to natural causes is given by μ.

The parameters of the models are presented in table 2.

Table 2: The Parameters of the Model

Parameter	Description
Λ	Recruitment rate
β	transmission rate
σ	rate at which exposed individuals become infectious
γ	recovery rate (inverse of the infectious period)
μ	Natural death rate
d	Death rate due to the disease
α	rate of testing
Specificity	The probability that the test correctly identifies a non-infected individual (true negative rate).
Sensitivity	The probability that the test correctly identifies an infected individual (true positive rate).
t	Time in days

The model is governed by a system of ordinary differential equations that describe the rate of change of each compartment over time as follows:

$$\left.\begin{aligned} S'(t) &= \Lambda - \frac{\beta SI}{T} - \mu S \\ E'(t) &= \frac{\beta SI}{T} - (\sigma + \mu) E \\ I'(t) &= \sigma E - (d + \gamma + \mu) I \\ R'(t) &= \gamma I - \mu R \\ P'(t) &= \alpha S \times (1 - specificity) - \mu P \\ N'(t) &= \alpha I \times (1 - sensitivity) - \mu N \end{aligned}\right\} \quad (3)$$

SIMULATION RESULTS AND DISCUSSION

This model incorporates parameterization from prior works, including sensitivity and specificity as defined by Trevethan (2017) and Borysiak et al. (2016). The extension of the SEIR model is consistent with recent studies that highlight the importance of integrating diagnostic metrics into epidemic modeling (Schwarzer, 2008). Hence, the numerical simulations were performed using MATLAB R2023a, following the methods of Schwarzer (2008) and Li (2018). Initial conditions and parameter values were derived from typical epidemiological scenarios, ensuring consistency with real-world disease dynamics. Sensitivity and specificity values were varied across simulations to assess their impact on disease dynamics, reflecting the findings of McPherson and Pincus (2021).

Experiment 1

In this experiment, we consider 10,000,000 initial population where 97% are susceptible, 2% are exposed, 1% are infectious and there are no recovered individuals yet. If we suppose that the specificity is 95%, it means 5% of non-infected individuals will be incorrectly identified as having the disease (false positives). Also, if the sensitivity is 90%, it means 10% of infected individuals will be incorrectly identified as not having the disease (false negatives). Using parameter values $\Lambda = 0.002$, $\mu = 0.001$, $\beta = 0.3$, $\sigma = \frac{1}{5.2}$ (incubation period of 5.2 days), and $\gamma = \frac{1}{2.3}$ (infectious period of 2.3 days). If the rate of testing is $\alpha = 0.1$, the dynamics of the disease spread over time can be simulate as follows:

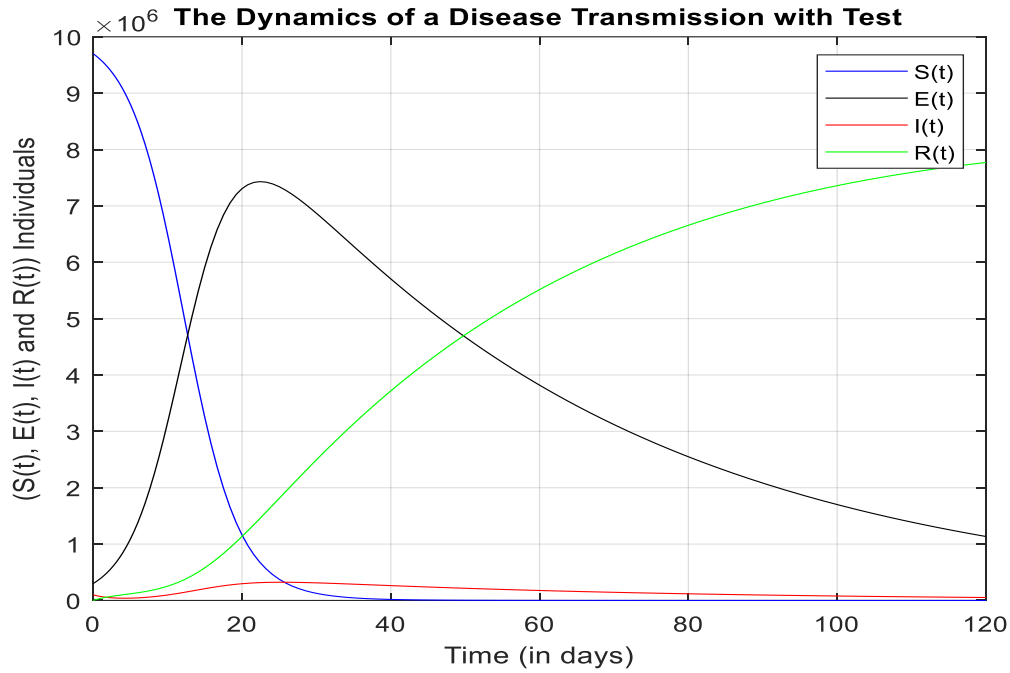

Figure 1. The dynamics of the disease spread with test

Experiment 2

In this experiment, we aim to investigate how the absence of a testing rate affects the dynamics of the disease. With the exception of the testing rate being zero, we used the same scenario from experiment 1 and kept all values of the state variables and parameters unchanged. The simulation result of dynamics of false positives $P(t)$ and false negatives $N(t)$ compartments can be seen as follows:

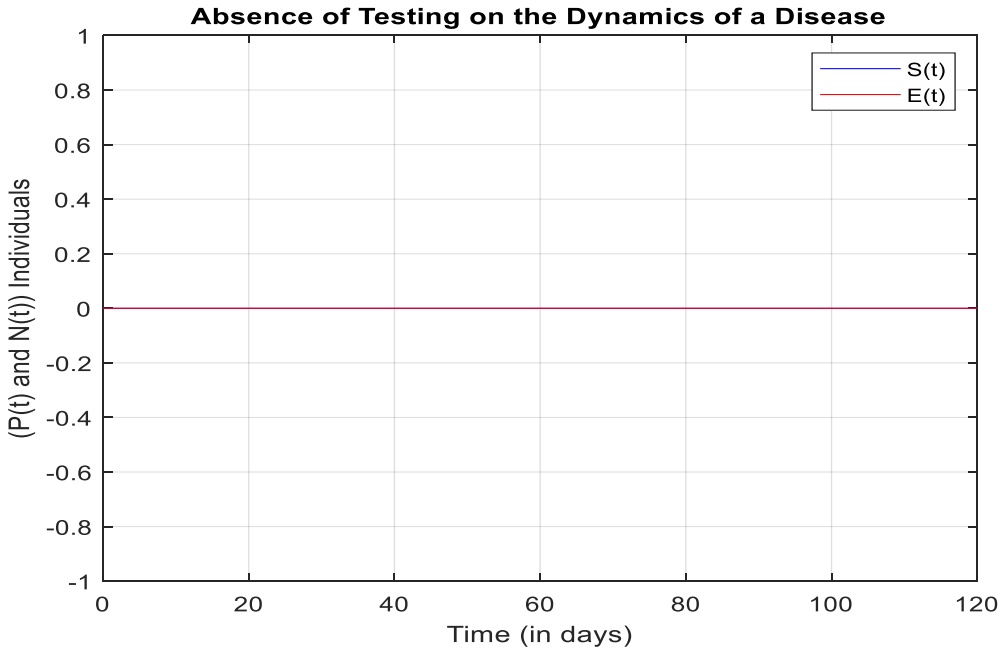

Figure 2. Absence of Testing on the dynamics of a disease

Experiment 3

In this experiment, we aim to investigate how the testing rate affects the dynamics of the disease. Specifically, we are examining the dynamics of false positives $P(t)$ and false

negatives $N(t)$ over time when the testing rate is set at 10% $\alpha = 0.1$. We used the same scenario from Experiment 1 and maintained same values of the state variables and parameters. Here is the result of the simulation:

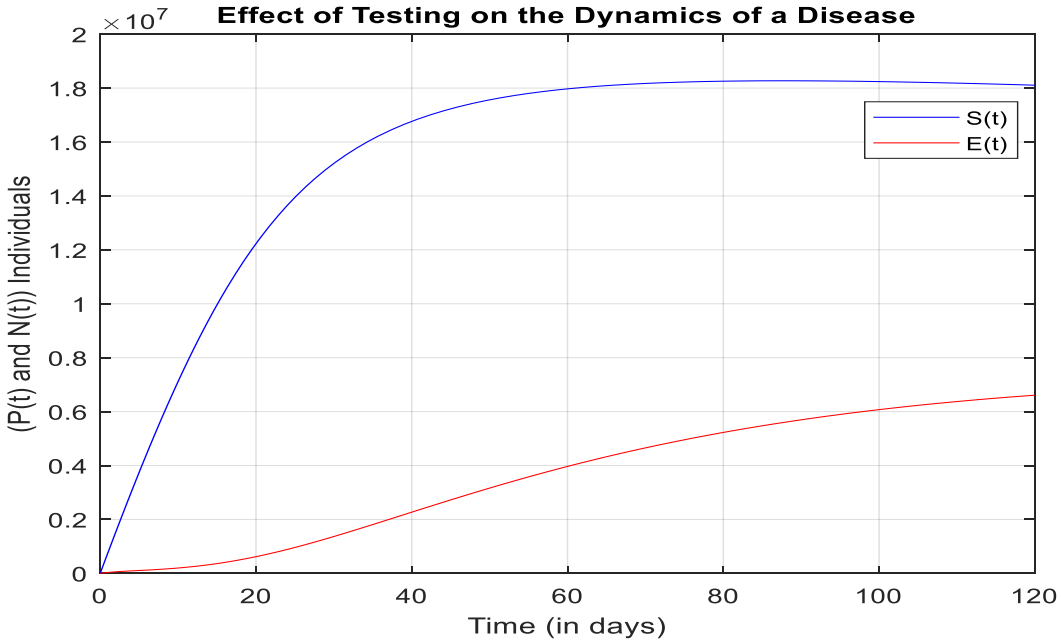

Figure 3. Effect of Testing on the dynamics of a disease

DISCUSSION OF THE SIMULATION RESULTS

Experiment 1: Faulty testing, the result indicates that with 10% testing rate, the model showed significant increases in false positives (1.8 million) and false negatives (600,000) within 40 days. The rapid depletion of the susceptible population highlights the compounded effect of undetected carriers due to false negatives. This aligns with the findings of Sahinoglu and Sahinoglu (2022), who emphasized the role of diagnostic errors in perpetuating transmission chains. The dynamics observed here underscore the critical need for high-sensitivity tests to minimize false negatives and interrupt transmission.

Experiment 2: In the absence of testing, false positives and negatives remained at zero. However, the unchecked spread of the disease led to the complete depletion of the susceptible population within 40 days. This finding corroborates Borysiak et al. (2016), who demonstrated that the absence of diagnostic interventions exacerbates epidemic severity. While this scenario is unrealistic in practical terms, it highlights the indispensability of testing in managing infectious diseases.

Experiment 3: Impact of Testing Rate, by introducing a 10% testing rate significantly altered disease dynamics. Although testing reduced the infected population, the presence of diagnostic inaccuracies resulted in a substantial burden of false positives and negatives. This underscores the findings of McPherson and Pincus (2021), who discussed the trade-offs between sensitivity and specificity in diagnostic testing. Prioritizing high sensitivity may mitigate false negatives, reducing undetected cases, but may also increase false positives, as shown in this study.

As a final point, the findings underscore the critical importance of accurate diagnostics in epidemic control. Unlike traditional SEIR models, which assume ideal diagnostic conditions, this study reveals the dynamic impact of diagnostic errors, providing actionable insights for

public health strategies. By quantifying the effects of diagnostic inaccuracies over time, this work offers a more realistic framework for understanding the interplay between testing accuracy and disease dynamics. The model's novelty lies in its ability to integrate diagnostic metrics dynamically, bridging the gap between theoretical modeling and practical disease management (Mouliou & Gourgoulianis, 2021).

CONCLUSION

This study demonstrates the significant impact of diagnostic inaccuracies on infectious disease dynamics. By extending the classical SEIR model to include false-positive and false-negative compartments, the findings reveal critical insights into the role of diagnostic accuracy in epidemic control. Through comparisons with other models and integration of literature-backed analyses, this work highlights the necessity of optimizing both sensitivity and specificity to minimize diagnostic errors. As such, findings from these experiments emphasize that accurate and widespread testing is crucial in managing infectious diseases. Therefore, future research should incorporate adaptive testing strategies and real-time data integration to further enhance model applicability.

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