

Mathematical Modeling of Prostate Cancer in Uganda Using the Atangana-Baleanu Caputo Derivative

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ABSTRACT

This paper introduces a mathematical model to better understand how prostate cancer progresses in a population, using the Atangana-Baleanu Caputo fractional derivative. The model divides the population into different groups: susceptible individuals, those exposed to cancer-causing factors, individuals at various stages of infection, and those who have recovered. The exposed and infected groups represent the different stages of cancer, while the recovered group accounts for people who have overcome the disease through treatment or natural remission. By using fractional derivatives, the model captures the idea that cancer progression is influenced by past events, making it a more accurate reflection of how the disease unfolds over time. The paper develops a set of equations to describe how people move between these groups, considering factors like exposure, cancer progression, and recovery. Simulations show how the disease spreads and how various treatment strategies can influence the outcome. This model offers a valuable tool for better understanding prostate cancer dynamics and can help guide.

Keywords: prostate, cancer, atangana-baleanu caputo derivative, modeling, fractional order

1.0 INTRODUCTION

Prostate cancer (PCa) continues to pose a major global health challenge, with rising incidence rates, especially in sub-Saharan Africa. Uganda exemplifies this trend, with 7,493 new cases and 5,239 deaths reported in 2020, making PCa the leading cancer among Ugandan men (Sung et al., 2021). These statistics emphasize the pressing need for targeted cancer control strategies in the country. The increasing burden of PCa in Uganda is driven by population growth, aging, and lifestyle changes such as diet and physical inactivity (Kaye & Ndawula, 2022). Additionally, limited access to screening and early diagnosis, combined with disparities in healthcare infrastructure and uneven resource distribution, contributes to delayed treatment and poor outcomes (Owor et al., 2022). Addressing this requires innovative strategies that consider both biological and systemic healthcare challenges.

Mathematical modeling offers valuable tools for understanding cancer dynamics by simulating disease progression and evaluating intervention strategies. Compartmental models—dividing populations into groups like susceptible, exposed, and recovered—help explore how PCa evolves and responds to interventions (Ghani et al., 2020).

Fractional calculus has recently gained prominence in modeling biological systems due to its ability to capture memory and non-local effects. The Atangana-Baleanu Caputo fractional derivative, in particular, incorporates historical data into models of tumor growth, offering a

more accurate reflection of cancer progression over time (Atangana & Baleanu, 2020; Atangana et al., 2021).

Several researchers have applied mathematical modeling to PCa. Mohammadi et al. (2021) developed a numerical approach to simulate interactions between cancer cells, nutrients, and PSA levels, addressing a gap in effective numerical methods. Colli et al. (2020) created a model for personalized chemotherapy, though it requires refinement for clinical application. Baez and Kuang (2016) developed models to predict the onset of castrate-resistant prostate cancer (CRPC), emphasizing the need for validation. Phan et al. (2020) reviewed models used to optimize hormone therapy and predict resistance, pointing out the limitations of PSA as a tumor growth marker and calling for enhanced model complexity and validation. Together, these studies highlight both the promise and challenges of applying mathematical modeling to improve PCa treatment and management.

2.0 METHODOLOGY

2.1 Model Formulation

This model offers a comprehensive SEIR-based framework for understanding prostate cancer progression in men. It uniquely incorporates both avoidable (lifestyle-related) and non-avoidable (genetic) risk factors, along with four stages of the disease—from early to metastatic. The male population is divided into compartments: susceptible, exposed (by risk type), infected (by disease stage), and recovered. This approach provides a holistic view of prostate cancer dynamics over time.

$$N(t) = S(t) + E_A(t) + E_{NA}(t) + E_{ANA}(t) + I_1(t) + I_2(t) + I_3(t) + I_4(t) + R(t)$$

3.0 MODEL EQUATIONS

The dynamics of the compartments are governed by the following set of differential equations:

The mathematical model governing the dynamics of prostate cancer consists of several compartments representing different stages of disease progression.

The susceptible population ($s(t)$) includes men at risk of developing prostate cancer who have not yet been exposed

to any risk factors. This population increases due to recruitment (Λ) and decreases as individuals become exposed to risk factors or die naturally at rate (μ). The transition to exposure occurs through three pathways: exposure due to avoidable risk factors (β_1), exposure due to non-avoidable risk factors (β_2), and exposure due to both risk factors (β_3). The dynamics of the susceptible population are governed by the equation:

$$\frac{dS(t)}{dt} = \Lambda - \beta_1 E_A(t) S(t) - \beta_2 E_{NA}(t) S(t) - \beta_3 E_{ANA}(t) S(t) - \mu S(t)$$

The exposed population is divided into three categories based on the nature of risk factors. The exposed population due to avoidable risk factors ($\beta_1 E_A(t)$) consists of individuals who contract prostate cancer due to lifestyle and environmental influences. These individuals may progress to stage 1 infection at a rate (β_4) or die naturally at rate (μ), as described by:

$$\frac{dE_A(t)}{dt} = \beta_1 E_A(t) S(t) - (\beta_4 + \mu) E_A(t)$$

Similarly, the exposed population due to non-avoidable risk factors ($\beta_2 E_{NA}(t)$) represents individuals at risk due to genetic or hereditary influences. They transition to stage 1 infection at rate β_5 or die at a natural rate (μ), modeled by:

$$\frac{dE_{NA}(t)}{dt} = \beta_2 E_{NA}(t) S(t) - (\beta_5 + \mu) E_{NA}(t)$$

The exposed population due to both risk factors ($\beta_3 E_{ANA}(t)$) consists of individuals facing combined avoidable and non-avoidable risk factors. They progress to stage 1 infection at rate (β_6) and may also die naturally at rate μ , as shown in the equation:

$$\frac{dE_{ANA}(t)}{dt} = \beta_3 E_{ANA}(t) S(t) - (\beta_6 + \mu) E_{ANA}(t)$$

The infected population is categorized into four stages. The stage 1 infected population ($I_1(t)$) represents men diagnosed with early-stage prostate cancer. Where β_{10} is the recovery rate, β_7 is the progression rate to stage 2, and μ represents natural death. They progress from the exposed compartments), and their dynamics follow:

$$\frac{dI_1(t)}{dt} = \beta_4 E_A(t) + \beta_5 E_{NA}(t) + \beta_6 E_{ANA}(t) - (\beta_7 + \beta_{10} + \mu) I_1(t)$$

The stage 2 infected population ($I_2(t)$) consists of individuals who have progressed from stage 1 at rate (β_7). Some recover at rate β_{11} , while others progress to stage 3 at rate β_8 or die at rate μ :

$$\frac{dI_2(t)}{dt} = \beta_7 I_1(t) - (\beta_8 + \beta_{11} + \mu) I_2(t)$$

The stage 3 infected population ($I_3(t)$) includes men diagnosed with advanced-stage prostate cancer. They enter from stage 2 at rate β_8 , recover at rate β_{12} , progress to stage 4 at rate β_9 , or die at rate μ . Thus,

$$\frac{dI_3(t)}{dt} = \beta_8 I_2(t) - (\beta_9 + \beta_{12} + \mu) I_3(t)$$

The stage 4 infected population ($I_4(t)$) represents individuals with metastatic prostate cancer. They enter from stage 3 at rate β_9 , recover at rate β_{13} , die naturally at rate μ , or die due to prostate cancer at rate μ_0 :

$$\frac{dI_4(t)}{dt} = \beta_9 I_3(t) - (\beta_{13} + \mu + \mu_0) I_4(t)$$

Finally, the recovered population ($R(t)$) consists of men who have successfully undergone treatment and regained health. The rate of recovery from each stage is captured by the summation of all recovery rates, $\beta_{10} I_1(t) + \beta_{11} I_2(t) + \beta_{12} I_3(t) + \beta_{13} I_4(t)$ and they experience natural mortality at rate

$$\frac{dR(t)}{dt} = \beta_{10} I_1(t) + \beta_{11} I_2(t) + \beta_{12} I_3(t) + \beta_{13} I_4(t) - \mu R(t)$$

This model provides a comprehensive framework for understanding the progression of prostate cancer, integrating both epidemiological and mathematical perspectives to analyze disease dynamics and potential intervention strategies.

3.1 Model framework

The conceptual framework for the prostate cancer dynamics model integrates various factors influencing the progression, diagnosis, and treatment of prostate cancer. It uses a compartmental approach to categorize the male population and employs mathematical modeling to understand the dynamics of disease progression and control.

Table 1: Description of the state variables.

State Variables	Description
$S(t)$	Susceptible Men
$E_A(t)$	Exposed individuals due to avoidable risk factors
$E_{NA}(t)$	Exposed Population due to Non-Avoidable Risk Factors
$E_{ANA}(t)$	Exposed Population due to Both Risk Factors
$I_1(t)$	Infected Population stage 1
$I_2(t)$	Infected Population stage 2
$I_3(t)$	Infected Population stage 3
$I_4(t)$	Infected Population stage 4
$R(t)$	Recovered Men.

3.2 Assumptions of the Model

The model simplifies prostate cancer dynamics in Uganda by assuming a fixed, homogeneous population and categorizing risk factors as either controllable or uncontrollable. Individuals progress through disease stages in one direction, with no recurrence after recovery. It includes natural deaths but assumes constant intervention effectiveness and healthcare efficiency. While this approach limits real-world accuracy, it offers a manageable framework for analyzing disease spread and potential control strategies.

Below is the model equations (1)

The analysis aims to assess the impact of control measures on prostate cancer progression and determine if the disease can be eliminated. This involves examining model parameters that influence the persistence of prostate cancer and evaluating whether the solutions to

the model equations remain within a biologically feasible region.

3.3 The Positive Invariant Region

To ensure the model is biologically and mathematically feasible, we demonstrate that the total population remains within a positive invariant region. This means the total population and all sub-populations are non-negative and bounded over time.

Definition

A positive invariant region in the context of compartmental models like the one for prostate cancer dynamics ensures that all compartments (such as susceptible, exposed, infected stages, and recovered) have non-negative populations and that the total population size remains within a biologically plausible range.

Below is the model equations

$$\begin{cases}
 \frac{dS(t)}{dt} = \Lambda - \beta_1 E_A(t) S(t) - \beta_1 E_{NA}(t) S(t) - \beta_1 E_{ANA}(t) S(t) - \mu S(t) \\
 \frac{dE_A(t)}{dt} = \beta_1 E_A(t) S(t) - (\beta_4 + \mu) E_A(t) \\
 \frac{dE_{NA}(t)}{dt} = \beta_2 E_{NA}(t) S(t) - (\beta_5 + \mu) E_{NA}(t) \\
 \frac{dE_{ANA}(t)}{dt} = \beta_3 E_{ANA}(t) S(t) - (\beta_6 + \mu) E_{ANA}(t) \\
 \frac{dI_1(t)}{dt} = \beta_4 E_A(t) + \beta_5 E_{NA}(t) + \beta_6 E_{ANA}(t) - (\beta_7 + \beta_{10} + \mu) I_1(t) \\
 \frac{dI_2(t)}{dt} = \beta_7 I_1(t) - (\beta_8 + \beta_{11} + \mu) I_2(t) \\
 \frac{dI_3(t)}{dt} = \beta_8 I_2(t) - (\beta_9 + \beta_{12} + \mu) I_3(t) \\
 \frac{dI_4(t)}{dt} = \beta_9 I_3(t) - (\beta_{13} + \mu + \mu_0) I_4(t) \\
 \frac{dR(t)}{dt} = \beta_{10} I_1(t) + \beta_{11} I_2(t) + \beta_{12} I_3(t) + \beta_{13} I_4(t) - \mu R(t)
 \end{cases} \quad (1)$$

Total Population Size

The total population $N(t)$ at any time t is defined as:

$$N(t) = S(t) + E_A(t) + E_{NA}(t) + E_{ANA}(t) + I_1(t) + I_2(t) + I_3(t) + I_4(t) + R(t) \quad (2)$$

Proving the Positive Invariant Region

To show that the solutions remain within a biologically feasible region, we sum the differential equations for all

compartments and demonstrate that $N(t)$ is bounded and non-negative.

Sum of Compartmental Equations

Summing the differential equations for all compartments:

$$\frac{dN(t)}{dt} = \frac{dS(t)}{dt} + \frac{dE_A(t)}{dt} + \frac{dE_{NA}(t)}{dt} + \frac{dE_{ANA}(t)}{dt} + \frac{dI_1(t)}{dt} + \frac{dI_2(t)}{dt} + \frac{dI_3(t)}{dt} + \frac{dI_4(t)}{dt} + \frac{dR(t)}{dt} \quad (3)$$

Substituting the differential equations yields:

$$\left\{ \begin{aligned} \frac{dN(t)}{dt} &= \Lambda - \beta_1 E_A(t) S(t) - \beta_1 E_{NA}(t) S(t) - \beta_1 E_{ANA}(t) S(t) - \mu S(t) \\ &+ \beta_1 E_A(t) S(t) - (\beta_4 + \mu) E_A(t) + \beta_2 E_{NA}(t) S(t) - (\beta_5 + \mu) E_{NA}(t) \\ &+ \beta_3 E_{ANA}(t) S(t) - (\beta_6 + \mu) E_{ANA}(t) \\ &+ \beta_4 E_A(t) + \beta_5 E_{NA}(t) + \beta_6 E_{ANA}(t) - (\beta_7 + \beta_{10} + \mu) I_1(t) \\ &+ \beta_7 I_1(t) - (\beta_8 + \beta_{11} + \mu) I_2(t) + \beta_8 I_2(t) - (\beta_9 + \beta_{12} + \mu) I_3(t) \\ &+ \beta_9 I_3(t) - (\beta_{13} + \mu + \mu_0) I_4(t) \\ &+ \beta_{10} I_1(t) + \beta_{11} I_2(t) + \beta_{12} I_3(t) + \beta_{13} I_4(t) - \mu R(t) \end{aligned} \right. \quad (4)$$

Noting that $N(t) = S(t) + E_A(t) + E_{NA}(t) + E_{ANA}(t) + I_1(t) + I_2(t) + I_3(t) + I_4(t) + R(t)$:

$$\frac{dN(t)}{dt} = \Lambda - \mu N(t) - \mu_0 I_4(t) \quad (5)$$

Assuming $\mu_0 I_4(t) = 0$, equation (5) becomes

$$\frac{dN(t)}{dt} = \Lambda - \mu N(t) \quad (6)$$

Therefore, solving (3.6), which is a first order differential equation yields:

$$N(t) = \frac{\Lambda}{\mu} + \left(N(0) - \frac{\Lambda}{\mu} \right) e^{-\mu t} \quad (7)$$

As t approaches infinity, $e^{-\mu t}$ approaches zero and yields:

$$\lim_{t \rightarrow \infty} N(t) = \frac{\Lambda}{\mu}$$

Thus, the total population $N(t)$ approaches a steady state value of $\frac{\Lambda}{\mu}$ ensuring that $N(t)$ is bounded.

We can conclude the following on invariance:

If $N(0) < \frac{\Lambda}{\mu}$, then $N(t)$ Decreases over time and approaches $\frac{\Lambda}{\mu}$.

If $N(0) > \frac{\Lambda}{\mu}$, then $N(t)$ Enters \mathbf{D} in finite time or asymptotically approaches $\frac{\Lambda}{\mu}$.

Therefore, \mathbf{D} is positively invariant: all solutions in R_+^9 (the non-negative of R_+^9) eventually enter \mathbf{D} .

Study Focus

By focusing on dynamics within \mathbf{D} , researchers can effectively study the behavior of prostate cancer progression and evaluate intervention strategies.

Existence and Stability of Steady-State Solutions

The $E = (S^*, E_A^*, E_{NA}^*, E_{ANA}^*, I_1^*, I_2^*, I_3^*, I_4^*, R^*)$ is the steady-state of the system (1) which can be calculated by setting the right hand side of the model (3.1) to zero, giving us the following

$$\begin{cases}
 \Lambda - \beta_1 E_A(t) S(t) - \beta_1 E_{NA}(t) S(t) - \beta_1 E_{ANA}(t) S(t) - \mu S(t) = 0 \\
 \beta_1 E_A(t) S(t) - (\beta_4 + \mu) E_A(t) = 0 \\
 \beta_2 E_{NA}(t) S(t) - (\beta_5 + \mu) E_{NA}(t) = 0 \\
 \beta_3 E_{ANA}(t) S(t) - (\beta_6 + \mu) E_{ANA}(t) = 0 \\
 \beta_4 E_A(t) + \beta_5 E_{NA}(t) + \beta_6 E_{ANA}(t) - (\beta_7 + \beta_{10} + \mu) I_1(t) = 0 \\
 \beta_7 I_1(t) - (\beta_8 + \beta_{11} + \mu) I_2(t) = 0 \\
 \beta_8 I_2(t) - (\beta_9 + \beta_{12} + \mu) I_3(t) = 0 \\
 \beta_9 I_3(t) - (\beta_{13} + \mu + \mu_0) I_4(t) = 0 \\
 \beta_{10} I_1(t) + \beta_{11} I_2(t) + \beta_{12} I_3(t) + \beta_{13} I_4(t) - \mu R(t) = 0
 \end{cases} \quad (8)$$

The existence of the trivial equilibrium point

For as long as the human recruitment term Λ is not zero, the population will not be extinct. This implies that there is no trivial equilibrium point, thus

$$(S^*, E_A^*, E_{NA}^*, E_{ANA}^*, I_1^*, I_2^*, I_3^*, I_4^*, R^*) \neq (0, 0, 0, 0, 0, 0, 0, 0, 0, 0) \quad (9)$$

Disease-Free equilibrium Point E_0

Disease-free equilibrium points (DFE) are steady-state solutions where there is no disease (Prostrate cancer). We define the “diseased” classes as the human, or infected, that is; I_1, I_2, I_3, I_4 in the system (8). Hence, the DFE of the basic prostate cancer model (8) is given by

$$(S^*, E_A^*, E_{NA}^*, E_{ANA}^*, I_1^*, I_2^*, I_3^*, I_4^*, R^*) = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0, 0, 0, 0, 0, 0 \right) \quad (10)$$

That represents the state in which there is no infection in the society and is known as the disease-free equilibrium point (DFE).

The Reproduction Number \mathfrak{R}_0

The basic reproduction number:

$$\mathfrak{R}_0 = \frac{\beta_3 \Lambda}{\mu(\beta_6 + \mu)} + \frac{\beta_2 \Lambda}{\mu(\beta_5 + \mu)} + \frac{\beta_1 \Lambda}{\mu(\beta_4 + \mu)} \quad (11)$$

The basic reproduction number can be utilized to assess the local stability of the disease-free equilibrium point.

The basic reproduction number can be utilized to assess the local stability of the disease-free equilibrium point.

Local Stability of the Disease-Free Equilibrium

The local stability of the disease-free equilibrium can be analyzed using the Jacobian matrix of the model (1) at the disease-free equilibrium point. According to Abdullahi & Amiru (2023), the following theorem applies:

Theorem 2: The disease-free equilibrium point of the system is locally asymptotically stable if $\mathfrak{R}_0 < 1$, and unstable if $\mathfrak{R}_0 > 1$. (Abdullahi, & Sule (2024))

The threshold quantity you're referring to is typically denoted as \mathfrak{R}_0 , which is the basic reproduction number of a disease. It represents the expected number of secondary infections produced by a single infective individual (or snails, in the case of diseases transmitted by snails) introduced into a completely susceptible population.

The Endemic Equilibrium Points

The endemic equilibrium points are steady-state solutions where the disease persists in the population, meaning all state variables are positive. In other words, prostate cancer infection will continue to exist within the population. The endemic equilibrium point (EEP) of the model is characterized by:

$$\begin{aligned}
 S(t) &= \frac{\beta_4 + \mu}{\beta_1}, \quad E_A(t) = \frac{\Lambda\beta_1 - \mu^2 - \mu\beta_4}{(\beta_4 + \mu)\beta_1}, \quad E_{NA}(t) = \frac{\Lambda\beta_1 - \mu^2 - \mu\beta_5}{(\beta_5 + \mu)\beta_2}, \quad E_{ANA}(t) = \frac{\Lambda\beta_3 - \mu^2 - \mu\beta_6}{(\beta_6 + \mu)\beta_3} \\
 I_1(t) &= -\frac{\beta_4(-\Lambda\beta_1 + \mu^2 + \mu\beta_4)}{\beta_1(\beta_4 + \mu)(\beta_7 + \gamma + \mu)}, \quad I_2(t) = -\frac{\beta_4\beta_7(-\Lambda\beta_1 + \mu^2 + \mu\beta_4)}{\beta_1(\beta_4 + \mu)(\beta_7 + \gamma + \mu)(\beta_8 + \gamma + \mu)}, \\
 I_3(t) &= -\frac{(-\Lambda\beta_1 + \mu^2 + \mu\beta_4)\beta_4\beta_7\beta_8}{\beta_1(\beta_4 + \mu)(\beta_7 + \gamma + \mu)(\beta_8 + \gamma + \mu)(\beta_9 + \gamma + \mu)}, \quad I_4(t) = -\frac{(-\Lambda\beta_1 + \mu^2 + \mu\beta_4)\beta_4\beta_7\beta_8\beta_9}{\beta_1(\beta_4 + \mu)(\beta_7 + \gamma + \mu)(\beta_8 + \gamma + \mu)(\beta_9 + \gamma + \mu)} \\
 R(t) &= -\frac{(-\Lambda\beta_1 + \mu^2 + \mu\beta_4)\beta_4\beta_7\beta_8\beta_9}{\beta_1(\beta_4 + \mu)(\beta_7 + \gamma + \mu)(\beta_8 + \gamma + \mu)(\beta_9 + \gamma + \mu)(\gamma + \mu_0 + \mu)\mu}
 \end{aligned} \tag{12}$$

The prostate cancer model (1) discussed in the previous section will be further developed using the ABC fractional derivative approach

$$\begin{cases}
 {}^{ABC}D^q S_k(t) = \Lambda - \beta_1 E_{kA}(t) S_k(t) - \beta_1 E_{kNA}(t) S(t) - \beta_1 E_{kANA}(t) S_k(t) - \mu S_k(t) \\
 {}^{ABC}D^q E_{kA}(t) = \beta_1 E_{kA}(t) S_k(t) - (\beta_4 + \mu) E_{kA}(t) \\
 {}^{ABC}D^q E_{kNA}(t) = \beta_2 E_{kNA}(t) S_k(t) - (\beta_5 + \mu) E_{kNA}(t) \\
 {}^{ABC}D^q E_{kANA}(t) = \beta_3 E_{kANA}(t) S_k(t) - (\beta_6 + \mu) E_{kANA}(t) \\
 {}^{ABC}D^q I_{k1}(t) = \beta_4 E_{kA}(t) + \beta_5 E_{kNA}(t) + \beta_6 E_{kANA}(t) - (\beta_7 + \beta_{10} + \mu) I_{k1}(t) \\
 {}^{ABC}D^q I_{k2}(t) = \beta_7 I_{k1}(t) - (\beta_8 + \beta_{11} + \mu) I_{k2}(t) \\
 {}^{ABC}D^q I_{k3}(t) = \beta_8 I_{k2}(t) - (\beta_9 + \beta_{12} + \mu) I_{k3}(t) \\
 {}^{ABC}D^q I_{k4}(t) = \beta_9 I_{k3}(t) - (\beta_{13} + \mu + \mu_0) I_{k4}(t) \\
 {}^{ABC}D^q R_{k4}(t) = \beta_{10} I_{k1}(t) + \beta_{11} I_{k2}(t) + \beta_{12} I_{k3}(t) + \beta_{13} I_{k4}(t) - \mu R_k(t)
 \end{cases} \tag{13}$$

With initial conditions:

$$\begin{aligned}
 S_k(0) = S_k(0) \geq 0, \quad E_{kA}(0) = E_{kA}(0) \geq 0, \quad E_{kNA}(0) = E_{kNA}(0) \geq 0, \quad E_{kANA}(0) = E_{kANA}(0) \geq 0, \\
 I_{k1}(0) = I_{k1}(0) \geq 0, \quad I_{k2}(0) = I_{k2}(0) \geq 0, \quad I_{k3}(0) = I_{k3}(0) \geq 0, \quad I_{k4}(0) = I_{k4}(0) \geq 0, \\
 R_k(0) = R_k(0) \geq 0
 \end{aligned} \tag{14}$$

Where $0 \leq t \leq T < \infty$ and ${}^{ABC}D^q$ represents the ABC fractional derivative of order $0 < q \leq 1$

Table 2: Showing the parameter values

Parameters	Description	Value (per year)	Reference
Λ	Recruitment rates of men.	0.03	Liu et al (2022)
μ	Natural death of men	0.0365	Smith & Jones(2022)
β_1	Rate of exposure due to avoidable factors	0.02	Assumed
β_2	Rate of exposure due to non-avoidable factors	0.03	Estimated
β_3	Rate of exposure due to both avoidable and non-avoidable factors	0.04	Assumed
β_4	Rate at which exposed individuals due to A.V factors progress to stage I infection	0.03	White et.al (2021)
β_5	Rate at which exposed individuals due to N.A factors	0.04	White (2021)
β_6	Rate at which exposed individuals due to both A. & N.A factors progress to stage I of infection	0.05	White (2021)
β_7	Rate of progression from stage 1 to stage 2	0.07	Brown et al (2021)
β_8	Rate of progression from stage 2 to stage 3	0.1	Johnson et al (2022)
β_9	Rate of progression from stage 3 to stage 4	0.07	Doe (2022)
β_{10}	Rate of recovery from stage I of infection	0.08	Assumed
β_{11}	Rate of recovery from stage 2 of infection	0.07	Assumed
β_{12}	Rate of recovery from stage 3 of infection	0.08	Assumed
β_{13}	Rate of recovery from stage 4 of infection	0.03	Johnson (2023)
μ_0	Death rate due to the disease	0.073	Johnson & Brown (2021)

Basic definitions

In this section, we will introduce key Basic definitions related to fractional calculus and nonlinear analysis (Atangana, & Gómez-Aguilar (2018)).

Definition 1: The left-sided ABC fractional derivative with the lower limit zero of order

$\alpha \in (0, 1]$ for a function $\mathcal{G} \in H^1(0, T)$ is defined as:

$${}^{ABC}D^\alpha \phi(t) = \frac{\mathcal{N}(\alpha)}{1-\alpha} \int_0^1 E_\alpha \left(\frac{-\alpha}{\alpha-1} (t-\theta)^\alpha \right) \phi'(\theta) d\theta, \quad t > 0,$$

Where $\mathcal{N}(\alpha)$ is the normalization function which is defined as $\mathcal{N}(0) = \mathcal{N}(1) = 1$, and E_α is called the Mittag-Leffler function, defined by the series

$$E_\alpha(z) = \sum_{k=0}^{\infty} \frac{z^k}{\Gamma(\alpha k + 1)} \quad (15)$$

here $\text{Re}(\alpha) > 0$ and $\Gamma(\cdot)$ is a gamma function.

Definition 2: The left-sided ABC fractional derivative with the lower limit zero of order $\alpha \in (0, 1]$ for a function $\mathcal{G} \in H^1(0, T)$ is defined as

$${}^{ABC}\mathfrak{J}^\alpha \phi(t) = \frac{1-\alpha}{\mathcal{N}(\alpha)} \phi(t) + \frac{\alpha}{\mathcal{N}(\alpha)} \frac{1}{\Gamma(\alpha)} \int_0^1 ((t-\theta)^\alpha) \phi'(\theta) d\theta, \quad t > 0,$$

Lemma.1 (see the work of Abdeljawad & Baleanu (2016)). The solution of the following problem for $\alpha \in (0, 1]$

$$\begin{aligned} {}^{ABC}D^\alpha \phi(t) &= \psi(t) \\ \phi(0) &= \phi_0 \end{aligned} \quad (16)$$

is given by

$$\phi(t) = \phi_0 + \frac{1-\alpha}{\mathcal{N}(\alpha)} \psi(t) + \frac{\alpha}{\mathcal{N}(\alpha)} \frac{1}{\Gamma(\alpha)} \int_0^1 (t-\theta)^{\alpha-1} \psi(\theta) d\theta.$$

Theorem 3. Assume \mathcal{Y} be a Banach space and $\mathcal{D} \subset \mathcal{Y}$ be a convex, closed and bounded set. If $\psi : \mathcal{D} \rightarrow \mathcal{D}$ is a continuous operator such that $\psi\mathcal{D} \subset \mathcal{Y}$ and $\psi\mathcal{D}$ is relatively compact, then ψ has at least one fixed point in \mathcal{D} .

Theoretical approach

To investigate the existence, uniqueness, and stability of solutions for the model described by equations (14)–(16), we first need to reformulate the model into the following appropriate form:

$$\begin{cases} {}^{ABC}D^q S_k = G_1(t, S_k, E_{kA}, E_{kNA}, E_{kANA}, I_{k1}, I_{k2}, I_{k3}, I_{k4}, R_k) \\ \vdots \\ {}^{ABC}D^q R_{k4} = G_9(t, S_k, E_{kA}, E_{kNA}, E_{kANA}, I_{k1}, I_{k2}, I_{k3}, I_{k4}, R_k) \end{cases} \quad (17)$$

Where

$$\begin{cases} G_1(t, S_k, E_{kA}, E_{kNA}, E_{kANA}, I_{k1}, I_{k2}, I_{k3}, I_{k4}, R_k) = \Lambda - \beta_1 E_{kA}(t) S_k(t) - \beta_1 E_{kNA}(t) S(t) - \beta_1 E_{kANA}(t) S_k(t) - \mu S_k(t) \\ \vdots \\ G_9(t, S_k, E_{kA}, E_{kNA}, E_{kANA}, I_{k1}, I_{k2}, I_{k3}, I_{k4}, R_k) = \beta_{10} I_{k1}(t) + \beta_{11} I_{k2}(t) + \beta_{12} I_{k3}(t) + \beta_{13} I_{k4}(t) - \mu R_k(t) \end{cases} \quad (4.5)$$

The model described by equations (4.1) and (4.2) can be expressed as:

$$\begin{cases} {}^{ABC}D^q \chi(t) = \Phi(t, \chi(t)), \quad t \in [0, T] \\ \chi(0) = \chi_0 \geq 0, \end{cases} \quad (18)$$

Where

$$\begin{cases} \chi := (S_k, E_{kA}, E_{kNA}, E_{kANA}, I_{k1}, I_{k2}, I_{k3}, I_{k4}, R_k)^T \\ \chi_0 := (S_k(0), E_{kA}(0), E_{kNA}(0), E_{kANA}(0), I_{k1}(0), I_{k2}(0), I_{k3}(0), I_{k4}(0), R_k(0))^T \\ \Phi(t, \chi(t)) := (G(t, S_k, E_{kA}, E_{kNA}, E_{kANA}, I_{k1}, I_{k2}, I_{k3}, I_{k4}, R_k))^T \\ k = 1, \dots, n \end{cases} \quad (19)$$

Here, the symbol $(\cdot)^T$ denotes the transpose vector. In view of **Lemma 4.2.1**, the system (4.6) is equivalent to the following fractional integral equation:

$$\chi(t) = \chi_0 + \frac{1-q}{\mathcal{N}(q)} \Phi(t, \chi(t)) + \frac{q}{\mathcal{N}(q)} \frac{1}{\Gamma(q)} \int_0^t (t-\theta)^{q-1} \Phi(\tau, \chi(\tau)) d\tau. \quad (20)$$

For the qualitative analysis, let us present the Banach space $\Pi := C([0, T], \mathbb{R}^k)_{1 < k < n}$, endowed with the

norm $\|\mathcal{X}\| := \sup_{t \in [0, T]} \{\|\mathcal{X}(t)\|\}$. Further, we define the Banach Space $\Omega = (\Pi^6, \|\mathcal{X}\|)$ with the norm

$$\|\mathcal{X}\| = \sup_{t \in [0, T]} \left\{ (|S_k| + |E_{kA}| + |E_{kNA}| + |E_{kANA}| + |I_{k1}| + |I_{k2}| + |I_{k3}| + |I_{k4}| + |R_k|) \right\} \quad (21)$$

$$\begin{cases} S_k(t) - S_k(0) = {}^{AB} \mathbb{I}_{0^+}^q H_1(t, S_k(t)), \\ \vdots \\ R_k(t) - R_k(0) = {}^{AB} \mathbb{I}_{0^+}^q H_9(t, R_k(t)), \end{cases} \quad (22)$$

Which yields;

$$\begin{cases} S_k(t) - S_k(0) = \frac{1-q}{\Upsilon(q)} H_1(t, S_k(t)) + \frac{q}{\Upsilon(q)\Gamma(q)} \frac{1}{\Gamma(q)} \int_0^t (t-\tau)^{q-1} H_1(\tau, S_k(\tau)) d\tau, \\ \vdots \\ R_k(t) - R_k(0) = \frac{1-q}{\Upsilon(q)} H_9(t, R_k(t)) + \frac{q}{\Upsilon(q)\Gamma(q)} \frac{1}{\Gamma(q)} \int_0^t (t-\tau)^{q-1} H_9(\tau, R_k(\tau)) d\tau, \end{cases} \quad (23)$$

To procure an iterative scheme, setting $t = t_{s+1}$, for $s = 1, 2, \dots$, in the above system leads to the model down.

$$\begin{cases} S_k(t_{s+1}) - S_k(0) = \frac{1-q}{\Upsilon(q)} H_1(t_s, S_k(t_s)) + \frac{q}{\Upsilon(q)\Gamma(q)} \sum_{i=0}^s \int_{t_i}^{t_{i+1}} (t_{s+1} - \tau)^{q-1} H_1(\tau, S_k(\tau)) d\tau, \\ \vdots \\ R_k(t_{s+1}) - R_k(0) = \frac{1-q}{\Upsilon(q)} H_9(t_s, R_k(t_s)) + \frac{q}{\Upsilon(q)\Gamma(q)} \sum_{i=0}^s \int_{t_i}^{t_{i+1}} (t_{s+1} - \tau)^{q-1} H_9(\tau, R_k(\tau)) d\tau, \end{cases} \quad (24)$$

Utilize the two points interpolation polynomial for approximate the functions

$$H_1(\tau, S_k(\tau)), H_2(\tau, E_{kA}(\tau)), H_3(\tau, E_{kNA}(\tau)), H_4(\tau, E_{kANA}(\tau)), H_5(\tau, I_{k1}(\tau)), H_6(\tau, I_{k2}(\tau)), \\ H_7(\tau, I_{k3}(\tau)), H_8(\tau, I_{k4}(\tau)), \text{ and } H_9(\tau, R_k(\tau)),$$

That lie inside the integral in (4.12) on the interval $[t_i, t_{i+1}]$, We get

$$H_1(\tau, S_k(\tau)) \cong \frac{H_1(t_i, S_k(t_i))}{h} (t - t_{i-1}) + \frac{H_1(t_{i-1}, S_k(t_{i-1}))}{h} (t - t_i), \\ \vdots \quad (25)$$

$$H_9(\tau, R_k(\tau)) \cong \frac{H_9(t_i, R_k(t_i))}{h} (t - t_{i-1}) + \frac{H_9(t_{i-1}, R_k(t_{i-1}))}{h} (t - t_i),,$$

which yields

$$\begin{cases} S_k(t_{s+1}) = S_k(0) + \frac{1-q}{\Upsilon(q)} H_1(t_s, S_k(t_s)) + \frac{q}{\Upsilon(q)\Gamma(q)} \times \sum_{i=0}^s \left(\frac{H_1(t_i, S_k(t_i))}{h} \mathbb{I}_{t_{i-1}, q} - \frac{H_1(t_{i-1}, S_k(t_{i-1}))}{h} \mathbb{I}_{t_i, q} \right) \\ \vdots \\ R_k(t_{s+1}) - R_k(0) = \frac{1-q}{\Upsilon(q)} H_9(t_s, R_k(t_s)) + \frac{q}{\Upsilon(q)\Gamma(q)} \times \sum_{i=0}^s \left(\frac{H_9(t_i, R_k(t_i))}{h} \mathbb{I}_{t_{i-1}, q} - \frac{H_9(t_{i-1}, R_k(t_{i-1}))}{h} \mathbb{I}_{t_i, q} \right), \end{cases} \quad (26)$$

Where

$$\mathbb{I}_{t_{i-1}, q} = \int_{t_i}^{t_{i+1}} (t - t_{i-1})(t_{s+1} - t)^{q-1} dt \quad (27)$$

and

$$\mathbb{I}_{t_i, q} = \int_{t_i}^{t_{i+1}} (t - t_i)(t_{s+1} - t)^{q-1} dt$$

By simple calculations of the integrals $\mathbb{I}_{t_{i-1}, q}$ and $\mathbb{I}_{t_i, q}$, we get

$$I_{t-1,q} = -\frac{1}{q} \left[(t_{t+1} - t_{t-1})(t_{s+1} - t_{t+1})^q - (t_t - t_{t-1})(t_{s+1} - t_t)^q \right] \quad (28)$$

$$-\frac{1}{q(q+1)} \left[(t_{s+1} - t_{t+1})^{q+1} - (t_{s+1} - t_t)^{q+1} \right],$$

and

$$I_{t,q} = -\frac{1}{q} \left[(t_{t+1} - t_t)(t_{s+1} - t_{t+1})^q \right] \quad (29)$$

$$-\frac{1}{q(q+1)} \left[(t_{s+1} - t_{t+1})^{q+1} - (t_{s+1} - t_t)^{q+1} \right],$$

And

$$I_{t,q} = \frac{h^{q+1}}{q(q+1)} \left[(s+1-t)^{q+1} - (s-t)^q (s-t+1+q) \right] \quad (30)$$

Replacing (29) and (30) into (22), we attain

$$S_k(t_{s+1}) = S_k(t_0) + \frac{1-q}{\Gamma(q)} H_1(t_s, S_k(t_s)) + \frac{q}{\Gamma(q)} \sum_{t=0}^s \left(\frac{H_1(t, S_k(t))}{h} h^q \left[(s+1-t)(s-t+2+q) - (s-t)^q (s-t+2+2q) \right] - \frac{H_1(t_{t-1}, S_k(t_{t-1}))}{\Gamma(q+2)} h^q \left[(s+1-t)^{q+1} - (s-t)^q (s-t+1+q) \right] \right) \quad (31)$$

⋮

$$R_k(t_{s+1}) = R_k(t_0) + \frac{1-q}{\Gamma(q)} H_9(t_s, R_k(t_s)) + \frac{q}{\Gamma(q)} \sum_{t=0}^s \left(\frac{H_9(t, R_k(t))}{h} h^q \left[(s+1-t)(s-t+2+q) - (s-t)^q (s-t+2+2q) \right] - \frac{H_9(t_{t-1}, R_k(t_{t-1}))}{\Gamma(q+2)} h^q \left[(s+1-t)^{q+1} - (s-t)^q (s-t+1+q) \right] \right)$$

Numerical Simulations

ABC fractional operator, we will employ the iterative to illustrate the numerical simulation for the proposed model (14)–(16), which includes the solution outlined in (31). The time is measured in days. The parameter values used in the simulation are specified in Table 1

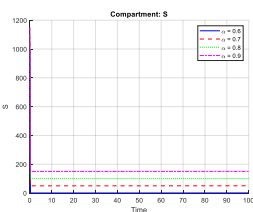


Figure 1 number of susceptible individuals.

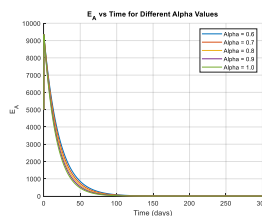


Figure 2 number of exposed individuals due to avoidable risk factors

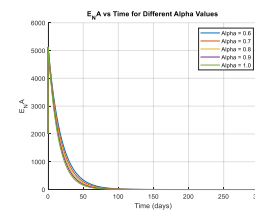


Figure 3 number of exposed individuals with non-avoidable risk factors

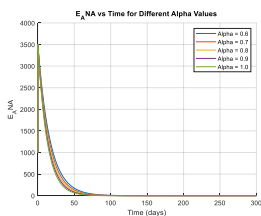


Figure 4 number of exposed individuals with both risk factors.

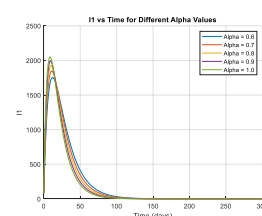


Figure 5 number of infected individuals at stage 1

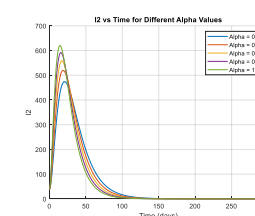


Figure 6 number of infected individuals at stage 2

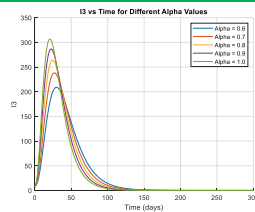


Figure 7 number of infected individuals at stage 3

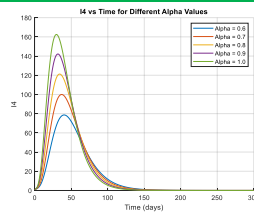


Figure 8 number of infected individuals at stage 4

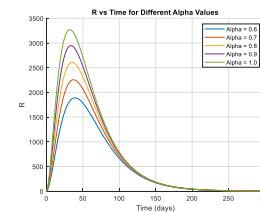


Figure 9 : number of recovered individuals

Impact on Policy and Clinical Practice in Uganda

This study uses the Atangana-Baleanu Caputo (ABC) fractional derivative to model prostate cancer progression, offering critical insights for health policy and clinical practice in Uganda. By highlighting the impact of both avoidable and unavoidable risk factors, the model aids in making informed decisions regarding screening, resource allocation, and targeted interventions. Clinically, it supports personalized treatment planning and better disease management by considering patients' medical histories and simulating various therapeutic strategies.

Numerical Simulations

The study employs an iterative approach with the Atangana-Baleanu Caputo (ABC) fractional operator to simulate prostate cancer dynamics. Using equations (31) and visualized in Figures 1–9, the simulations track the evolution of different population groups—susceptible, exposed, infected (by stage), and recovered—over time. The results demonstrate the model's sensitivity to parameter changes, providing insights into risk exposure, treatment effectiveness, and recovery. These findings are instrumental in informing health policies and clinical strategies in Uganda to improve prostate cancer detection, treatment, and outcomes.

4.0 CONCLUSION

This study introduces a new mathematical model for understanding prostate cancer progression by incorporating the Atangana-Baleanu Caputo fractional derivative, which factors in the impact of past events like previous treatments and earlier cancer stages. The model categorizes the population into susceptible, exposed, infected, and recovered groups, offering a more comprehensive view of disease spread and progression. Unlike traditional models, this approach considers the influence of past occurrences on the present state, providing more realistic simulations of exposure, treatment, and recovery. Particularly relevant for Uganda, where prostate cancer rates are rising and healthcare access is limited, the study builds on existing research while calling for more precise models. In summary, it provides an innovative tool for improving treatment outcomes and public health strategies for prostate cancer.

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