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Analysis of a Nonlinear Mathematical Model Related to Type 1 Diabetes and Growth Hormone

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Abstract

This research investigates a nonlinear ordinary differential equation (ODE) model characterizing the interactions between β-cells and Growth Hormone (G_H). By employing the Localization of Compact Invariant Set (LCIS) method, we define a bounded positive invariant domain that reflects the physiological limits of the human body. The study aims to clarify the hyperglycemic effects of G_H on glucose variation, particularly in Type 1 Diabetes (DM-1) contexts. Our results provide a mathematical physiological cage that explains how hormonal regulation maintains stability despite pathological disturbances.

Keywords— Diabetes, β-cells, Growth Hormone, Localization of Compact Invariant Sets, Stability

1 Introduction

Type-1 Diabetes (DM-1) is a chronic autoimmune disease that consists mainly of the loss of pancreatic beta cells, resulting in persistent hyperglycemia [1]. As a result of this, various complications appear, such as microvascular and macrovascular diseases developing, which affect the lifestyle of people with DM-1 [2]. To understand its complexity, the role of counter-regulatory hormones such as Growth Hormone (G_H) must be considered. Produced in the anterior pituitary gland by specialized somatotrophs, G_H release is stimulated by Growth Hormone-Releasing Hormone (GHRH) and inhibited by somatostatin (SS). The physiological impact of G_H varies across the human lifespan: in children, it facilitates linear skeletal growth by stimulating hepatic somatomedins (IGF family), while in adults, it promotes protein synthesis and fatty acid release. Crucially, G_H inhibits muscle glucose uptake while promoting amino acid uptake, forcing muscles to utilize fatty acids as an energy source. Consequently, elevated G_H levels lead to hyperglycemia, representing a causative factor in diabetic complications for both DM-1 and DM-2 patients.

The physiological mechanism of G_H operates through a highly regulated hypothalamic-pituitary-liver axis, characterized by episodic pulses where GHRH regulates amplitude and SS determines frequency. Clinical evidence highlights that G_H alterations vary significantly between diabetes types. According to Álvarez-Castro *et al.* [3], DM-1 patients typically exhibit higher basal G_H concentrations and exaggerated responses to stimuli compared to healthy subjects. Conversely, in DM-2 patients, the G_H response to GHRH is often reduced, particularly in cases involving obesity. Distinguishing these dynamics is vital for the biological accuracy of our model, as chronic G_H-induced hyperglycemic stress is a defining characteristic of the DM-1 metabolic profile.

Over the past five decades, more than 250 mathematical models have been developed to describe glucose and insulin dynamics, such as those in [4, 5, 6]. Modeling DM-1 through Ordinary Differential Equations (ODEs) provides significant advantages for understanding the disease evolution [7]. In this work, we analyze a nonlinear model to demonstrate the interactions between β-cells, insulin, glucose, and G_H levels. Specifically, the Localization of Compact Invariant Sets (LCIS) method is applied to establish the ultimate dynamics and evaluate the reliability of treatments aimed at strengthening β-cell mass.

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2 Mathematical Model and Methodology

The mathematical framework of this research is fundamentally anchored in the seminal work of Topp *et al.* [8], which introduced a robust three-dimensional nonlinear system of ODEs. This original model was designed to capture the multi-scale temporal dynamics of the glucose-insulin feedback loop, specifically emphasizing the slow-scale evolution of β-cell mass in response to fast-scale glycemic fluctuations. By characterizing the pathways to diabetes through cellular replication and apoptosis, the Topp model provided a physiological basis for understanding metabolic failure. However, to address the complexities of hormonal counter-regulation in DM-1, this framework was subsequently expanded by Al Ali *et al.* [9]. This enhancement involved the integration of a fourth state variable representing G_H dynamics, transforming the system into a more comprehensive somatotropic-pancreatic model.

The model is structured around four primary state variables. The interactions and the role of each parameter are summarized below.

Beta-Cell Mass Dynamics (β)

$$\frac{d\beta}{dt} = \left(-g + \xi G_L - iG_L^2\right)\beta \tag{1}$$

This equation describes the glucose-dependent growth of beta cells. It includes natural apoptosis (g), glucose-stimulated replication (ξ), and glucotoxicity (iG_L^2), which dominates at high glucose concentrations.

Insulin Dynamics (I)

$$\frac{dI}{dt} = \frac{dG_L^2}{e + G_L^2}\beta - fI \tag{2}$$

Insulin secretion is modeled as a Hill function of the glucose concentration, scaled by the total beta-cell mass β. The parameter f represents the first-order insulin clearance rate.

Glucose Dynamics (G_L)

$$\frac{dG_L}{dt} = a - (b + cI)G_L + cG_H \tag{3}$$

Here, a represents the constant hepatic glucose production rate. The term $-(b + cI)G_L$ accounts for both insulin-independent (b) and insulin-dependent (c) glucose uptake. The term $+cG_H$ represents the hyperglycemic effect of G_H, which inhibits peripheral glucose uptake.

Growth Hormone Dynamics (G_H)

$$\frac{dG_H}{dt} = \rho - \zeta G_H \tag{4}$$

G_H is produced at a rate ρ and cleared at a rate ζ. Its primary role in this model is to act as a forcing term in the glucose equation.

For a better understanding of the system's differential equations and the relation with the parameters presented in Table 1, a representative diagram is presented in Figure 1.

2.1 Physiological Relevance of Parameters

The parametric structure of the proposed four-dimensional system represents the metabolic reserves and regulatory limits of the somatotropic-pancreatic axis. A critical indicator is parameter d, which quantifies the maximum insulin secretory rate relative to β-cell mass; this reflects the functional reserve of the pancreas when subjected to chronic glycemic stress. Unlike simplified models, our framework distinguishes between the adaptive and pathological responses of β-cells through parameters ξ and i. Specifically, ξ acts as the linear glucose tolerance factor facilitating cellular replication, whereas i represents the quadratic exhaustion rate, or glucotoxicit effect.

This quadratic term is vital for the model's biological accuracy, as it accounts for the oxidative stress and cellular failure that occur when glucose levels exceed a sustainable threshold. Together with the natural death rate g, these parameters establish a metabolic window where the body can maintain homeostasis. By defining these interactions, the model transitions from idealized growth to a realistic representation of DM-1 progression, where the somatotropic influence of G_H acts as a persistent stressor on insulin sensitivity. This parametric configuration ensures that the localization bounds derived in the following section correspond to authentic physiological limits rather than mere mathematical artifacts.

Table 1: Model parameters, symbols, values and units used [9].

Parameter	Symbol	Value	Unit
Biological parameters			
Glucose production rate by liver	a	45.28	mg/dL min
Glucose clearance rate independent of insulin	b	0.13	min^{-1}
Insulin induced glucose uptake rate	c	0.85	mL/mIU min
β-cell maximum insulin secretory rate	d	43.2	mIU/mL min mg
Sigmoidal inflection point	e	20×10^3	mg^2/dL^2
Whole body insulin clearance rate	f	72.19	min^{-1}
β-cell natural death rate	g	0.03	min^{-1}
Determines β-cell glucose tolerance range factor	ξ	0.5727×10^{-3}	dL/mg min
Determines β-cell glucose tolerance range factor	i	1.91×10^{-6}	dL^2/mg^2 min
Growth hormone production rate by somatotropic cells	ρ	15.06	mIU/mL min
Growth hormone clearance rate by the liver	ζ	1958.4	min^{-1}
Model response parameters			
β-cells	β	800	mg
Insulin	I	20	mIU/mL
Glucose	G_L	80	mg/dL
Growth Hormone	G_H	30	mIU/mL

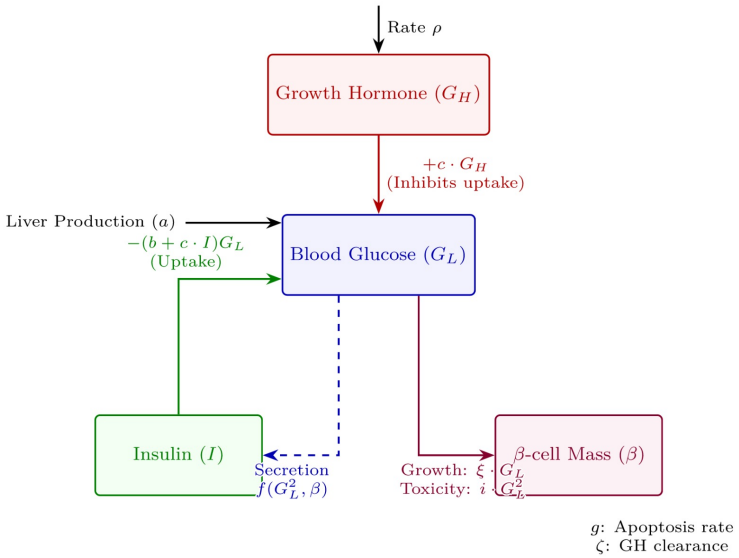

Figure 1: The visual representation utilizes a color-coded hierarchy: red for the G_H axis, blue for glucose, green for insulin, and purple for β-cell mass. The red arrow from G_H indicates a counter-regulatory pressure $+cG_H$, which inhibits insulin-mediated glucose uptake. This stimulates an increase in blood glucose (G_L), shown in the central blue block. In response, a dashed blue arrow illustrates how glucose stimulates insulin (I) secretion through the function $f(G_L^2, \beta)$, while a solid purple arrow shows glucose driving β-cell variation via linear growth (ξG_L) and quadratic toxicity ($-iG_L^2$) . Homeostasis is represented by the solid green arrow signifying insulin-induced uptake ($-cIG_L$), which lowers glucose levels.

2.2 Localization Bounds and the "Physiological Cage"

The LCIS method facilitates the derivation of G_{Hmax}, G_{Lmax}, β_{max}, and I_{max}, establishing what we define as the physiological cage. These bounds represent the systemic capacity for metabolic containment, delineating the maximum hormonal and glycemic concentrations the human body can endure before reaching irreversible pathological states. Mathematically, these invariant domains prove that the system is dissipative and globally stable within a compact set. This ensures that the trajectories of DM-1 dynamics are naturally confined to biologically survivable regions, providing a rigorous framework to predict long-term disease evolution and its inherent resistance to unbounded divergence under stress.

3 Main Results

3.1 Stability of Equilibrium Points

The local stability analysis of the system (1)-(4), conducted via the indirect Lyapunov method and the evaluation of the Jacobian matrix, reveals the existence of three distinct equilibrium points representing unique metabolic states within the somatotropic-pancreatic axis. As detailed in Table 2, equilibrium point P_2 is the only locally asymptotically stable state, characterized by eigenvalues with strictly negative real parts. Biologically, P_2 represents a stable metabolic basin where the endocrine system successfully manages glucose concentrations despite the counter-regulatory influence of G_H. In this state, the compensatory mechanisms of β-cell replication and insulin secretion are sufficient to counteract G_H-induced hyperglycemic effects, providing the system with the intrinsic resilience to return to homeostasis following minor metabolic disturbances.

In contrast, P_1 and P_3 are mathematically classified as unstable saddle points, which effectively act as physiological tipping points. The instability of P_1, where β-cell mass and insulin levels are depleted, signifies a critical systemic collapse typical of advanced, untreated DM-1. Similarly, P_3 represents a non-sustainable state of severe hyperglycemia; although some β-cell mass remains, the rates of cellular exhaustion and apoptosis outweigh replication, making this condition unsustainable without exogenous intervention.

The current parameter set is calibrated to represent the metabolic profile of a DM-1 patient. The saddle nature of P_1 and P_3 confirms that unless the patient's state remains within the basin of attraction of P_2, the system will naturally drift toward pathological extremes. By analyzing the vector field near these equilibria, we visualize trajectories pushing the biological state away from stability, emphasizing that maintaining the system within the vicinity of P_2 is fundamental for metabolic survival. This underscores the necessity of the localization domains discussed in the following section, which establish the global boundaries for these trajectories.

Table 2: Equilibrium points stability analysis.

Point	Coordinates (β, I, G_L, G_H)	Stability
P_1	$(0, 0, 348.36, 7.69 \times 10^{-3})$	Unstable
P_2	$(5.69, 0.63, 67.64, 7.69 \times 10^{-3})$	Stable
P_3	$(0.17, 7.6 \times 10^{-3}, 232.2, 7.69 \times 10^{-3})$	Unstable

3.2 Stability Analysis and Biological Implications

The system yields three equilibrium points, but only P_2 is locally asymptotically stable. The presence of two unstable points, P_1 and P_3, signifies critical physiological thresholds. Biologically, P_1 (where $\beta = 0$) represents the total collapse of the pancreatic function, while P_3 represents a precarious "tipping point" where insulin production is insufficient to overcome hyperglycemia. These points are mathematically characterized as saddle points, meaning that unless the system is within the basin of attraction of P_2, the trajectories will diverge toward pathological states.

3.3 LCIS Method and Invariant Sets

The existence of the localization domain is contingent upon the condition $4ig > \xi^2$. Physiologically, this inequality implies that the product of the β-cell exhaustion rate (i) and the natural death rate (g) must be greater than the square of the glucose-induced replication factor (ξ). This ensures that the biological cost of high glucose concentrations

(death and exhaustion) eventually outweighs the replication rate, preventing an unrealistic, infinite expansion of the β-cell mass and ensuring the system remains within a bounded.

To determine if the model fulfills the physiological criteria, it is necessary to apply the positivity test on the model. The following is obtained:

$$\frac{d\beta}{dt}|_{\beta=0} = \left(\xi G_L - i{G_L}^2 - g\right)(0) = 0, \tag{5}$$

$$\frac{dI}{dt}|_{I=0} = \left(\frac{\beta d{G_L}^2}{e + {G_L}^2}\right) - f(0) = 0, \tag{6}$$

$$\frac{dG_L}{dt}|_{G_L=0} = a - (b + cI)(0) + cG_H = a + c\rho, \tag{7}$$

$$\frac{dG_H}{dt}|_{G_H=0} = \rho - \zeta(0) = \rho, \tag{8}$$

Having verified the system through positivity analysis, the lower and upper limits need to be established. For this, it is necessary to apply the LCIS method. Applying the method, the upper limits ($G_{Hmax}, G_{Lmax}, \beta_{max}, I_{max}$) are obtained through propositions of localization functions, while the lower limits are given by ($G_{Hmin} = 0, G_{Lmin} = 0, \beta_{min} = 0, I_{min} = 0$).

Continuing with the method, the localization function $\mathbf{h_1} = \mathbf{G_H}$ is proposed, and the following localization domain is obtained:

$$K_1 = \left\{G_H \leq G_{H\max} := \frac{\rho}{\zeta}\right\} \tag{9}$$

Subsequently, the second localization function $\mathbf{h_2} = \mathbf{G_L}$ is proposed; the following localization domain is obtained:

$$K_2 = \left\{G_L \cap K_1 \leq G_{L\max} := \frac{a}{b} + \frac{c}{b}G_{H_{\max}}\right\} \tag{10}$$

Hence, the localization function $\mathbf{h_3} = \mathbf{G_L} + \boldsymbol{\beta}$ is proposed, from this function the set $S(h_3)$ is obtained:

$$S(h_3) = \left\{\left(\frac{4ig - \xi^2}{4i}\right)\beta = a - bG_L - cIG_L + cG_H - i\beta\left(G_L - \frac{\xi}{2i}\right)^2\right\} \tag{11}$$

From Equation (11), the following condition is obtained:

$$4ig > \xi^2$$

Having this condition and if it satisfied, the following localization domain is obtained:

$$K_3 = \left\{h_3\,|_{S(h_3)} \cap K_1 \cap K_2 \leq G_{L\max} + \left(\frac{4i}{4ig - \xi^2}\right)(a + cG_{H\max})\right\} \tag{12}$$

For the fourth localization function $\mathbf{h_4} = \mathbf{I}$ is proposed, the localization domain is obtained:

$$K_4 = \left\{I \cap K_2 \cap K_3 \leq I_{\max} := \frac{d}{fe}\beta_{\max}G_{L\max}^2\right\} \tag{13}$$

Theorem 3.1. *Through the proposition of localization functions, the localization of compact invariant sets are determined, which the set for the domain of interest is given by $K = K_1 \bigcap K_2 \bigcap K_3 \bigcap K_4$. Where the localization region is satisfied under the constraint of $R^4_{+,0}$. As presented in Table 3.*

3.4 Biological Constraints and LCIS Conditions

The application of the LCIS method provides a global perspective on the system's behavior, establishing the ultimate dynamics through the definition of a bounded, positive invariant domain. A pivotal result of this method is the derivation of the algebraic condition $4ig > \xi^2$, which acts as a fundamental biological feasibility constraint. This inequality governs the parabolic nature of the β-cell mass equation; mathematically, it ensures that the localization function remains negative for large values of glucose, thereby preventing the trajectories from escaping to infinity.

Table 3: System localization domain.

	Localization functions	Localization domains
$\mathbf{K_1}$	$h_1 = G_H$	$G_H \leq G_{H\max} := \frac{\rho}{\zeta}$
$\mathbf{K_2}$	$h_2 = G_L$	$G_L \cap K_1 \leq G_{L\max} := \frac{a}{b} + \frac{c}{b} G_{H_{\max}}$
$\mathbf{K_3}$	$h_3 = G_L + \beta$	$h_3 \mid_{S(h_3)} \cap K_1 \cap K_2 \leq G_{L\max} + \left(\frac{4i}{4ig-\zeta^2}\right)(a + cG_{H\max})$
$\mathbf{K_4}$	$h_4 = I$	$I \cap K_2 \cap K_3 \leq I_{\max} := \frac{d}{fe}\beta_{\max} G_{L\max}^2$

Physiologically, this condition reflects a vital balance within the pancreas: the product of the β-cell exhaustion rate (i) and the natural death rate (g) must be sufficiently larger than the square of the glucose-induced replication factor (ξ). If this constraint were violated, the model would predict an unrealistic and biologically impossible infinite expansion of pancreatic tissue. In reality, the metabolic cost of chronic hyperglycemia—manifested as oxidative stress and cellular exhaustion—eventually limits the regenerative capacity of β-cells, ensuring a bounded population.

Furthermore, the invariant domains K_1 through K_4 establish the physiological cage, defining the maximum hormonal and glycemic ceilings (G_{Hmax}, G_{Lmax}, β_{max}, and I_{max}) that a human subject can realistically reach. For instance, $G_{Hmax} = \rho/\zeta$ illustrates that the peak concentration of G_H is strictly limited by the ratio between its pituitary production rate and its hepatic clearance rate. Similarly, the glucose bound G_{Lmax} accounts for the synergy between endogenous production and the inhibitory effect of G_H on insulin sensitivity. These localization sets prove that the interaction between the somatotropic axis and glucose-insulin kinetics is dissipative. This means that, regardless of the initial diabetic state or the severity of the initial hormonal surge, all trajectories will eventually be trapped within this compact set K. This finding is of paramount clinical importance, as it provides a rigorous proof that the disease dynamics are contained within survivable ranges, offering a definitive mathematical boundary for the evaluation of chronic complications and the long-term effectiveness of glycemic control strategies.

3.5 Numerical Simulations

The numerical simulations, illustrated in Figure 2, were conducted using the stable equilibrium point P_2 with initial conditions $G_L(0) = 80$, $I(0) = 20$, $\beta(0) = 800$, and $G_H(0) = 30$. The biological rates in Table 1 are expressed in minutes to represent rapid insulin-glucose kinetics, the simulation results reflect the chronic evolution of DM-1. The observed convergence to P_2 over approximately 200 minutes carries significant biological weight, representing the long-term adaptation period where the β-cell population undergoes a gradual process of replication or exhaustion until a homeostatic balance is established.

To further elucidate the model's behavior, we analyzed the sensitivity of the system to the insulin-induced glucose uptake rate (c) and the G_H clearance rate (ζ). Variations in c directly influence the "tightness" of the localization domain K_2; specifically, a decrease in insulin sensitivity expands the glycemic bound G_{Lmax}, shifting P_2 toward more hyperglycemic values. Similarly, alterations in the G_H clearance rate ζ or production rate ρ modify the magnitude of hormonal pulses. Since G_H inhibits glucose uptake, an increase in the ρ/ζ ratio results in a sustained elevation of baseline glucose, forcing β-cells to operate at a higher compensatory rate. These scenarios demonstrate that the model effectively captures the metabolic stress imposed by hormonal counter-regulation, providing a robust analytical framework for observing the progression of chronic complications.

For these numeric simulations, the command ODE45 was used to verify the obtained results through the model analysis, this command applies the Runge-Kutta algorithm.
Using Figure (3), the localization domain for each variable is validated, for $K = K_1 \bigcap K_2 \bigcap K_3 \bigcap K_4$ which is represented with its respective associated maximums, this is possible if the condition $4ig > \xi^2$ is satisfied using the Table 1. The graph of the maximum of the G_H function was not added because the maximum value coincided with the constant value of the system response for G_H.

4 Discussion

The findings of this research provide a significant advancement in the dynamical understanding of DM-1 by incorporating the somatotropic axis as a fundamental modulator of glucose homeostasis. The analysis transcends a simple stability study by integrating the LCIS method to define a global physiological cage, which serves as a

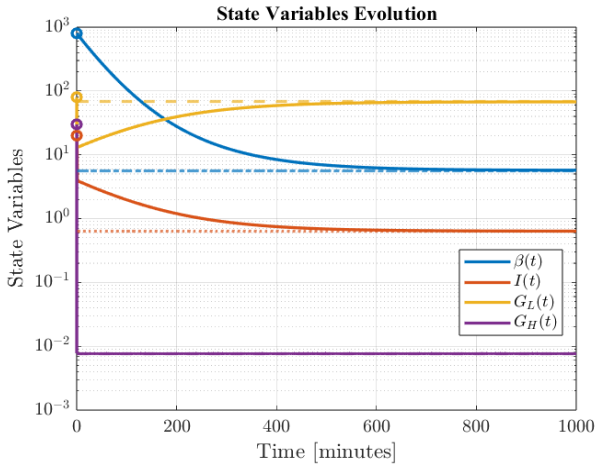

Figure 2: Trajectories dynamics towards the equilibrium point P_2, when initial conditions are $G_L(0) = 80$, $I(0) = 20$, $\beta(0) = 800$, $G_H(0) = 30$.

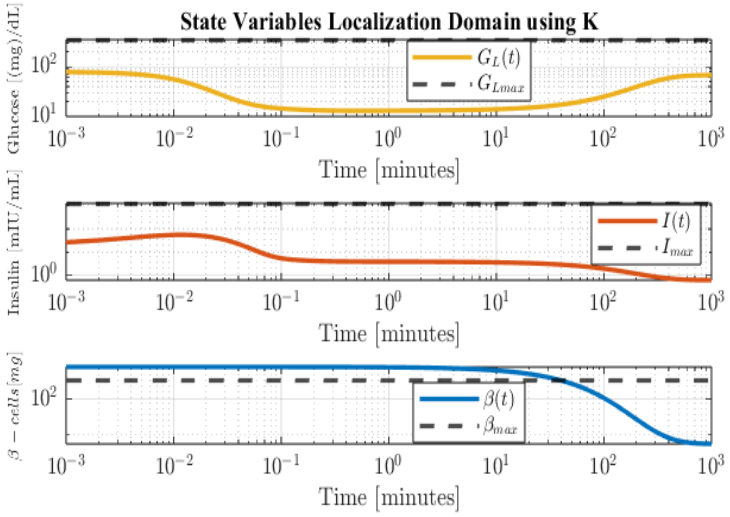

Figure 3: Model localization domains (9)-(13) implying that G_{Lmax}, I_{max} and β_{max} are located.

mathematical guarantee that the biological variables remain within life-sustaining limits despite the chronic stress of the disease. This is particularly relevant in the context of G_H, whose hyperglycemic effects are often overlooked in simpler glucose-insulin models. Our results demonstrate that the interaction between G_H and glucose is naturally bounded and dissipative; this means that regardless of initial metabolic spikes or growth spurts, the body's state will eventually be trapped within a compact set, preventing the trajectories from diverging toward biologically impossible or fatal values.

Furthermore, the characterization of the stable basin of attraction surrounding P_2 offers a quantitative measure of metabolic resilience. While the local stability indicates the system's ability to recover from minor fluctuations, the global localization domains provide a framework for evaluating long-term disease progression. The identified pathological thresholds, represented by the unstable equilibria P_1 and P_3, underscore the inherent risks of G_H-induced insulin resistance. From a clinical perspective, the fact that the system remains within the invariant sets K_i provides a definitive analytical boundary for designing therapeutic interventions. Future control strategies can utilize these bounds to ensure that exogenous insulin delivery not only targets a specific set point but also guarantees that the system's state never exits the physiological cage. By aligning mathematical dissipation with biological containment, this work establishes a rigorous foundation for the development of personalized treatments that account for the complex interplay between growth, metabolism, and endocrine regulation in diabetic patients.

5 Conclusions

The comprehensive analysis conducted in this research underscores the critical role of G_H as a fundamental modulator in the glycemic dynamics of DM-1. By integrating the somatotropic axis into the classical glucose-insulin framework, we have demonstrated that metabolic stability is not merely a product of pancreatic function but a systemic balance influenced by counter-regulatory hormonal stress. The application of the method serves as the mathematical cornerstone of this study, providing a rigorous proof of the system's global dissipativity. This approach transcends traditional local stability analysis by establishing a definitive physiological cage that guarantees the containment of state variables within biologically viable bounds. In the context of diabetes research, the LCIS method strengthens the mathematical foundation of the model, ensuring that long-term predictions remain consistent with human physiological limits and do not diverge into pathological impossibilities, thereby offering a reliable analytical tool for predicting disease evolution under various clinical scenarios.

The LCIS method establishes the ultimate dynamics of the system by defining a physiological cage within which all trajectories remain. A fundamental result of this localization is the condition:

$$4ig > \xi^2 \tag{14}$$

This inequality is not merely a mathematical requirement for the existence of the compact set K, but it carries a profound biological implication. The parameters ξ and i characterize the β-cell glucose tolerance range; ξ represents the replication rate in response to glucose, while i represents the quadratic rate of exhaustion or "glucotoxicity."

The condition $4ig > \xi^2$ implies that the combined effect of cellular exhaustion (i) and natural death (g) must eventually dominate the replication stimulus (ξ) at high glucose concentrations. Biologically, if this condition were not met, the model would predict an unbounded and unrealistic expansion of pancreatic tissue. In a real physiological context, the regenerative capacity of β-cells is limited, and chronic hyperglycemia eventually leads to a decline in mass due to metabolic stress. Thus, this constraint ensures that the model remains consistent with the limited homeostatic capacity of the human body. For a detailed mathematical derivation of the sets K_1 to K_4, the reader is referred to Appendix A.

Looking forward, the insights gained from this localization analysis provide a strategic bridge toward the integration of modern Artificial Intelligence (AI) and advanced simulation frameworks, such as the UVA-Padova Type 1 Diabetes Simulator. The mathematical bounds identified herein can serve as robust constraints for machine learning algorithms and reinforcement learning agents tasked with optimizing insulin delivery. By embedding these physiological safety boundaries into AI-driven controllers, future developments can minimize the risk of hypoglycemic or hyperglycemic events, ensuring that automated treatments operate within a strictly defined metabolic safety zone. Future work will focus on incorporating exogenous control variables to simulate personalized therapy, aiming to align the rigorous containment of the LCIS method with the predictive power of neural networks. This synergy between nonlinear dynamical analysis and AI-based modeling represents a promising frontier for the development of the next generation of artificial pancreas systems and personalized endocrine management.

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7 Appendix A. Derivation of Invariant Sets K_i

The LCIS method utilizes the Lie derivative $L_f h(x)$ to find the bounds of the system. For a reader unfamiliar with this framework, the sets are obtained by ensuring that outside a certain boundary, the "direction" of the system always points inward toward the homeostatic state.

1. **Set K_1 (Growth Hormone):** By choosing $h_1 = G_H$, we find that $\dot{G}_H = \rho - \zeta G_H$. The system cannot exceed $G_{Hmax} = \rho/\zeta$, as the clearance rate ζ would eventually overcome the production ρ.
2. **Set K_2 (Glucose):** Using $h_2 = G_L$, we find the upper glycemic bound G_{Lmax}. This represents the maximum glucose level reachable when hepatic production and G_H-induced suppression of insulin uptake are at their peaks.
3. **Sets K_3 and K_4 (β-cells and Insulin):** These sets are derived by combining the variables to find a bounded region for cellular mass and insulin secretion. The condition $4ig > \xi^2$ ensures that the quadratic term $-iG_L^2$ in the β-cell equation acts as a stabilizing "sink," preventing numerical divergence.

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