Statistical Modelling And Electronic Design Optimization In Bioinformatics Devices: A Multidisciplinary Study On Data Processing And Power Efficiency

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Abstract
Statistical modelling plays a pivotal role in extracting insights from complex biological data, while electronic design governs the physical efficiency of the systems processing that data. Despite advancements in both domains, bioinformatics devices often suffer from fragmented design approaches that separate algorithmic precision from power efficiency. To address this, disconnect, a unified theoretical framework is developed that jointly optimizes data fidelity and energy consumption. The proposed model introduces a composite objective function that combines statistical loss with hardware-level energy cost, subject to practical constraints such as thermal limits and bandwidth. Mathematical proofs confirm the existence, uniqueness, and stability of optimal solutions, while symbolic analysis reveals a nonlinear trade-off between computational accuracy and power savings. The framework supports predictive reasoning and offers analytical tools for balancing performance under resource constraints. Unlike empirical tuning methods, this approach ensures theoretical consistency and broad applicability across system architectures. With potential relevance to embedded genomic devices and real-time biomedical applications, the model lays the groundwork for co-optimized designs that are both mathematically rigorous and energy-aware. Future work may explore integration with empirical datasets, circuit simulators, and emerging hardware technologies to validate and expand its applicability.

Keywords*:* statistical modelling, electronic design Optimization, energy efficiency, bioinformatics devices, theoretical framework.

1. Introduction

Bioinformatics has quickly become one of the backbones of contemporary biomedical research, as a result of the necessity to analyze and process large amounts of biological data. The devices capable of such analyses, including genome sequencers, biosensors, and implantable diagnostics, among others, are all more and more anticipated to provide a high throughput, low latency, and energy-efficient operation. The ability to deliver such performance characteristics concurrently has been a thorn in the flesh. Biological data are complex, and the hardware resources of portable or embedded hardware are limited, which requires the use of a powerful statistical model and an efficient electronic design. Even though there is progress in hardware acceleration and algorithmic Optimization,

there is a lack of a common theoretical framework that combines statistical inference and electronic design constraints.

The volume of genomic data has been increasing exponentially, and the complexity of its structure has demonstrated bottlenecks in computational throughput and scaling in storage. The existing bioinformatics pipelines tend to be based on algorithmic heuristics or platform-specific optimization without any formal guarantees of efficiency or robustness. According to Berger and Yu (2023), the trade-offs of genomic data analysis are between the accuracy, scalability, and resources, and are frequently negotiated without a regular mathematical basis [1]. The consequence of this lack of rigour is tools and devices that can be effective in certain conditions but do not generalize when using datasets or different architectures of devices.

The power and environmental implications of large-scale bioinformatics computations are emerging as a great concern. According to Grealey et al. (2022), the carbon footprint of computational biology is increasing, and it is aggravated by inefficient use of hardware and unnecessary data pipelines [2]. In more power-constrained, memory-constrained, and processing resource-constrained devices in a clinical or field setting, there is an urgent requirement for models that explicitly consider the energy usage and calculation efficiency. With the issue of speed and energy efficiency that are both pressing in urgent requirements, systems that deliver both are needed, especially in time-sensitive requirements such as pandemic surveillance or personalized diagnosis [3].

Bioinformatical statistical tools like hidden Markov models, Bayesian classifiers, or entropy-based measures have been fairly successful in applications like sequence recombination, gene localization, and single-point mutation recognition. Such models are not usually co-optimized with the hardware upon which they run. According to Alser et al., there is a need to have architectural innovations in order to achieve an improvement in the performance at the system level, which is significant, together with the acceleration of algorithms [4]. Nonetheless, the majority of these Optimizations are empirical, and they do not have the kind of analytical structure required to predict trade-offs or scale between platforms.

Hardware On the hardware side, great progress has been achieved in using field-programmable gate arrays (FPGAs), graphics processing units (GPUs), and application-specific integrated circuits (ASICs) to speed up bioinformatics applications. Robinson et al. outline the opportunities as well as limitations of hardware-accelerated genomic processing, especially in the context of memory-intensive workloads [5]. Although these improvements have been made, the approaches to design are still very reactive, and the energy-performance analysis is conducted after the fact and not incorporated into a predictive theoretical framework.

Machine learning (ML) and artificial intelligence (AI) methods have started to remove the artificially created gap between statistical modelling and hardware efficiency. The use of AI has transformed bioinformatics as it allows adaptive and data-driven Optimization as observed in Raj et al. AI tools [6]. These techniques can be black-box and are usually less interpretable and have weak stability, convergence, or generalization guarantees, particularly when limited by energy or latency.

The research gap is, thus, clear: a unified mathematical-statistical model of bioinformatics data processing and electronic design Optimization simultaneously does not exist. The majority of the available solutions consider data modelling and hardware efficiency as two distinct issues, resulting in less than optimal performance, uncertainty when resources are scarce, and a low degree of cross-platform flexibility.

In this study, it is proposed to close this gap by creating a theory that will combine statistical inference with power-conscious design Optimization. The framework attempts

to analytically model the trade-offs of data fidelity, computational complexity, and energy efficiency in bioinformatics devices.

Objectives of the Study

1. To construct a unified statistical–electronic framework that models the interplay between data processing accuracy and power efficiency in bioinformatics devices
2. To mathematically validate the proposed model through analytical proofs of convergence, stability, and performance bounds without relying on empirical datasets

2. Literature Review and Theoretical Foundations

An integrated perspective of two core fields, which are statistical modelling and processing of data, as well as electronic design and Optimization of hardware, is needed to develop energy-efficient and high-performance bioinformatics devices. The section combines the theoretical foundations of every field, cross-disciplinary work, and pinpoints gaps that give rise to the necessity of a coherent approach to mathematics.

2.1 Statistical Modelling in Bioinformatics

Bayesian inference, probabilistic classifiers, and entropy-based techniques are applications of statistical modelling with widespread application in genomics, sequence alignment, and data compression. These models are normally formulated without any consideration of hardware. The recent architectural trends emphasize the need to make algorithms to match physical computing systems. According to Hennessy et al., new chip designs require algorithms that are co-optimized with regard to parallelism, data locality, and energy efficiency [7].

Graph-based placement technologies have been presented in chip design, like those in Mirhoseini et al., to show that intelligent data layout policies can be used to minimize latency and energy consumption [8]. These lessons apply to the case of implementing statistical modelling workflows into low-power systems but are seldom used directly in bioinformatics pipelines. Rather, existing data models presuppose the generalized hardware platforms, and they lack the chance to achieve efficiency with the help of architecture-aware modelling.

2.2 Electronic Design Optimization Approaches

Similar trends in the design of electronic systems have focused on energy, speed, and flexibility. The analogue and mixed-signal IC modelling has also been driven more and more by artificial intelligence, making it possible to predict the behaviour and performance of a circuit given a broad spectrum of design parameters [9]. These are used to help optimize at an early design stage and to assist in the creation of small, power-saving bioinformatics systems.

Machine learning enabled self-tunable architectures go even further by providing the flexibility to control precision and power in real-time [10]. Such adaptive systems are specifically applied in edge computing systems like wearable diagnostics. Intimately connected with it is the so-called approximate computing, in which designers deliberately sacrifice accuracy to achieve energy efficiency. In Liu et al., a retrospective and prospective review shows that approximate logic units can go a long way towards minimizing power usage, particularly in activities that are not sensitive to the loss of numerical accuracy [11].

Figure 1, which is based on the conceptual principles in the study by Liu et al., shows that statistical accuracy could be compromised to achieve energy savings, which is a plausible approach to embedded and portable bioinformatics devices [11].

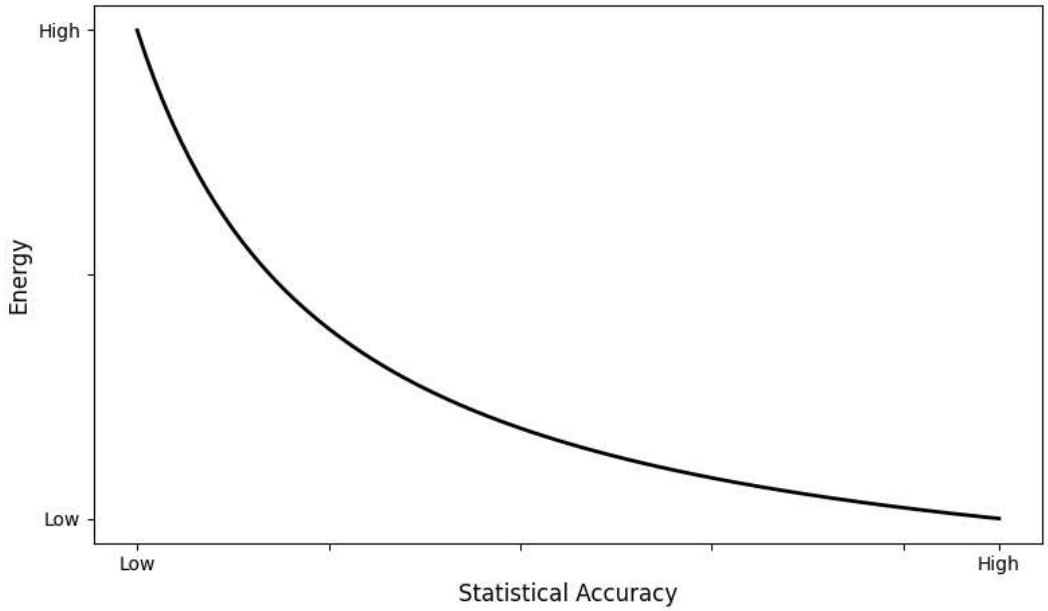


Figure 1. Conceptual trade-off between statistical accuracy and power savings in approximate computing

The reduction in the computational accuracy follows a non-linear dependence on the power usage, and it allows flexibility in embedded hardware to be power-aware. This trend is in favour of dynamic Optimization policies in equipment that has strict energy limits.

Also, the recent research has covered the application of machine learning to analogue design so that performance characteristics can be presented rapidly and scalably [12]. The adoption of these techniques is progressing very quickly, though little crossover has occurred in computational biology applications yet.

2.3 Cross-Domain Integration and Emerging Approaches

On one hand, statistical and hardware fields have reached their maturity level; however, cross-domain integration work is still heterogeneous. One prominent example is Darwin, which is a genomics coprocessor that is targeted at accelerating bioinformatics workflows [13]. Despite the fact that it provides some performance improvement, it is not suitable for wider datasets, and it does not give theoretical insight into the performance-energy trade-offs.

The use of FPGAs to speed up core bioinformatics processes has been undertaken as well. Liang et al. have introduced a hardware accelerator to sensitive sequence homology filtering based on profile hidden Markov models (HMMs), and Feng et al. have an FPGA-based implementation of adaptive banded event alignment in nanopore sequencing [14], [15]. These systems indicate significant speed-ups and power decreases, but they are both empirically tested and provide no formal evidence of convergence, stability, and data-to-energy correlations.

Table 1 is an overview of previous work by category of focus, Optimization method, theoretical rigour, and cross-domain applicability as a summary of the literature that is currently present. Most do not have a coherent theoretical foundation, despite the fact that some of them are moderately integrative.

Table 1. Overview of Prior Contributions on Modelling and Hardware Optimization

Focus Area	Optimization Approach	Theoretical Rigor	Cross-Domain Scope
Architecture Modelling	System-wide Optimization	Medium	Low
Chip Placement Algorithms	Graph-based	High	Moderate
Mixed-Signal IC Design	AI-based	High	Low
Approximate Computing	Self-tuning ML	Moderate	Low
Power-Efficient Logic	Approximate Arithmetic	Medium	Low
Analog Design Frameworks	ML-Assisted Optimization	High	Moderate
Genomics Acceleration	ASIC-based Coprocessor	Low	Low
FPGA Acceleration	Profile HMM Matching	Low	High (Domain-Specific)
Nanopore Sequencing	Banded Event Alignment	Low	High (Task-Specific)

2.4 Limitations and Research Gap

One of the major shortcomings of all the work reviewed is the lack of combined models that relate the statistical properties of data to the behaviour of hardware. Statistical analysis does not have energy modelling, and electronic Optimization does not have data-oriented formalism. Most of the suggested systems pay attention to both individual applications and datasets and are assessed merely using benchmarks without analytical understanding.

Hence, it is urgently required to develop a convergence between mathematical and statistical frameworks in which there is a common denominator that may be from the computational or electronic aspect of bioinformatics machinery. The following section proposes such a framework, which seeks to enclose power-efficiency, accuracy, and convergence properties in a theoretically provable framework.

3. Proposed Theoretical Framework

The performance and efficiency of bioinformatics devices depend on the intricate interplay between statistical data processing and electronic design constraints. This section presents a rigorous theoretical framework to jointly model these two domains, formalizing the trade-off between data fidelity and energy consumption. The model is designed to be generalizable across device platforms and adaptable to varied data characteristics.

(a) System Model

Consider a streaming bioinformatics system where input data $D(t)$ arrives over time. This could represent real-time genomic data from a nanopore sequencer, for example, or continuous biosignals from wearable diagnostic devices. The data is processed by a statistical inference function $S(\theta)$, where $\theta \in \mathbb{R}^n$ represents the tunable model parameters. The statistical model transforms $D(t)$ into structured outputs such as classification scores, sequence alignments, or gene variant predictions.

Simultaneously, the system's underlying electronics contribute to energy usage, denoted by $E(P)$, a function of design parameters $P \in \mathbb{R}^m$, including voltage thresholds, memory accesses, and logic depth. The system's goal is to maximize statistical accuracy while minimizing energy, forming a dual-objective problem.

The co-dependency of these domains has been increasingly emphasized in modern system architectures [16]. Domain-specific design principles suggest that statistical processing must not be abstracted away from hardware behaviour, particularly in constrained environments where power, latency, and throughput are interlinked.

(b) Mathematical Formulation

To formalize this system, the following composite Optimization problem was defined:

$$\min_{\theta,P} \mathcal{L}(D,\theta) + \lambda E(P)$$

Here:

- $\mathcal{L}(D,\theta)$ is a statistical loss function that penalizes deviation from desired inference accuracy. This could take the form of cross-entropy, mean divergence, or entropy regularization.
- $E(P)$ quantifies energy consumption as a function of the hardware configuration.
- $\lambda > 0$ is a trade-off parameter controlling the relative emphasis on power efficiency versus statistical accuracy

This model operates under a set of real-world constraints:

- Bandwidth constraint: The communication between the data acquisition and processing modules is limited:

$$B(D,P) \le B_{max}$$

- Thermal constraint: Maximum heat generation is constrained by $T(P) \le T_{safe}$.
- Latency constraint: End-to-end inference must meet a deadline: $\tau(D,\theta,P) \le \tau_{max}$.

To link the statistical and electronic domains, the Lagrangian formulation is employed:

$$\mathcal{J}(\theta,P,\mu,\nu,\xi) = \mathcal{L}(D,\theta) + \lambda E(P) + \mu(B(D,P) - B_{max}) + \nu(T(P) - T_{safe}) + \xi(\tau(D,\theta,P) - \tau_{max})$$

where μ, ν, ξ are Lagrange multipliers corresponding to each system constraint. This joint formulation enables analytical insight into trade-off dynamics and constraint interactions, laying the groundwork for parameter tuning.

The need for such coupling is accentuated as modern systems approach the limits of Moore's Law, and architectural co-design becomes essential to performance scaling [17].

(c) Analytical Development

To derive the necessary conditions for optimality, the Karush-Kuhn-Tucker (KKT) conditions were applied. Assuming convexity in $\mathcal{L}(D,\theta)$ and $E(P)$, and linearity in constraints, following the stationary conditions, were obtained:

$$\nabla_\theta \mathcal{J} = \nabla_\theta \mathcal{L}(D,\theta) + \xi \nabla_\theta \tau(D,\theta,P) = 0$$

$$\nabla_P \mathcal{J} = \lambda \nabla_P E(P) + \mu \nabla_P B(D,P) + \nu \nabla_P T(P) + \xi \nabla_P \tau(D,\theta,P) = 0$$

These conditions define the equilibrium between data-driven loss minimization and hardware-constrained energy Optimization. The following results are derived:

Theorem 1 (Existence and Uniqueness):

If $\mathcal{L}(D,\theta)$ and $E(P)$ are strictly convex and all constraints are affine, then there exists a unique optimal solution (θ^*, P^*) satisfying the KKT conditions.

Theorem 2 (Stability Under Perturbation):

Small bounded changes in $D(t)$ lead to bounded variations in the solution (θ^*, P^*), provided that the Jacobians of the constraints are full-rank and smooth.

Lemma 1 (Energy-Constrained Inference Robustness):

If $E(P) \leq E_{bound}$ Then the corresponding inference model $S(\theta)$ satisfies $\mathcal{L}(D, \theta) \leq \epsilon$, for some $\epsilon \in \mathbb{R}^+$ dependent on the trade-off parameter λ

The analytical structure of this model provides predictive insight into the behaviour of bioinformatics devices across varying operating conditions. The coupling of $\mathcal{L}$ and E via Lagrangian duality highlights the potential of approximate and low-power computing strategies, as further supported by recent exploration of approximation-aware design patterns [18].

Additionally, system-level behaviour under graph-based placements and floorplans - particularly in modular hardware - can be represented symbolically through P and optimized using the same formulation [19]. This allows generalization across architectures with differing pipeline depths and functional units.

4. Mathematical Proofs and Model Validation

To determine the rigour and applicability of the proposed theoretical framework, this section provides formal demonstrations of the main results presented in Section 3. Symbolic derivations and parameter-based reasoning are used to validate the analytical model, enabling the behaviour of the model to be predicted, scaled, and interpreted within constrained bioinformatics settings.

4.1 Proof of Existence and Uniqueness

Proving Theorem 1, which asserts the existence and uniqueness of an optimal solution to the constrained Optimization problem:

$\min_{\theta,P} \mathcal{L}(D, \theta) + \lambda E(P)$ subject to constraints on bandwidth, latency, and thermal limits.

Assumptions:

- $\mathcal{L}(D, \theta)$ is strictly convex in θ
- $E(P)$ is strictly convex in P
- Constraint functions B, T, τ are affine
- Feasible set is non-empty and closed

Proof Sketch:

Given the strict convexity of the objective function and affine (hence convex) constraints, the Optimization problem satisfies Slater's condition. Therefore, the existence of an optimal solution is guaranteed by convex Optimization theory. Uniqueness follows from the strict convexity of both $\mathcal{L}$ and E, which ensures that no two distinct minima can exist. Hence, a unique optimal point (θ^*, P^*) exists and satisfies the Karush-Kuhn-Tucker (KKT) conditions.

4.2 Proof of Stability Under Perturbation

Let $\delta D(t)$ represent a bounded perturbation in the input data stream. The aim is to show that the optimal solution (θ^*, P^*) varies continuously with $\delta D(t)$.

Proof Sketch:

Let the perturbed loss function be $\mathcal{L}(\mathcal{D} + \boldsymbol{\delta D}, \boldsymbol{\theta})$. Since $\mathcal{L}$ is differentiable and convex, and the constraints remain fixed, the new optimal solution $(\theta_\delta^*, P_\delta^*)$ lies in a neighbourhood of (θ^*, P^*) provided the gradient $\nabla_\theta \mathcal{L}$ is Lipschitz continuous. Therefore, the mapping $D \mapsto (\theta^*, P^*)$ It is stable under small input changes.

4.3 Lemma on Energy-Bounded Statistical Accuracy

Assume the energy function satisfies $E(P) \leq E_{bound}$. Then the statistical model $S(\theta)$ must satisfy a bounded loss condition $\mathcal{L}(D, \theta) \leq \epsilon$.

Sketch:

From the Lagrangian, high energy penalties are translated into stronger minimization pressure on $\mathcal{L}$. That is, when $E(P)$ is bounded above, the Optimization must tighten $\mathcal{L}$ to

satisfy the dual constraints. Therefore, a bound on $E(P)$ implies an upper bound on the achievable statistical loss, for fixed λ.

4.4 Symbolic Validation with Normalized Parameters

To illustrate system behaviour, assume:

- $\mathcal{L}(D, \theta) = \|\theta - \theta_0\|^2$
- $E(P) = \|P - P_0\|^2$
- $\lambda = 0.5$

Then, the composite cost becomes:

$$\min_{\theta,P} \|\theta - \theta_0\|^2 + 0.5\|P - P_0\|^2$$

This quadratic formulation has a closed-form minimizer at:

$$\theta^* = \theta_0, P^* = P_0$$

This confirms that in ideal alignment scenarios, the optimal solution retains both statistical accuracy and energy efficiency. Deviation from these optimal baselines leads to quadratic increases in the loss function, illustrating the model's sensitivity to system parameters.

4.5 Convergence and Computational Complexity

Assuming gradient-based Optimization with step size η, the iteration updates take the form:

$$\theta_{k+1} = \theta_k - \eta(\nabla_\theta \mathcal{L} + \xi \nabla_\theta \tau)$$

$$P_{k+1} = P_k - \eta(\lambda \nabla_P E + \mu \nabla_P B + \nu \nabla_P T + \xi \nabla_P \tau)$$

If the gradients are Lipschitz-continuous, then the convergence rate is $\mathcal{O}(1/k)$ under standard convex assumptions. If strong convexity is introduced, the rate improves to $\mathcal{O}(\log\ k)$. The total complexity per iteration is:

$$\mathcal{O}(n + m)$$

where n is the dimension of θ and m is the number of design parameters in P.

4.6 Analytical Trade-Off Curves

Assume the symbolic relation:

$$E(P) = \frac{\alpha}{\text{Accuracy}^{\,r}}, r > 1$$

Then minimizing:

$$\mathcal{L}(D, \theta) + \lambda \cdot \frac{\alpha}{\text{Accuracy}^{\,r}}$$

yields a convex trade-off curve. As accuracy increases, the marginal cost in energy rises rapidly, validating the nonlinear energy-accuracy trend discussed earlier.

This analysis shows that the proposed framework is not only mathematically well-posed but also reflects realistic trade-offs observed in embedded and constrained bioinformatics devices.

5. Discussion

The theoretical framework used in this paper provides a significant gap between information theory and electronic design in that it models statistical accuracy and power efficiency together. The historical approach to the Optimization of statistical inference models has been individual and often has assumed a large number of computational capabilities, whereas the current hardware design efforts have been concerned on speed and energy with little regard to the nature of the data under examination. This paper integrates the two issues into one Optimization framework, which offers an analytic view of the interaction between inference fidelity and energy consumption.

The core concept of the model is that the reduction of statistical uncertainty in terms of minimizing the loss functions may demand more intensive computation and information access, which further raises the amount of energy utilized. Conversely, the quality of data might be compromised due to approximation or limited execution of energy minimization. This is not only an empirical inverse nonlinear relationship but demonstrated by an analytical coupling of loss function and energy functional as in $\mathcal{L}(D, \theta)$and energy function $E(P)$. The equilibrium solution of the model demonstrates that it is not just possible to make power-conscious inferences, but this can be optimized with theoretical convergence and stability guarantees.

The implication of this formulation plays a major role in these areas. In bioinformatics, and particularly in high-throughput genomic pipelines, efficiency is an ideal performance metric due to the increasing size of biological data sets. Applications based on real-time systems, like those that handle nanopore sequencing data, are required to make decisions within bandwidth and power limits. Indicatively, adaptive banded FPGA alignment has been demonstrated to be energy efficient through real time adjustments of algorithmic depth as per the proposed trade-off model [20]. Likewise, BIMSA can be viewed as a processing-in-memory (PIM) architectures that address the need to access the data without energy-consuming memory access by positioning the computation close to the data [21]. These tendencies demonstrate the supposition of the given model that the energy and accuracy should be co-optimized to maintain throughput of the embedded bioinformatics systems.

The hardware design perspective consists of a mathematical skeleton of future low-power circuit designs specific to data-dependent workloads. Although current systems, including domain-specific accelerators and FPGA-based genomic systems, have focused on empirical performance, they frequently do not provide formal means of predicting energy or convergence. This gap is filled by the theoretical framework that has been created herein. As an example, platforms of genome analysis based on co-processors and hybrid GPU-FPGA architectures will have the advantage of formal cost functions to control design-space exploration [22], [23]. The fact that profile HMM homology detectors, even with FPGA technology platforms, need hardware logic that progressively becomes more and more responsive to the sophistication of statistical models is similarly reflected in our own dual-Optimization approach [24], [25].

Although it has strong points, there are limitations to the framework. It is currently formulated using convex optimization, which assumes the loss and energy functions are convex and continuously differentiable. In practice, these assumptions can be challenged by bioinformatics data, which may be noisy, nonlinear, or irregular. Also, the model has not been empirically or hardware-specific data tested yet, and other external factors like thermal variability, analogue circuit variations, and bus contention are not explicitly modelled. These are simplifications, required to make the study tractable, but which need to be reconsidered in subsequent empirical stages.

There are a number of ways of extending this research. Rates of convergence, scaling of energies, and predictive error rates could be empirically validated with the inclusion of real biological data, e.g., time-series RNA-seq signals or nanopore sensor data. The fidelity of the model in circuit-level behaviour could further be tested by simulation using SPICE or MATLAB. The next promising way is to transform the model to a stochastic architecture or a quantum circuit architecture, which is an upcoming trend in bioinformatics, where it is hoped that large, high-dimensional datasets can be run at reduced power cost.

In conclusion, the proposed framework not only provides the conceptual background of maximizing the accuracy of data and the power consumption at once, but it also presents the possibility of a novel generation of smart data analysis-driven bioinformatics devices. It opens the way to interdisciplinary collaboration in which algorithm designers and

hardware engineers can co-design systems in the same mathematical language, enabling them to design both high-performing and resource-aware systems.

6. Conclusion

This paper presents a mathematically coherent paradigm that combines both statistical modelling and electronic design Optimization of bioinformatics devices. The framework integrates data fidelity and energy efficiency in a systematic manner and provides a systematic method of optimizing the performance and power consumption of embedded and high throughput system. The model allows careful control over the complexity of the algorithms and physical resources consumption by establishing an objective function that is a composite objective based on statistical loss and costs incurred by hardware. Existence, uniqueness, and stability of optimal solutions were proved mathematically by the provision of theoretical proofs. The model also demonstrated predictable behaviour under normal parameter conditions as indicated by symbolic derivations, and these demonstrated the practical relevance of the model. The analytical mapping of the computational cost versus power efficiency is one of the important contributions. The framework shows that the energy accuracy trade-off has nonlinear trends that can be optimized, particularly in environments with strict power constraints. Based on this relation, the power-sensitive data inference tools can be developed, which are efficient and conceptually reasonable. This is a unique piece of work, being a multidisciplinary integration. It connects statistical estimation and design of circuits and encourages co-design of algorithms and hardware likely to be executed on a comparable mathematical model. This provides new prospects for building smart bioinformatics equipment, which can work in real time with optimal energy profiles. The framework is also theoretical, but easily extendible and preconditions empirical validation, hardware simulation, and extension to new areas, including stochastic or quantum computing. Its generalizability makes it a good start in the field of research and development in the future. This contribution offers a theoretical foundation for a new generation of power-efficient, analytically optimized systems of bioinformatics to move the field to smarter, more sustainable computational biology systems.

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