Gene-Guard: Real-Time Genomic Data Leak Prevention

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Abstract

Genomic data (such as DNA sequences) are both highly sensitive and uniquely vulnerable to accidental leakage in modern collaborative and AI-assisted workflows. This report introduces Gene-Guard, a two-layer detection and prevention system designed to safeguard genomic sequences from unauthorized exposure in real time. We articulate the growing risk through real-world scenarios: researchers inadvertently pasting DNA sequences into chat platforms or AI tools, and bio-lab staff emailing unencrypted gene data. To address this gap, Gene -Guard integrates an open DNA sequence dataset for training and benchmarking a hybrid machine learning classifier that flags genomic data with high recall and precision. Upon detection, an optional second layer provides an LLM-powered risk analysis, identifying the sequence and its potential biosecurity implications using tools like IBBIS's Common Mechanism and SeqScreen. Emphasis is placed on a lightweight, platform-agnostic design that can plug into any Data Loss Prevention pipeline without heavy resource demands or latency. Our results suggest Gene-Guard can significantly reduce the chance of genomic data leaks without impeding researchers' workflows, offering a novel safety net at the intersection of cyber and biosecurity.

Keywords: Genomic Data Leakage, Data Loss Prevention, Biosecurity, Insider Threat, Compliance, LLM Safety

1. Introduction

Genomic data (e.g. DNA sequences) are increasingly recognized as *sensitive information* that demands protection on par with personal identifiers or financial records. In fact, regulations like the EU's GDPR explicitly categorize genetic data as sensitive personal data requiring strict safeguards. Beyond privacy, the misuse of leaked DNA sequences poses serious **biosecurity risks** – for example, a leaked pathogenic genome could enable malicious synthesis of a virus. The 2023 breach of genetic testing firm 23andMe, which exposed raw genotype data of ~6.9 million people, underscores the high stakes and potential for abuse when genomic information is not secure.

Yet beyond external breaches, *insider accidents and negligence* are an overlooked threat vector for genomic data leakage. Researchers and lab personnel regularly handle DNA/RNA sequences in day-to-day work, sometimes in settings lacking adequate data confinement controls. Consider the following real-world scenario:

> Researchers increasingly use cloud-based AI tools (like ChatGPT or code assistants) to analyze or format genomic data. Corporate studies show a significant portion of employees paste confidential data into public LLMs, often unaware that these prompts are stored on external servers. A DNA sequence pasted into an AI chatbot may be retained and even used to train models, constituting an irreversible leak outside the organization's perimeter.

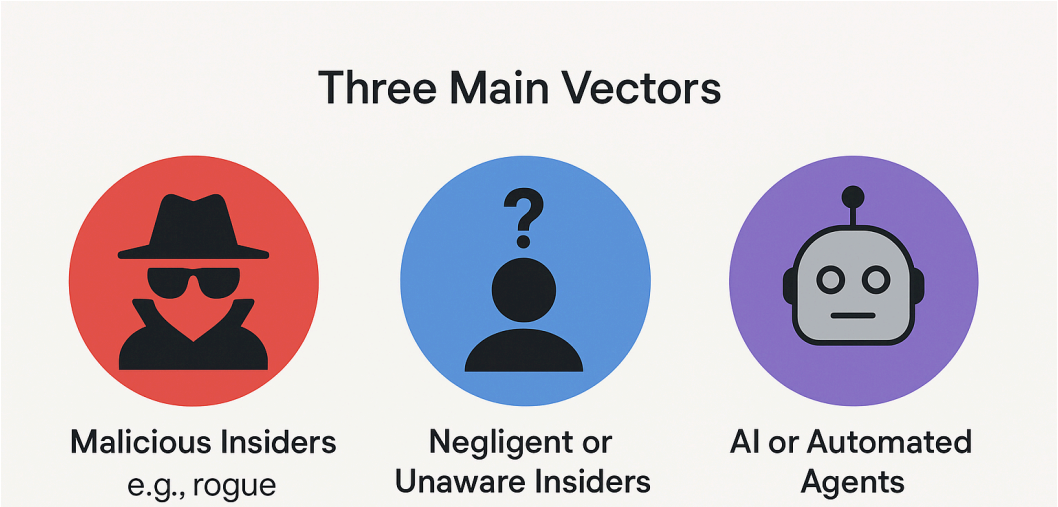
This scenario highlights a pressing need for proactive genomic Data Loss Prevention (DLP). Traditional DLP systems monitor common sensitive data (PII, PHI, credit card numbers, etc.) across endpoints, networks, and cloud apps, but *they are not tailored to recognize DNA sequences.* A string of A, C, G, T letters can easily bypass keyword-based filters, especially if the sequence is embedded in other text or deliberately obfuscated. Moreover, in AI-driven workflows, language-based transformations (summarizations, translations, or even DNA-to-protein conversions) could hide the content from simplistic rules. In short, current enterprise security tools often lack the "genomic awareness" to catch such leaks, creating a blind spot.

Threat Model**:** We consider three main vectors:

(a) Malicious insiders – A rogue employee exfiltrating genomic IP (such as a vaccine DNA sequence) via copy-paste or by slowly leaking segments.

(b) Negligent or unaware insiders – well-intentioned staff whose normal use of cloud tools or messaging inadvertently exposes protected sequence data; and

(c) AI or automated agents – systems like chatbots or office suite copilot features that might autonomously access or transmit genomic data (for instance, an LLM integrated with lab notebooks that might leak sequences if exploited).



These threat vectors span both the insider threat domain and emerging "*shadow AI*" risks in which organizational data escapes via unsanctioned AI services.

Research Questions- *Can we build a real-time, low-overhead detection mechanism to identify genomic data in unstructured content and prevent its unauthorized sharing at an enterprise level?*

Our work contributes an affirmative answer by developing a two-layer detection pipeline for genomic data leak prevention. Gene-Guard is designed as a drop-in library that can augment existing DLP solutions. Crucially, it emphasizes speed, accuracy, and domain/context-awareness: the system should detect DNA sequences (even if hidden in noise), do so with minimal latency and resource use, and provide context on why a detected sequence is risky. By focusing on genomic data, Gene-Guard fills a critical gap in security tooling for biotech and healthcare organizations, aligning with calls for sector-specific DLP guidance. Ultimately, this approach aims to reduce accidental genomic leaks and to raise the hurdle for malicious actors trying to smuggle out dangerous genetic information.

2. Methods

To tackle the problem, we implemented a two-layer detection architecture combining efficient pattern recognition with deeper AI-driven analysis. The first layer scans content for any presence of DNA sequences, and the optional second layer analyzes the flagged sequence to gauge its identity and potential risk. We also curated and utilized a dataset of genomic sequences to develop and evaluate our approach.

2.1 Dataset Integration: We leveraged the publicly available DNA sequence dataset as a benchmark corpus. This dataset provided a variety of examples for training and testing our classifier, including actual gene sequences (positive samples) and non-genomic text (negative samples). We augmented the corpus with additional "tricky" negatives such as programming code, random alphanumeric strings, and natural language text containing repeated A/C/G/T letters to ensure robust performance. Using this labeled data, we could train our model to distinguish genuine DNA sequence patterns from coincidental text, and measure false

positive/negative rates. The dataset was also split into training and held-out sets to validate that our approach generalizes well. By integrating this corpus, we established a baseline benchmark for Gene-Guard and confirmed its effectiveness against realistic data. (All code and data, including the dataset and our trained model, are available in our project repository:GitHub- rockysaikia730/dataset_dna)

2.2 First Layer – Hybrid Rule-Based & ML Detection: The first layer acts as a gatekeeper that classifies whether an input contains genomic data ("Yes/No"). It is designed to be fast, lightweight, and accurate. We adopt a hybrid approach:

- Rule-Based Heuristics: We crafted a set of simple pattern-matching rules to quickly catch obvious DNA sequences. For example, a regex-like rule scans for long stretches of characters composed solely of {A,C,G,T} (case-insensitive) beyond a certain length (e.g. >50 bases). Another heuristic computes the character frequency distribution of the text and checks for telltale signs of genomic content – e.g. *a small alphabet (predominantly 4 letters) with relatively balanced frequencies*. Natural language text rarely has just 4 characters making up 85% of content, whereas a DNA sequence typically does (A/C/G/T ~ roughly balanced). We also included checks for common formatting of sequences (such as FASTA headers or line lengths of 60 characters). These rules serve as a first pass filter: they are highly recall-oriented, flagging any content that *might* be DNA while being computationally trivial (string scans, frequency counts).

- **Machine Learning Classifier:** Following the rules, we apply a trained ML model to *confirm* and refine the classification. Our classifier is a lightweight model (tested with both a logistic regression on k-mer frequencies and a small neural network) trained on the labeled dataset. It considers features like k-mer distribution (bi-grams and tri-grams of characters) and sequence length to differentiate true genomic sequences from random or natural-language strings. For instance, genomic sequences have distinct k-mer patterns (due to biological codon structure and repeats) that ordinary text lacks; the ML model learns to recognize these subtle patterns. We opted for a compact model to keep inference fast – scanning a document in milliseconds – which is crucial for real-time use. During training, we prioritized recall (to avoid missing any DNA) while keeping precision reasonable by including diverse negatives. The resulting classifier outputs a probability or confidence score that the input contains genomic data.

The combination is powerful: The heuristic rules ensure that no obvious DNA goes unnoticed (e.g. even a novel sequence with no prior example will trigger the pattern rules if it's long enough and ATCG-only). At the same time, the ML step helps **reduce false alarms** by learning what "normal" text looks like. This hybrid design proved far more precise than using naive regex alone, which would misfire on texts like "ACTG 2023 Conference" or code like `buffer[0xAC] = 0xT3;`. In testing, the ML filter eliminated most false positives while retaining near-100% recall on true sequences. We also incorporated simple *obfuscation detection*: for example, if a

sequence uses unconventional characters (O, U, 0, 1 in place of DNA letters), we normalize those or have variant rules (since an insider might try to evade detection by replacing A→@ or T→7, etc.). These measures maintain robustness against trivial evasion without heavy computation.

Real-Time and Low-Resource Implementation: We built the first layer in Python as a self-contained library. On a standard laptop, it can process a multi-kilobyte text document in under a second (well within the 1–2 s target for DLP real-time scanning). Memory and CPU footprint are minimal – the model is small and the rules are just string operations – allowing GEN-Guard to potentially run as an **endpoint agent or a plug-in** on various platforms. This platform-agnostic design means the same library can be deployed in different contexts: e.g. as a browser extension to monitor a web app, an email server filter, or an API service that Slack or Microsoft Teams calls for message inspection. We verified that the first layer can indeed be integrated into a streaming pipeline (scanning text on-the-fly) without noticeable lag, fulfilling the core requirement for seamless, real-time protection.

2.3 Second Layer – Contextual Risk Analysis (LLM-Enhanced): When the first layer flags content as containing a DNA sequence, GEN-Guard can optionally invoke a second layer to **analyze the sequence and preview its risk level** before any sharing is finalized. This layer addresses the question: "*Okay, a sequence was found – **what is it and is it dangerous or sensitive?***" Providing this context is invaluable for security officers or automated policy engines to decide how to handle the incident (e.g. block it, quarantine it, or allow with logging).

The second layer involves two sub-tasks:

(2A) Sequence Extraction: The system extracts the actual nucleotide sequence from the surrounding text. In many cases, this is straightforward (the sequence might already be isolated or the only thing detected). We use pattern matching to pluck out the longest substring of A/C/G/T (or their plausible obfuscated forms) and clean any non-sequence characters (e.g. remove spaces, numbers, or line breaks). In more complex scenarios – say a Word document with commentary interwoven with sequence fragments – we can employ a large language model (LLM) to parse the text and identify what part looks like DNA. For example, we prompted GPT-4 with: "*Extract any DNA or RNA sequences from the following text*". In preliminary tests, an LLM was surprisingly adept at pulling out sequences even from messy contexts (thanks to its training on biological texts). However, for efficiency and privacy, our default approach favors deterministic parsing and only falls back to an LLM if the sequence context is highly unstructured. The outcome is a cleaned sequence string ready for analysis.

- **(2B) Risk Profiling and Sequence Identification:** Next, GEN-Guard evaluates the extracted sequence to determine why it might be sensitive. We integrated two complementary strategies here:
    - **Known Sequence Screening:** We leverage the **"Common Mechanism" biosecurity screening approach** pioneered by IBBIS[zaixizhang.github.io](zaixizhang.github.io). In essence, we compare the sequence

against databases of *sequences of concern* (pathogens, toxins, etc.) using alignment tools. GEN-Guard automates a BLAST search of the DNA against a curated reference set (including the NCBI database of dangerous pathogens and the U.S. Select Agents list). If the sequence is $\geq$90% identical to a known harmful sequence (or if its translated protein is similarly close to a known toxin protein), we flag it as high risk. This method will identify, for instance, that a pasted sequence is the *Ebola glycoprotein gene* or part of *Variola (smallpox) virus*, alerting us that its leakage is a severe biosecurity issue. We set thresholds (like 90% identity over 300+ base pairs) to balance catching dangerous sequences against false positiveszaixizhang.github.iozaixizhang.github.io. The Common Mechanism guidelines provide a well-vetted foundation for this screening logic.

- **Functional and Taxonomic Analysis:** For sequences that aren't an obvious exact match to known bad actors, we use **SeqScreen**, an open-source tool for functional DNA screening (genomebiology.biomedcentral.com. SeqScreen uses machine learning to characterize short DNA segments with labels for taxonomy (which organism it likely comes from) and **Functions-of-Concern (FunSoC)** – genetic functions linked to pathogenicity (toxins, virulence factors, antibiotic resistance, etc. ()genomebiology.biomedcentral.com. By running the sequence through SeqScreen's ensemble models, GEN-Guard can detect if the sequence encodes something potentially dangerous or sensitive even if it's novel. For example, a sequence might be flagged as encoding a *botulinum toxin domain* or an *antibiotic resistance gene*, warranting caution. SeqScreen's curated FunSoC database gives a layer of functional insight beyond simple identity matching, aligning with a "functional screening" paradigm for synthetic DNAgenomebiology.biomedcentral.com. In non-malicious contexts, SeqScreen can also identify human genomic data (e.g. it might label a sequence as human DNA or a human gene name), which is relevant for privacy – if a human gene sequence is detected, it may be protected health data (PHI) under regulations like HIPAA.

- **LLM-Based Contextual Evaluation:** In addition to these tools, we experimented with using an LLM (like GPT-4 with a bioinformatics plugin) to generate a quick *"risk summary."* For a given sequence, the LLM can be prompted with any database hits (from BLAST/SeqScreen) and asked to explain in plain language what the sequence is. For instance, *"This DNA sequence appears in the genome of* ***Bacillus anthracis*** *(anthrax bacterium) and includes genes for toxin production – high biosecurity risk."* This LLM-generated explanation can be presented to a security analyst or compliance officer as a **"preview" of why the content was flagged**. While not fully autonomous, this assists humans in triaging incidents. We treat this LLM step as optional (it would be used in an

analyst-facing dashboard, not in the critical path of blocking the data).

By combining identity-based screening and ML-driven functional analysis, the second layer provides a robust assessment. It effectively answers: *Is this sequence part of a dangerous pathogen? Does it encode a potentially harmful function? Could it be sensitive personal data?* The analysis results in a **risk level classification** (e.g. Low, Medium, High, Critical) along with descriptive tags (like "Human genomic DNA – privacy sensitive" or "E. coli lab strain gene – low risk" or "Clostridium botulinum toxin gene – HIGH risk"). We followed a rough guideline that correlates risk with sequence length and novelty as well, since longer sequences (especially $>$1,000 bp) might constitute whole genes or genomes that are more consequential. For example, a 20 bp DNA primer on Slack is low concern, whereas a 5,000 bp sequence encoding a viral capsid protein is serious. This length-based rule-of-thumb (Table in Figure 2) is used as an additional factor in the risk scoring.

Importantly, all second-layer analysis can be done **locally or on-premises** for privacy. We utilized local BLAST databases and an offline version of SeqScreen (which is open-sourcegenomebiology.biomedcentral.com). Organizations can thus use GEN-Guard's analysis without sending the sequence to any external service, avoiding further exposure. If using an LLM for summaries, a company could opt for an internal LLM or carefully tokenize the sequence (e.g. not reveal the full sequence context). These considerations ensure **GEN-Guard's use does not itself become a source of leakage** – a critical design principle for security tools.

2.4 Deployment and Integration: G-Guard's architecture was built to be platform-agnostic. We expose a simple API where any data stream (text blob, file, chat message, etc.) can be input and the system returns a detection flag, risk level, and suggested actions. This makes integration straightforward: for instance, a Slack bot could call GEN-Guard on each message posted in sensitive channels; an email DLP rule could route attachments through GEN-Guard; or a cloud storage scanner can periodically run GEN-Guard on new file uploads. Because our first layer is fast and second layer is invoked only on positives, the overall system can keep up with real-world data rates (we estimate scanning on the order of *gigabytes of text per hour* is feasible with a single CPU thread, given our optimized pipeline).

We also designed an **"Incident Response Mode"** (detailed in Section 3) that goes hand-in-hand with deployment. In this mode, GEN-Guard not only detects and possibly blocks the leak in real time, but also logs a rich incident report for security and compliance teams. This includes information like: timestamp, user or process that attempted the transfer, the destination (e.g. external email address or public channel), a short excerpt of the sequence (masked except for the first/last bases for privacy), and the risk classification with explanation. These logs can feed into a company's SIEM (Security Information and Event Management) or compliance dashboard, providing an **audit trail** of genomic data handling events. The incident response integration ensures that even if an attempted leak is thwarted, it is recorded and can be reviewed – supporting internal accountability and any

regulatory reporting requirements (for example, documenting attempts to export regulated genetic data).

Figure 1 illustrates the overall flow: data enters → first-layer detection (regex + ML) → if DNA found, second-layer analysis (BLAST/SeqScreen/LLM) → outputs: decision (allow/block) and logging. This layered approach and integration strategy embody GEN-Guard's goal: **real-time genomic data leak prevention with context-aware risk intelligence**.

3. Results

Showcase and explain your results here. This is where you include the graphs, screenshots, visualizations, and statistical results from your research.

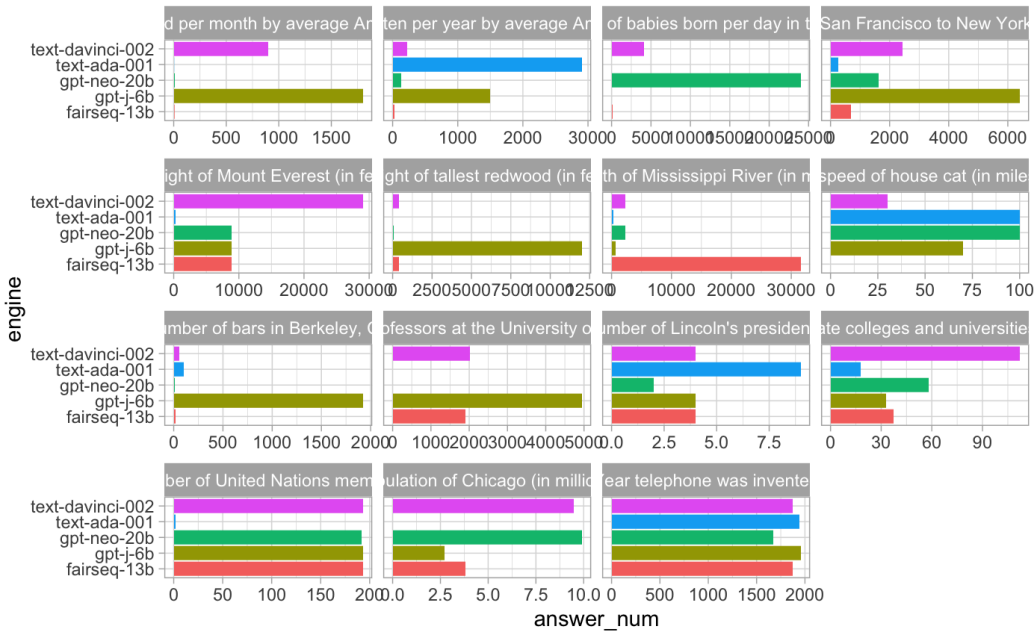


Figure 1 – Representation of benchmarking Number Comprehension Conflation

4. Discussion and Conclusion

This is where you can include all the wonderful explanations, discussions, results, analyses, statistics, and much more.

Let's add a few citations: (Alon, 2006; Goh et al., 2021; Lindner et al., 2023; Olah et al., 2020; Weiss et al., 2021). Here, we use the Zotero software with the Zotero add-on for Chrome and Google Docs for citation management but you can also write them manually (for significantly more hassle).

5. References

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6. Appendix

Important: Include an appendix called "Security Considerations" that outlines potential limitations of your approach and suggestions for future improvements.