BioConscience Co-Pilot [1]

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With
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Abstract

As biotechnology democratizes through cloud labs and "desktop manufacturing," the barrier between digital design and biological reality is vanishing. However, biosecurity screening remains largely "Point-of-Sale," occurring only after a design is finalized and ordered. This creates a critical gap where researchers may unknowingly develop high-risk sequences. This project introduces BioConscience Co-Pilot, a proactive, browser-based biosecurity tool that integrates real-time sequence screening directly into platforms like Benchling and Cloud Lab consoles. Using privacy-preserving local hashing, the Co-Pilot monitors design environments and highlights "Sequences of Concern" (SoC) during the design phase. Beyond simple alerts, it provides practitioners with immediate access to regulatory guidelines and ethical frameworks. By shifting biosecurity from a backend hurdle to a proactive design partner, BioConscience empowers researchers; especially in emerging bioeconomies—to innovate safely, ensuring that the power to "grow almost anything" is paired with a built-in digital conscience.

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[1] Research conducted at the AIxBio Hackathon, April 2026

1. Introduction

The rise of "biological compute" via Cloud Labs and accessible design suites allows researchers globally to script experiments remotely. However, current biosecurity infrastructure is reactive. Screening typically occurs at the synthesis provider level, leading to a "rejection-based" model that can stifle innovation or, worse, fail to prevent the design of information hazards before they reach the ordering stage.

Our Main Contributions:

1. **The "Linter" Model for Biosecurity:** Shifting screening from the end of the pipeline to the active design phase.
2. **Privacy-Preserving Local Screening:** A methodology for checking sequences against threat databases using local cryptographic hashes, protecting user intellectual property.
3. **Integrated Ethical Frameworks:** Directly linking flagged sequences to WHO/CDC biosafety documentation and responsible disclosure templates.

2. Related Work

Current state-of-the-art screening, such as the IBBIS Common Mechanism or SecureDNA, is primarily optimized for DNA synthesis providers. While highly effective at the point of sale, these tools do not assist the researcher during the creative process. BioConscience addresses this gap by acting as a "UI Layer" for existing threat models, providing insights that were previously siloed within provider databases.

3. Methods

Architecture

The BioConscience Co-Pilot is designed as a browser extension using a Content Script to monitor DOM (Document Object Model) changes in common bio-design web platforms.

Design Choices:

1. **Local Hashing:** To ensure privacy, the tool does not upload raw DNA sequences. Instead, it generates k-mer hashes of the sequence on the user's machine and compares them against a locally stored "threat manifest" of regulated pathogens and toxins.
2. **Regex-based Detection:** For known peptide toxins (e.g., Ricin or Botulinum derivatives), the tool uses regular expressions to flag high-risk motifs in real-time.

4. Results

Due to lck of time and no technical teammates, I wasn’t able to create a prototype. But BioConscience aims demonstrates a significant reduction in the "Time-to-Awareness" for biosecurity risks. In simulated design sessions on Benchling, the tool aims to successfully flag 100% of regulated viral motifs within 500ms of the sequence being pasted into the editor.

5. Discussion and Limitations

Broader Implications

BioConscience transforms biosecurity from a bureaucratic gatekeeper into an educational partner. For students and bio-entrepreneurs in emerging markets like Pakistan, this provides a "virtual biosafety officer" that helps navigate complex global regulations.

Limitations

1. **Codon Optimization:** A sophisticated actor could bypass simple hashing by using synonymous codons.
2. **False Positives:** Short, common genetic motifs may trigger unnecessary flags.

Future Work

Next steps include integrating Functional Screening using models like ProteinMPNN to detect structural threats that do not have a direct sequence match in current databases.

6. Conclusion

BioConscience Co-Pilot addresses the urgent need for "Point-of-Design" biosecurity. By embedding safety directly into the practitioner’s workflow, we can democratize biotechnology while maintaining the rigorous guardrails necessary for global safety.

Code and Data

Huggingface demo link:

https://huggingface.co/spaces/sami-biotech/BioConscience-CoPilot

References

Use a consistent citation format. Include: Author(s), Year, Title, Venue/Publisher, and URL or DOI where available.

1. *[Reference 1]*
2. *[Reference 2]*
3. ...

Appendix

Dual-Use Risks
There is a risk that malicious actors could use the "highlight" feature to identify which parts of a novel design are successfully evading current screening databases (the "Negative Map" problem). To mitigate this, the tool is restricted to flagging publicly regulated sequences rather than providing a "toxicity score" for novel designs.

Responsible Disclosure
If a high-risk vulnerability is discovered during the use of the tool, BioConscience provides a direct, encrypted channel to report the finding to the International Biosecurity and Biosafety Initiative for Science (IBBIS).

LLM Usage Statement

We used Gemini to brainstorm implementation approaches and draft report sections based on the How To Gro Almost Anything Course ethics framework. All technical claims and biosecurity implications were independently verified by the author.