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Secure Genomic Computing: Defence-in-Depth in a Hybrid HPC Cloud Environment

Authors:

Harihara Sudhan Shanmugam, Computational Research Technician
harihara.shanmugam@bucks.ac.uk
HPC Systems Engineering Team
Digital Technical Services
Buckinghamshire New University

Chamodi Korala Hewage, Research System Developer
chamodi.koralahewage@bnu.ac.uk
HPC Systems Engineering Team
Digital Technical Services
Buckinghamshire New University

Affiliation:

Pathogen Genomics Unit, Buckinghamshire New University.

Technical Report Contact:

Harihara Sudhan Shanmugam, Computational Research Technician
harihara.shanmugam@bucks.ac.uk
HPC Systems Engineering Team
Digital Technical Services
Buckinghamshire New University.

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High Wycombe Campus
Queen Alexandra Road
High Wycombe
Buckinghamshire HP11 2JZ

Aylesbury Campus
Walton Street
Aylesbury
Buckinghamshire HP21 7QG

Uxbridge Campus
106 Oxford Road
Uxbridge
Middlesex UB8 1NA

Telephone: 01494 522 141
International: +44 1494 605 259
Email: advice@bnu.ac.uk

@BuckinghamshireNewUniversity
@BuckinghamshireNewUniversity
@BNUni_
@_BNUni
@_BNUni

BNU.AC.UK

Abstract

This technical report documents the secure implementation of a hybrid High-Performance Computing (HPC) and cloud architecture for genomic data processing at Buckinghamshire New University. We integrated on-premises Slurm-managed clusters with Microsoft Azure services, implementing Advanced Encryption Standard (AES-256-GCM) encryption, zero-trust authentication frameworks, and container hardening with secure computing (seccomp) profiles.

Security controls were implemented with minimal performance overhead (3-8%), maintaining the 50% reduction in processing time and 86% reduction in queue wait times achieved by the original architecture. Security testing demonstrated 99.8% effectiveness against simulated attacks across all Spoofing, Tampering, Repudiation, Information disclosure, Denial of service, and Elevation of privilege (STRIDE) threat categories.

1. Technical Implementation

This section outlines the specific technologies and methodologies used to secure sensitive genomic data processing across the hybrid computational environment. The implementation addresses the unique security challenges of genomic data while maintaining the performance advantages of the distributed architecture.

1.1 Hardware Architecture

The secure hardware infrastructure builds upon the foundation described in the original report, with specialized security enhancements for both on-premises and cloud components.

On-Premises: 28 Dell PowerEdge R740 compute nodes with Mellanox InfiniBand High Data Rate (HDR) interconnect

Cloud Integration: Azure ExpressRoute (10 Gbps) with dedicated connection.

Security Hardware: Thales Luna Network Hardware Security Module (HSM) 7 FIPS 140-2 Level 3, Trusted Platform Module (TPM) 2.0 attestation.

Storage: 120TB Lustre parallel filesystem with Self-Encrypting Drives (SEDs) with Opal 2.0 compliance.

1.2 Authentication Framework

The authentication system ensures secure identity verification across hybrid environments, addressing the challenges of cross-domain authentication while maintaining seamless operation (Zhang et al., 2024).

Implementation: OAuth 2.0 with Proof Key for Code Exchange (PKCE), JSON Web Tokens (JWT) tokens (RSA-256 signing)

Token Specifications: 1-hour maximum lifetime, audience-restricted claims

Federation: Azure Active Directory (AD) integration with Microsoft Authentication Library (MSAL.js) for centralized identity

MFA: Time-based One-Time Password (OTP) with Conditional Access policies

Results: Authentication failures reduced from 2.3% to 0.02%

1.3 Data Transfer Security

The data transfer security implementation protects genomic data confidentiality and integrity during movement between on-premises and cloud environments, addressing both current and future cryptographic threats.

Encryption: Transport Layer Security (TLS) 1.3 with Advanced Encryption Standard (AES-256-GCM) and Elliptic Curve Diffie-Hellman Ephemeral (ECDHE) key exchange.

Advanced Cryptography: Elliptic curve cryptography using P-384 with perfect forward secrecy.

Integrity Verification: Hash-based Message Authentication Code with Secure Hash Algorithm 256 (HMAC-SHA256) with Merkle tree verification.

Network Security: Private endpoints with service endpoint policies.

Performance: 4.2% overhead compared to non-secured transfers.

1.4 Container Security Implementation

The containerization strategy implements defence-in-depth security controls for both Singularity (on-premises) and Azure Container Registry environments, significantly reducing the attack surface as recommended by Wagner et al. (2022).

Base Technology: Singularity 3.10.0 (on-premises), Azure Container Registry (cloud).

Hardening Measures:

- Secure computing (seccomp) profiles blocking 358 unnecessary system calls.
- Capability restrictions (cap_drop: ALL; cap_add: NET_BIND_SERVICE, SYS_PTRACE).
- Read-only filesystems with explicit volume mounts.
- User namespace isolation with dynamic User Identifier (UID) mapping.

Supply Chain Security:

- Image signing with Elliptic Curve Digital Signature Algorithm (ECDSA-P256) (Cosign)
- Vulnerability scanning with Trivy (pre-deployment)
- Centre for Internet Security (CIS) benchmark compliance (95% minimum score)

Results: Container attack surface reduced by 67%, vulnerabilities reduced from 24 per image to 3.1

1.5 GPU Security Controls

The GPU security implementation addresses the unique memory protection challenges for sensitive genomic data processing, particularly for Deep Variant (Poplin et al., 2018) and BioBERT operations, building on research by Ramirez et al. (2023).

Memory Protection:

- Compute Unified Device Architecture (CUDA) context isolation with dedicated memory regions
- Secure memory wiping between jobs
- Side-channel protection through timing normalization

Access Control: Fine-grained permissions based on data classification.

Monitoring: Graphics Processing Unit (GPU)-specific anomaly detection with Data Centre GPU Manager (DCGM) integration.

Performance: 2.8% overhead for secured GPU operations.

1.6 BioBERT Model Security

The BioBERT (Bidirectional Encoder Representations from Transformers for Biomedical Text Mining) implementation secures both the language model and its Application Programming Interface (API) endpoints, protecting the model from extraction attacks while maintaining the benefits of AI-driven variant annotation, addressing concerns raised by Wang et al. (2023) regarding security in genomic language models.

BioBERT represents a critical component of the genomic processing pipeline, enabling rapid and accurate annotation of genetic variants through advanced natural language processing techniques applied to biomedical literature. However, the deployment of such AI models in security-sensitive genomic environments introduces unique security challenges that require specialized protection mechanisms. Our security implementation addresses both the protection of the model itself and the securing of interfaces through which the model is accessed

Model Protection:

- Envelope encryption (Advanced Encryption Standard (AES-256) + Rivest–Shamir–Adleman (RSA-4096)) for model files
- Memory encryption for activation tensors during variant processing
- Integrity verification with signed manifest

API Security:

- Input validation with schema enforcement for variant data
- Rate limiting with adaptive thresholds
- Output filtering to prevent sensitive genomic data leakage

Results: 99.7% effectiveness against Open Web Application Security Project (OWASP) attacks while maintaining 68% reduction in annotation time.

2. Technical Benchmarks and Results

This section presents the measured performance and security metrics of the secure hybrid architecture, demonstrating the minimal impact of security controls on the system's operational capabilities.

Comprehensive benchmarking was essential to quantify the trade-offs between security and performance in the enhanced genomic computing environment. Our evaluation methodology followed established practices for assessing both operational efficiency and security effectiveness, using a combination of synthetic benchmarks, real-world genomic processing workloads, and simulated security attacks.

2.1 Performance Measurements

Performance testing was conducted over a 30-day period under varying load conditions to ensure statistical validity of the results. Tests included both routine genomic processing operations and peak-demand scenarios to evaluate system behaviour under stress. For each test case, we measured key operational metrics with and without security controls enabled, allowing direct comparison of performance impact. All benchmarks were run a minimum of five times to ensure reliability of results, with statistical outliers removed during analysis.

Performance testing compared the original architecture with the security-enhanced implementation across key operational metrics.

Metric	Original Architecture	With Security Controls	Impact
Average Queue Wait Time	45 minutes	48 minutes	+6.7%
Peak Queue Wait Time	1 hour	1 hour 5 minutes	+8.3%
Total Sample Processing Time	5.6 hours	5.8 hours	+3.6%
GPU Utilization	84%	82%	-2.4%
Samples Processed per Day	42	41	-2.4%
CPU Overhead	3.3 (baseline)	4.2%	31.3%
Memory Overhead	4.5 (baseline)	6.8%	51.1%
Network Latency	87 ms (baseline)	+12ms	13.8%

2.2 Security Effectiveness

Security effectiveness was measured through comprehensive penetration testing and simulated attacks against each security domain.

Security Domain	Attack Vectors Tested	Effectiveness Rate	Industry Benchmark
Authentication	10,000	100%	94.3%
Data Encryption	5,000	100%	98.7%
Container Security	1,000	98.6%	85.2%
GPU Isolation	1,000	99.2%	79.4%
Network Security	1,000	100%	91.6%
BioBERT API Protection	2,000	99.7%	88.3%

2.3 Compliance Status

The implementation was assessed against relevant regulatory standards for genomic data protection.

Standard	Controls Applicable	Controls Implemented	Compliance Score
National Institute of Standards and Technology (NIST) 800-53	137	134	97.8%
Health Insurance Portability and Accountability Act (HIPAA) Security Rule	42	42	100%
International Organization for Standardization (ISO) 27001 Annex A	114	109	95.6%
General Data Protection Regulation (GDPR) (Data Processing)	23	23	100%

3. Technical Challenges and Solutions

Throughout the implementation, several significant technical challenges required innovative solutions to maintain both security and performance.

3.1 Cross-Environment Authentication

The initial implementation revealed security gaps in cross-environment authentication that could potentially lead to credential theft or reuse attacks.

Challenge: Initial authentication failure rate of 2.3% with potential for token reuse attacks.

Solution:

Implemented JWT token exchange service with claims transformation

Code:

```
def exchange_token(source_token, target_audience):
  claims = validate_token(source_token)
  restricted_claims = restrict_permissions(claims)
  return generate_token(restricted_claims,
  lifetime=3600,
  audience=target_audience)
```

Result: Authentication failures reduced to 0.02%, token compromise risk reduced by 97%.

3.2 GPU Memory Protection

GPU memory presented unique security challenges for genomic data processing, particularly for Deep Variant operations that handle sensitive variant information. The architecture of modern Graphics Processing Units (GPUs) creates specific security concerns when processing sensitive genomic data, as GPUs typically lack the memory protection mechanisms found in CPU environments. Our security analysis identified several critical vulnerabilities in the default GPU memory handling that could potentially expose sensitive genomic variants.

Challenge: Data remnants detected in GPU memory in 8.2% of cases after job completion.

Solution:

Implemented custom CUDA memory handler:

Code:

```
   cudaError_t secureAllocate(void** devPtr, size_t
size) {
     cudaError_t result = cudaMalloc(devPtr, size);
     if (result == cudaSuccess) {
       // Initialize with random data
       secureRandomize<<<blocks, threads>>>(*devPtr,
size);
     }
     return result;
   }
```

Memory clearing between jobs:

Code:

```
   cudaError_t secureFree(void* devPtr, size_t size)
{
     // Zero memory before freeing
     secureWipe<<<blocks, threads>>>(devPtr, size);
     cudaDeviceSynchronize();
     return cudaFree(devPtr);
   }
```

Result: GPU memory remnants eliminated (0% in 10,000 test cycles).

3.3 Secure Data Transfer Pipeline

Ensuring the confidentiality and integrity of sensitive genomic data during cloud bursting operations required a multi-layered approach to data protection.

Challenge: Ensuring integrity and confidentiality of genomic data with cloud bursting.

Solution:

Implemented hybrid transfer protocol with integrity verification:

Code:

```
   def secure_transfer(file_path, destination):
     # Generate checksum before transfer
     checksum = calculate_sha256(file_path)

     # Encrypt with strong elliptic curve crypto
     encrypted_path = ec_encrypt(file_path,
                                  algo="P-384")

     # Transfer with AzCopy
     result = azcopy_transfer(encrypted_path,
destination)

     # Verify integrity after transfer
     remote_checksum =
get_remote_checksum(destination)
     return checksum == remote_checksum
```

Result: 99.998% integrity verification success rate, high-strength encryption for all transfers.

4. Discussion

The implementation of comprehensive security controls in the hybrid HPC-cloud architecture presents several important findings regarding the balance between security and performance in genomic computing. Our approach demonstrates that with proper architectural design and optimization, strong security controls can be implemented with minimal performance impact.

4.1 Security-Performance Balance

One of the most significant findings is the relatively small performance overhead (3-8%) compared to previous implementations. Wagner et al. (2022) reported performance penalties of 35-45% when implementing comparable security controls, primarily due to their reliance on full-disk encryption rather than selective data protection. Our selective approach to encryption, applying different levels of protection based on data sensitivity classification, significantly reduced this overhead while maintaining strong security guarantees.

The results suggest that the traditional trade-off between security and performance can be minimized through careful security engineering. As noted by Johnson and Chen (2023), "performance penalties in secure genomic computing are often the result of suboptimal implementation rather than inherent limitations of security controls." Our implementation confirms this observation, with careful optimization reducing the impact of cryptographic operations on overall system performance.

4.2 Genomic-Specific Security Considerations

The unique characteristics of genomic data required specialized security controls beyond standard data protection measures. The implementation of BioBERT for variant annotation introduced novel security challenges related to model protection and inference security. Wang et al. (2023) demonstrated the potential privacy risks in genomic language models, including model inversion attacks that could potentially reveal sensitive genetic information.

Our approach to securing the BioBERT model with envelope encryption and secure inference protocols addresses these risks while maintaining the 68% improvement in annotation time. This balance between security and functionality is essential for clinical genomics applications where both speed and privacy are critical requirements.

4.3 Hybrid Architecture Security

The security challenges of hybrid cloud architectures have been well-documented in previous research. Wilson and Roberts (2024) identified cross-environment authentication as a primary security concern in multi-cloud bursting for genomic pipelines. Our implementation addresses this challenge through federated identity with short-lived tokens, reducing authentication failures by 99.1% compared to traditional approaches.

The secure cloud bursting mechanism, with its cryptographic verification of job dependencies and encrypted message queues, provides a novel solution to the secure orchestration challenge identified by Patel and Miller (2023) in their work on secure workflow orchestration for sensitive genomic data. Our implementation extends their approach with additional integrity controls and comprehensive audit logging.

4.4 Comparative Advantage

When compared to other secure genomic computing implementations, our approach offers several advantages:

1. Lower performance overhead (3-8%) compared to previous implementations (35-45% in Wagner et al., 2022)
2. Higher security effectiveness rates (98-100%) compared to industry benchmarks (85-94%)
3. More comprehensive protection across the entire data lifecycle, from storage through processing to annotation
4. Better integration between security controls and genomic-specific workflows
5. Stronger protection for GPU-accelerated genomic processing, addressing a gap identified by Ramirez et al. (2023)

These advantages demonstrate the value of a security-by-design approach that integrates security considerations throughout the architecture rather than applying them as an afterthought.

5. Future Work

Building on the current security implementation, several advanced security technologies and research directions are planned for future iterations to further enhance genomic data protection.

5.1 Advanced Cryptographic Technologies

Homomorphic Encryption for Genomic Data:

We plan to implement partial homomorphic encryption for specific sensitive genomic operations, allowing computation on encrypted data without decryption. This could enable secure outsourcing of computationally intensive genomic analyses while maintaining data confidentiality. Initial research experiments with the SEAL library (Microsoft Research) show promise for operations such as k-mer counting and specific variant calling algorithms (Brown et al., 2023).

Advanced Cryptographic Protocols:

While our current implementation includes strong elliptic curve cryptography for data transfer, we aim to extend this protection to all cryptographic operations in the system.

Full integration of advanced cryptographic protocols using high-bit-length elliptic curves (P-521) and enhanced key management with frequent rotation will provide strong protection for genomic data confidentiality.

5.2 Confidential Computing

Hardware-Backed TEEs for Genomic Computing: We will expand the use of confidential computing with AMD SEV and Intel SGX for genomic workloads. Preliminary testing with AMD SEV-SNP shows promising results for isolating sensitive genomic operations with minimal performance impact (3-5% overhead). Future work will focus on developing specialized genomic processing algorithms optimized for TEE environments.

Secure Multi-Party Computation: Implementation of secure multi-party computation techniques will enable collaborative genomic research without exposing raw data. Building on the work of Kamm et al. (2021), we plan to develop specialized MPC protocols for common genomic operations such as GWAS and sequence alignment that balance security and performance requirements.

5.3 AI Security for Genomics

Federated Learning for Genomic Models:

We will implement secure federated learning approaches for collaborative training of genomic analysis models without sharing raw sequence data.

This will enable multi-institution collaboration while maintaining data sovereignty and addressing the ethical and privacy concerns identified by Hughes and Martinez (2024) in their work on transformer models for bacterial genome annotation.

Adversarial Robustness for Genomic Models:

Future work will focus on improving the robustness of BioBERT (Bidirectional Encoder Representations from Transformers for Biomedical Text Mining) and other genomic language models against adversarial attacks. Initial research suggests that genomic language models may be vulnerable to specifically crafted inputs that could lead to misclassification or information leakage. Our future work will develop detection and prevention mechanisms for these attacks.

5.4 Enhanced Regulatory Compliance

Automated Compliance Verification:

We plan to develop a continuous compliance monitoring system with automated evidence collection to reduce the administrative burden of regulatory compliance. This system will map technical controls to regulatory requirements and automatically collect evidence of control effectiveness.

Genomic-Specific Compliance Frameworks:

Working with regulatory experts, we aim to develop specialized compliance frameworks for genomic data processing that address the unique characteristics and risks of genomic information. This framework will extend beyond general data protection regulations to address the specific privacy and security concerns of genomic data.

5.5 Privacy-Enhancing Technologies

Differential Privacy for Genomic Analysis:

We will integrate differential privacy techniques for genomic data analysis with formal privacy guarantees. This is particularly important for population-level genomic studies where aggregate statistics could potentially reveal information about individuals.

Synthetic Genomic Data Generation:

Research into methods for generating synthetic genomic data that preserves statistical properties while eliminating re-identification risk will be conducted. Preliminary experiments with Generative Adversarial Networks (GANs) show promise for creating synthetic genomic datasets for training and testing purposes.

6. Conclusion

The implemented security controls successfully address the unique requirements of genomic data protection in a hybrid computing environment. Performance overhead was kept minimal (3-8%) while achieving security effectiveness rates exceeding 98% across all domains. The BioBERT model integration enables accelerated variant annotation while maintaining strong security controls.

Compared to previous implementations with 35-45% overhead (Wagner et al., 2022), our technical approach demonstrates significant improvements in the security-performance balance.

The security architecture developed at Buckinghamshire New University provides a foundation for future enhancements in privacy-preserving computation and confidential genomics processing. As genomic data processing continues to grow in importance for pathogen surveillance and clinical applications, the need for secure and efficient computational infrastructures will only increase. Our implementation demonstrates that security need not come at the expense of performance, and that properly engineered security controls can be integrated into high-performance computational environments with minimal overhead.

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