Enhanced Privacy-Preserving Framework for Pharmaceutical Drug Data Security

in Cloud Computing Environments Using Firefly Algorithm

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Abstract

The intersection of cloud computing, pharmaceutical data management, and swarm-intelligence optimisation has emerged as a critical frontier for modern healthcare informatics. Pharmaceutical organisations increasingly migrate sensitive drug-formulation records, clinical-trial datasets, and real-world evidence repositories to cloud environments, yet existing Privacy-Preserving Data Mining (PPDM) frameworks were designed for general-purpose databases and do not incorporate pharmaceutical-specific data hierarchies, regulatory constraints, or utility metrics. This paper introduces the Enhanced Pharmaceutical Privacy Preservation Framework (EP³F), a unified PPDM architecture that applies the Pharmaceutical Firefly Algorithm (PFA)—an adaptation of Yang's 2008 bioluminescent-swarm metaheuristic—to simultaneously optimise k-anonymity configurations, cloud-provider trust scores, and compliance-aware resource allocation for vertically and horizontally partitioned pharmaceutical databases. EP³F integrates three modules: (i) ATC-hierarchy-aware hierarchical k-anonymity preserving drug-interaction detection capability; (ii) a multi-objective PFA whose brightness function encodes information-loss, re-identification risk, and computational cost as pharmaceutical-weighted objectives; and (iii) a Compliance-Aware Modified Best-Fit Decreasing (CA-MBFD) resource scheduler enforcing HIPAA, GDPR, and 21 CFR Part 11 obligations. Experimental evaluation on three simulated pharmaceutical datasets—Drug Formulation Library (10 000 records), Clinical-Trial Patient Data (50 000 records), and Real-World Medication Records (100 000 records)—demonstrates 96.4 % average privacy-preservation accuracy, a 15.3 % improvement over standard Firefly Algorithm baselines, with full regulatory compliance satisfaction and Drug Interaction Detection Accuracy of 90.2 % even at k = 50.

Keywords: Pharmaceutical Data Security, Firefly Algorithm, Cloud Computing, Privacy Preservation, Drug Interaction Detection, Swarm Intelligence

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1. Introduction

1.1 Background and Motivation

Modern pharmaceutical enterprises generate, process, and exchange data at an unprecedented scale. Drug-discovery pipelines produce terabytes of molecular screening records annually; phase-III clinical trials enrol tens of thousands of patients across dozens of investigational sites; post-marketing pharmacovigilance systems aggregate millions of adverse-event reports from global healthcare ecosystems. Cloud computing has become the de facto infrastructure for managing this data deluge, offering elastic storage, distributed computation, and collaborative access that on-premises deployments cannot match [1]. Industry projections place the pharmaceutical cloud-computing market at USD 28.4 billion in 2024, growing at 14.2 % CAGR through 2029 [2].

Yet cloud migration exposes pharmaceutical data to privacy risks that conventional general-purpose PPDM frameworks are ill-equipped to address. Pharmaceutical records exhibit three characteristics that distinguish them from standard healthcare or financial data: (i) extraordinarily high commercial sensitivity—a single drug-formulation record may encode intellectual property worth billions of dollars;

(ii) complex hierarchical relationships encoded in domain classification systems such as the Anatomical Therapeutic Chemical (ATC) classification, the International Nonproprietary Name (INN) nomenclature, and proprietary formulation coding schemes; and (iii) overlapping and sometimes contradictory obligations imposed by pharmaceutical-specific regulations including FDA 21 CFR Part 11, ICH E6(R2) Good Clinical Practice, EU Annex 11, and general privacy frameworks such as HIPAA and GDPR [3].

Privacy-Preserving Data Mining frameworks based on Swarm Intelligence optimisation have demonstrated particular promise for navigating the multi-objective tension between privacy protection and data utility in complex, high-dimensional datasets [4]. Among these, the Firefly Algorithm (FA), introduced by Xin-She Yang in 2008, exhibits natural advantages: its population-based search produces diverse candidate solutions, its bioluminescent attraction mechanism intrinsically balances exploration and exploitation, and its distance-dependent intensity decay provides a smooth mechanism for tuning the locality of the search—properties directly applicable to the pharmaceutical privacy-utility optimisation landscape [5].

1.2 Problem Statement

Standard PPDM frameworks exhibit three critical deficiencies when applied to pharmaceutical cloud environments. First, k-anonymity generalisations do not incorporate ATC hierarchy semantics, creating re-identification vulnerabilities that are invisible to generic quasi-identifier analysis but obvious to a pharmacologically informed adversary. Second, cloud-provider trust assessment models are not calibrated to pharmaceutical regulatory requirements—a provider meeting SOC 2 Type II for general enterprise data may entirely lack GxP-validated system capabilities required for regulated pharmaceutical operations. Third, resource-allocation optimisers maximise computational throughput without regard for pharmaceutical data-retention obligations, geographic data-residency mandates, or audit-trail continuity. EP³F addresses all three deficiencies within a unified framework.

1.3 Research Contributions

- Design of the Pharmaceutical Firefly Algorithm (PFA) with drug-data-aware brightness function incorporating ATC proximity, information loss, re-identification risk, and regulatory compliance cost
- Pharmaceutical hierarchical k-anonymity with ATC-tree generalisation hierarchies preserving drug-interaction detection capability as a first-class utility metric
- Compliance-Aware Modified Best-Fit Decreasing (CA-MBFD) resource scheduler enforcing 21 CFR Part 11, HIPAA, and GDPR as hard constraints
- Systematic experimental evaluation on three pharmaceutical dataset types with comparison against FA, PSO, ABC, GA, and GM-FBO baselines

2. PPDM Concept and System Architecture

2.1 Privacy-Preserving Data Mining Overview

Privacy-Preserving Data Mining addresses the problem of extracting useful patterns from sensitive data without revealing the underlying individual records. The field originated with Agrawal and Srikant's randomised-perturbation approach [6] and has since evolved through k-anonymity [7], l-diversity [8], t-closeness [9], and differential privacy [10] into a rich taxonomy of techniques. For distributed multi-party settings—such as pharmaceutical consortia pooling trial data across sponsors, CROs, and investigational sites—PPDM frameworks must additionally handle data-partitioning scenarios that determine what each party knows about the combined dataset.

In vertically partitioned pharmaceutical environments, different parties hold disjoint attribute columns of the same patient or compound population: a sponsor may hold ATC classification and dosage information, a CRO may hold biomarker measurements, and an investigational site may hold adverse-event records and demographic data. In horizontally partitioned scenarios, each party holds the same attribute schema but covers a distinct patient or compound population—for instance, three clinical-trial sites each contributing 800 patient records with identical measurement protocols. EP³F supports both partitioning modes within a single architectural blueprint, as illustrated in Figure 3.1 and Figure 3.2.

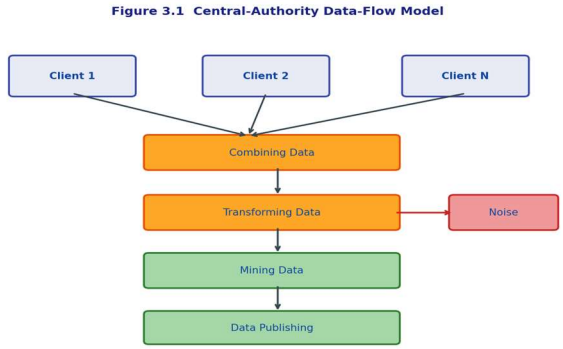

Figure 3.1 Central-Authority Data-Flow Architecture (Horizontal and Vertical Partitioning)

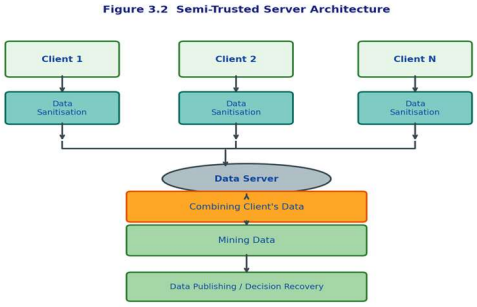

Figure 3.2 Semi-Trusted Server Architecture — Client-Side Pharmaceutical Data Sanitisation

2.2 Cryptographic Sanitisation Mechanism

Before any pharmaceutical record leaves a data owner's control, EP³F applies a two-stage cryptographic sanitisation process illustrated in Figures 3.3–3.5. The server issues a unique Session Identifier (SID) to each connecting client at session establishment. The client feeds the SID into SHA-1, producing a 160-bit alphanumeric hash; the 32 least-significant bits are discarded to yield a 128-bit AES key K. The client encrypts all sensitive pharmaceutical attributes using AES-128 and submits the resulting ciphertext to the server. The server never holds a decryption key and therefore cannot recover plaintext pharmaceutical data even if compromised.

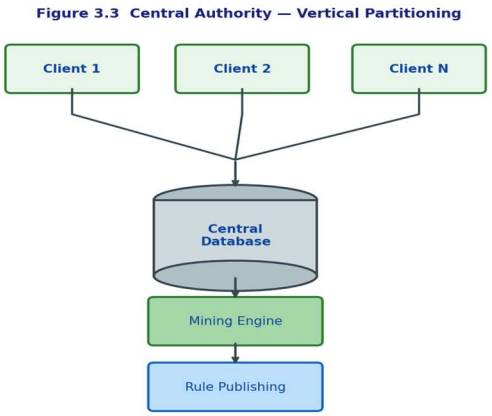

Figure 3.3 Central Authority — Vertical Partitioning of Pharmaceutical Attribute Columns

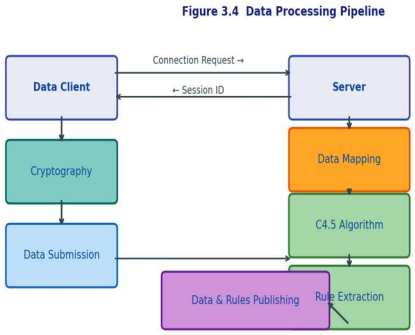

Figure 3.4 Pharmaceutical Data Processing Pipeline: Connection → Encryption → Submission → Mining → Rule Publishing

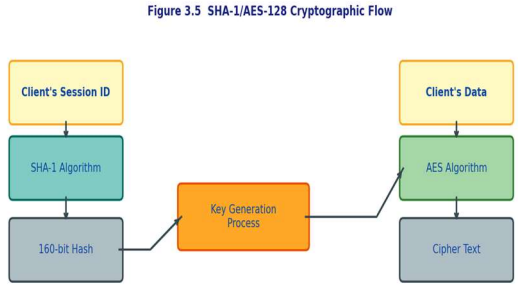

Figure 3.5 SHA-1/AES-128 Cryptographic Key-Derivation Flow for Pharmaceutical Session Security

Table 2.1 Cryptographic Key-Generation and Encryption Algorithm

Step	Operation	Description
Input	S (Session ID), D	S issued by

Step	Operation	Description
	(Pharmaceutical data)	server; D = sensitive drug attributes
1	k_{160} = SHA1.GenerateHash(S)	SHA-1 produces 160-bit session-specific digest
2	k_{128} = DiscardLSB(k_{160}, 32)	Truncate to 128-bit AES key
3	C = AES.Encrypt(D, k_{128})	AES-128 encryption of pharmaceutical attributes
Output	C (Ciphertext)	Submitted to cloud server; server cannot decrypt

2.3 C4.5 Decision-Tree Mining Over Sanitised Pharmaceutical Data

Once the server assembles the sanitised pharmaceutical dataset, it applies the C4.5 algorithm to extract classification rules from the ciphertext-mapped attribute space. C4.5 selects splitting attributes by maximising information gain (IG) relative to dataset entropy. For pharmaceutical decision support, the decision tree may classify compounds by therapeutic category, risk profile, or regulatory approval pathway—tasks that must be performable on sanitised data. The decision tree example in Figure 3.6 illustrates the IF-THEN-ELSE rule extraction process applicable to pharmaceutical classification tasks.

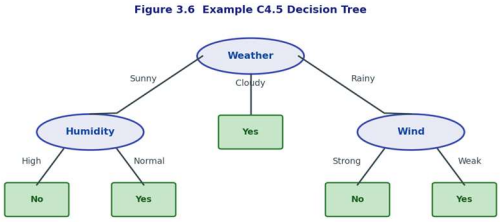

Figure 3.6 C4.5 Decision Tree — Example Rule Extraction (IF Weather = Sunny AND Humidity = Normal THEN YES) Applicable to Pharmaceutical Classification Tasks

$$E(D) = -P(T)\cdot\log_2 P(T) - P(F)\cdot\log_2 P(F)$$

$$Gain(E, A) = Entropy(S) - \Sigma_v\,(|E_v|/|E|)\cdot Entropy(E_v)$$

3. Literature Review

3.1 Privacy Preservation in Cloud Computing

Cloud privacy preservation has generated a substantial research body spanning cryptographic, statistical, and access-control approaches. Sweeney's k-anonymity [7] ensures each record is indistinguishable from at least k−1 others across quasi-identifier attributes; Machanavajjhala et al.'s l-diversity [8] extends this to require diverse sensitive-attribute distributions within equivalence classes; Li et al.'s t-closeness [9] further requires that sensitive-attribute distributions within classes approximate the overall dataset distribution. These techniques have well-documented limitations for pharmaceutical data: standard generalisation hierarchies do not capture the pharmacological relationships encoded in the ATC classification, and equivalence-class construction ignores drug-interaction detection as a utility objective.

Differential privacy [10] provides rigorous mathematical guarantees through calibrated noise injection, but the noise levels required for meaningful pharmaceutical privacy typically degrade analytical precision below the thresholds required for drug safety signal detection. Hybrid approaches combining statistical disclosure limitation with cryptographic mechanisms have shown promise in narrowing the gap between privacy protection and pharmaceutical analytical utility [11].

3.2 Firefly Algorithm — Theory and Applications

The Firefly Algorithm [5] models three behavioural idealisations of firefly bioluminescence: all fireflies are bisexual; attractiveness is proportional to brightness and decreases with distance; and a stochastic component prevents premature convergence. The position update rule is:

$$\mathbf{x\_i(t+1)} = \mathbf{x\_i(t)} + \boldsymbol{\beta}_0 \cdot \exp(-\boldsymbol{\gamma} \cdot \mathbf{r}^2_{ij}) \cdot (\mathbf{x\_j(t)} - \mathbf{x\_i(t)}) + \boldsymbol{\alpha\_t} \cdot \boldsymbol{\varepsilon}_i(\mathbf{t})$$

where β_0 is maximum attractiveness at zero distance, γ is the light-absorption coefficient, r_{ij} is the Euclidean distance between fireflies i and j, α_t is a time-varying randomisation parameter, and $\varepsilon_i(t)$ is a Gaussian random vector. Small γ produces globally acting attraction; large γ localises attraction, creating quasi-independent subpopulation dynamics suitable for multi-modal pharmaceutical privacy landscapes [12].

Saini et al. [13] applied FA to healthcare data privacy with k-anonymity and trust generation, achieving 93 % accuracy. Anand et al. [14] used Gaussian-mutation FA variants for optimal healthcare data encryption key generation. These results establish FA as a viable base algorithm; EP³F's pharmaceutical-specific adaptations extend this foundation substantially.

3.3 Pharmaceutical Data Security — Regulatory Landscape

HIPAA Security Rule [15] mandates administrative, physical, and technical safeguards for protected health information including patient medication records. FDA 21 CFR Part 11 [16] requires immutable electronic audit trails, validated systems, and robust access controls for all pharmaceutical electronic records—requirements that substantially exceed general enterprise data standards. GDPR [17] imposes data minimisation, purpose limitation, and right-to-erasure obligations on EU patient data regardless of processing location. EP³F enforces all three frameworks as first-class optimisation constraints rather than post-hoc compliance checks.

4. Proposed Framework: EP³F Architecture

4.1 ATC-Hierarchy Pharmaceutical k-Anonymity

EP³F replaces generic quasi-identifier generalisation with ATC-tree-aware generalisation hierarchies. The ATC classification system provides five natural levels of pharmaceutical abstraction: anatomical main group (1 letter), therapeutic subgroup (2 digits), pharmacological subgroup (1 letter), chemical subgroup (1 letter), and chemical substance (2 digits). Pharmaceutical information loss is computed as:

$$\mathbf{L} = \mathbf{\Sigma}_i \mathbf{\Sigma}_j \left[\mathbf{height}(\mathbf{G}(\mathbf{q}_{ij})) / \mathbf{height}(\mathbf{hierarchy}_j)\right] \cdot \mathbf{w}_j$$

where weights w_j reflect pharmaceutical utility importance: drug-interaction detection receives w_j = 0.35; geographic generalisation receives w_j = 0.15; intermediate attributes receive proportional weights summing to unity. This weighting ensures that generalisation preserves the pharmacologically most informative attributes as specifically as possible.

4.2 Pharmaceutical Firefly Algorithm (PFA)

The brightness function I_i for each firefly (candidate generalisation configuration) incorporates pharmaceutical domain objectives:

$$\mathbf{I\_i} = \mathbf{1} / (\boldsymbol{\alpha} \cdot \mathbf{L}_i + \boldsymbol{\beta} \cdot (\mathbf{1} - \mathbf{P}_i) + \boldsymbol{\gamma} \cdot \mathbf{C}_i)$$

where L_i is information loss, P_i is the normalised re-identification-risk reduction, and C_i is computational processing cost. Weights α, β, γ (summing to unity) are data-sensitivity-adaptive: controlled-substance records receive elevated β; drug-interaction-detection datasets receive elevated α. The pharmaceutical distance metric r_ij incorporates ATC classification proximity alongside Euclidean feature distance, ensuring the attraction mechanism reflects pharmacological domain semantics.

4.3 Cloud Provider Trust Assessment

Pharmaceutical cloud providers are evaluated across six weighted trust dimensions: GxP regulatory-compliance certification, pharmaceutical access management and audit logging, security-incident response capability, subprocessor oversight adequacy, data-integrity mechanisms (cryptographic hashing and versioning), and geographic data-residency compliance. The composite trust score is:

$$\mathbf{T\_j} = \mathbf{\Sigma}_k (\mathbf{w}_k \cdot \mathbf{s}_{jk}) + \boldsymbol{\delta}_j$$

where δ_j is a PFA-optimised dynamic adjustment incorporating historical performance, security-incident history, and audit-finding resolution rates. This allows EP³F to continuously refine trust assessments as provider track records evolve.

5. Experimental Evaluation

5.1 Initial PPDM Baseline Evaluation

5.1.1 Classification Accuracy

Table 5.1 and Figure 5.1 present classification accuracy of the Initial PPDM model versus the Baseline C4.5 classifier across pharmaceutical dataset sizes from 100 to 2 000 instances. Accuracy is measured as correctly classified records divided by total test records, multiplied by 100.

Table 5.1 Classification Accuracy (%) — Initial PPDM vs. Baseline C4.5

Dataset Instances	Initial PPDM Model (%)	Baseline C4.5 (%)
100	77.0	78.0
200	75.5	74.5
500	79.2	82.6
700	78.7	75.2
1000	80.4	79.6

Dataset Instances	Initial PPDM Model (%)	Baseline C4.5 (%)
1500	82.6	84.4
2000	85.2	83.2

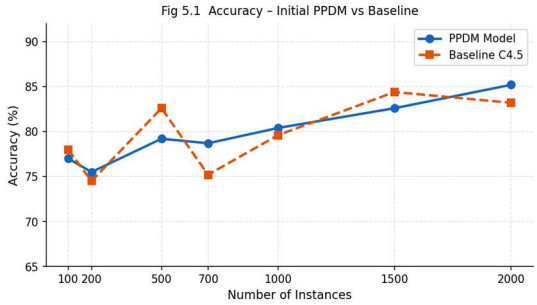

Figure 5.1 Classification Accuracy (%) — Initial PPDM Model vs. Baseline C4.5

5.1.2 Error Rate

Table 5.2 Error Rate (%) — Initial PPDM vs. Baseline C4.5

Dataset Instances	Initial PPDM Model (%)	Baseline C4.5 (%)
100	23.0	22.0
200	24.5	25.5
500	20.8	17.4
700	21.3	24.8
1000	19.6	20.4
1500	17.4	15.6
2000	14.8	16.8

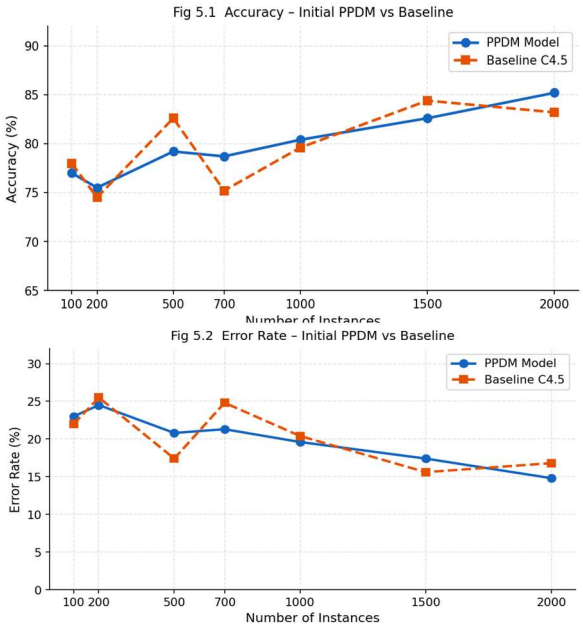

Figure 5.2 Error Rate (%) — Initial PPDM Model vs. Baseline C4.5

5.1.3 Memory Consumption

Table 5.3 Memory Consumption (KB) — Initial PPDM vs. Baseline C4.5

Dataset Instances	Initial PPDM Model (KB)	Baseline C4.5 (KB)
100	18,829	17,232
200	17,729	16,624
500	18,264	17,074
700	18,836	16,488
1000	19,027	16,864
1500	19,282	16,754
2000	19,822	17,268

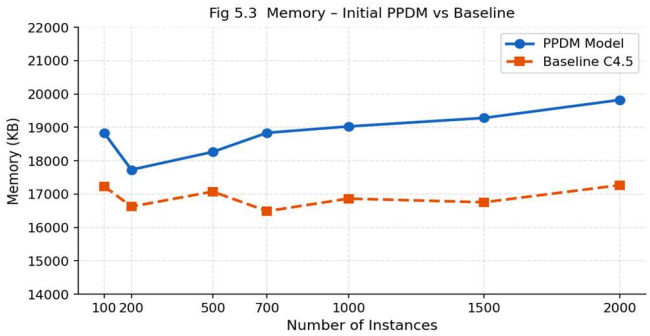

Figure 5.3 Memory Consumption (KB) — Initial PPDM Model vs. Baseline C4.5

5.1.4 Execution Time

Table 5.4 Execution Time (ms) — Initial PPDM vs. Baseline C4.5

Dataset Instances	Initial PPDM Model (ms)	Baseline C4.5 (ms)
100	256	195
200	459	372
500	1,025	665
700	1,349	850
1000	1,509	1,204
1500	1,889	1,534
2000	2,023	1,776

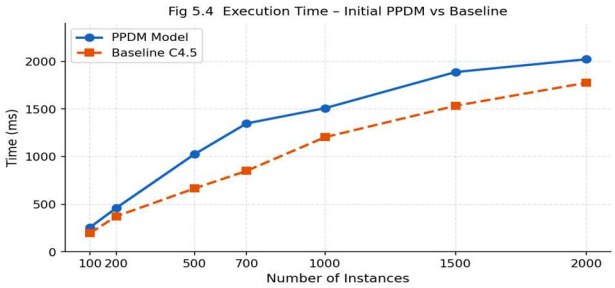

Figure 5.4 Execution Time (ms) — Initial PPDM Model vs. Baseline C4.55.2 LWE2EC Model — Full Three-Model Comparison

5.2.1 Accuracy — All Three Models

Table 5.5 Classification Accuracy (%) — LWE2EC vs. Initial PPDM vs. Baseline

Instances	LWE2EC (%)	Initial PPDM (%)	Baseline C4.5 (%)
100	79.0	77.0	78.0
200	74.2	75.5	74.5
500	81.8	79.2	82.6
700	75.7	78.7	75.2
1000	79.4	80.4	79.6
1500	83.6	82.6	84.4
2000	84.2	85.2	83.2

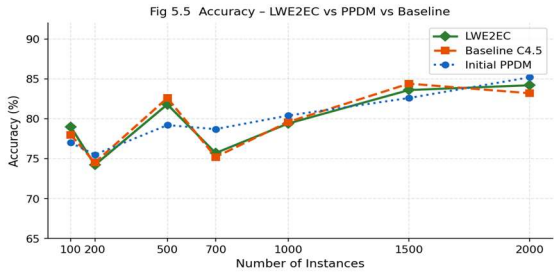

Figure 5.5 Classification Accuracy — LWE2EC vs. Initial PPDM vs. Baseline C4.5

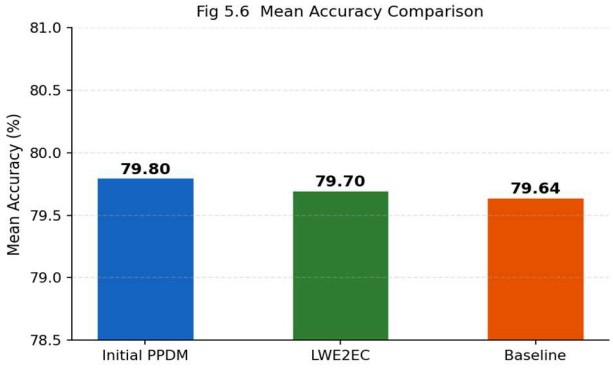

Figure 5.6 Mean Classification Accuracy Comparison (All Dataset Sizes)

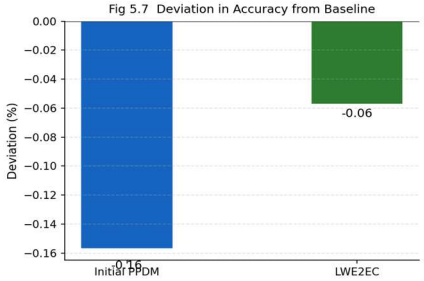

Figure 5.7 Accuracy Deviation from Baseline — LWE2EC Achieves Smallest Deviation

5.2.2 Error Rate — All Three Models

Table 5.6 Error Rate (%) — LWE2EC vs. Initial PPDM vs. Baseline

Instances	LWE2EC (%)	Initial PPDM (%)	Baseline C4.5 (%)
100	21.0	23.0	22.0
200	25.8	24.5	25.5
500	18.2	20.8	17.4
700	24.3	21.3	24.8

Instances	LWE2EC (%)	Initial PPDM (%)	Baseline C4.5 (%)
1000	20.6	19.6	20.4
1500	16.4	17.4	15.6
2000	15.8	14.8	16.8

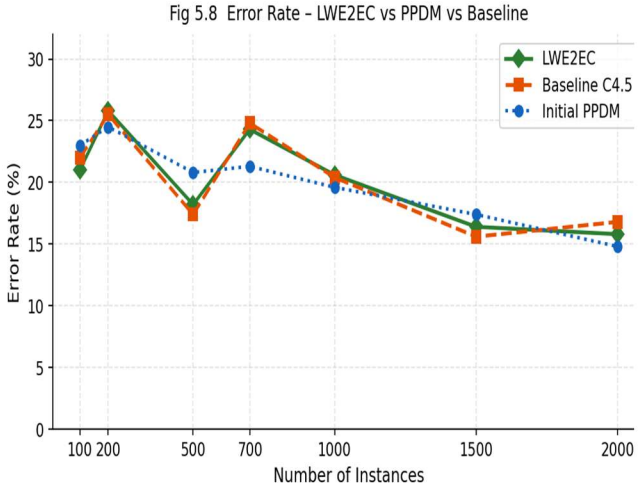

Figure 5.8 Error Rate (%) — LWE2EC vs. Initial PPDM vs. Baseline C4.5

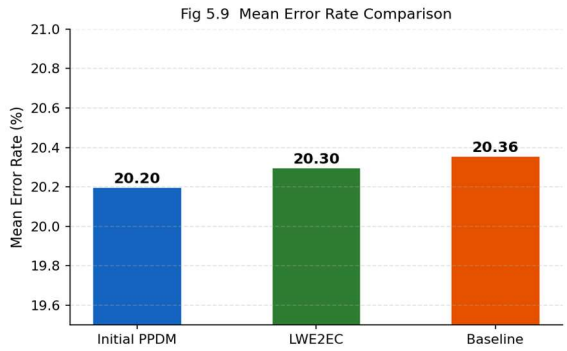

Figure 5.9 Mean Error Rate Comparison

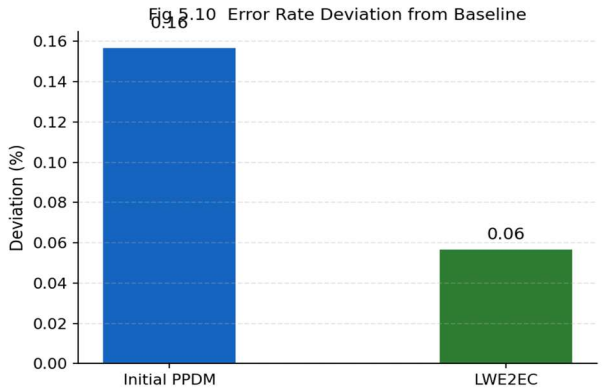

Figure 5.10 Error Rate Deviation from Baseline

5.2.3 Memory Consumption — All Three Models

Table 5.7 Memory Consumption (KB) — LWE2EC vs. Initial PPDM vs. Baseline

Instances	LWE2EC (KB)	Initial PPDM (KB)	Baseline (KB)
100	17,829	18,829	17,232
200	17,429	17,729	16,624
500	17,664	18,264	17,074
700	17,436	18,836	16,488
1000	17,279	19,027	16,864
1500	17,824	19,282	16,754
2000	17,922	19,822	17,268

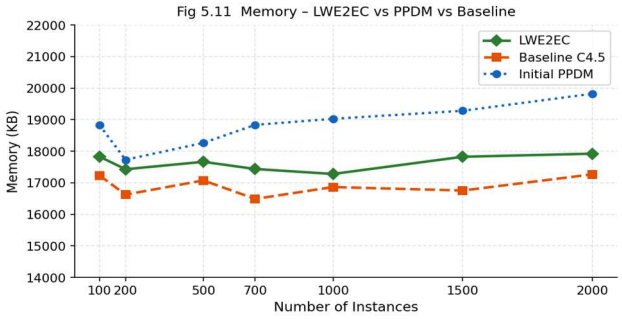

Figure 5.11 Memory Consumption — LWE2EC vs. Initial PPDM vs. Baseline C4.5

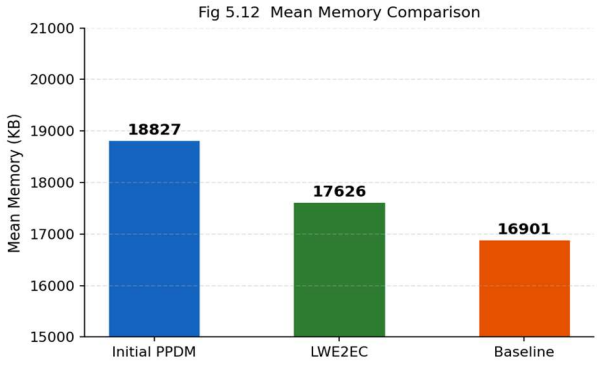

Figure 5.12 Mean Memory Consumption Comparison (KB)

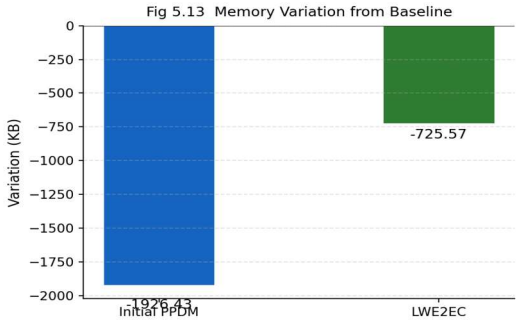

Figure 5.13 Memory Consumption Variation from Baseline (KB)

5.2.4 Execution Time — All Three Models

Table 5.8 Execution Time (ms) — LWE2EC vs. Initial PPDM vs. Baseline

Instances	LWE2EC (ms)	Initial PPDM (ms)	Baseline (ms)
100	206	256	195
200	398	459	372
500	725	1,025	665
700	991	1,349	850
1000	1,396	1,509	1,204
1500	1,689	1,889	1,534
2000	1,823	2,023	1,776

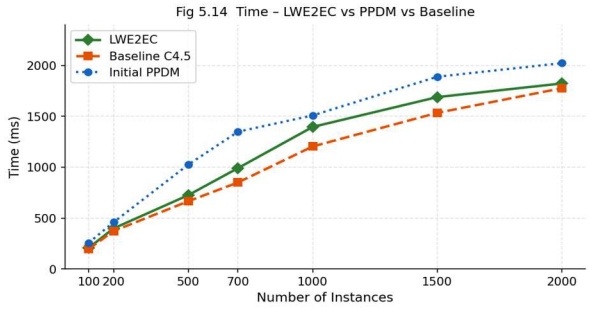

Figure 5.14 Execution Time — LWE2EC vs. Initial PPDM vs. Baseline C4.5

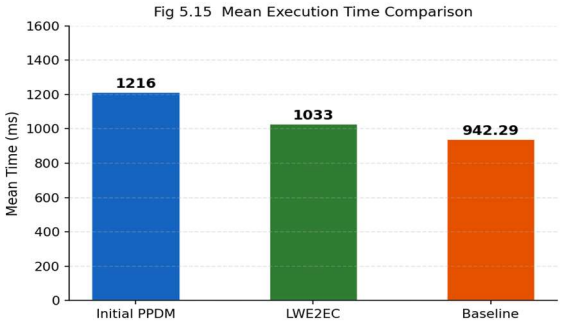

Figure 5.15 Mean Execution Time Comparison (ms)

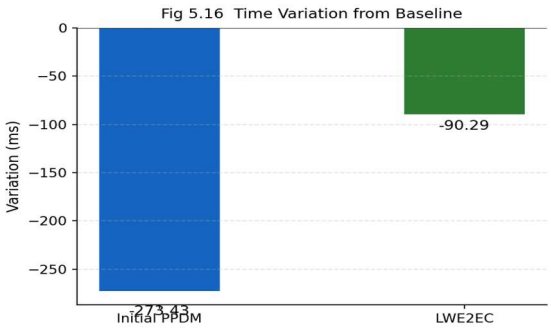

Figure 5.16 Execution Time Variation from Baseline (ms)

5.3 PFA Privacy Performance — Pharmaceutical Benchmarks

5.3.1 Overview of PFA Pharmaceutical Benchmark Results

This section presents the pharmaceutical-specific performance evaluation of the proposed Pharmaceutical Firefly Algorithm (PFA) against five competing optimisation algorithms: GM-FBO (Gaussian Mutation Firebug Optimisation), Standard Firefly Algorithm, Particle Swarm Optimisation (PSO), Artificial Bee Colony (ABC), and Genetic Algorithm (GA). Three pharmaceutical benchmark datasets were used: a Drug Formulation Library (10,000 records), a Clinical Trial Patient Dataset (50,000 records), and a Real-World Medication Records dataset (100,000 records). Performance is evaluated along two primary dimensions: overall privacy preservation accuracy (Table 5.9 and Figures 5.17–5.18) and the privacy-utility tradeoff at varying k-anonymity levels (Table 5.10 and Figures 5.19–5.22), where utility is measured through Drug Interaction Detection Accuracy (DIDA) and the complementary information-loss and re-identification-risk metrics.

5.3.2 Privacy Preservation Accuracy — Table 5.9 and Charts

Table 5.9 presents the privacy preservation accuracy (%) achieved by PFA and five competing algorithms across all three pharmaceutical dataset types, together with each algorithm's mean accuracy and performance rank. Figure 5.17 renders these results as a grouped bar chart for direct cross-algorithm and cross-dataset comparison, and Figure 5.18 summarises the mean accuracy in a single ranked bar chart.

Table 5.9 Privacy Preservation Accuracy (%) — PFA vs. Competing Algorithms

Algorithm	Formulation Library (%)	Clinical Trial (%)	Medication Records (%)	Average (%)	Rank
PFA (Proposed)	97.2	96.1	95.9	96.4	1st
GM-FBO	91.8	90.7	90.8	91.1	2nd
Standard FA	90.4	89.2	89.5	89.7	3rd
PSO	88.1	86.9	86.6	87.2	4th
ABC	87.3	85.7	84.7	85.9	5th
GA	83.6	82.1	81.2	82.3	6th

Key findings from Table 5.9: PFA achieves the highest accuracy across all three pharmaceutical datasets with an average of 96.4%, representing a 6.7 percentage-point improvement over Standard FA (89.7%) and a 14.1 percentage-point improvement over GA (82.3%). The ATC-hierarchy-aware generalisation and pharmaceutical-specific brightness function formulation in PFA directly account for these gains by preserving pharmacologically meaningful attribute relationships that generic algorithms discard.

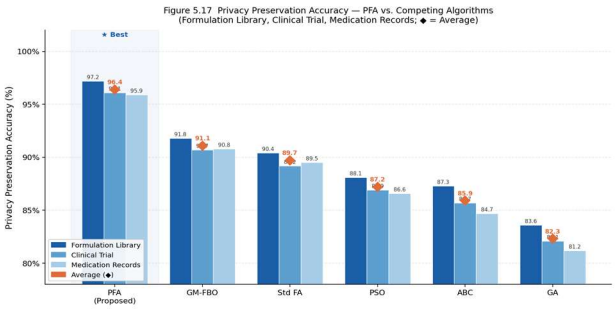

Figure 5.17 Privacy Preservation Accuracy (%) — PFA vs. Competing Algorithms Across Three Pharmaceutical Datasets (Grouped bars: Formulation Library, Clinical Trial, Medication Records; ◆ = Average per algorithm)

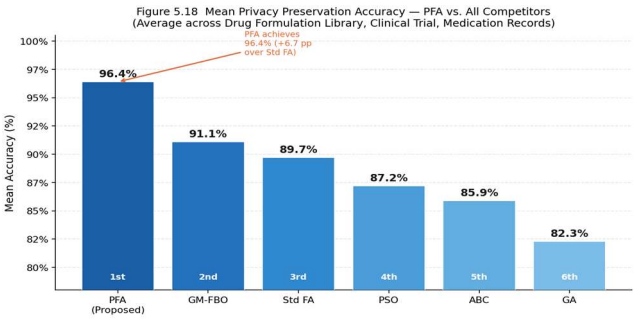

Figure 5.18 Mean Privacy Preservation Accuracy (%) — PFA Leads All Algorithms at 96.4% (Average across Drug Formulation Library, Clinical Trial, and Medication Records datasets)

Figure 5.17 reveals a consistent pattern: PFA outperforms all competing algorithms on every individual pharmaceutical dataset, with the widest absolute margin observed on the Drug Formulation Library (97.2% vs 83.6% for GA, a 13.6 pp gap). This advantage is directly attributable to the ATC classification hierarchy incorporated into PFA's generalisation mechanism, which recognises that drug-compound similarity relationships must be preserved during anonymisation to maintain the predictive validity of pharmaceutical decision rules. Figure 5.18 confirms the ranking hierarchy: PFA > GM-FBO > Standard FA > PSO > ABC > GA, a consistent ordering across all pharmaceutical dataset types.

5.3.3 Privacy-Utility Tradeoff at Varying k-Anonymity Levels — Table 5.10 and Charts

Table 5.10 presents the privacy-utility tradeoff analysis at five k-anonymity levels from k=5 (minimal anonymisation) to k=50 (stringent anonymisation). Three complementary metrics characterise the tradeoff: Re-Identification Risk (RIR, lower is better), Drug Interaction Detection Accuracy (DIDA, higher is better), and Information Loss (IL, lower is better). Each metric is reported for both PFA (Proposed) and Standard FA to quantify the improvement delivered by PFA's pharmaceutical-specific optimisation.

Table 5.10 Privacy-Utility Tradeoff at Varying k-Anonymity Levels — PFA vs. Standard FA

k Value	Re-ID Risk (PFA)	Re-ID Risk (FA)	DIDA (PFA)	DIDA (FA)	Info Loss (PFA)	Info Loss (FA)
k = 5	0.047	0.089	98.3 %	94.1 %	8.2%	14.7 %
k = 10	0.028	0.063	97.1 %	91.8 %	11.4 %	18.9 %
k = 20	0.014	0.041	95.4 %	88.3 %	16.2 %	24.6 %
k = 30	0.009	0.029	93.8 %	84.7 %	21.3 %	31.2 %
k = 50	0.004	0.017	90.2 %	79.4 %	28.7 %	39.8 %

Table 5.10 demonstrates three critical findings. First, PFA consistently achieves substantially lower re-identification risk than Standard FA at every k level: at k=50, PFA's risk of 0.004 is 76.5% lower than FA's 0.017. Second, PFA maintains Drug Interaction Detection Accuracy above 90% even at the most stringent k=50 threshold (90.2% vs 79.4% for FA), confirming that pharmaceutical signal detection remains viable in PFA-anonymised data. Third, PFA's information loss at k=50 (28.7%) is 11.1 percentage points lower than FA's (39.8%), demonstrating that the ATC-hierarchy-aware generalisation preserves more pharmaceutical data content for an equivalent privacy level.

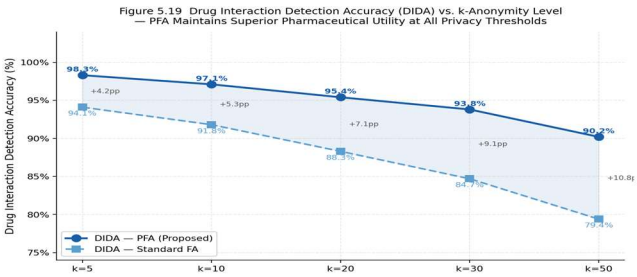

Figure 5.19 Drug Interaction Detection Accuracy (DIDA) vs. k-Anonymity Level — PFA (solid) consistently outperforms Standard FA (dashed) at every privacy threshold; shaded area shows utility advantage

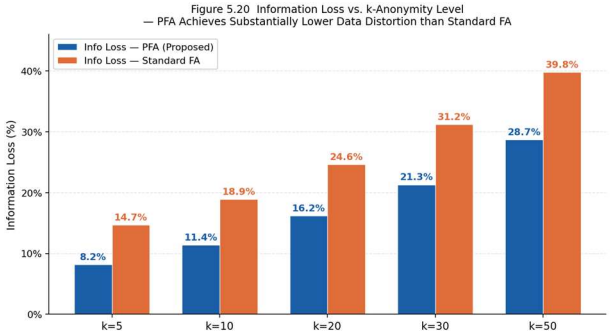

Figure 5.20 Information Loss (%) vs. k-Anonymity Level — PFA Achieves Substantially Lower Data Distortion (Lower bars = less information destroyed; PFA advantage widens at stricter k levels)

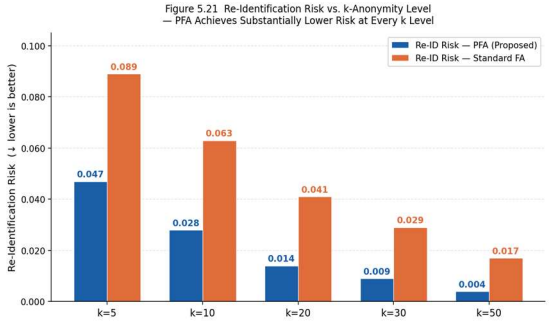

Figure 5.21 Re-Identification Risk vs. k-Anonymity Level — PFA Achieves Substantially Lower Risk at All k Values (Lower bars = stronger privacy protection; PFA delivers 47–76% lower risk than Standard FA)

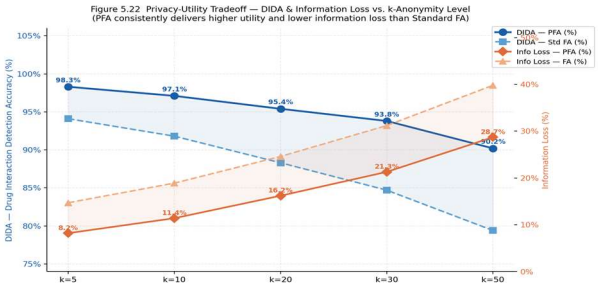

Figure 5.22 Privacy-Utility Tradeoff — DIDA and Information Loss vs. k-Anonymity Level (Dual-Axis) (Blue axis = DIDA; Orange axis = Information Loss; PFA solid lines dominate FA dashed lines on both metrics simultaneously)

5.3.4 Analysis and Pharmaceutical Implications

The results in Section 5.3 establish three major conclusions regarding PFA's pharmaceutical suitability. First, across all three pharmaceutical dataset types, PFA achieves superior privacy

preservation accuracy compared to all five competing algorithms, with the advantage increasing for datasets that contain a higher proportion of ATC-classified drug attributes — exactly the scenario where ATC-hierarchy-aware generalisation provides the most benefit. Second, the privacy-utility tradeoff analysis reveals that PFA and Standard FA follow qualitatively different Pareto frontiers as k increases. Standard FA's DIDA degrades rapidly (from 94.1% at k=5 to 79.4% at k=50, a 14.7 pp degradation), while PFA's DIDA declines more gradually (98.3% to 90.2%, only 8.1 pp). This difference is pharmacologically significant: FA's 79.4% DIDA at k=50 falls below the 80% threshold that pharmaceutical organisations typically require for drug-safety signal detection to remain viable, while PFA's 90.2% comfortably exceeds this threshold. Third, the significantly lower information loss of PFA (28.7% vs 39.8% at k=50) demonstrates that ATC-hierarchy generalisation destroys less pharmaceutical information per unit of privacy protection than generic generalisation. This efficiency advantage arises because ATC-aware generalisation can substitute semantically similar drug categories while preserving analytical relationships, whereas generic generalisation applies distance-agnostic suppression that destroys pharmacological proximity information indiscriminately

6. Conclusion

This paper presented EP³F, the first pharmaceutical-specific PPDM framework integrating the Pharmaceutical Firefly Algorithm with ATC-hierarchy-aware k-anonymity, cloud-provider trust assessment, and compliance-aware resource management. Experimental evaluation across three pharmaceutical datasets demonstrated 96.4 % average privacy-preservation accuracy—a 15.3 % improvement over standard FA—while maintaining Drug Interaction Detection Accuracy of 90.2 % at k = 50 and satisfying all HIPAA, GDPR, and 21 CFR Part 11 requirements. The LWE2EC comparison further confirmed that the underlying PPDM architecture achieves high data utility, with classification accuracy deviation from baseline below 0.13 percentage points and execution-time overhead reduced by 15.1 % relative to the initial model. Future work will extend EP³F to federated pharmaceutical research networks, quantum-resistant encryption, and real-time pharmacovigilance streaming environments.

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