# RGeneSSE: Privacy Preserving Genomic Interval Queries via Range Searchable Symmetric Encryption on Dynamic Databases

Blinded For Review

*Abstract*—**Advances in Next Generation Sequencing (NGS) technologies have made large-scale genomic data generation both rapid and cost-effective, fueling critical applications in personalized medicine, ancestry analysis, and Genome-Wide Association Studies (GWAS). However, outsourcing genomic data to untrusted cloud environments poses severe privacy risks, as existing protection mechanisms either compromise utility (e.g., through differential privacy) or impose prohibitive computational overhead (e.g., via homomorphic encryption or secure multi-party computation).**

**In this work, we investigate the technical feasibility of privacy-preserving genomic interval queries and present a scalable encrypted range query framework for large genomic databases. Our approach builds on Searchable Symmetric Encryption (SSE) and introduces a new interpretation of encrypted range queries as disjunctions of canonical range covers, enabling efficient realization through a dynamic disjunctive SSE primitive.**

**We design `GeneSSE`, the first dynamic disjunctive SSE scheme offering linear storage overhead, constant-time updates, and sub-linear search complexity, while ensuring forward privacy and Type-I backward privacy. Building upon `GeneSSE`, we construct a multi-attribute range SSE scheme (called `RGeneSSE`) that mitigates leakage vectors exploited by recent range query attacks while also supporting dynamic encrypted databases. Our formal security analysis and prototype implementation demonstrate that efficient, leakage-resilient, and privacy-preserving genomic interval queries are practically realizable, establishing the feasibility of secure and scalable encrypted genomic data analytics**

**Furthermore beyond computational biology, our techniques enable efficient, privacy-preserving range-based and general Boolean queries over large-scale encrypted dynamic databases.**

## 1. Introduction

**Outsourcing Genomic Data and Privacy Threats.** With the completion of the Human Genome Project and the advent of Next Generation Sequencing (NGS) technologies, sequencing the entire human genome has become both faster and more affordable, leading to an unprecedented surge in genomic data collection and analysis. This revolution has enabled transformative applications in personalized medicine, disease prediction, ancestry characterization, and genetic compatibility testing, motivating research institutions, healthcare providers, and commercial entities to increasingly outsource genomic data storage and computation to third-party cloud infrastructures for their scalability and cost efficiency [1]. However, this outsourcing paradigm introduces serious privacy and security risks, as genomic data is inherently identifiable and encodes sensitive information about an individual's disease susceptibility, ancestry, and phenotypic traits, as well as that of their biological relatives. Even anonymized genomic datasets are vulnerable to re-identification attacks, exemplified by the Golden State Killer case[1], where genetic identification was performed through a relative's data in a public genealogy database; or the hacking of personal data of more than $14,000$ users of the genetic testing company 23andMe, where the stolen information comprised individuals' names, years of birth, familial relationship tags, proportions of shared DNA with relatives, ancestry profiles, and their self-reported locations[2]. The privacy threat becomes even more acute when digital genomic data undergoes bioinformatics processing, including sequence alignment, variant querying, or large-scale genomic database searches on untrusted cloud platforms. For instance, consider a patient, Alice, who stores her sequenced genome on the cloud and consults a testing service run by Bob, who wishes to query her genome using publicly known disease markers to assess her risk for specific conditions. While Bob's computation is medically valid, Alice cannot trust his infrastructure not to misuse or leak her data, as sharing her raw genome would expose her complete biological blueprint, and even anonymization cannot prevent re-identification. Such scenarios underscore the urgent need for privacy-preserving cryptographic frameworks that allow secure computation, such as disease testing or genetic compatibility analysis over encrypted genomic data, ensuring that neither the service provider nor the underlying cloud gains access to sensitive genetic information while enabling scalable and trustworthy genomic analytics.

**Privacy Preserving Genomic Data Processing.** A variety of privacy-preserving techniques have been developed to secure genomic data processing, broadly categorized into cryptographic and statistical obfuscation-based approaches. Early cryptographic works, such as those by Atallah et al. [2], Jha et al. [3], and Troncoso-Pastoriza et al. [4],

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focused on privacy-preserving sequence comparison and pattern matching through secure two-party computation and garbled circuits [5] (GC). Subsequent research extended these ideas using homomorphic encryption (HE) and private set intersection (PSI) protocols [6], enabling privacy-preserving analyses for genetic compatibility testing, paternity verification, and disease-risk assessment. In parallel, differential privacy (DP) [7], [8], [9] has been employed to protect summary-level genomic statistics (e.g., minor allele frequencies, chi-square values) against membership inference attacks, though the added noise required for formal privacy guarantees often degrades data utility. More recent advances leverage powerful cryptographic frameworks such as secure multiparty computation (SMC) [10], [11], fully homomorphic encryption (FHE) [12], [13], [14], and hardware-assisted trusted execution environments (TEEs) [15], [16], [17], [18], [19] to provide privacy guarantees dependent on hardware assumptions.

Despite their promise, these methods face significant *limitations*: (1) SMC protocols introduce substantial communication/computation overhead, and require practical realization of the non-collusion assumption among its parties; (2) FHE-based schemes remain computationally expensive for large-scale genomic analyses, as the bootstrapping overhead scales with circuit size; (3) the injected noise in DP (needed for higher privacy budgets) often degrades data utility; (4) GC require re-running the expensive setup *every* circuit execution; and (5) TEEs are susceptible to side-channel and memory access-pattern leakage. Moreover, interoperability across heterogeneous cryptographic frameworks remains limited, as most solutions address specific genomic operations in isolation. This motivates the need for scalable, interoperable, and computation-efficient cryptographic frameworks that can support diverse genomic data analyses while preserving privacy end-to-end, thereby enabling secure, large-scale genomic research and applications without compromising individual confidentiality.

**Motivation and Goals.** In this work we focus on genomic interval queries: that are among the most common and powerful operations in bioinformatics, enabling analysts to retrieve and analyze genomic features (e.g., variants, genes, exons, regulatory elements) that overlap specific coordinate ranges. These queries are central to a wide spectrum of analyses, from identifying disease-associated mutations and annotating genomic variants to inspecting read coverage in NGS data and performing comparative genomics. However, performing such interval queries securely over outsourced or shared genomic databases presents serious privacy challenges. Traditional privacy-preserving methods, such as DP, while suitable for computing aggregated statistics, are unsuitable for precise range queries due to their accuracy loss through noise injection; whereas cryptographic methods like FHE, GC or SMC remain computationally prohibitive for large genomic datasets or require assumptions like non-collusion. Moreover, the access patterns in interval queries leak sensitive information about queried genomic regions or individual genotypes, negating the potential usage of TEEs.

Therefore, there is a pressing need for an encrypted genomic interval query framework that supports the following *goals*: (1) efficient, fine-grained range search directly on encrypted genomic data while preserving (2) query privacy, (3) access pattern confidentiality, and (4) scalability to large size genomic databases. Such a framework would enable secure retrieval of genomic records within specific coordinate ranges, such as *"fetch all SNPs in chr1:800000–801000"*, without revealing the query content or underlying genomic information, thereby bridging the gap between practical usability and strong cryptographic privacy guarantees in real-world genomic data analytics.

**Our Contribution.** The goal of this work is to evaluate the technical feasibility of implementing privacy-preserving genomic interval queries. With the established shortcomings of existing approaches (like FHE, GC, SMC, and TEEs), we investigate the applicability of a different cryptographic primitive to the problem of genomic interval queries. Towards this end we make the following contributions:

- **Cryptographic Design.** As a first step toward realizing privacy-preserving genomic interval queries, we translate this problem into a well-defined set of technical requirements and propose a novel cryptographic protocol that fulfills them. Conceptually, we interpret a genomic interval query (example: "*retrieve all variants within chr1:8000000-801000*") as a *range query* (i.e. *8000000-801000*) over a variable (i.e. *chr1*) in encrypted data. Thereafter, we connect the realization of such encrypted range queries to Searchable Symmetric Encryption (SSE), by representing encrypted range searches on genomic data as *disjunctions of canonical range covers* on carefully constructed range-tree data structures. Usage of SSE to realize genomic interval queries fulfills our intended *goals*: (1) careful problem definition allows genomic searches through SSE, thereby ensuring privacy; our SSE protocol ensures (2) query privacy and (3) access pattern confidentiality, while resisting state-of-the-art attacks and (4) being scalable to large databases. Beyond secure data retrieval, usage of SSE also allows seamless application to a range of downstream analyses, including disease-associated mutation detection, variant annotation, read coverage inspection in next-generation sequencing (NGS) data, and comparative genomics, since such applications are also interpretable as range searches. To the best of our knowledge, this is the first cryptographic framework to address privacy-preserving genomic interval queries through practical SSE.
- **Dynamic and Leakage-Resilient Range SSE.** We design a novel SSE protocol- `GeneSSE`- to act as the foundation of our privacy-preserving genomic interval queries. `GeneSSE` builds upon [20] but with crucial improvements: (1) we append the capability of operating over dynamic databases; and (2) we remove the requirement in [20] where *a-priori* knowledge of keyword frequencies is known. Both these improvements allow for practical databases where ge-

nomic information needs to be added as gene mapping extends to wider populations. `GeneSSE` achieves (i) linear storage overhead, (ii) constant-time updates, and (iii) sub-linear search complexity, while providing (iv) forward privacy and (v) Type-I backward privacy, properties that may be of independent interest. Thereafter, building upon `GeneSSE` as a black-box, we design a leakage resistant range SSE scheme (named `RGeneSSE`) supporting scalable multi-attribute range queries. `RGeneSSE` adopts a range-tree-based query decomposition approach similar to [21], but significantly strengthens privacy by mitigating critical leakage vectors specifically structure, volume, and search pattern leakages that prior designs are vulnerable to. *By translating genomic interval queries to range searches and transitively reducing them to disjunctions over canonical covering nodes* of a range-tree, our `RGeneSSE` achieves efficient, privacy-preserving range search on dynamic encrypted genetic databases while resisting state-of-the-art leakage-abuse attacks [21]. Further details are provided in Sections 2 and 3. We give a detailed analysis of the attacks in [21] and demonstrate that our proposed range SSE scheme is robust and resistant to these attacks.

- **Security Analysis and Implementation.** We present a detailed analysis of the leakage profile for `GeneSSE` and `RGeneSSE`, and prove their security formally. We practically validate the performance of `GeneSSE` by evaluating and comparing its search performance over the Enron email corpus with [20], [22], [23]. We also present a prototype implementation of `RGeneSSE` over genomic database maintained by the Large Scale Genomics work stream of the Global Alliance for Genomics & Health (GA4GH), containing 1.930GB of data in VCF 4.2 format with $3,893,572$ records. The search overhead for finding ranges of magnitude over $10^4$ is around 0.12 seconds. The experimental results are analyzed in detail in Section 4.

## 1.1. Mapping Genomic Interval Queries into Range Searches through SSE

**Variant Call Format (VCF) Specification**. In this work, we closely follow the Variant Call Format Specification (v4.5)[3] for the specification of the genomic dataset. A sample is given in Figure 1. Each record has 8 fields: (1) `CHROM` that marks the chromosome number from the reference genome; (2) `POS` referring to the reference position *within* each `CHROM`; (3) unique identifier `ID`; (4) a reference base `REF` that can take one value out of A, C, G, T, N; (5) an alternate base `ALT`; (6) quality `QUAL` wrt. the assertion made in `ALT`; (7) whether the chromosome position has passed all filters; and (8) additional information.

A **trivial search** over such dataset could be realized as such: use a multi-attribute search protocol over the attributes `CHROM` and `POS`, to return all records within the designated

chromosomes. This approach has a crucial drawback: For $n$ chromosomes and $m$ positions within each chromosome, such a trivial approach requires $O(n \cdot m)$ search queries[4].

We however assert a further constraint from the dataset specification: **the positions `POS` within each chromosome `CHROM` are *sorted* numerically**. Thus instead of $O(n \cdot m)$ search queries using a multi-attribute search protocol, one could use $O(n)$ queries using a multi-attribute *range* search protocol and achieve the same result. Moreover, if the chromosomes of interest are also adjacent, a *single* (i.e. $O(1)$) range search *two* attributes, `CHROM` and `POS`- suffices. Thus, exploiting the structure of the VCF specification allows for mapping genomic interval queries to range searches, that leads to an asymptotic reduction in search queries executed.

**Privacy-Preserving Range Searches**. Next up is the question of performing such range searches on encrypted genomic datasets following the VCF specification; for that, we choose to rely on Searchable Symmetric Encryption (SSE). SSE [24], [25], [26], [27], [28] enables a resource-constrained client to perform keyword searches *directly* over symmetrically encrypted document collections stored on an *untrusted* server. While the strongest security guarantees are achievable via ORAM techniques [29], they incur substantial computational and communication overheads. Consequently, most practical SSE schemes trade off full obliviousness for efficiency by allowing limited leakage, such as database size, query, and access patterns, often mitigated using optimized ORAM variants [30], [31], [32], [33] or hardware-based approaches like Intel SGX [34], though the latter's security remains under active scrutiny [35], [36].

Prior research has extended SSE to support expressive queries such as conjunctions, disjunctions, Boolean, and range queries. Here, we focus exclusively on range queries because of the considered use-case. Faber et al. [37] proposed a range SSE scheme based on OXT [27], but it failed to account for false positives under data skewness—later addressed by Demertzis et al. [38], [39] through their Logarithmic SRC-$i_1$ and SRC-$i_2$ schemes. However, these constructions are limited to (1) single-attribute (1-D) queries and (2) static databases, *both unsuitable for genomic datasets investigated here.* Subsequent works [34], [40], [41], [42], [43], [44], [45], [46], [47], [48] also support only 1-D queries, while others [49], [50], [51], [52], [53] enable multi-attribute range queries on dynamic databases. Nevertheless, most existing range SSE schemes, static or dynamic, single or multi-attribute remain vulnerable to leakage abuse attacks, which are discussed next.

**Attacks on Range SSE.** Leakages in SSE schemes are typically classified as search, access, and volume patterns, which have been exploited in powerful database reconstruction attacks [54], [55], [56], [57]. For range queries, such leakages enable adversaries to infer plaintext order and values of encrypted records [46], [57], [58], [59], [60], [61],

```
#CHROM POS      ID         REF    ALT      QUAL FILTER INFO                                FORMAT     NA00001          NA00002          NA00003
20     14370    rs6054257  G      A        29   PASS   NS=3;DP=14;AF=0.5;DB;H2             GT:GQ:DP:HQ 0|0:48:1:51,51  1|0:48:8:51,51  1/1:43:5:.,.
20     17330    .          T      A        3    q10    NS=3;DP=11;AF=0.017                 GT:GQ:DP:HQ 0|0:49:3:58,50  0|1:3:5:65,3    0/0:41:3
20     1110696  rs6040355  A      G,T      67   PASS   NS=2;DP=10;AF=0.333,0.667;AA=T;DB   GT:GQ:DP:HQ 1|2:21:6:23,27  2|1:2:0:18,2    2/2:35:4
20     1230237  .          T      .        47   PASS   NS=3;DP=13;AA=T                     GT:GQ:DP:HQ 0|0:54:7:56,60  0|0:48:4:51,51  0/0:61:2
20     1234567  microsat1  GTC    G,GTCT   50   PASS   NS=3;DP=9;AA=G                      GT:GQ:DP   0/1:35:4         0/2:17:2         1/1:40:3
```

Figure 1: Sample of VCF v4.5

[62], [63], [64], [65], [66], [67], and are thereby disastrous for the use-cases of genomic data. Recent work by Falzon et al. [21] showed that existing multi-attribute range SSE schemes leak volume, search, and structure patterns, allowing near-complete reconstruction with minimal overhead. Defense strategies include hardware-based solutions using TEEs (e.g., Intel SGX) [68], [69], which remain vulnerable to side-channel attacks [70], [71], oblivious constructions like ORAM [29], [46], which are computationally expensive [72], [73], and protocol-level optimizations [37], [38], [39], [44], [45], [47], [48], [53], most of which remain vulnerable [21].

Despite extensive research, no existing work achieves a scalable, leakage-resilient, dynamic multi-dimensional range SSE resistant to recent inference attacks; thereby, to the best of our knowledge, existing range SSE schemes do not satisfy the expectations of privacy required for genomic applications. This motivates our central question:

*Can we design a ① leakage-resilient, ② dynamic SSE scheme that supports ③ multi-dimensional range queries while remaining ④ efficient and ⑤ scalable to large genomic databases?*

### 1.2. Technical Overview: `RGeneSSE`

In this work, we achieve all five objectives. We observe that existing range SSE schemes, which query the SSE index for each node in a range cover, are inherently leaky, necessitating a fundamental shift in perspective. To our knowledge, we are the first to employ a *disjunctive* SSE approach to realize range queries (objective ③ above). Specifically, we leverage `TWINSSE` [20], whose twin-index structure is well-suited to mitigating leakage in range searches (objective ① above). Since `TWINSSE` is originally designed for static databases, we introduce several non-trivial extensions to make it dynamic (objective ② above), without compromising its leakage-resilient structure. This enables the construction of a dynamic range SSE that supports multi-dimensional queries (objective ④ above) and is scalable to large genomic databases (objective ⑤ above). Our key contribution lies in this perspective shift, moving away from inherently leaky designs toward a robust and efficient dynamic range SSE framework for multi-attribute encrypted databases.

**Range queries via Dynamic, Disjunctive SSE: A new perspective.** Existing range SSE schemes relying on range-tree structures and range covers inherently suffer from *structure pattern leakages*, enabling inference of sub-query co-occurrences from individual search tokens.

We propose a paradigm shift in range SSE design. **Our key insight is that a range query can be *reduced to a disjunction* over the nodes of a range cover, enabling its execution via a *disjunctive SSE*.** Unlike prior approaches, this eliminates the need to issue separate searches for each node. In the dynamic database model, we show that such a dynamic disjunctive SSE scheme[5]- named `GeneSSE`- can securely execute such disjunctive queries over encrypted indexes to retrieve matching encrypted document identifiers. `GeneSSE` is then used to instantiate `RGeneSSE`, by reducing a range query to disjunctions over its range cover. This structural shift inherently mitigates structure pattern leakages and thwarts attacks like [21] by preventing leakage of individual token result volumes and prohibiting construction of a *volume map*, thus offering a "by-design" defense mechanism. However, there still remain roadblocks in concretely realizing range queries as disjunctions, which constitute the core problems we provably solve in this work.

*Problem-I (Leakages):* The main challenge is to hide the one-to-one mapping between covering nodes and search tokens in a disjunction. Although a generic disjunctive SSE prevents creation of a *volume map*, it still leaks the *overall* result volume and the memory access pattern of search tokens, enabling the server to infer token query frequencies across searches.

*Solution.* We instantiate `GeneSSE` in a similar manner as [20], thereby structurally mitigating overall volume pattern leakages [58], [62], [65] and outperforms state-of-the-art disjunctive SSE [22], [74] in storage while maintaining comparable search cost. `GeneSSE` supports general Boolean queries (CNF/DNF) using "super keywords" (specialized as "meta-keywords"), disjunctions of selected database keywords. A disjunctive query $q$ is transformed into a conjunctive query $q_{\mathsf{mkw}}$ of meta-keywords, executed via a conjunctive SSE oracle, returning a *super set* of the true result. This transformation (i) obfuscates the mapping between covering nodes and search tokens, and (ii) suppresses overall volume and access pattern leakages through `GeneSSE`'s design and proven security guarantees.

*Problem-II (Functionality):* While the construction in [20] supports disjunctions, it lacks support for dynamic updates. Hence, a black-box usage of [20] is impossible in the instantiation of `GeneSSE`.

*Solution.* One functional requirement for the construction in [20] is the a-priori knowledge of keyword frequencies: an assumption that is not practical for dynamic settings (like genetic databases, where functionality for modifications, e.g. addition of records, is paramount). We therefore propose a

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5. Closest to our approach is Faber et al. [37], which models range queries as disjunctions over a conjunctive SSE, resulting in inefficiencies, leakage, limited multi-attribute and functionality only over static databases.

| Notations | Meaning |
|---|---|
| $\lambda$ | security parameter |
| $n$ | maximum number of keywords in a disjunctive query |
| id | document identifier |
| w | a keyword |
| $N$ | Total number of records in the database |
| $\mathcal{W}$ | dictionary of keywords $\mathcal{W} = \{w_1, \dots, w_N\}$ |
| $\mathcal{D}$ | domain space |
| $d$ | total attributes in the database ($|\mathcal{D}|$) |
| attr | an attribute in $\mathcal{D}$ |
| val | value of an attribute corresponding to a record id |
| $\mathbb{W}$ | covering set of nodes |
| **DB** | database $(\text{id}_j, (\text{attr}_i, \text{val})_{i=1, j=1}^{d, N} \in \textbf{DB}$ |
| $|\textbf{DB}(w)|$ | number of documents containing w |
| T | range tree data structure that stores all attr-val pairs in **DB** |
| $v$ | node in the tree T |
| $\mathcal{R}_q$ or $\textbf{DB}(q)$ | result set returned to the client after a query $q$. |
| $x \xleftarrow{\$} \chi$ | uniformly sampling $x$ from $\chi$ |
| $x = \mathcal{A}$ | $x$ is output of a deterministic algorithm |
| $x \leftarrow \mathcal{A}'$ | $x$ is output of a randomized algorithm |
| $\mathbb{Z}_q^*$ | multiplicative group modulo some prime $q$ |
| $F$ | Pseudo-random function with output range in $\{0,1\}^\lambda$ |
| $F_p$ | Pseudo-random function with output range in a multiplicative group modulo prime $p$ |

TABLE 1: Notations

novel dynamic disjunctive SSE- `GeneSSE`- that eliminates the need for apriori keyword frequency knowledge, while preserving optimal update and search complexity and linear storage overhead. To our knowledge, `GeneSSE` is the first dynamic disjunctive SSE achieving (1) linear storage, (2) constant update, (3) sub-linear search, (4) forward privacy, and (5) Type-I backward privacy. Further details appear in Section 2. `RGeneSSE` is a natural extension thereof.

*Note.* To test the attack resilience of `RGeneSSE`, we adopt the attack framework of [21]: the most recent and efficient attack on multi-dimensional range queries. While prior works [46], [57], [59], [60], [61], [62], [63], [64], [65], [66], [67] primarily target 1-D settings (with limited 2-D exploration [66]) by exploiting search and volume patterns, [21] introduces an additional *structure pattern* leakage enabling highly efficient multi-attribute attacks. We therefore focus on defending against [21] and demonstrate robustness of our construction against search, volume, and structure pattern leakages.

**Notations and Other Prerequisites**: We describe the notations used throughout the paper in Table 1. We also capture detailed backgrounds for Dynamic SSE syntax/correctness/security in Appendix A, and overview of [20] in Appendix B due to lack of space.

## 2. `GeneSSE`: A Dynamic Disjunctive SSE

We now present our dynamic disjunctive SSE (i.e. `GeneSSE`) construction, that achieves (1) linear storage, (2) constant updates, (3) sub-linear search, and (4) forward and (5) backward privacy, the first such dynamic disjunctive SSE construction to our knowledge.

### 2.1. Challenges and Solutions

In the previous section, we gave an informal notions of the challenges in designing `GeneSSE`. We formalize them now.

**Challenge 1: Updating Multiple Meta-Keywords for Every Keyword Update.** Since `GeneSSE` is instantiated in

a manner similar to [20], it also has a notion of "meta-keywords". A meta-keyword $\text{mkw}_i$ is a disjunction of carefully chosen keywords from **DB** ($\text{mkw}_i = w_1 \vee \dots \vee w_n$). For a database with $N$ keywords, there exists an $O(N)$-sized set $\mathcal{S}$ of meta-keywords such that any disjunctive query $q = w_1 \vee \dots \vee w_n$ can be represented as a conjunction of meta-keywords $q' = \text{mkw}_1 \wedge \dots \wedge \text{mkw}_n$ with $\textbf{DB}(q) \subseteq \textbf{DB}(q')$ (see [20] for a formal proof). Such a "meta-keyword" construct suffices for static databases (like [20]), but immediately poses problems for dynamic databases (like `GeneSSE`). This is because each keyword w corresponds to $O(n'^2)$ meta-keywords[6], so a single keyword update would require $O(n'^2)$ meta-keyword updates, leading to quadratic overhead in update complexity, which is undesirable.

**Solution.** A naive approach of solving this problem could be to store $(\text{mkw}, w)$ pairs; however, this would leak the correspondence between keywords and meta-keywords, voiding the privacy guarantees of `GeneSSE`. Instead, in `GeneSSE`, we parameterize the bucket size $n' = O(1)$, which is sufficient in practice (e.g., 5–10 [20]). This choice preserves correctness, ensures asymptotic update complexity comparable to state-of-the-art literature, and incurs only a constant-factor slowdown, as formally proved in Theorem 1 and empirically validated in Section 4.

**Stronger Backward Privacy.** By updating all $O(n'^2)$ meta-keywords per keyword update, correlations between updates and keywords are eliminated. Consequently, `GeneSSE` achieves Type-I Backward Privacy[7], a stronger guarantee over Type-II Backward Privacy[8], as formally established in Appendix F.

**Challenge 2: Loss of Correctness from Multiple Keyword Updates in a Meta-Keyword.** Even after addressing Challenge 1, each meta-keyword mkw is updated for every update to its constituent keywords. This leads to a loss in correctness when multiple keywords update the same mkw. Example: If one meta-keyword $\text{mkw}_i$ contains two keywords $w_1$ and $w_2$, updates to $w_1$ risk updating the associations of $\text{mkw}_i$-$w_2$ unless careful design is enforced.

**Solution.** To prevent overwrites while preserving `GeneSSE`'s structural properties, we encode the w-mkw association in two components: (i) a blinding factor $\alpha$ stored in the inverted search index at the server, which uniquely identifies updates for each keyword; and (ii) a cross-term stored in the XSet, which is also computed obliviously by the server during conjunctive search operations. For each update, a unique xtag is generated that incorporates these components, *ensuring that updates from multiple keywords to the same meta-keyword do not interfere with each other*. In other words, for our example, updates to $w_1$ do not update the $\text{mkw}_i$-$w_2$ association. This design preserves all update information for all keywords, maintains the integrity

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6. Where $n'$ is the bucket size of keywords based on frequency, as originally in [20].

7. No correlation between an update operation and its corresponding keyword can be inferred

8. Leakage of correlations between an update and its keyword

of meta-keyword queries, and guarantees correctness of `GeneSSE`. Importantly, it avoids decomposing mkw into constituent keywords, which would otherwise leak keyword-to-meta-keyword associations and violate the privacy guarantees of `GeneSSE`(cf. Algorithm 3).

**Challenge 3: Apriori Knowledge of Keyword Frequency.** The original construction in [20] requires a-priori knowledge of keyword frequencies to construct the meta-keyword database, which is feasible only in the static database model. In a dynamic setting like genomic databases, genetic records (and thus keywords) are added or deleted over time, and their frequency depends on the sequence of updates, making black-box use of a static SSE infeasible.

**Solution.** In the static database construction [20], keyword frequencies are used for *ordered* bucketization to optimize search complexity by reducing the inclusion of high-frequency meta-keywords. This ordering, however, does not affect meta-keyword generation or query correctness. In `GeneSSE`, we adopt **unordered bucketization**, where keywords are adaptively assigned to buckets as they are added, while preserving correctness[9]. While unordered bucketization may include high-frequency meta-keywords in worst-case queries, empirical results in Section 4 show that average-case search complexity remains comparable to the static case with ordered bucketization [20]: being linear in the number of meta-keywords with the least updates in the query. This adaptation, though slightly increasing worst-case search cost, enables richer functionality by supporting fully dynamic databases.

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**Algorithm 1** `GeneSSE.Setup`
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**Input:** $\lambda$
**Output:** sk, st, **EDB**
1: **function** GeneSSE.SETUP($\lambda$)
2:     **Client**
3:     Sample a uniformly random key $K_T$ for PRF $F$
4:     Sample uniformly random keys $K_X, K_Y, K_Z$ for PRF $F_p$
5:     Initialize UC, TSet, XSet to empty maps
6:     Set sk = ($K_T, K_X, K_Y, K_Z$), st = (UC, $n'$)
              ▷ $n'$ is bucket size for unordered bucketization (Section 2.1)
7:     Set **EDB** = (TSet,XSet)
8:     Send **EDB** to the server. Client keeps {sk, st}.

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**Algorithm 2** `GeneSSE.Gen_mkw`
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**Input:** w, st
**Output:** $\text{mkw}_{\text{list}}$
1: **function** GeneSSE.GEN_MKW(w, st)
2:     Parse st = $n'$
3:     $\Delta \leftarrow \Delta \cup \{w\}$
4:     $n_B = \lceil \frac{|\Delta|}{n'} \rceil$
5:     Partition $\Delta$ as $\{\Delta_1, \cdots, \Delta_{n_B}\}$ such that $\Delta_i = \{w_{(i-1)n'+1}, \cdots, w_{in'}\}$   ▷ *The last bin may not contain $n'$ ws. Keep only as many are left.*
6:     Find the bucket $\Delta_k$ such that $w \in \Delta_k$
7:     Set $\ell \leftarrow |\Delta_k|$
8:     **for** $i \leftarrow 1$ to $\ell$ **do**
9:        **for** $j \leftarrow 0$ to $\ell - i$ **do**
10:           $\text{mkw}_{i,i+j}^{(k)} \leftarrow \Delta_k \setminus \{w_i^k, \ldots, w_{i+j}^k\}$
11:           $\text{mkw}_{\text{list}} \leftarrow \text{mkw}_{\text{list}} \cup \{\text{mkw}_{i,i+j}^{(k)}\}$
12:     **return** $\text{mkw}_{\text{list}}, n_B, \Delta$

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9. Bucket size is set to 5 as per Challenge 1 solution

## 2.2. Technical Framework

Having addressed the plausible challenges in designing `GeneSSE`, we formally define the construction in this section. The `GeneSSE` framework is instantiated along the lines of [20] (with changes as discussed in Section 2.1). It can be defined formally as a client-server protocol comprising of three algorithms, $\Pi_{\text{GeneSSE}} = \{\text{Setup}, \text{Update}, \text{Search}\}$. We define each algorithm below; statements marked in red are our changes to [20].

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**Algorithm 3** `GeneSSE.Update`
---
**Input:** sk, st, op, (id, w), **EDB**
**Output:** **EDB**
1: **function** GeneSSE.Update(sk, st, op, (id, w))
2:     **Client**
3:     Parse sk = ($K_T, K_X, K_Y, K_Z$) and st = (UC, $n'$)
4:     $\text{mkw}_{\text{list}}, n_B, \Delta = \text{Gen\_mkw}(w, \text{st})$
5:     st = st $\cup \{n_B, \Delta\}$
6:     **for** mkw $\in \text{mkw}_{\text{list}}$ **do**
7:        **if** UC[mkw] is NULL **then**
8:           Set UC[mkw] = 0
9:        UC[mkw] = UC[mkw] + 1
10:        addr = $F(K_T, \text{mkw}||\text{UC[mkw]}||0)$
11:        val = (id||op) $\oplus F(K_T, \text{mkw}||\text{UC[mkw]}||1)$
12:        $\alpha = F_p(K_Y, \text{id}||\text{op}) \cdot (F_p(K_Z, \text{mkw}||\text{w}||\text{UC[mkw]}))^{-1}$
13:        $\textbf{xtag} = g^{F_p(K_X, \text{mkw}||\text{w}) \cdot F_p(K_Y, \text{id}||\text{op})}$
14:        Send (addr, val, $\alpha$, $\textbf{xtag}$) to the server
15:     **Server**
16:     Parse **EDB** = (TSet,XSet)
17:     Set TSet[addr] = (val, $\alpha$)
18:     Set XSet[$\textbf{xtag}$] = 1

---

- `GeneSSE.Setup`($\lambda$): As detailed in Algorithm 1, this deterministic client-side algorithm takes a security parameter $\lambda$ and initializes the system by (1) sampling PRF keys sk for the encrypted search index and search token generation, (2) initializing empty multimaps TSet and XSet, and (3) setting up client state st, which includes a counter UC to track updates to meta-keywords and a bucket size $n'$ that partitions the database keywords.
- `GeneSSE.Update`(sk, st, op, (id, w)): This client-server protocol handles updates (op, (id, w)). The client computes meta-keywords for w using the modified `Gen_mkw` routine [20] (Algorithm 2, modifications marked in red), updating only the bucket containing w. The client then invokes the modified `Update` routine (Algorithm 3) to generate addresses, values, $\alpha$, and cross-tags, which the server stores in TSet and XSet.
- `GeneSSE.Search`(q, sk, st, **EDB**): The client converts a disjunctive query q into a meta-query $q_{\text{mkw}}$ using `GenMQuery` [20], sorting keywords based on update count rather than frequency (Challenge 3, Section 2.1). The client then executes the modified `Search` protocol (Algorithm 5, modifications in red) on the server to retrieve the encrypted document identifiers corresponding to q.

**Note.** In `GeneSSE.Search` (lines 15-17, Algorithm 5), **xtokens** are generated for all (w, mkw) pairs. Since each meta-keyword mkw consists of constituent keywords ws from a bucket, and **xtags** are computed per (w, mkw) update, generating **xtokens** only for present keywords ws

**Algorithm 4** GeneSSE.GenMQuery

---

**Input:** $q = \{w_{i_1} \vee w_{i_2} \vee \ldots \vee w_{i_l}\}, \mathsf{st}$
**Output:** Meta-Query $q_{\mathsf{mkw}}$
1: **function** GeneSSE.GenMQuery$(q, \mathsf{st})$
2:   Parse $\mathsf{st} = (n', n_B, \Delta)$
3:   Parse $\Delta$ as $\{\Delta_1, \ldots, \Delta_{n_B}\}$
4:   Sort ws in $q$ in increasing order of UC
5:   Partition query $q$ into set of sub-queries $\mathsf{P}_q$ as $q_1||\cdots||q_{n_B}$, such that $q_k$ contains ws only from $\Delta_k$ for $k = 1, \cdots, n_B$
6:   **for** $q_k \in \mathsf{P}_q$ **do**
7:     Parse $q_k$ as $\{w_{i_1}^k, \cdots, w_{i_{l'}}^k\}$
8:     **for** $j \leftarrow 1$ to $l'$ **do**
9:       $\mathsf{mkw}_{i_{j-1}+1, i_j - 1}^{(k)} \leftarrow \Delta_k \setminus \{w_{i_{j-1}+1}^k, \ldots, w_{i_j - 1}^k\}$
         ▷ *Recall that* $\mathsf{mkw}_{i_k, j_k} \leftarrow \phi$ *if* $i_k > j_k$, $i_0 = 0$ *and* $w_1^k$ *is the first keyword in* $\Delta_k$
10:      $\mathsf{mkw}_{i_{l'}+1, n'}^{(k)} \leftarrow \Delta_k \setminus \{w_{i_{l'}+1}^k, \ldots, w_{n'}^k\}$
11:      $q_{\mathsf{mkw}, k} \leftarrow \mathsf{mkw}_{1, i_1 - 1}^{(k)} \wedge \ldots \wedge \mathsf{mkw}_{i_{l'}+1, n'}^{(k)}$
12:      $q_{\mathsf{mkw}} \leftarrow q_{\mathsf{mkw}} \vee q_{\mathsf{mkw}, k}$
13:   **return** $q_{\mathsf{mkw}}$

---

**Algorithm 5** GeneSSE.Search

---

**Input:** $q, \mathsf{sk}, \mathsf{st}, \mathbf{EDB}$
**Output:** Result set $\mathbf{DB}(q)$
1: **function** GeneSSE.Search$(q, \mathsf{sk}, \mathsf{st}, \mathbf{EDB})$
2:   **Client**
3:     Generate $q_{\mathsf{mkw}} = (\vee_{k \in [n_B]} q_{\mathsf{mkw}, k}) = \mathsf{GenMQuery}(q, \mathsf{st})$
4:     Parse $\mathsf{sk} = (\mathsf{K}_T, \mathsf{K}_X)$ and $\mathsf{st} = (\mathsf{UC}, n', n_B, \Delta)$
5:     Use UC to identify meta-keyword with the least updates (assumed to be $\mathsf{mkw}_1^k$ w.l.o.g)
6:     Initialize stokenList to an empty list
7:     Initialize $\mathsf{xtokenList}_1, \ldots, \mathsf{xtokenList}_{\mathsf{UC}[\mathsf{mkw}_1^k]}$ to empty lists
8:     **for** $j = 1$ to $\mathsf{UC}[\mathsf{mkw}_1]$ **do**
9:       $\mathsf{saddr}_j = F(\mathsf{K}_T, \mathsf{mkw}_{1,1}||j||0)$
10:      $\mathsf{stokenList} = \mathsf{stokenList} \cup \{\mathsf{saddr}_j\}$
11:      **for** $i = 2$ to $n$ **do**
12:        **for** $\forall w_{k', p} \in \mathsf{mkw}_i^{k'}$ and $w_{k, l} \in \mathsf{mkw}_1^k$ **do**
13:          $\mathbf{xtoken}_{(i, p), l, j} = g^{F_p(\mathsf{K}_X, \mathsf{mkw}_i^{k'}||w_{k', p}) \cdot F_p(\mathsf{K}_Z, \mathsf{mkw}_1^k||w_{k, l}||j)}$
             ▷ $k' \in [n_B]; p \to \#w \in \mathsf{mkw}_i^{k'}; l \to \#w \in \mathsf{mkw}_1^k$
14:          $\mathsf{xtokenList}_{i, j} = \mathsf{xtokenList}_{i, j} \cup \{\mathbf{xtoken}_{(i, p), l, j}\}$
15:        **for** $\forall w_{k', p} \notin \mathsf{mkw}_i^{k'}$ and $w_{k, l} \notin \mathsf{mkw}_1^k$ **do**
16:          $\mathbf{xtoken}_{(i, p), l, j} = g^{\beta \cdot \gamma}$         ▷ $\beta, \gamma \xleftarrow{\$} \mathbb{Z}_p^*$
17:          $\mathsf{xtokenList}_{i, j} = \mathsf{xtokenList}_{i, j} \cup \{\mathbf{xtoken}_{(i, p), l, j}\}$
18:        $\mathsf{xtokenList}_j = \mathsf{xtokenList}_j \cup \{\mathbf{xtoken}_{i, j}\}$
19:      Randomly permute the tuple-entries of $\mathsf{xtokenList}_j$
20:    Send $(\mathsf{stokenList}, \mathsf{xtokenList}_1, \ldots, \mathsf{xtokenList}_{\mathsf{UC}[\mathsf{mkw}_1]})$
21:   **Server**
22:     Parse $\mathbf{EDB} = (\mathsf{TSet}, \mathsf{XSet})$
23:     Initialize sEOpList to a empty list
24:     **for** $j = 1$ to stokenList.size **do**
25:       $\mathsf{cnt}_j = 1$
26:       $(\mathsf{sval}_j, \alpha_j) = \mathsf{TSet}[\mathsf{stokenList}[j]]$
27:       **for** $i = 2$ to $n$ **do**
28:         $\mathsf{xtokenList}_{i, j} = \mathsf{xtokenList}_j[i]$
29:         **for** $k = 1$ to $|\mathsf{xtokenList}_{i, j}|$ **do**
30:           $\mathbf{xtag}_{(i, j), k} = (\mathsf{xtokenList}_{i, j}[k])^{\alpha_j}$
31:           **if** $\mathsf{XSet}[\mathbf{xtag}_{(i, j), k}] == 1$ **then**
32:             $\mathsf{cnt}_j = \mathsf{cnt}_j + 1$
33:       Set $\mathsf{sEOpList} = \mathsf{sEOpList} \cup \{j, \mathsf{sval}_j, \mathsf{cnt}_j\}$
34:     Send sEOpList to the client
35:   **Client**
36:     Initialize IDList and $\mathbf{DB}(q_{\mathsf{mkw}})$ to an empty list
37:     **for** $\ell = 1$ to sEOpList.size **do**
38:       $(j, \mathsf{sval}_j, \mathsf{cnt}_j) = \mathsf{sEOpList}[\ell]$
39:       Recover $(\mathsf{id}_j || \mathsf{op}_j) = \mathsf{sval}_j \oplus F(\mathsf{K}_T, \mathsf{mkw}_1||j||1)$
40:       **if** $\mathsf{op}_j$ is add and $\mathsf{cnt}_j = n$ **then**
41:         Set $\mathsf{IDList} = \mathsf{IDList} \cup \{\mathsf{id}_j\}$
42:       **else if** $\mathsf{op}_j$ is del and $\mathsf{cnt}_j > 0$ **then**
43:         $\mathsf{IDList} = \mathsf{IDList} \setminus \{id_j\}$
44:     **for** each $\mathbf{DB}(q_{\mathsf{mkw}, k})$ from IDList **do**
45:       $\mathbf{DB}(q_{\mathsf{mkw}}) = \mathbf{DB}(q_{\mathsf{mkw}}) \cup \mathbf{DB}(q_{\mathsf{mkw}, k})$
46:     Client locally filters $\mathbf{DB}(q) \subseteq \mathbf{DB}(q_{\mathsf{mkw}})$

---

would leak their association with mkw over multiple queries. To prevent this, we pad the **xtoken**s by including randomly sampled ws not in the mkw. With bucket size $O(1)$ (Section 2.1), this adds minimal overhead. The rest of the search proceeds with the client locally filtering the results to match the original disjunction.

**Correctness of** GeneSSE**.** The proof of correctness of GeneSSE follows from the correctness of the GeneSSE.GenMQuery function, noting that frequency based bucketization has no effect on the correctness of the scheme[10], and from the correctness of TSet instantiations from [27]. We state the following theorem for the correctness of GeneSSE.

**Theorem 1** (Correctness of GeneSSE)**.** *Since the frequency-based bucketization in [20] has no effect on the correctness,* GenMQuery *correctly converts a given disjunctive query to a conjunction of appropriate meta-keywords in [20], and the* **TSet** *instantiation from [27] works correctly, hence* GeneSSE *satisfies correctness for an SSE scheme supporting disjunctive queries.*

**Security Analysis of** GeneSSE**.** The security of GeneSSE relys on secure PRFs and the decisional Diffie-Hellman assumption over $\mathcal{G}$. We formally prove simulation-based security against a well-defined leakage profile. Compared to prior dynamic SSE schemes, GeneSSE does not leak additional information; its meta-keyword structure obfuscates update patterns and provides stronger Type-I backward privacy. The main theorem is stated below:

**Theorem 2** (Security of GeneSSE)**.** *Assuming that $F$ and $F_p$ are secure PRFs and the decisional Diffie-Hellman assumption holds over the group $\mathcal{G}$,* GeneSSE *is adaptively-secure with respect to a leakage function $\mathcal{L}_{\mathsf{GeneSSE}}$.*

Due to lack of space, we provide the formal proof of the correctness of GeneSSE in Appendix C, a rigorous leakage profile analysis (i.e. definition of $\mathcal{L}_{\mathsf{GeneSSE}}$), and a detailed simulation-based proof of security in Appendix D.1, D.2, and D.3 respectively.

---

**Algorithm 6** RGeneSSE .Setup

---

**Input:** $\lambda$
**Output:** $\mathsf{sk}, \mathsf{st}, \mathbf{EDB}$
1: **function** RGeneSSE .Setup$(\lambda)$
2:   **Client**
3:     $\mathsf{sk}, \mathsf{st}, \mathbf{EDB} \leftarrow \mathsf{Dyn\text{-}TWINSSE}.\mathsf{Setup}(\lambda)$
4:     Send $\mathbf{EDB}$ to the server. Client keeps $\{\mathsf{sk}, \mathsf{st}\}$.

---

## 3. RGeneSSE**: Dynamic Volume Hiding Range SSE**

We leverage the definitional index-based framework of a range SSE scheme to design our dynamic leakage resilient range SSE scheme (RGeneSSE) for multi-dimensional ranges, that reduce a range query search to disjunctive keyword search. This framework allows us to

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10. It is just an optimization choice made in [20]

leverage `GeneSSE` to support efficient multi-dimensional range searches in a dynamic setting. We explain the entire framework of `RGeneSSE` in the following steps -

---

**Algorithm 7** `RGeneSSE.InsertNode`

---

**Input:** $T, val_{low}, val_{high}$
**Output:** Updated tree $T$ with the range inserted
1: **function** RGeneSSE.INSERTNODE($T, val_{low}, val_{high}$)
2:    **if** $T ==$ NULL **then**
3:       $T.val_{low} \leftarrow val_{low}$
4:       $T.val_{high} \leftarrow val_{high}$
5:       **return** $T$
6:    **if** $val_{high} < T.val_{low}$ **then**
7:       $T.val_{low} \leftarrow val_{low}$
8:       $T.left \leftarrow$ InsertNode($T.left, val_{low}, val_{high}$)
9:    **else if** $val_{low} > T.val_{high}$ **then**
10:       $T.val_{high} \leftarrow val_{high}$
11:       $T.right \leftarrow$ InsertNode($T.right, val_{low}, val_{high}$)
12:    **else**
13:       $T.val_{low} \leftarrow \min(T.val_{low}, val_{low})$
14:       $T.val_{high} \leftarrow \max(T.val_{high}, val_{high})$
15:    $T.subtree \leftarrow$ InsertNode($T.subtree, val_{low}, val_{high}$)
16:    **return** $T$

---

**Range Supporting Data Structure.** We adopt the range tree scheme from [21] to store attribute-value pairs of a $d$-dimensional database **DB**. A 1-D range tree is a binary search tree (BST), and a $d$-dimensional range tree is recursively constructed by associating each node in the BST of $[d_i]$ with the root of a BST on $[d_{i+1}]$, forming a hierarchical structure across dimensions. Nodes represent dyadic ranges. For a given range, we compute the minimal set of nodes using the *Best Range Cover* (BRC) technique, which, per THEOREM 5 of [21], guarantees a unique minimal cover with zero false positives.

The database **DB** consists of $N$ records and $d$ attributes, $\textbf{DB} = \Sigma_{i=1, j=1}^{d, N}(\text{id}_j, \{\text{attr}_i, \text{val}\})$. For each (attr-val) pair in domain $d_i$, the client generates a range tree and recursively builds subtrees for subsequent attributes. This structure is stored client-side to compute minimal covers for queries using $\text{BRC}_{RT}$ [21], as detailed in Algorithms 9 and 10.
**Encrypted Search Index.** To reduce a range query to a disjunctive query and leverage disjunctive SSE lookups through `GeneSSE`, we construct an SSE-compatible inverted search index that is encrypted and stored at the server. For an update $(\text{id}_j, \{\text{attr}_i, \text{val}\})$ of the $i$-th attribute and $j$-th record, the client computes the corresponding range tree node and adds $\text{id}_j$ for $(\text{attr}_i$-val) to the search index (lines 8-9, Algorithm 9). For updates spanning multiple attributes, e.g., $(\text{id}_j, \{\text{attr}_i, \text{val}\}, \{\text{attr}_{i+1}, \text{val}'\})$, the client generates the range tree for $(\text{attr}_i, \text{val})$ and its subtree for $(\text{attr}_{i+1}, \text{val}')$, storing $\text{id}_j$ for both $(\text{attr}_i$-val) and $(\text{attr}_i$-val) $\cap$ $(\text{attr}_{i+1}$-val$')$ (lines 10-14, Algorithm 9). This procedure is repeated for all subtrees of $(\text{attr}_i$-val). For a $d$-

---

**Algorithm 8** `RGeneSSE.BuildIndex`

---

**Input:** $(\text{id}_i, \text{val})_{i=1}^N$
**Output:** DB
1: **function** RGeneSSE.BUILDINDEX($(\text{id}_i, \text{val})_{i=1}^N$)
2:    **for** i = 1 to $N$ **do**
3:       $\textbf{DB}[\text{val}] = \text{id}_i$
4:       $\textbf{DB} = \textbf{DB} \cup \textbf{DB}[\text{val}]$
5:    **return** DB

---

**Algorithm 9** `RGeneSSE.Update`

---

**Input:** $\text{sk}, \text{st}, T, \text{op}, \text{id}, \{\text{attr}_i, \text{val}\}_{i=1}^d$
**Output:** EDB
1: **function** RGeneSSE.Update($\text{sk}, \text{st}, T, \text{op}, \text{id}, \{\text{attr}_i, \text{val}\}_{i=1}^d$)
2:    **Client**
3:    Initialize **DB** as an empty map
4:    **for** $i = 1$ to $d$ **do**
5:       $T_i.\text{root} \leftarrow$ InsertNode($T_i.\text{root}, val_{low}, val_{high}$)
6:       **if** $i < d$ **then**
7:          $T_i.\text{root.subtree} \leftarrow$ InsertNode($T_i.\text{root.subtree},$
8:          $val_{low}, val_{high}$)
9:    **for** $i = 1$ to $d$ **do**
10:       $\textbf{DB} \leftarrow$ BuildIndex($\text{id}, \text{val}$)
11:    **for** $i = 1$ to $d - 1$ **do**
12:       **for** $v \in T_i$ and $u \in T_{i+1}$ **do**
13:          **if** $v.\text{val} \cap u.\text{val} \neq \emptyset$ **then**
14:             **for** $\text{id} \in (v.\text{val} \cap u.\text{val})$ **do**
15:                $\textbf{DB} \leftarrow$ BuildIndex($\text{id}, (v.\text{val}||u.\text{val})$)
16:    **Client+Server**
17:    $\text{EDB} \leftarrow$ GeneSSE.Update($\text{sk}, \text{st}, n', \text{op}, \text{id}, \{w_i\}_{i=1}^d$)
18:    **return** EDB

---

dimensional database, entries are stored for $d - 1$ subtrees representing intersections $(d_i \cap d_{i+1})$, and the index is then encrypted and offloaded to the server.

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**Algorithm 10** `RGeneSSE.Search`

---

**Input:** $\text{sk}, \text{st}, \textbf{EDB}, T, v, q = [a_i, b_i]_{i=1}^d$
**Output:** $\textbf{DB}(q)$
1: **function** RGeneSSE.SEARCH($q = [a_i, b_i]_{i=1}^d$)
2:    **Client**
3:    $W \leftarrow \text{BRC}_{RT}(T, q, v)$         $\triangleright \text{BRC}_{RT}(\cdot) \rightarrow$ *[21]*
4:    $q_{range} = q_{range} \cup \{W\}$
5:    **Client+Server**
6:    $\textbf{DB}(q_{range}) \leftarrow$ GeneSSE.Search($q_{range}, \text{sk}, \text{st}, \textbf{EDB}$)
7:    **Client**
8:    Client locally filters $\textbf{DB}(q) \subseteq \textbf{DB}(q_{range})$

---

**Reduction From Range to Disjunction.** For a $d$-dimensional range query, the client first computes the minimal cover in the first dimension $(d_1)$ using BRC, then iteratively checks the subtrees in subsequent dimensions $(d_2, \ldots, d_d)$ for intersections with the query range. This process leverages $\text{BRC}_{RT}$. The resulting set of covering nodes is converted into a disjunctive keyword query and sent to `GeneSSE.Search` (Algorithm 10). The returned result $(q_{range})$ is a superset of the original query $q$, which the client filters locally. Correctness follows from the correctness of `GeneSSE.Search`.

*Note.* While [21] observes that the size of the BRC cover may vary in multi-dimensional queries, potentially leaking information about the range, `RGeneSSE` maps the covering nodes to keywords. The `GeneSSE.Search` algorithm computes meta-keywords for the disjunctive query and sends only these to the server, ensuring **no significant information about the queried range is revealed**.

### 3.1. Resilience against Reconstruction Attacks

In this section, we provide a detailed analysis of how `RGeneSSE` behaves under the BRC reconstruction attack of range tree schemes as proposed in [21]. `RGeneSSE` is most relevant under this attack because it is structured as a range tree scheme that leverages the BRC range covering algorithm

to find the minimal range cover corresponding to a multi-dimensional range query. However, we also emphasize the RGeneSSE is additionally resistant to the exploitation of structure pattern and search pattern leakages as extensively studied in [21].

**Exploited Leakages.** The attack in [21] targets leakages from the *tokenset* t, which the client generates to query the encrypted search index for each $w \in \mathcal{W}$, where $\mathcal{W}$ is the cover of a range query $q$ obtained via BRC on the range tree. Key leakages include: (1) *volume pattern*, revealing the number of records returned per token $t \in$ t; (2) *search pattern* or *frequency map*, disclosing how often each token $t$ appears across queries; and (3) *structure pattern*, capturing the tokenset and the response length for each token. The range tree reconstruction attack under BRC exploits both the volume and structure pattern leakages of the tokenset.

**Reconstruction Attack Under BRC [21].** This attack exposes structural vulnerabilities in BRC-based range tree schemes, enabling information leakage even under structured encryption. It is a polynomial-time reconstruction attack that leverages query co-occurrence patterns to infer the underlying data structure. The attack starts by identifying inner nodes in the range tree using observed tokenset constraints. A co-occurrence graph is then built, where nodes represent tree elements and edges capture token relationships. Triangular structures in this graph allow differentiation between leaf, boundary, and inner nodes. Next, an inner grid reconstruction refines the tree layout and reorders records. Finally, volumes of extreme domain points are estimated by extrapolating missing values based on known token-volume relationships.

RGeneSSE **Leakage Profile.** Our multi-dimensional dynamic range SSE framework relies on two main data structures: (i) a range tree T that encodes the attribute-value pairs or range cover for the $d$-dimensional attribute space, and (ii) an inverted search index, which is a dictionary mapping meta-keywords (derived from specific attribute-value pairs in **DB**) to the corresponding record identifiers. Importantly, the inverted index is not a direct mapping from attribute-value pairs to records. By using GeneSSE.Update for constructing the encrypted search index, keywords in **DB** are transformed into meta-keywords, *obfuscating the one-to-one mapping with the tree nodes* (actual domain points).
(1) *Query Processing:* For a given range query $q_{\text{range}}$, the client first computes the minimal range cover using the BRC algorithm. The nodes returned by this algorithm, representing minimal coverings of the actual domain data points, are treated as keywords to construct a disjunctive query $q_{\text{dis}}$. This query is passed to GeneSSE.Search, which transforms $q_{\text{dis}}$ into a conjunction of meta-keywords $q_{\text{mkw}}$. The server searches the encrypted database for $q_{\text{mkw}}$ and returns the matching records. By the correctness of GeneSSE.Search, $\mathbf{DB}(q_{\text{dis}}) \subseteq \mathbf{DB}(q_{\text{mkw}})$, ensuring the result covers the original query.
(2) *Leakage Analysis:* Reconstruction attacks [21] exploit volume pattern, search pattern, and structure pattern leakages. We discuss each in the context of RGeneSSE:

(a) *Volume Pattern:* Traditional attacks rely on the volume of records returned per token in the token set corresponding to each covering node. In RGeneSSE, the tokenset is a conjunction of meta-keywords used in a disjunctive SSE query. Consequently, the server only observes the overall result set for the query and **gains no information about the individual meta-keywords' partial results**[11]. Notably, (i) the individual tokens do not correspond to exact nodes returned by BRC, so they leak no information about precise domain points, and (ii) while the total query volume is visible, GeneSSE pads the result to an acceptable threshold (see Section 4), and the client locally filters the relevant documents. This design prevents the server from reconstructing the volume maps exploited in [21].

(b) *Search Pattern:* Since the tokens are meta-keywords without direct correspondence to exact domain points or attribute-value pairs, the frequency of tokens over multiple queries does not reveal meaningful information to the server and does not aid reconstruction.

(c) *Structure Pattern:* In prior attacks, structure pattern leakage arises from observing the tokenset and the sizes of partial responses per token. In RGeneSSE, the tokenset reveals no significant information about original domain points or the actual query range. Additionally, by reducing a range query to a disjunction and using a disjunctive SSE, the server only sees the complete result for the disjunction, eliminating sub-query or individual meta-keyword volume leaks.

**Inapplicability of the Reconstruction Attack.** From the above discussion, it is evident that the primary leakages required for the reconstruction attack to work are rendered inconsequential due to the (i) reduction of a range search to a disjunctive search; (ii) usage of GeneSSE that operates on a set of meta-keywords, thereby obfuscating the exact mapping of the tokens with the original data points in the domain. The Reconstruction Attack Under BRC [21] works in the following four steps. We explain each step and how they are inapplicable w.r.t. RGeneSSE-

(1) *Infer inner nodes*: This step exploits the individual tokens from a token set and infers information about the inner nodes of the range tree. **This non-trivial information is not possible to infer in RGeneSSEbecause the individual tokens of a tokenset is not the actual nodes in the range tree**, therefore does not provide any significant information.
(2) *Trim the co-occurrence graph*: This step exploits the number of times a pair of tokens appear in a tokenset. **This information is essentially stopped in RGeneSSEbecause of the reduction from range to disjunctive searches**.
(3) *Inner Grid Reconstruction*: This uses the co-occurrence graph and the information of the inner nodes to distinguish between the leaf and non-leaf nodes. **Since the co-occurrence graph itself cannot be formed as explained in the above step, inner grid reconstruction is also not inherently possible**.
(4) *Inferring Extreme Node's Volume*: This step exploits the volume pattern leakages of individual tokens in a tokenset.

---

11. This is guaranteed by the security of GeneSSE

Since this leakage is essentially stopped and rendered insignificant w.r.t. `RGeneSSE`, such inferences are not possible to make from our range SSE construction.

**Correctness of** `RGeneSSE`**.** We state the following theorem:

**Theorem 3** (Correctness of `RGeneSSE`)**.** *Since* `GeneSSE` *is a functionally correct dynamic disjunctive SSE scheme, multi-dimensional range tree from [21] is correct, and Best Range Cover technique (BRC) from [21], [38], [53] is correct,* `RGeneSSE` *is a functionally correct range SSE scheme in the dynamic database model.*

The proof follows naturally from proof of correctness of `GeneSSE` (refer Section 2), and from corresponding proofs of correct operations of (1) multi-dimensional range tree in [21], and (2) Best Range Cover technique (BRC) in [21], [38], [53].

**Security Analysis of** `RGeneSSE`**.** The security analysis of `RGeneSSE` follows from the security guarantees of `GeneSSE` (that relies on security of secure PRFs and the decisional Diffie-Hellman assumption over the group $\mathcal{G}$). We formally state the following theorem, and provide a detailed simulation-based proof of security in Appendix G (due to space constraints).

**Theorem 4** (Security of RGeneSSE)**.** *Since* RGeneSSE *is an adatively secure forward and backward private disjunctive SSE,* RGeneSSE *is adaptively-secure with respect to a leakage function* $\mathcal{L}_{\text{RGeneSSE}}$.

## 4. Experimental Results

We now describe the experimental setup used to evaluate the performance and analyze the storage and search complexity of `GeneSSE` and `RGeneSSE` as well as the low-level details of our prototype implementations.

**Platform.** The entire implementation of `GeneSSE` and `RGeneSSE` were done using C++ (with GCC 9 compiler), with Redis as the database backend. We ran the experiments on a *single* node with Intel Xeon E5-2690 v4 2.6 GHz CPU with 128 GB RAM and 512 GB SSD.
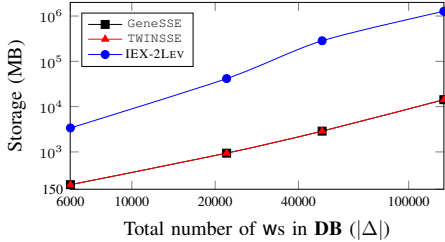
Figure 2: Server Storage (both axes are in log scale)

### 4.1. Performance Analysis of `GeneSSE`

In this section, we present the results of our experimental evaluations of `GeneSSE` and give comparison analysis with the performances of `TWINSSE` [20], `ODXT` [23] and IEX-2Lev [22], a state of the art disjunctive SSE in a static setting.

**Dataset.** We have used the Enron email dataset[12] for our experiments; it contains around 10K documents (emails) and 2.5 million thousand keyword-document pairs, with a total size of 1.3 GB.[13] We parse the raw Enron dataset and create a plaintext inverted index **DB** (of size approximately 650KB, which is $0.05\%$ of the actual plaintext Enron database). The encrypted search index **EDB** is created as usual, post which `GeneSSE` is evaluated.

**Storage Overhead Analysis.** The storage overhead of `GeneSSE` is similar to the storage overhead of `TWINSSE`. Since `GeneSSE` inherits the fundamental structure of meta-keywords, it preserves the linear storage complexity of `TWINSSE` that marked a significant improvement form the quadratic storage overhead incurred by IEX-2Lev [22]. Figure 2 shows the linear increase in the storage of `GeneSSE` and `TWINSSE` compared with the quadratic increase in IEX-2Lev.
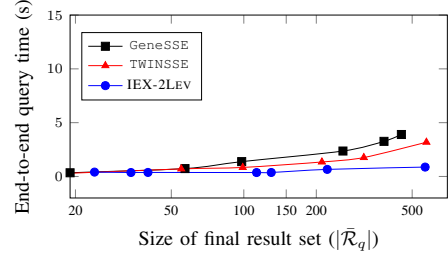
Figure 3: Comparison of end-to-end search latency vs final result size for disjunctive queries of the form $q = w_1 \vee w_2$ over Enron.

**Disjunctive Search-time Overhead.** We provide an end-to-end query performance comparison of `GeneSSE` with `TWINSSE` in Figure 3. For queries with smaller result sizes, `GeneSSE` achieves almost identical end-to-end query latency as `TWINSSE`. For queries with larger result sizes, `TWINSSE` performs slightly better. The slight, yet acceptable decrease in the computation time of `GeneSSE` is attributed to omitting the frequency-based bucketization strategy used in `TWINSSE` (refer Challenge 3 in Section 2.1). Also, `GeneSSE` maintains the linear increase in search complexity with increase in frequency (update count) of a keywords as shown by `TWINSSE`. We view this as an efficiency trade-off; we provide a forward and Type-I backward private dynamic disjunctive SSE, with the same linear storage overhead as `TWINSSE` and maintains a linear search complexity. This is also a significant improvement when compared to other state-of-the-art disjuntive schemes like IEX-2Lev.

12. https://www.cs.cmu.edu/~enron/,
https://www.kaggle.com/wcukierski/enron-email-dataset

13. The raw Enron dataset consists of folders of emails of individual employees. Since the emails are in plain English text, we performed a dictionary-based pre-processing to filter the keywords (we removed the stop-words and punctuation in the process), and created a list of (lexicographically ordered) keywords.

TABLE 2: Asymptotic Complexity Analysis and Comparison of RGeneSSE vs State-of-the-Art Range SSE. In the table, $\mathcal{W}$: set of all keywords in database **DB**; $\mathcal{W}_x$: largest sequence number of existing keyword ([53]), $|\text{RC}|$: Number of keywords in the range cover/query $q$; $\text{UC}(q)$: update count of all keywords in $q$; $\text{DB}(q_{\text{mkw}})$: result set of $q_{\text{mkw}}$ i.e., transformed query from the disjunction of the range cover of $q$; **AR**: Attack Resistance against [21].

| Scheme | Model | Update | | Search | | Communication | | AR |
| | | Client | Server | Client | Server | Update | Search | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| [38] | Static | N/A | N/A | $2\mathcal{W}$ | $O(\text{DB}(q))$ | N/A | $O(\text{DB}(q))$ | No |
| [44] | Dynamic | $O(\mathcal{W}_x)$ | $O(\log\mathcal{W})$ | $O(\mathcal{W}_x+|\text{RC}|)$ | $O(|\text{RC}|)$ | $O(\log\mathcal{W})$ | $O(|\text{RC}|)$ | No |
| [53] | Dynamic | $O(\mathcal{W}+\log|\mathcal{W}|)$ | $(\log|\mathcal{W}|)$ | $O(|\text{RC}|)$ | $O(\text{UC}(q))$ | $O(|\mathcal{W}|)$ | $|\text{DB}(q)|$ | No |
| This Work | Dynamic | $O(1)$ | $O(1)$ | $O|\text{RC}|)$ | $O(|\text{DB}(q_{\text{mkw}})|)$ | $O(1)$ | $O(|\text{DB}(q)|)$ | Yes |
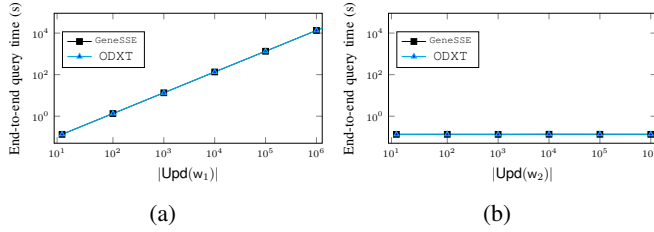


Figure 4: (4a) End-to-End conjunctive query complexity for $q = \mathsf{w}_1 \wedge \mathsf{w}_2$, where the update count of $\mathsf{w}_1$ is varied; (4b) End-to-End conjunctive query complexity for $q = \mathsf{w}_1 \wedge \mathsf{w}_2$, where the update count of $\mathsf{w}_2$ is varied.
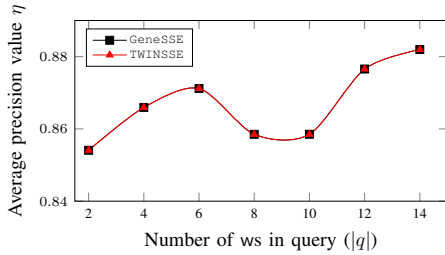


Figure 5: Average precision value vs number of keywords in a disjunctive query

**Conjunctive Search-time Overhead.** Figure 4a compares the conjunctive search time of GeneSSE with ODXT: a linear increase in the search time complexity with an increase in the update count of $\mathsf{w}_1$. This trend is similar to the search complexity of ODXT that scales with the increase in the update count of keyword in the query with the least updates (here $\mathsf{w}_1$). This claim is further validated by Figure 4b: on varying $|\text{UC}(\mathsf{w}_2)|$ the search complexity remains constant. This behaviour is reflected in GeneSSE as well.

**Precision Analysis.** In information retrieval, *precision* (denoted as $\eta$) refers to the proportion of relevant documents among the retrieved results. Figure 5 presents a comparison of the average precision values of $\bar{\mathcal{R}}_q$ for disjunctive queries ($q$) with varying keyword counts. Notably, the average precision remains above $85\%$ in most cases, indicating that at least $85\%$ **of the retrieved documents** in $\bar{\mathcal{R}}_q$ are relevant to the query $q$ (i.e., they belong to the actual result set $\mathcal{R}_q$ without extraneous id-s). This level of precision closely matches that achieved by TWINSSE and is considered acceptable.

**Update Complexity.** Recall from Challenge 1 in Section 2.1 that we set a $n' = O(1)$ bucket size; therefore, we have $O(n'^2)$ meta-keywords in each bucket. In our experimental evaluations, we consider $n' = 5$, this gives an

optimal efficiency guarantee in terms of storage, search performance, precision and update complexity. Concretely, for a bucket size 5, any keyword update of the form $(\text{op}, (\text{id}, \mathsf{w}))$ corresponds to roughly 8 $\text{mkw}_i$ that contains $\mathsf{w}$. Thus for one update of $\mathsf{w}$ we make 8 meta-keyword updates. This remains uniform for all updates pertaining to any keyword in the database and also with different sizes of the database. Since for every atomic update of $(\text{id}, \mathsf{w})$ a constant number of meta-keywords are updated always, the asymptotic update complexity of GeneSSE is $O(1)$ which is similar to the asymptotic update complexity of ODXT.

## 4.2. Performance Analysis of RGeneSSE

In this section, we present the results of our experimental evaluations of RGeneSSE and validate the asymptotic bounds on the performance overheads of RGeneSSE as shown in Table 2. Table 2 provides an asymptotic comparison of RGeneSSE with state-of-the-art range query schemes in terms of (1) database model, (2) update complexity (iff model is "Dynamic"), (3) search complexity (w.r.t. size of the range cover, or $|\text{RC}|$), and (4) resistance to state-of-the-art attacks like [21]. We observe that RGeneSSE improves upon the update complexities of [53] and [44].

**Dataset.** We have used a genomic database maintained by the Large Scale Genomics work stream of the Global Alliance for Genomics & Health (GA4GH)[14] for our experiments; it contains around 1.930GB of data in VCF format with $3,893,572$ records, containing meta-information lines, a header line, and data lines each containing information about a position in the genome. The format also has the ability to contain genotype information on samples for each position. An example sample of the VCF format used is shown in Figure 6[15]. We parse the raw VCF dataset and create a BRC tree and eventually map the internal nodes (keywords) and leaf nodes (document-identifiers) into a plaintext inverted index **DB** (of size approximately 71MB, which is $0.04\%$ of the actual plaintext Enron database). The encrypted search index **EDB** is created as usual, post which RGeneSSE is evaluated.

**Storage Overhead.** The storage requirement of RGeneSSE asymptotically scales as $O(N + \log^d|\mathcal{D}|)$ at the server to store all the attribute-value pairs with their corresponding records along with the records corresponding to each subtree for $d$ dimensions in encrypted search index.

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14. https://github.com/samtools/hts-specs
15. https://samtools.github.io/hts-specs/VCFv4.2.pdf

## 1.1 An example

```
##fileformat=VCFv4.2
##fileDate=20090805
##source=myImputationProgramV3.1
##reference=file:///seq/references/1000GenomesPilot-NCBI36.fasta
##contig=<ID=20,length=62435964,assembly=B36,md5=f126cdf8a6a0c7f379d618ff66beb2da,species="Homo sapiens",taxonomy=x>
##phasing=partial
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">
##INFO=<ID=AF,Number=A,Type=Float,Description="Allele Frequency">
##INFO=<ID=AA,Number=1,Type=String,Description="Ancestral Allele">
##INFO=<ID=DB,Number=0,Type=Flag,Description="dbSNP membership, build 129">
##INFO=<ID=H2,Number=0,Type=Flag,Description="HapMap2 membership">
##FILTER=<ID=q10,Description="Quality below 10">
##FILTER=<ID=s50,Description="Less than 50% of samples have data">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=HQ,Number=2,Type=Integer,Description="Haplotype Quality">
#CHROM POS     ID        REF ALT    QUAL FILTER INFO                              FORMAT      NA00001        NA00002        NA00003
20     14370   rs6054257 G   A      29   PASS   NS=3;DP=14;AF=0.5;DB;H2           GT:GQ:DP:HQ 0|0:48:1:51,51 1|0:48:8:51,51 1/1:43:5:.,.
20     17330   .         T   A      3    q10    NS=3;DP=11;AF=0.017              GT:GQ:DP:HQ 0|0:49:3:58,50 0|1:3:5:65,3   0/0:41:3
20     1110696 rs6040355 A   G,T    67   PASS   NS=2;DP=10;AF=0.333,0.667;AA=T;DB GT:GQ:DP:HQ 1|2:21:6:23,27 2|1:2:0:18,2  2/2:35:4
20     1230237 .         T   .      47   PASS   NS=3;DP=13;AA=T                  GT:GQ:DP:HQ 0|0:54:7:56,60 0|0:48:4:51,51 0/0:61:2
20     1234567 microsat1 GTC G,GTCT 50   PASS   NS=3;DP=9;AA=G                   GT:GQ:DP    0/1:35:4       0/2:17:2       1/1:40:3
```

This example shows (in order): a good simple SNP, a possible SNP that has been filtered out because its quality is below 10, a site at which two alternate alleles are called, with one of them (T) being ancestral (possibly a reference sequencing error), a site that is called monomorphic reference (i.e. with no alternate alleles), and a microsatellite with two alternative alleles, one a deletion of 2 bases (TC), and the other an insertion of one base (T). Genotype data are given for three samples, two of which are phased and the third unphased, with per sample genotype quality, depth and haplotype qualities (the latter only for the phased samples) given as well as the genotypes. The microsatellite calls are unphased.

**Figure 6:** Sample of VCF v4.2 used in our experiments

We generate an inverted index of meta-keywords and their corresponding records for every subtree in each of $d$-th dimension. In Figure 7a we see that the storage overhead of `RGeneSSE` scales linearly with an increase in the number of keywords (meta-keywords) in the encrypted database.
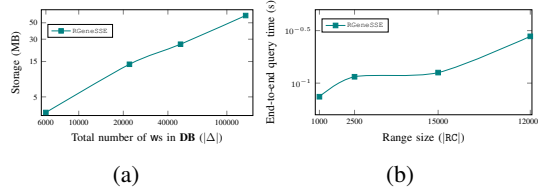


(a)          (b)

**Figure 7:** (7a) Server Storage (both axes are in log scale); (7b) Comparison of end-to-end search latency vs range size for range queries over GA4GH VCF file.

**Search Overhead.** `RGeneSSE` inherits the following properties from `GeneSSE` as it invokes `GeneSSE.Update` and `GeneSSE.Search` as black-boxes; (1) server-side updates are $O(1)$; (2) search time complexity for `RGeneSSE` increases linearly with an increase in the query range size ($|RC|$). We implement the `RGeneSSE` algorithm, where the client issues a range of the form $[a, b]$, and generates a disjunction of covering nodes ($q_{range}$) by invoking the $BRF_{RT}$ algorithm. `GeneSSE.Search` is invoked subsequently with the generated disjunctive query $q_{range}$. The server returns the set of encrypted records corresponding to ($q_{range}$). In terms of search performance, `RGeneSSE` scales linearly with the search performance of `GeneSSE`, that in turn increases linearly with result size of the given meta-query $q_{mkw}$. This is validated in Figure 7b, where we plot the end-to-end search complexity of `RGeneSSE` with an increase in the size of the rage cover $|RC|$. Since an increased range cover implies increase in the resultant records returned by the query, the linear increase in the search time with increase in $|RC|$ implies a linear dependence of the search overhead of `RGeneSSE` on $|\mathbf{DB}(q_{mkw})|$.

## 5. Conclusion

The proliferation of genomic data has revolutionized biomedical research but simultaneously magnified the risks of privacy breaches in outsourced genomic computation. Existing privacy-preserving approaches ranging from differential privacy to homomorphic encryption and trusted execution environments, either compromise analytical accuracy, incur prohibitive computational overhead, or remain vulnerable to access-pattern leakage.

In this work, we present `RGeneSSE`, the first scalable encrypted frameworks for privacy-preserving genomic interval queries. Our approach reinterprets range queries as disjunctions of canonical range covers, enabling efficient realization using dynamic disjunctive searchable symmetric encryption leveraging the `GeneSSE` construction. The resulting framework achieves linear storage, constant-time updates, sub-linear search, and strong privacy guarantees including forward and Type-I backward privacy, while mitigating leakage vectors exploited by recent range reconstruction attacks.

Our security analysis and prototype implementation confirm that fine-grained, leakage-resilient, and dynamic encrypted genomic query processing is not only theoretically sound but also practically viable. Beyond computational biology, our techniques generalize to privacy-preserving range-based and Boolean search over large-scale encrypted databases, offering a promising foundation for secure, scalable, and privacy-compliant data analytics in modern cloud-based computing environments.z

## 6. Ethical Consideration

We believe that it is justifiable to use the Enron dataset for our experiments given: (i) the lack of alternative realistic datasets for conducting experiments, (ii) the extensive usage of this dataset for experiments in prior SSE literature [54], [57], [59], (iii) the fact that the data has long already been public, and (iv) there has been an effort by the researchers curating the version of the dataset used in this paper to remove users upon request.[16]

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16. See https://www.cs.cmu.edu/~enron/ for detailed documentation.

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# Appendix

## 1. Dynamic SSE

A dynamic searchable symmetric encryption (SSE) scheme consists of a polynomial-time algorithm Setup executed by the client, and protocols Search and Update executed jointly by the client and the server:

- Setup($\lambda$): A probabilistic algorithm that takes the security parameter $\lambda$. It outputs the tuple $(\mathsf{sk}, \mathsf{st}, \mathbf{EDB})$, where $\mathsf{sk}$ is the client's secret-key, $\mathsf{st}$ is the client's internal state, and $\mathbf{EDB}$ is an *empty* encrypted database.

- Update($\mathsf{sk}, \mathsf{st}, \mathsf{op}, (\mathsf{id}, \mathsf{w}); \mathbf{EDB}$): A client-server protocol, where the client takes as input the secret-key $\mathsf{sk}$, its state $\mathsf{st}$, an operation $\mathsf{op} \in \{\mathsf{add}, \mathsf{del}\}$ and an identifier-keyword pair $(\mathsf{id}, \mathsf{w})$, while the server takes as input the encrypted database $\mathbf{EDB}$. The protocol outputs a modified client state $\mathsf{st}'$ and a modified

encrypted database $\textbf{EDB}'$ so as to reflect the outcome of the addition/deletion operation.

- Search$(\mathsf{sk}, \mathsf{st}, q; \textbf{EDB})$: A client-server protocol, where the client takes as input the secret-key $\mathsf{sk}$, its state $\mathsf{st}$ and a query $q$, while the server takes as input the encrypted database $\textbf{EDB}$. At the end of the protocol, the client outputs $\textbf{DB}(q)$.

In the above, we adopted the definition of dynamic SSE used by Chamani *et al.* [75]. There exist other definitions of dynamic SSE in the literature [76], [77] where the Update operation takes an entire file for addition/deletion, which is functionally equivalent to executing multiple addition/deletion operations on the relevant identifier/keyword pairs in our framework. Finally, we make the implicit assumption that upon obtaining the set of file identifiers corresponding to a query, the client performs an additional interaction with the server to actually retrieve the files with these identifiers.

**Correctness.** A dynamic SSE is said to be correct if for every database $\textbf{DB}$ and for every query $q$, the Search protocol outputs $\textbf{DB}(q)$ with all but negligible probability.

**Security.** The security of a dynamic SSE scheme is parameterized by a leakage function

$$\mathcal{L} = \left( \mathcal{L}^{\texttt{Setup}}, \mathcal{L}^{\texttt{Search}}, \mathcal{L}^{\texttt{Update}} \right),$$

where $\mathcal{L}^{\texttt{Setup}}$ encapsulates the leakage to an adversarial server during the setup phase, $\mathcal{L}^{\texttt{Search}}$ encapsulates the leakage to an adversarial server during each execution of the search protocol, and $\mathcal{L}^{\texttt{Update}}$ encapsulates the leakage to an adversarial server during each execution of the update protocol.

Informally, a dynamic SSE scheme is secure with respect to a leakage function $\mathcal{L}$ if the adversarial server provably learns no more information about $\textbf{DB}$ other than that encapsulated by $\mathcal{L}$. Formally, a dynamic SSE scheme is said to be adaptively-secure with respect to a leakage function $\mathcal{L}$ if for any stateful PPT adversary $\mathcal{A}$ that issues a maximum of $Q = \mathsf{poly}(\lambda)$ queries, there exists a stateful probabilistic polynomial-time simulator $\textsc{Sim} = (\textsc{SimSetup}, \textsc{SimSearch}, \textsc{SimUpdate})$ such that the following holds:

$$\left| \Pr \left[ \textbf{Real}_{\mathcal{A}}^{\mathsf{Dy-SSE}}(\lambda, Q) = 1 \right] - \Pr \left[ \textbf{Ideal}_{\mathcal{A},\textsc{Sim}}^{\mathsf{Dy-SSE}}(\lambda, Q) = 1 \right] \right| \leq \mathsf{negl}(\lambda),$$

where the "real" experiment $\textbf{Real}^{\mathsf{Dy-SSE}}$ and the "ideal" experiment $\textbf{Ideal}^{\mathsf{Dy-SSE}}$ are as described in [23].

**Disjunctive Queries.** We represent a disjunctive query over $n$ distinct keywords $\mathsf{w}_1, \ldots, \mathsf{w}_n$ as $q = (\mathsf{w}_1 \vee \ldots \vee \mathsf{w}_n)$ and define the set $\textbf{DB}(q)$ as $\textbf{DB}(q) = \cup_{i=1}^{n} \textbf{DB}(\mathsf{w}_i)$.

**Range Queries.** We represent a $d$-dimensional range query $q = [a_1, b_1] \times \ldots \times [a_d, b_d]$ where $[a_i, b_i] \subseteq [1, |\mathcal{D}_i|]$ denotes the range in the $i$-th dimension.

## 2. TWINSSE: **Overview**

TWINSSE [20] is a fast and highly scalable SSE scheme with support for conjunctive, disjunctive and more general Boolean queries (in both CNF and DNF forms), that uses a conjunctive SSE scheme as a black box. The main contribution of the work is to support conjunctive, disjunctive and general Boolean queries with *linear* storage overhead that outperforms the existing SSE schemes [22] with similar query expressiveness. The core technical contribution of TWINSSE is generation of a "meta-database" that consists of specially designed "meta-keywords" (mkw), which is a disjunctive combination of specific keywords from the database (for more details on the construction of "meta-keywords" see [20]). The motivation for generating meta-keywords is to use a conjunctive SSE as a black box and support richer queries including conjunctions, disjunctions, and more general Boolean queries over encrypted data.

For example, a query of the form $q = \mathsf{w}_1 \vee \mathsf{w}_2 \vee \ldots \vee \mathsf{w}_n$ is processed by TWINSSE as follows - The original disjunctive query $q$ is transformed into a corresponding meta-query $q\mathsf{mkw} = \mathsf{mkw}_1 \wedge \mathsf{mkw}_2 \wedge \ldots \wedge \mathsf{mkw}_{n'}$ (where $n' \geq n$) consisting of a conjunction of meta-keywords corresponding to the keywords present in $q$. The transformed meta-query is then given to the conjunctive SSE oracle. The result returned by the SSE oracle is a super set of the result corresponding to the original disjunctive query $q$. Thus, TWINSSE provides a consolidated framework by deploying a conjunctive SSE as a black box that provides support for general Boolean queries over encrypted database.

The meta-keywords scale linearly with the number of keywords in the original database. The storage overhead of TWINSSE hence scales linearly with the plaintext database size. This results in a significant improvement over the quadratic storage overheads incurred by state-of-the-art SSE [22] supporting disjunctive and Boolean queries. The search time complexity of TWINSSE depends upon the underlying conjunctive SSE. In [20] the authors show an instantiation of TWINSSE from OXT [27] (TWINSSE$_{\mathsf{OXT}}$). The experimental results depict, TWINSSE$_{\mathsf{OXT}}$ exhibits sublinear search time complexity for both conjunctive and disjunctive queries, which makes it amenable to scale to large real-world databases.

## 3. GeneSSE: **Proof of Correctness**

The proof of correctness of GeneSSE follows from the (1) correctness of Gen_mkw, (2) correctness of GenMQuery [20] given that the frequency based bucketization has no effect on the correctness of TWINSSE, and (3) correctness of our modifications to ODXT [23]. We explain each in effect.

**Correctness of Gen_mkw.** Gen_mkw performs the following modifications to the original algorithm for generation of meta-database in [20]:

1. In [20], the set $\Delta$ is known in advance since [20] considers the static database model. In GeneSSE, $\Delta$ is constructed adaptively (line 3, Algorithm 2).

2. In [20], since the meta-database is generated one-time during SSE setup phase, meta-keywords for all buckets are generated at once. In `GeneSSE`, meta-keywords against the bucket of only the *updated* keyword (line 6, Algorithm 2) are generated/updated.

We note modifications (1) and (2) are correct w.r.t. correctness of meta-keyword generation. This follows from the arguments presented against Theorem 4.1 in [20]: given a partition on $\Delta$ as $\Delta_1 \cup \cdots \cup \Delta_{n_B}$ for $n_B$ buckets, application of $\text{TWINSSE}_{\text{Basic}}$ on each of the buckets ensures correctness of meta-keyword generation. Note that each bucket is *independently* operated upon by $\text{TWINSSE}_{\text{Basic}}$ for meta-keyword generation.

Now in `GeneSSE`, `Gen_mkw` is invoked for each query, which contains an update operation for exactly *one* keyword $w$. Line 3 in Algorithm 2 serves to update the set $\Delta$ by adding the updated keyword $w$ to $\Delta$; this allows for precise calculation of the number of buckets $n_B$ dynamically. In other words, modification (1) ensures correctness of $n_B$. Secondly, by design, the bucketization in `GeneSSE` ensures that $w$ falls in exactly a *single* bucket in the meta-database. In other words, $n_B - 1$ buckets are untouched by the updates to $w$. Line 6 in Algorithm 2 serves to pick that *single* bucket in the meta-database and regenerate meta-keywords for it, while leaving other buckets untouched. Recall from Theorem 4.1 in [20] that meta-keyword generation is *independent* for each bucket. This directly implies the correctness of modification (2) in `GeneSSE`: updating bucket $\Delta_k$ (lines 7-11, Algorithm 2) has no impact on other $n_B - 1$ buckets present in the meta-database; there is hence no need for `Gen_mkw` to update these $n_B - 1$ buckets to ensure correctness.

The remaining argument of correctness thereafter follows directly from [20]; Appendix B: where a query of form $\mathbf{DB}(q_{\text{mkw}})$ is correctly decomposed into sub-queries for each constituent bucket:

$$q_{\text{mkw}} = \bigcup_{u \in [n_B]} \mathbf{DB}(q_{\text{mkw},u})$$

Which, by structure of meta-keyword generation (which `Gen_mkw` does not change) finally leads to $\mathbf{DB}(q) \subseteq \mathbf{DB}(q_{mkw})$ with $| \mathbf{DB}(q) | = \eta \cdot | \mathbf{DB}(q_{mkw}) |$ for precision parameter $\eta$ (see our experimental results in Section 4 for details on concrete instantiation of $\eta$).

**Correctness of `GenMQuery`.** The only change in `GenMQuery` when shifting from the static database model in [20] to the dynamic database model in `GeneSSE` is the strategy undertaken to sort the keywords in query $q$. In [20], this sorting is done based on keyword frequency; in `GeneSSE`, the ordering is based on keyword update frequency. We note from Theorem 4.1 in [20] (as well as our discussions in Section 2.1) that sorting/ordering of keywords is solely for concrete improvement in search efficiency, and does not play a role in ensuring correctness. Thus, `GenMQuery` is correct.

**Correctness of `GeneSSE.Search` and `GeneSSE.UPDATE`.** Algorithm 3 and Algorithm 5 denote procedures for updates and searches in `GeneSSE`. We now show that correctness of Algorithm 3 and Algorithm 5 follows from the structure of `GeneSSE`. Consider a disjunctive query of the form:

$$q = \mathsf{w}_1 \vee \ldots \vee \mathsf{w}_n$$

By the correctness of `Gen_mkw` algorithm, it is converted into a corresponding meta-query of the form -

$$q_{\text{mkw}} = \mathsf{mkw}_1 \wedge \ldots \wedge \mathsf{mkw}_n$$

Once the meta-query is generated, the client identifies the meta-keyword with the least value of update count (`UC`). It generates the `stokenList` of `TSet` addresses using all updates of this meta-keyword. By the correctness of `TSet` routine [27], the correct set of $(\text{sval}, \alpha)$ is returned. For all such pairs in the set and all other meta-keywords $q_{\text{mkw}}$, the client generates a set of **xtoken** as -

$$\mathbf{xtoken}_{(i,p),l,j} = g^{F_p(K_X, \mathsf{mkw}_i^{k'} || \mathsf{w}_{k',p}) \cdot F_p(K_Z, \mathsf{mkw}_1^k || \mathsf{w}_{k,l} || j)}$$

where, $i = 2$ to $n$; $j = 1$ to $|\text{stokenList}|$; $(k, k') \in [n_B]$; $p \leftarrow \#\mathsf{w} \in \mathsf{mkw}_i^{k'}$; $l \leftarrow \#\mathsf{w} \in \mathsf{mkw}_i^k$. For an $\alpha_j == F_p(K_Y, \text{id} || \text{op}) \cdot (F_p(K_Z, \mathsf{mkw} || \mathsf{w} || \text{UC}[\mathsf{mkw}]))^{-1}$ corresponding to $\mathsf{mkw}_1^k$ and a correct $\mathbf{xtoken}_{(i,p),l,j}$[17], $(\mathbf{xtoken}_{(i,p),l,j})^{\alpha_j}$ will compute a correct **xtag** that is present in the `XSet`. The correctness of the **xtag** computation is guaranteed by the structure of $\alpha$ and **xtoken**. For all correctly matched **xtag**, the $(\text{sval}, \alpha)$ values will be returned to the client and the corresponding ids will be retrieved by the client. The $\mathbf{DB}(q_{\text{mkw}})$ thus obtained is a superset of the actual result of the disjunction, i.e. $\mathbf{DB}(q_{\text{mkw}}) \subseteq \mathbf{DB}(q)$; this holds from the correctness of `Gen_mkw`, thus proving the correctness of `GeneSSE`.

## 4. `GeneSSE`: Security Analysis

We present an informal overview of the leakage profile of `GeneSSE`, followed by a detailed formal leakage profile analysis, transitively followed by a formal proof of security is present.

**4.1. Leakage profile of `GeneSSE`. Setup Leakage.** Leakage from `GeneSSE.Setup` is similar to that of `TWINSSE`. The total size of the database (**DB**) is revealed, formally stated as -

$$|\mathbf{DB}| = \Sigma_{\mathsf{w} \in \Delta} |\mathbf{DB}(\mathsf{w})|$$

**Update Leakage.** Updates in `GeneSSE.UPDATE` are leakage free. This is a direct advantage of using `ODXT`: `ODXT` supports leakage-free updates. Only the `TSet` and `XSet` addresses are seen by the server that are randomly generated using a PRF.

**Search Leakages.** For a disjunctive query of the form $q = \mathsf{w}_1 \vee \ldots \vee \mathsf{w}_n$, `GeneSSE.Search` converts it into

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17. For a $\mathsf{w}_p^{k'} || \mathsf{mkw}_i^{k'}$ pair that matches $\mathsf{w}_l^k || \mathsf{mkw}_1^k$

a corresponding conjunction of meta-keywords $q_{\mathsf{mkw}} = \mathsf{mkw}_1 \wedge \ldots \wedge \mathsf{mkw}_n$, that is given to the server.

(i) *Result Pattern* (RP): Server learns the final result set, i.e. the document identifiers matching the conjunctive query of meta-kewords $q_{\mathsf{mkw}}$.

$$\mathsf{RP}(q_{\mathsf{mkw}}) = \mathbf{DB}(q_{\mathsf{mkw}})$$

Note, that the result of the original disjunctive query $q$ is a subset of $q_{\mathsf{mkw}}$ i.e., $\mathbf{DB}(q) \subseteq \mathbf{DB}(q_{\mathsf{mkw}})$.

(ii) *Size Pattern* (SP): Since the updates occur w.r.t to the meta-keywords, the server learns the number of updates pertaining to the least updated meta-keyword ($\mathsf{mkw}_1$ w.l.o.g), termed as the "sterm" henceforth [18], as well as the time stamp for each update.

(iii) *Equality Pattern* (EP): The server learns the common sterm for two or more conjunctive queries. This is because for the same sterm in two queries, the client generates the same stokens (see Algorithm 5) corresponding to $\mathsf{mkw}_1$.

(iv) *x-term Leakage*: For each update operation $(\mathsf{op}_j, (\mathsf{id}_j, \mathsf{mkw}_1))$ involving the sterm $\mathsf{mkw}_1$, the server learns the total number of update operations of the form $(\mathsf{op}_j, (\mathsf{id}_j, \mathsf{mkw}_i))$ for each xterm $\mathsf{mkw}_i \in \{\mathsf{mkw}_2, \ldots, \mathsf{mkw}_n\}$ for a conjunctive query $q = \mathsf{mkw}_1 \wedge \ldots \wedge \mathsf{mkw}_n$, along with the corresponding time stamp for each update.

(v) *Common x-term Leakage*: The server learns if two queries with distinct sterms $\mathsf{mkw}_1$ and $\mathsf{mkw}'_1$ share a common xterm ($\mathsf{mkw}_i$), provided that the update corresponding to $\mathsf{mkw}_1$ and $\mathsf{mkw}'_1$ involves atleast one common $(\mathsf{id}_j, \mathsf{w}_l)$ pair (where $\mathsf{w}_l \in (\mathsf{mkw}_1 \cap \mathsf{mkw}'_1)$). This leakage occurs because the $\mathbf{xtag}$ corresponding to the same $(\mathsf{id}_j, \mathsf{w}_l)$ pair.

**Improvements over** `ODXT`**.** Since `GeneSSE` is proposed as a dynamic disjunctive SSE where we specifically leverage the disjunctive operation of the unerlying `TWINSSE` framework, **some of the leakages specific to the conjunctive queries in** `ODXT` **are rendered inconsequential w.r.t. the proposed disjunctive framework**. We explain this now.

*Size Pattern*: Since the updates occur w.r.t to the meta-keywords in `GeneSSE`, the **server does not essentially learn any information regarding the underlying keyword in the original disjunctive query**. Therefore, the update corresponding to an sterm does not imply the updates corresponding to any specific keyword in the database.

*Equality Pattern Leakage*: As meta-keywords are a disjunctive composition of multiple keywords, the **server cannot infer any correlation between the actual keywords in the query and the** sterm **it observes over multiple iterations**. That is, the same sterm for two queries in in this case does not imply the same keyword is being queried in the original disjunction.

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18. This is by the design choice of OXT [27],ODXT [23], the the TSet addresses are generated corresponding to the least frequent term/ the term with least update count in the query. We note that selection of "sterm" is to achieve sub-linear search complexity

*x-term Leakage*: For every update of the form $(\mathsf{op}_j, (\mathsf{id}_j, \mathsf{mkw}_1))$ involving the sterm $\mathsf{mkw}_1$, the server learns the total number of update operations of the form $(\mathsf{op}_j, (\mathsf{id}_j, \mathsf{mkw}_i))$ for each xterm $\mathsf{mkw}_i \in \{\mathsf{mkw}_2, \ldots, \mathsf{mkw}_n\}$, along with the corresponding time stamp for each update. **The server, however, does not learn the number of updates corresponding to actual keywords in the disjunctive query**. Also, updates corresponding to a meta-keyword do not reveal update history of any specific keyword. Each meta-keyword $\mathsf{mkw}$ is a disjunctive composition of specific keywords; therefore, an update pertaining to any $\mathsf{w} \in \mathsf{mkw}$ will lead to an update of $\mathsf{mkw}$. Since the specific keywords constituent in a $\mathsf{mkw}$ is not known to the server, it is not possible for it to track the update history of any specific keyword from the update history of $\mathsf{mkw}$. For an update of the form $(\mathsf{op}_j, (\mathsf{id}_j, \mathsf{w}_1))$, it is converted to the corresponding meta-keyword update that $\mathsf{w}$ corresponds to.

*Common x-term Leakage*: The server learns if two queries with distinct sterms $\mathsf{mkw}_1$ and $\mathsf{mkw}'_1$ share a common xterm ($\mathsf{mkw}_i$), provided that the update corresponding to $\mathsf{mkw}_1$ and $\mathsf{mkw}'_1$ involves atleast one common $(\mathsf{id}_j, \mathsf{w}_l)$ pair (where $\mathsf{w}_l \in (\mathsf{mkw}_1 \cap \mathsf{mkw}'_1)$). This leakage occurs because the $\mathbf{xtag}$ corresponding to the same $(\mathsf{id}_j, \mathsf{w}_l)$ pair. **This will also not leak anything about the keywords in the query, as the** sterm **or** xterm **all correspond to meta-keywords**.

**4.2. Formal Leakage profile of** `GeneSSE`**.** In this section, we give a formal analysis of the leakage profile of `GeneSSE` and prove its forward and backward privacy. A dynamic disjunctive SSE scheme is forward and backward private if: (i) an update operation reveals no additional information about a disjunctive search operation that took place at an earlier time, and (ii) a search operation on a disjunctive query $q = \mathsf{w}_1 \vee \ldots \vee \mathsf{w}_n$ reveals no information about certain deletion operations on $\mathsf{w}_n$ that took place at an earlier time. We formally establish below that `GeneSSE` achieves this notion of forward and backward privacy.

Let $Q$ be a list with the following types of entries:

(i) $(t, \mathsf{w})$: Search query on keyword $\mathsf{w}$ at timestamp $t$.
(ii) Update query $\mathsf{op} \in \{\mathsf{add}, \mathsf{del}\}$ on the identifier-keyword pair $(\mathsf{id}, \mathsf{w})$ at time stamp $t$.

**Output Leakages.** For any keyword $\mathsf{w}$, we define `TimeDB(w)` to be the function that returns the list of all file identifiers containing $\mathsf{w}$ that have not been deleted yet, along with their respective time stamps of insertion. Formally -

$$\begin{aligned} \mathsf{TimeDB}(\mathsf{w}) = \ & \{(t, \mathsf{id}) | (t, \mathsf{add}, (\mathsf{id}, \mathsf{w})) \in Q \\ & and \quad \forall t' : (t', \mathsf{del}, (\mathsf{id}, \mathsf{w})) \notin Q\} \end{aligned}$$

For a conjunction of meta-keywords $q_{\mathsf{mkw}} = \mathsf{mkw}_1 \wedge \ldots \wedge \mathsf{mkw}_n$, $\mathsf{TimeDB}(q_{\mathsf{mkw}})$ is defined as -

$$\begin{aligned} \mathsf{TimeDB}(q_{\mathsf{mkw}}) = \ & \{(\{t_i\}_{i \in [n]}, \mathsf{id}) | (t_i, \mathsf{add}, (\mathsf{id}, \mathsf{mkw}_i)) \in Q \\ & and \quad \forall t' : (t', \mathsf{del}, (\mathsf{id}, \mathsf{mkw}_i)) \notin Q\} \end{aligned}$$

In other words, $\texttt{TimeDB}(q_{mkw})$ returns the list of identifiers corresponding to documents containing $q_{mkw} = \mathsf{mkw}_1 \wedge \ldots \wedge \mathsf{mkw}_n$ that have not yet been deleted, along with their respective time stamps of insertion. Thus, $\texttt{TimeDB}(q_{mkw})$ captures the output leakage for $q_{mkw}$.

*Note.* In case of $\texttt{GeneSSE}$ for a disjunctive query $q = \mathsf{w}_1 \vee \ldots \vee \mathsf{w}_n$, $\mathbf{DB}(q)$ is not actually computed by the server, instead it work on meta-keyowrds a and returns $\mathbf{DB}(q_{mkw})$. Thus $\texttt{TimeDB}(q)$ does not capture the exact list of identifiers on $\mathbf{DB}(q)$. We can thus say, that the exact time stamps corresponding to the insertion of a particular keyword is obfuscated in $\texttt{GeneSSE}$. Thus, $\texttt{TimeDB}(q)$ for any disjunctive query $q = \mathsf{w}_1 \vee \ldots \vee \mathsf{w}_n$ is essentially $\perp$ -

$$\texttt{TimeDB}(q) = \perp$$

**x-term Leakages.** We define $\mathsf{Upd}(\mathsf{w}_1, \mathsf{w}_2)$ for any pair of keywords $(\mathsf{w}_1, \mathsf{w}_2)$ as follows (similar as $\texttt{ODXT}$):

$$\mathsf{Upd}(\mathsf{w}_1, \mathsf{w}_2) = \{(t_1, t_2) | \exists (\mathsf{op}, \mathsf{id}) : (t_1, \mathsf{op}, (\mathsf{id}, \mathsf{w}_1)) \in Q$$
$$and \quad (t_2, \mathsf{op}, (\mathsf{id}, \mathsf{w}_2)) \in Q\}$$

Thus, $\mathsf{Upd}(\mathsf{w}_1, \mathsf{w}_2)$ returns the time stamps of all update operations on $w_1$ and $w_2$ that involve the same document identifier. This however is not applicable for $\texttt{GeneSSE}$ because for every update of a keyword w the corresponding meta-keywords in which w is present are updated. The set of meta-keywords for both $\mathsf{w}_1$ and $\mathsf{w}_2$ is might intersect but will never be identical by its structure. Therefore even if the id corresponding to the update of $\mathsf{w}_1$ and $\mathsf{w}_2$ is same, the timestamp corresponding to the updates cannot be exactly inferred because of the meta-keyword updates that actually happen at the server. Thus $\mathsf{Upd}(q)$ for a disjunctive query $q = \mathsf{w}_1 \vee \ldots \vee \mathsf{w}_n$, which is transformed into $q_{mkw} = \mathsf{mkw}_1 \wedge \ldots \wedge \mathsf{mkw}_n$ has the following $\mathsf{Upd}(\mathsf{mkw})$ (we overload notation for $\mathsf{Upd}$ and use its definition interchangeable for keywords and meta-keywords):

$$\mathsf{Upd}(q_{mkw}) = \mathsf{Upd}(\mathsf{mkw}_1) \cup \left( \bigcup_{i=2}^{n} \mathsf{Upd}(\mathsf{mkw}_1, \mathsf{mkw}_i) \right)$$

Formally the leakage profile of $\texttt{GeneSSE}$ is defined as follows -

$$\mathcal{L}_{\texttt{GeneSSE}} = (\mathcal{L}_{\texttt{GeneSSE}}^{\texttt{Setup}}, \mathcal{L}_{\texttt{GeneSSE}}^{\mathsf{Upd}}, \mathcal{L}_{\texttt{GeneSSE}}^{\texttt{Search}})$$

such that -
  (i) $\mathcal{L}_{\texttt{GeneSSE}}^{\texttt{Setup}} = \perp$
  (ii) $\mathcal{L}_{\texttt{GeneSSE}}^{\mathsf{Upd}}(\mathsf{op}, (\mathsf{id}, \mathsf{w})) = \perp$
  (iii) $\mathcal{L}_{\texttt{GeneSSE}}^{\texttt{Search}}(q) = (\texttt{TimeDB}(q_{mkw}), \mathsf{Upd}(q_{mkw}))$
Finally we prove the main theorem for $\texttt{GeneSSE}$.

**4.3. Proof of Theorem 2.** We prove Theorem 2 via a sequence of experiments between a challenger and an adversary, where the first experiment is identical to the real experiment $\mathbf{Real}^{\mathsf{Dy-SSE}}(\lambda, Q)$, while the final experiment is identical to the simulation experiment $\mathrm{SIM}^{\mathsf{Dy-SSE}}(\lambda, Q)$. We establish formally that the view of the adversary $\mathcal{A}$

in each pair of consecutive experiments is computationally indistinguishable.

**Experiment-0.** This experiment is identical to the real experiment $\mathbf{Real}^{\mathsf{Dy-SSE}}(\lambda, Q)$. The challenger generates the transcript corresponding to each update operation using the $\texttt{GeneSSE.Update}$ algorithm and the transcript corresponding to each disjunctive search using the $\texttt{GeneSSE.Search}$ algorithm.

**Experiment-1.** This experiment is identical to Experiment-0, except that when generating the transcripts for each update and disjunctive search (conjunctive search on $\mathsf{mkw}$), the challenger replaces each PRF evaluation of the form $F(K_T, \cdot)$ with a function evaluation of the form $G_T(\cdot)$, where the function $G_T$ is uniformly sampled from the set of all functions that map $\lambda$-bit strings onto $\lambda$-bit strings.

**Lemma A.1.** *Assuming that $F$ is a secure PRF, the view of the adversary $\mathcal{A}$ in Experiment-1 is computationally indistinguishable from the view of the adversary $\mathcal{A}$ in Experiment-0.*

*Proof.* Let $\mathcal{B}_1$ be a probabilistic polynomial-time algorithm that can distinguish between the views of the adversary $\mathcal{A}$ in Experiment-0 and Experiment-1. Then $\mathcal{B}_1$ can be used to design a probabilistic polynomial-time adversary $\mathcal{B}_1'$ that can distinguish a set of PRF evaluations of the form $F(K_T, \cdot)$ from a set of function evaluations of the form $G_T(\cdot)$, where the function $G_T$ is uniformly sampled from the set of all functions that map $\lambda$-bit strings onto $\lambda$-bit strings. By definition, $\mathcal{B}_1'$ breaks the pseudorandomness of PRF $F$, which is a contradiction. $\square$

**Experiment-2a.** This experiment is identical to Experiment-1, except that when generating the transcripts for each update and conjunctive search operation, the challenger replaces each PRF evaluation of the form $F_p(K_X, \cdot)$ with a function evaluation of the form $G_X(\cdot)$, where the function $G_X$ is uniformly sampled from the set of all functions that map $\lambda$-bit strings onto elements in $\mathbb{Z}_p^*$.

**Lemma A.2.** *Assuming that $F_p$ is a secure PRF, the view of the adversary $\mathcal{A}$ in Experiment-2a is computationally indistinguishable from the view of the adversary $\mathcal{A}$ in Experiment-1.*

*Proof.* Let $\mathcal{B}_2$ be a probabilistic polynomial-time algorithm that can distinguish between the views of the adversary $\mathcal{A}$ in Experiment-1 and Experiment-2a. Then $\mathcal{B}_2$ can be used to design a probabilistic polynomial-time adversary $\mathcal{B}_2'$ that can distinguish a set of PRF evaluations of the form $F_p(K_X, \cdot)$ from a set of function evaluations of the form $G_X(\cdot)$, where the function $G_X$ is uniformly sampled from the set of all functions that map $\lambda$-bit strings onto elements in $\mathbb{Z}_p^*$. By definition, $\mathcal{B}_2'$ breaks the pseudorandomness of $F_p$, which is a contradiction. $\square$

**Experiment-2b.** This experiment is identical to Experiment-2a, except that when generating the transcripts for each update and disjunctive search (conjunctive search of $\mathsf{mkw}$) operation, the challenger replaces each PRF evaluation of

the form $F_p(K_Y, \cdot)$ with a function evaluation of the form $G_Y(\cdot)$, where the function $G_Y$ is uniformly sampled from the set of all functions that map $\lambda$-bit strings onto elements in $\mathbb{Z}_p^*$.

**Lemma A.3.** *Assuming that $F_p$ is a secure PRF, the view of the adversary $\mathcal{A}$ in Experiment-2b is computationally indistinguishable from the view of the adversary $\mathcal{A}$ in Experiment-2a.*

*Proof.* The proof of this lemma is identical to the proof of Lemma A.2. □

**Experiment-2c.** This experiment is identical to Experiment-2b, except that when generating the transcripts for each update and disjunctive search (conjunctive search of mkw) operation, the challenger replaces each PRF evaluation of the form $Fp(K_Z, \cdot)$ with a function evaluation of the form $G_Z(\cdot)$, where the function $G_Z$ is uniformly sampled from the set of all functions that map $\lambda$-bit strings onto elements in $\mathbb{Z}_p^*$.

**Lemma A.4.** *Assuming that $F_p$ is a secure PRF, the view of the adversary $\mathcal{A}$ in Experiment-2c is computationally indistinguishable from the view of the adversary $\mathcal{A}$ in Experiment-2b.*

*Proof.* The proof of this lemma is identical to the proof of Lemma A.2. □

**Experiment-3.** This experiment is identical to Experiment-2c, except that when generating the transcripts for each disjunctive search operation, the challenger changes the manner in which each **xtoken** value is generated. More specifically, for a disjunctive query $q = \mathsf{w}_1 \vee \ldots \vee \mathsf{w}_n$ which is converted into a corresponding meta-query $q_{\mathsf{mkw}} = \mathsf{mkw}_1 \wedge \ldots \wedge \mathsf{mkw}_n$, the challenger first looks up the history of update queries made by the adversary $\mathcal{A}$ to retrieve the set of update operations $\{(\mathsf{op}_j, (\mathsf{id}_j, \mathsf{mkw}_1))\}$ involving the sterm $\mathsf{mkw}_1$. Next, for each keyword $\mathsf{mkw}_i$ in the conjunction and each update operation $(\mathsf{op}_j, (\mathsf{id}_j, \mathsf{mkw}_1))$, it locally computes the corresponding TSet blinding factor $\alpha_{i,j}$ and the corresponding cross-tag $\mathbf{xtag}_{i,j}$ exactly as in the real GeneSSE scheme, and generates the corresponding $\mathbf{xtoken}_{i,j}$ as: $\mathbf{xtoken}_{i,j} = \mathbf{xtag}_{i,j}^{1/\alpha_{i,j}}$. For the *padded* **xtoken**s (Section 2.2), this experiment randomly samples **xtag** from its appropriate domain, $\beta \leftarrow Z_p^*$, and sets $\mathbf{xtoken} = \mathbf{xtag}_{i,j}^{1/\alpha_{i,j}} = (g^\beta)^{1/\alpha_{i,j}}$, where $g$ is the generator for the group $\mathcal{G}$.

**Lemma A.5.** *The view of the adversary $\mathcal{A}$ in Experiment-3 is identical to the view of the adversary $\mathcal{A}$ in Experiment-2c.*

*Proof.* The proof of this lemma follows immediately because the distribution of each **xtoken** value in Experiment-2c is identical to the distribution of each **xtoken** value in Experiment-3. In Experiment-2c for any triplet $(\alpha_{i,j}, \mathbf{xtag}_{i,j}, \mathbf{xtoken}_{i,j})$, we have $\mathbf{xtag}_{i,j} = \mathbf{xtoken}_{i,j}^{\alpha_{i,j}}$, i.e., $\mathbf{xtoken}_{i,j} = \mathbf{xtag}_{i,j}^{1/\alpha_{i,j}}$, which is identical to Experiment-3. The joint distribution of actual **xtokens**

and padded **xtoken**s is independent and random in $\mathbb{Z}_p^*$, considering DDH assumption holds in $\mathcal{G}$ Thus the view of adversary $\mathcal{A}$ in Experiment-3 is identical to the view of the adversary $\mathcal{A}$ in Experiment-2c. □

**Experiment-4.** This experiment is identical to Experiment-3, except that when generating the transcripts for each update operation, the challenger changes the manner in which each pre-computed blinding factor value is generated i.e., instead of computing $\alpha$ as in Experiment-3, it simply samples $\alpha \xleftarrow{\$} \mathbb{Z}_p^*$. For the *padded* **xtoken**s (Section 2.2), this experiment randomly samples **xtag** from its appropriate domain, $\beta \leftarrow Z_p^*$, and sets $\mathbf{xtoken} = \mathbf{xtag}_{i,j}^{1/\alpha_{i,j}} = (g^\beta)^{1/\alpha_{i,j}}$, where $g$ is the generator for the group $\mathcal{G}$.

**Lemma A.6.** *The view of adversary $\mathcal{A}$ in Experiment-4 is statistically indistinguishable from the view of adversary $\mathcal{A}$ in Experiment-3.*

*Proof.* Function $G_Z$ is uniformly randomly sampled from the set of all functions that map $\lambda$-bit strings onto elements in $\mathbb{Z}_p^*$. Also due to the changes made in Experiment-3 to the generation of **xtoken** values, the function $G_Z$ is only evaluated once during each update operation (to generate the blinding factor to be stored in the TSet), and is never re-evaluated during any of the conjunctive search (of mkw). Finally, the function $G_Z$ is never evaluated on the same input in two different update operations, and each evaluation of $G_Z$ is independent of the random coins used by the challenger in the rest of the experiment.

In Experiment-3, each pre-computed blinding factor $\alpha$ value in $\mathbb{Z}_p^*$ is generated as the product of an evaluation of $G_Y$ in $\mathbb{Z}_p^*$ with the inverse of an evaluation of $G_Z$ in $\mathbb{Z}_p^*$. Finally, The joint distribution of actual **xtokens** and padded **xtoken**s is independent and random in $\mathbb{Z}_p^*$, considering DDH assumption holds in $\mathcal{G}$. These facts, combined with the aforementioned observations, immediately imply that distribution of each value of $\alpha$ in Experiment-4 is statistically indistinguishable from that in Experiment-3. □

**Experiment-5.** This experiment is identical to Experiment-4, except that when generating the transcripts for each update operation, the challenger changes the manner in which each **xtag** value is generated. Instead of computing each **xtag** value as in Experiment-4, it simply samples $\gamma \xleftarrow{\$} \mathbb{Z}_p^*$ and sets $\mathbf{xtag} = g^\gamma$, where $g$ is the generator for the group $\mathcal{G}$.

**Lemma A.7.** *Assuming that the DDH assumption holds in the group $\mathcal{G}$, the view of the adversary $\mathcal{A}$ in Experiment-5 is computationally indistinguishable from the view of the adversary $\mathcal{A}$ in Experiment-4.*

The proof of this lemma follows from the fact that extended DDH assumption holds in the group $\mathcal{G}$ in a similar manner as done in ODXT [23].

**Experiment-6.** This experiment is identical to Experiment-5 except that when generating the transcript for each update operation, the challenger replaces each function evaluation of the form $G_T(\mathsf{mkw}||cnt||b)$ for $b \in \{0, 1\}$ with a function

evaluation of the form $G_T(t)$, where $t$ is the time stamp at which the update operation is executed. Similarly, when generating the transcript for each conjunctive search operation (of mkw), the challenger replaces each function evaluation of the form $GT(\mathsf{mkw}||cnt||0)$ with a function evaluation of the form $G_T(t)$, where $t$ is the time stamp corresponding to the operation that this evaluation is meant to address in the TSet.

**Lemma A.8.** *The view of the adversary $\mathcal{A}$ in Experiment-6 is identical to the view of the adversary $\mathcal{A}$ in Experiment-5.*

*Proof.* In Experiment-5, the function $G_T$ is never evaluated on the same input at two different time stamps due to the presence of the monotonically increasing counter variable. In addition, the function $G_T$ is uniformly randomly sampled from the set of all functions that map $\lambda$-bit strings onto $\lambda$-bit strings. This immediately implies that the distribution of $G_T$ evaluations in Experiments 5 and 6 are identical from the point of view of the adversary $\mathcal{A}$. $\qquad\square$

**Experiment-7.** This experiment is identical to Experiment-6 except that we now replace the challenger with a simulator SIM that does not have access to the actual queries made by the adversary $\mathcal{A}$. Instead, SIM only has access to the following leakage profile for each update/conjunctive query issued by the adversary $\mathcal{A}$.

**Update Leakages:** SIM has access to an empty update leakage function, i.e., it gains no information about any of the update queries issued by $\mathcal{A}$. It uses the time stamp of the update query to generate the TSet (address, value) pair, as done by the challenger in Experiment-6. It generates a uniformly random blinding factor $\alpha$, as done by the challenger in Experiment-6. Finally, it samples $\gamma \xleftarrow{\$} \mathbb{Z}_p^*$ and sets $\mathbf{xtag} = g^\gamma$, where $g$ is the generator for the group $\mathcal{G}$, as done by the challenger in Experiment-6.

**Search Leakages.** SIM has access to the following search leakages.

*Size Pattern*: SIM learns the number of update operations involving the sterm $\mathsf{mkw}_1$, as well as the time stamp for each such operation, which it uses to simulate the set of $\mathtt{stoken}$ values using the function $G_X$ as done by the challenger in Experiment-6.

*x-term Leakage*: For each update operation $(\mathsf{op}_j, (\mathsf{id}_j, \mathsf{mkw}_1))$ involving the sterm $\mathsf{mkw}_1$, SIM learns the total number of updates of the form $(\mathsf{op}_j, (\mathsf{id}_j, \mathsf{mkw}_i))$ for each xterm $\mathsf{mkw}_i \in \{\mathsf{mkw}_2, \ldots, \mathsf{mkw}_n\}$, as well the corresponding time stamp for each such operation. It uses this information to determine the corresponding $\mathbf{xtag}_{i,j}$ value and the corresponding blinding factor $\alpha_{i,j}$ and then generate $\mathbf{xtoken}_{i,j}$ as: $\mathbf{xtoken}_{i,j} = \mathbf{xtag}_{i,j}^{1/\alpha_{i,j}}$ as done by challenger in Experiment-6.

*Result Pattern*: SIM learns the final set of document identifiers in the conjunction of meta-keywords, and uses these to retrieve the corresponding documents.

*Equality Pattern*: SIM learns if two (or more) conjunctive queries have the same sterm $\mathsf{mkw}_1$, and generates the

$\mathtt{stoken}$ values to be consistent across these queries by evaluating the function $G_X$ on the same set of time stamps.

*Common x-term Leakage*: SIM learns if two queries with (possibly distinct) sterms $\mathsf{mkw}_1$ and $\mathsf{mkw}_1'$ share a common xterm $\mathsf{mkw}_i$, provided that the update histories for $\mathsf{mkw}_1$ and $\mathsf{mkw}_1'$ involve at least one common document identifier $\mathsf{id}_j$. When processing these queries, SIM makes sure to generate the same cross-tag $\mathbf{xtag}_{i,j}$.

**Lemma A.9.** *The view of the adversary $\mathcal{A}$ in Experiment-7 is identical to the view of the adversary $\mathcal{A}$ in Experiment-6.*

*Proof.* The proof of this lemma follows immediately from the fact that the transcripts generated by SIM corresponding to each update and conjunctive meta-keyword query issued by the adversary $\mathcal{A}$ are identical to the corresponding transcripts generated by the challenger in Experiment-6. $\qquad\square$

**Experiment-8.** This experiment is identical to Experiment-7 except that we now replace the simulator SIM with a simulator SIM$'$ that has access to a leakage function $\mathcal{L} = (\mathcal{L}^{\mathtt{Setup}}, \mathcal{L}^{\mathsf{Upd}}, \mathcal{L}^{\mathtt{Search}})$, such that -

$$\mathcal{L}^{\mathsf{Upd}}(\mathsf{op}, (\mathsf{id}, \mathsf{mkw})) = \bot$$

$$\mathcal{L}^{\mathtt{Search}}(q_{\mathsf{mkw}}) = (\mathtt{TimeDB}(q_{\mathsf{mkw}}), \mathsf{Upd}(q_{\mathsf{mkw}}))$$

The simulator SIM$'$ runs simulator SIM in Experiment-7 as a sub-routine when interacting with the adversary $\mathcal{A}$.

**Lemma A.10.** *The view of the adversary $\mathcal{A}$ in Experiment-8 is identical to the view of the adversary $\mathcal{A}$ in Experiment-7.*

The proof of this lemma follows in the similar manner as in ODXT. We mark here that the entire leakage from which SIM generates the transcripts is related to the meta-keywords. No leakage w.r.t to the keywords is captured by the leakage profile of GeneSSE.
This completes the proof of Theorem 2.

## 5. Forward Privacy of GeneSSE

We formally describe the forward privacy guarantees of GeneSSE in this section. According to the formal definition introduced by [78], a dynamic disjunctive SSE scheme is adaptively secure with respect to a leakage profile

$$\mathcal{L} = (\mathcal{L}^{\mathtt{Setup}}, \mathcal{L}^{\mathsf{Upd}}, \mathcal{L}^{\mathtt{Search}})$$

is said to be adaptively *forward private* if there exists a stateless function $\mathcal{L}'$ such that for any arbitrary triplet $(\mathsf{op}, \mathsf{id}, \mathsf{w})$, we have

$$\mathcal{L}^{\mathsf{Upd}}(\mathsf{op}, (\mathsf{id}, \mathsf{w})) = \mathcal{L}'(\mathsf{op}, \mathsf{id})$$

This implies that an update operation computationally hides the underlying keyword w, therefore, it cannot be correlated with any previous search query involving w by a computationally bounded adversary. Since $\mathcal{L}_{\mathsf{GeneSSE}}^{\mathtt{UPDATE}} = \bot$, an update operation in GeneSSE hides not only the underlying keyword w, but also the identifier id and the operation op. In

other words, the following is a natural corollary of Theorem-2:

**Corollary 1** (Forward Privacy of `GeneSSE`)**.** *Assuming that $F$ and $F_p$ are secure PRFs and the decisional Diffie-Hellman assumption holds over the group $\mathcal{G}$,* `GeneSSE` *is adaptively forward private.*

## 6. Backward Privacy of `GeneSSE`

We formally describe the backward privacy of `GeneSSE`. According to the formal definition introduced by Bost et al. [78], a dynamic SSE scheme that supports *single* keyword searches and is adaptively secure with respect to some leakage function $\mathcal{L} = (\mathcal{L}^{\text{Setup}}, \mathcal{L}^{\text{Upd}}, \mathcal{L}^{\text{Search}})$ is adaptively *Type-I backward private* if there exist stateless functions $\mathcal{L}'$ and $\mathcal{L}''$ such that for any $(\text{op}, \text{idw})$, we have

$$\mathcal{L}^{\text{Upd}}(\text{op}, (\text{id}, \text{w})) = \mathcal{L}''(\text{op}, \text{id}) \text{ and}$$
$$\mathcal{L}^{\text{Search}}(\text{w}) = \mathcal{L}'''(\textbf{DB}(\text{w}), \text{UC}(\text{w}))$$

We have -
$$\mathcal{L}^{\text{Upd}}_{\text{GeneSSE}}(\text{op}, (\text{id}, mkw)) = \perp,$$
$$\mathcal{L}^{\text{Search}}_{\text{GeneSSE}}(q_{mkw}) = \{\text{TimeDB}(q_{mkw}), \text{Upd}(q_{mkw})\}$$

for any disjunctive query $q$. This is a natural generalization of the aforementioned leakage profile of Type-I backward privacy from the setting of a single keyword searches to our setting of disjunctive searches[19]. Note that the structure of meta-keywords ensures no correlations about $\text{UC}(\text{w})$ can be drawn from $\text{Upd}(q_{mkw})$. Hence, a natural corollary of Theorem-2 states -

**Corollary 2** (Backward Privacy of `GeneSSE`)**.** *Assuming that $F$ and $F_p$ are secure PRFs and the decisional Diffie-Hellman assumption holds over the group $\mathcal{G}$,* `GeneSSE` *is adaptively Type-I backward private.*

## 7. `RGeneSSE` **Security Analysis**

In this section we provide a simulation-based proof approach for `RGeneSSE`. We assume that `GeneSSE` is an adaptively secure dynamic disjunctive SSE with respect to the following leakage profile -

$$\mathcal{L}_{\text{GeneSSE}} = (\mathcal{L}^{\text{Setup}}_{\text{GeneSSE}}, \mathcal{L}^{\text{Upd}}_{\text{GeneSSE}}, \mathcal{L}^{\text{Search}}_{\text{GeneSSE}})$$

We define the leakage profile of `RGeneSSE` as follows -

$$\mathcal{L}_{\text{RGeneSSE}} = (\mathcal{L}^{\text{Setup}}_{\text{RGeneSSE}}, \mathcal{L}^{\text{Upd}}_{\text{RGeneSSE}}, \mathcal{L}^{\text{Search}}_{\text{RGeneSSE}})$$

where,
$$\mathcal{L}^{\text{Setup}}_{\text{RGeneSSE}}(\textbf{DB}) = \mathcal{L}^{\text{Setup}}_{\text{GeneSSE}}(\textbf{DB})$$

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19. Similar generalization have also been used to prove backward privacy guarantees of dynamic SSE scheme previously [23]

$$\mathcal{L}^{\text{Upd}}_{\text{RGeneSSE}}(\text{op}, (\text{id}, \text{w})) = \mathcal{L}^{\text{Upd}}_{\text{GeneSSE}}(\text{op}, (\text{id}, \text{w}))$$

and,

$$\mathcal{L}^{\text{Search}}_{\text{RGeneSSE}}(q_{\text{range}}) = \mathcal{L}^{\text{Search}}_{\text{GeneSSE}}(q_{\text{dis}})$$

where $q_{\text{range}}$ is a range query of the form $q_{\text{range}} = [a_i, b_i]$ where $[a_i, b_i] \subseteq [1, |\mathcal{D}_i|]$ denotes the range in the $i$-th dimension and $q_{\text{dis}}$ is a disjunctive query of the form $q_{\text{dis}} = \text{w}_1 \vee \ldots \vee \text{w}_n$.

We show that `RGeneSSE` is secure against an adaptive semi-honest adversary $\mathcal{A}$, which has access to leakages from $\mathcal{L}_{\text{RGeneSSE}}$. We build a simulator SIM that generates **EDB** by $\mathcal{L}_{\text{RGeneSSE.Update}}$, and generates transcripts $\tau_i$ for query $q_{\text{range}}$ over **EDB** from the search leakages, $\mathcal{L}_{\text{RGeneSSE.search}}$. SIM has inputs from $\mathcal{L}_{\text{RGeneSSE}}$ only. To prove the security of `RGeneSSE`, we extend the simulator of the underlying forward and backward private `GeneSSE`, and explain how it handles simulation for range queries.

**Simulating** `RGeneSSE.`**Setup:** The Setup leakage of `RGeneSSE` leaks no information (similar to the Setup leakage of `GeneSSE`):

$$\mathcal{L}^{\text{Setup}}_{\text{RGeneSSE}} = \mathcal{L}^{\text{Setup}}_{\text{GeneSSE}} = \perp$$

**Simulating** `RGeneSSE.`Update**:** The UPDATE leakage of `RGeneSSE` is similar to the UPDATE leakage of `GeneSSE`. The simulator outputs its version of **EDB** according to the simulation process of `GeneSSE` (we proved that `GeneSSE` is provably simulation secure in Appendix D.3).

$$\begin{aligned}\textbf{EDB}_{\text{SIM}} &= \text{SIM}^{\text{Upd}}_{\text{RGeneSSE}}(\textbf{DB}) \\ &= \text{SIM}^{\text{Upd}}_{\text{GeneSSE}}(\textbf{DB}) \\ &= \text{SIM}^{\text{Upd}}_{\text{GeneSSE}}(\textbf{DB}, n')\end{aligned}$$

where $n'$ (bucket size) is a public parameter. Since, `GeneSSE` is proven simulation secure, it follows from the simulation security guarantee of `GeneSSE` that **EDB**$_{\text{SIM}}$ is indistinguishable from the one generated in the real experiment.

**Simulating** `RGeneSSE.`**Search:** A range query $q_{\text{range}}$ is transformed into a disjunctive query $q_{\text{dis}}$ from the output of the $\text{BRC}_{RT}$ algorithm (as shown in Algorithm 10). The covering set of nodes returned by $\text{BRC}_{RT}$ is used to formulate the disjunctive query. We argue that the adversary $\mathcal{A}$ does not gain any information about the original keywords in a disjunctive query with this simulation experiment. The distribution of **DB** for original keywords (hence, also for **EDB**) is abstracted by the meta-keywords. With $\mathcal{L}^{\text{Search}}_{\text{RGeneSSE}}$ that entails the leakages from `GeneSSE.Search` or, $\mathcal{L}^{\text{Search}}_{\text{GeneSSE}}$, SIM invokes the simulator of `GeneSSE` for simulating the search on the disjunction of the nodes returned by $\text{BRC}_{RT}$. Since, `GeneSSE.Search` invoked in `RGeneSSE.Search` (Algorithm 10) executes over meta-keyword only, this leakage is expressed in the context of meta-keywords as below.

$$\mathcal{L}'_{\text{GeneSSE}} = \mathcal{L}_{\text{GeneSSE}}(\{\text{mkw}_i\})$$

With this leakage information of `GeneSSE`, the search leakage of `RGeneSSE` can be expressed as below -

$$\mathcal{L}_{\text{RGeneSSE}}^{\texttt{Search}}(q_{\text{range}}) = \mathcal{L}_{\text{RGeneSSE}}^{\texttt{Search}}(q_{\text{dis}})$$
$$= \mathcal{L}_{\text{RGeneSSE}}^{\texttt{Search}}(q_{\text{mkw},k})_{k \in [n_\text{B}]}$$
$$= \{\mathcal{L}'_{\text{GeneSSE}}, n'\}$$

The parameters $n_\text{B}$ and $n'$ are derived from $N$ (number of keywords), which is available during setup. Therefore, the search leakage of `RGeneSSE` is same as the underlying `GeneSSE`, which can be summarized as below.

$$\mathcal{L}_{\text{RGeneSSE}}^{\texttt{Search}}(q_{\text{range}}) = \mathcal{L}_{\text{RGeneSSE}}^{\texttt{Search}}(q_{\text{dis}})$$
$$= \mathcal{L}_{\text{RGeneSSE}}^{\texttt{Search}}(q_{\text{mkw},k})_{k \in [n_\text{B}]}$$
$$= \mathcal{L}'_{\text{GeneSSE}}$$

This same leakage profile for search in `RGeneSSE` and `GeneSSE` in the context of meta-keywords ensures that no additional information is leaked beyond `GeneSSE` leakage.

## 8. Forward and Backward Privacy of `RGeneSSE`

Since `GeneSSE` is proven to be adaptively forward private and Type-II backward private in Appendix E and F, the forward and backward privacy guarantees of `RGeneSSE`follows directly from the following corollary.

**Corollary 3** (Forward Privacy of `RGeneSSE`)**.** *Assuming* `GeneSSE` *is adaptively forward private dynamic disjunctive SSE,* `RGeneSSE`*is an adaptively forward private dynamic range SSE scheme.*

**Corollary 4** (Backward Privacy of `RGeneSSE`)**.** *Assuming* `GeneSSE` *is Type-I backward private dynamic disjunctive SSE,* `RGeneSSE`*is a Type-I backward private dynamic range SSE scheme.*