

Exploring Distributed Vector Databases Performance on HPC Platforms: A Study with Qdrant

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Abstract

Vector databases have rapidly grown in popularity, enabling efficient similarity search over data such as text, images, and video. They now play a central role in modern AI workflows, aiding large language models by grounding model outputs in external literature through retrieval-augmented generation. Despite their importance, little is known about the performance characteristics of vector databases in high-performance computing (HPC) systems that drive large-scale science. This work presents an empirical study of distributed vector database performance on the Polaris supercomputer in the Argonne Leadership Computing Facility. We construct a realistic biological-text workload from BV-BRC and generate embeddings from the pes2o corpus using Qwen3-Embedding-4B. We select Qdrant to evaluate insertion, index construction, and query latency with up to 32 workers. Informed by practical lessons from our experience, this work takes a first step toward characterizing vector database performance on HPC platforms to guide future research and optimization.¹

1 Introduction

Vector databases enable efficient search over encoded representations of embedded data known as vectors. Amid the rapid advancement of modern AI systems, they have become an integral component of scientific workflows [18, 34, 52], particularly those leveraging retrieval-augmented generation (RAG) [3, 5, 8, 38, 50]. As large-scale workflows are increasingly executed on high-performance computing (HPC) systems, vector databases must be adapted to the unique characteristics of these environments, which include specialized interconnects, parallel file systems, deep memory hierarchies, and heterogeneous hardware architectures [13, 20–22, 29, 41]. While prior work has studied the performance and trade-offs of vector databases [39] in the context of single-GPU RAG, to the best of our knowledge no studies have focused on understanding or optimizing vector database performance in the context of scientific

workloads and HPC systems, which remain the primary environment for large-scale scientific computation. A deeper understanding of how distributed vector databases perform on HPC architectures is necessary to inform system design, improve performance, and guide future research.

This work presents an early evaluation of vector database performance on an HPC system; we characterize the runtime performance of Qdrant [37], a popular distributed vector database, on the Polaris supercomputer in the Argonne Leadership Computing Facility² using a realistic biological workflow. We generate embeddings based on the pes2o [42] scientific text corpus using Qwen3-Embedding-4B [51]. We provide insight and recommendations for future work from our deployment experience on Polaris (see section 4). In summary, we make the following contributions.

- We evaluate Qdrant’s distributed performance on Polaris, testing insertion, index-building, and query performance with up to 32 Qdrant workers that span 8 compute nodes.
- We provide a first step toward characterizing vector database performance on HPC platforms, detailing the lessons learned from our experience.
- We publish a scientific embedding dataset and query workload for future use.³

2 Distributed Vector Databases

Section 2.1 provides the necessary background to understand the distributed vector database landscape. Section 2.2 discusses a few of the popular distributed vector databases and their features.

2.1 Background

Vector databases are specialized data management systems designed to store, index, and search high-dimensional vector representations of data [16, 25]. These vectors, also known as embeddings [26, 36], are numerical representations of data such as text, images, or audio. Embeddings capture semantic or structural relationships between data such that similar items are represented by vectors that are

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²<https://www.alcf.anl.gov/polaris>

³<https://doi.org/10.5281/zenodo.17101276>

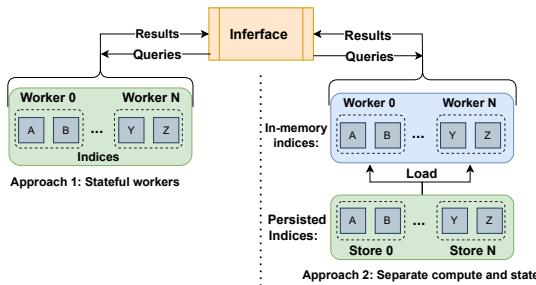


Figure 1: Two example distributed vector database configurations. Blue boxes represent stateless workers, and green boxes denote the presence of a state.

close together in the embedding space [23, 51]. This process enables efficient similarity search via (approximate) nearest neighbor search [9, 28]: Given a query encoded as a vector, the system computes its distance (e.g., cosine similarity, euclidean, inner product) to all stored embeddings and returns the top N closest vectors as the most similar results.

As the number of embeddings grows, searching the entire database becomes intractable [28]. To address this challenge, vector databases employ specialized data structures known as indexes [4, 16, 25] to enable efficient approximate nearest neighbor (ANN) search. These indexes reduce the number of required distance computations by pruning large portions of the search space while aiming to maximize accuracy. Common index types include graph-based approaches such as Hierarchical Navigable Small World (HNSW) graphs [25], inverted file structures often paired with product quantization [17], and tree-based methods such as KD-trees [4]. The choice of index depends on dataset size, dimensionality, latency requirements, and the desired trade-off between accuracy and query or insertion time. For details on algorithms and trade-offs, we refer readers to Ma et al. [24].

To achieve even greater scalability and support thousands of concurrent queries, practitioners employ distributed vector databases [37, 45–48]. Distributed vector databases divide coordination, computation, and data storage among multiple workers while presenting a single unified interface to users. In order to accomplish this, the data is sharded into independent indexes built for each shard [11, 37, 45–48]. Sharding is one of the primary techniques for achieving horizontal scalability in vector databases. There are two dominant sharding approaches: stateful (approach 1 of fig. 1) and stateless with compute/storage separation (approach 2 of fig. 1). In a stateful architecture, each worker stores state such as indexes or data and performs the needed computation to serve queries for its shard. In essence, the worker both “owns” and is responsible for a portion of the dataset. This paradigm is used by vector databases such as Qdrant [37], Vald [45], and Weaviate [48]. Alternatively, in a stateless architecture, workers perform computation but do not persistently store the dataset or indexes locally. Instead, data is stored in a separate, durable storage layer (often an object storage or file system) and loaded into a cache layer when needed. This approach is used by distributed vector databases such as Vespa [46] and Milvus [47]. Regardless of the specific architecture, a distributed vector

database must support search across all data shards. To do so, the query is broadcast to all workers,⁴ and each worker performs an ANN search over its shards. The partial results are then aggregated, and the top results are returned.

2.2 State of the Art

A few popular distributed vector databases include Vespa [46], Vald [45], Weaviate [48], Milvus [11, 47], and Qdrant [37]. Table 1 shows an overview of a few of their notable features. All the listed databases support parallel reading/writing, multicore acceleration, elasticity, and shard replication for increased availability and reliability. However, only a subset—Vespa and Milvus—support compute-storage separation, while only Vald, Weaviate, and Milvus support GPU-accelerated ANN search. The ability to scale compute independently of state allows the workflow to add more workers without repartitioning persisted data—traditionally an expensive process [6, 27, 43] that requires both data transfer and the reconstruction of impacted indexes. The degree to which compute-storage separation is critical depends on the workload. While all the described vector databases support elastic addition/subtraction of workers, stateful architectures require data rebalancing before the new resources can be fully utilized. For relatively static query and update patterns, there is little need to rapidly scale the number of workers independently of data storage. However, recent work [27] showed that real-world workloads (e.g., Wikipedia) often exhibit dynamic and skewed access/update patterns, highlighting the advantages of compute-storage separation.

2.3 Related Work

The rapid adoption of vector databases in large language model (LLM) workflows and other data-intensive applications has led to several recent surveys [12, 15, 19, 35, 44] that review LLM architectures, storage/retrieval mechanisms, use cases, and open challenges. Although these works include feature-level comparisons of widely used systems, none provides empirical performance evaluations, particularly in HPC settings [30]. Shen et al. [39] evaluated multiple index types in the context of single-GPU RAG but did not evaluate distributed vector database systems or test in an HPC environment. Xu et al. [49] proposed a distributed vector database designed for scalability and benchmarked it against FAISS [7], but they did not benchmark against existing distributed systems or perform experiments in an HPC setting.

3 Performance Evaluation

We consider an end-to-end workflow that leverages vector databases to contextualize raw data records with information from papers, which is intended to be used in biological RAGs. This synthetic data could also be used in a variety of ways to improve LLM performance: pretraining/fine-tuning the model [10], training a cross-modal adapter [1], or better grounding the output of the system with tools (see [33]). The target workload uses a small subset of 22,723 terms related to genomes available through BV-BRC [31]—a

⁴In the case of queries that filter based on a condition (predicated queries), some vector databases perform prefiltering to reduce the shard search space. To the best of our knowledge, however, for non-predicated ANN search, all the systems discussed in this work follow a broadcast-reduce workflow.

System	Parallel Read/Write	Compute/Storage Separation	Load Balanced	Autoscaling	GPU Indexing	GPU ANN
Vespa	✓	✓	✓	✓	✗	✗
Vald	✓	✗	✓	✓	✓	✓
Weaviate	✓	✗	✓	✓	✓	✓
Qdrant	✓	✗	✓	✓	✓	✗
Milvus	✓	✓	✓	✓	✓	✓

Table 1: Comparison of features among state-of-the-art distributed vector databases. Some of the listed features are available only in the paid cloud offerings of the respective vector database; such entries are denoted as ✓.

comprehensive bioinformatics resource developed to support biological research. Each term is used to generate a query that searches the papers contained within the pes2o dataset [42] (comprising up to 8 million full-text papers) for data related to the term. The intuition is that searching across a collection of research papers allows one to find data directly related to the target term, thereby providing better context for the information that would be supplied to a RAG system. This approach mimics prior work on synthetic data generation [10]. Although pes2o is not a dedicated biological corpus, it serves as a proxy for an internal large corpus containing biological papers. In this work we focus on runtime performance rather than correctness, for which pes2o is sufficient. Our analysis examines embedding generation, data insertion, index-building, and query behavior. We perform all testing on Polaris. Each compute node features a 2.8 GHz AMD EPYC Milan 7543P 32-core CPU, 512 GB of DDR4 RAM, and four NVIDIA A100 GPUs. The system is interconnected using HPE Slingshot 11 and uses a Dragonfly topology. We select Qdrant as the vector database system for our initial evaluation.

3.1 Embedding Generation

We generate embeddings using the collection of full academic papers in the pes2o dataset, comprising a total of 8,293,485 embeddings. We generate a single embedding per paper by feeding each paper’s full text into the Qwen3-Embedding-4B model, a state-of-the-art embedding model that fits within a single 40 GB GPU. In future work we could apply chunking techniques [40], which would likely improve retrieval quality but increase the number of entities in the database, stressing performance further. To ensure efficiency, we design an adaptive pipeline overseen by an orchestrator. Based on user-controlled parameters, the orchestrator batches the input text into single-node jobs to minimize queue wait time and monitors a user-defined set of queues. As availability within a queue opens, the orchestrator submits the next batch. The orchestrator can be paused and resumed as needed, with the flexibility to adjust target queues and the number of jobs per queue. Within a single job, multiprocessing is used to process papers concurrently, splitting work among all available GPUs. Each GPU uses a simple heuristic—based on limits for total characters and the number of papers per batch—to determine how many papers to process in each batch. Based on empirical observations, we define each batch as 4,000 papers and set the total batch character limit and maximum batch size to 150,000 and 8, respectively. In the event of an OOM error, the GPU falls back to sequential processing for that individual batch,

Model Loading	I/O	Inference
28.17	7.49	2381.97

Table 2: Mean embedding generation runtime in seconds across $N=2,079$ batches of approximately 4,000 papers. Model loading refers to loading the model weights from disk and transferring them to the GPU; I/O denotes the time spent loading the raw text from disk; and inference refers to the period spent generating embeddings.

ensuring that there is no possibility of truncated papers.

Results: Across all jobs, embedding generation (model inference) dominates overall runtime (see table 2), with a mean runtime that comprises 98.5% of total runtime ($2,417.84 \pm 113.92$ s). Notably, the batching heuristic was highly successful at preventing memory errors while promoting parallelism, processing less than 0.10% of the papers sequentially. These findings indicate that for datasets that fit comfortably within an HPC compute node’s memory, embedding generation efforts should prioritize improving the efficiency of model inference rather than I/O or model loading.

3.2 Data Insertion

After embedding generation, the data must be uploaded to the Qdrant workers. To optimize insertion performance, we tune the batch size (i.e., number of vectors per upload request) and the number of allowed concurrent upload requests on a 1 GB subset of the full dataset. Although the effects of changing batch size and concurrency may interact, for brevity in this work we fix the batch size to the optimal value discovered during batch size tuning while adjusting the degree of concurrency. To perform multiple concurrent upload requests, we use Qdrant’s asynchronous client implementation and Python’s asyncio library. After tuning, we upload the full dataset to a Qdrant cluster with the following number of workers: 1, 4, 8, 16, and 32. The data is partitioned across workers, with each worker responsible for approximately 80 GB/#Workers of data. We employ multiprocessing to assign one client to each Qdrant worker. Each client is configured with the optimal batch size and degree of concurrency determined during tuning. All clients run on a single compute node, while the Qdrant servers are deployed on separate compute nodes, with four Qdrant workers per machine.

Results: Figure 2 presents the insertion time for a 1 GB subset of the full dataset, measured using a single Qdrant worker with varying parameter settings. Batch size exhibits a clear optimization curve, with performance improving from 468 s (size 1) to a minimum of 381 s (size 32) before gradually degrading at larger batch

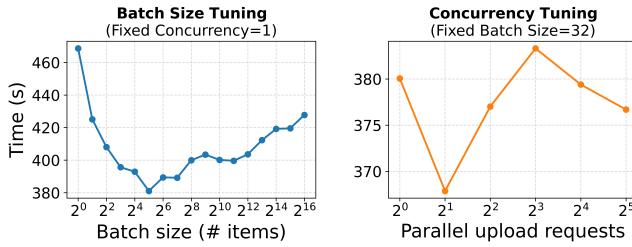


Figure 2: Data insertion time for a 1 GB dataset into a single-worker Qdrant cluster on Polaris using varying batch sizes and parallel requests. The optimal discovered batch size was used while tuning the number of parallel requests.

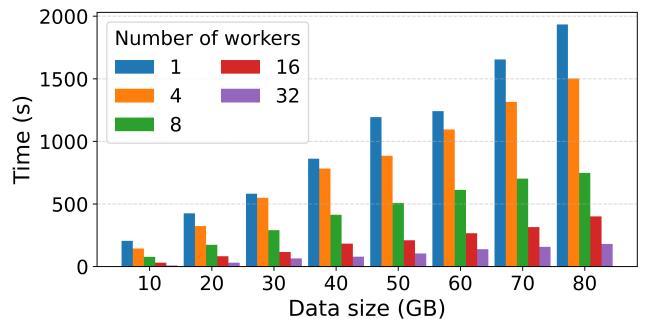


Figure 3: Index build time versus dataset size for varying numbers of Qdrant workers.

Workers	1	4	8	16	32
Time	8.22 h	2.11 h	1.14 h	35.92 m	21.67 m

Table 3: Full dataset (~80 GB) insertion time as a function of the number of Qdrant workers.

sizes. Increasing the number of concurrent insertion requests shows diminishing returns: insertion time decreases from 381 s (1 request) to 367 s (2 requests) but increases thereafter. This trend reflects the constraints of `asyncio` when applied directly to data insertion without further customization. By default Python’s `asyncio` library runs tasks in a single synchronous thread, with each task yielding control only when it hits the `await` keyword during data upload; CPU-bound tasks are not performed in parallel. Profiling reveals that, on average, with a batch size of 32, converting the batch into a Qdrant batch object—a CPU task—for upload requires 45.64 ms, while data insertion requires only 14.86 ms. Thus, the potential speedup from allowing multiple concurrent upload requests is minimal, defined at a maximum of 1.31× by Amdahl’s law [2]. Qdrant’s asynchronous approach to single-client parallelism yields limited speedup during data upload, as CPU-bound tasks dominate runtime. Consequently, **multiprocessing may be better suited than asyncio for single-client parallelism during data insertion**. The scaling is more favorable as we increase the number of Qdrant workers and correspondingly total clients. The total insertion time decreases from approximately 8.22 hours with 1 Qdrant worker to 21.67 minutes with 32 Qdrant workers (see table 3). While the upload speed is significantly below the theoretical network bandwidth, this is expected; during data insertion, in addition to the data being communicated over the network, Qdrant is storing the data, optimizing the data layout to minimize memory usage, and building indexes in the background. While a more detailed profile of I/O, data communication, and CPU operations is needed to understand the cause, the rate of **data insertion has the potential to become a bottleneck for large-scale, scientific HPC workloads** that need to continually insert, index, and search new data. Further optimizations to data insertion should be a high priority for the HPC community.

3.3 Index-Building

To evaluate the index-building phase, we measure index construction time with various amounts of data. Although indexes are typically built incrementally as data arrives, Qdrant’s documentation⁵ suggests deferring index construction to accelerate insertion in certain cases, necessitating a complete index rebuild. We mimic this scenario and use the default HNSW index settings. For this work we focus on CPU evaluation; future work will explore Qdrant’s performance with GPU-enabled index-building.

Results: As the number of Qdrant workers increases, the index build time decreases, with a maximum speedup of 21.32× using 32 workers relative to a single-worker Qdrant. This scaling behavior is expected because each index can be constructed independently; partitioning the data across workers proportionally reduces the workload per worker and enables substantial performance gains. However, as shown in fig. 3, the scaling falls short of linear. This is likely due to interworker communication overhead and resource contention, as each group of four workers shares a single compute node. This limitation is most apparent when scaling from one to four workers, which displays a maximum speedup of 1.27x. Profiling reveals that a single worker already utilizes 90–97% of the compute node’s CPU capacity during index construction, indicating that **deploying multiple Qdrant workers per node is unnecessary to achieve CPU saturation during index-building**. To better exploit per-node resources and leverage multiple Qdrant workers per node, index-building could be offloaded to GPUs. Future work will test different cluster configurations and GPU-based index construction.

3.4 Query

To optimize query performance, we tune the query batch size and number of concurrent batches in flight in the same manner as described in section 3.2. We set the query to return the 10 most similar results. After tuning, we test our biological query workload with Qdrant clusters of 1, 4, 8, 16, and 32 workers, utilizing the parameters discovered through tuning.

⁵<https://qdrant.tech/documentation/database-tutorials/bulk-upload/>

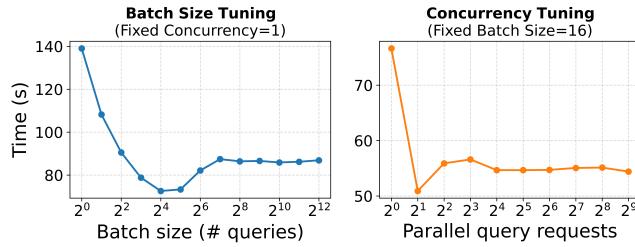


Figure 4: Query running time for a 1 GB dataset into a single-worker Qdrant cluster on Polaris using varying batch sizes and parallel requests.

Results: Figure 4 shows query time using a single Qdrant worker with varying parameter settings on a 1 GB subset of the data. We observe that increasing the batch size reduces runtime until a batch size of 16 (from 139 s to 73 s) before further increases yield minimal benefit. Similar to the results shown in table 3, the shortest runtime is observed when only two parallel query requests are allowed. Follow-up testing revealed that as the number of parallel batch requests increases past 2, the average time spent waiting for the result from the worker grows correspondingly. For example, the average per-batch call time rises from 30.7 ms with 2 concurrent requests to 76.4 ms with 4 requests, and further to 170 ms with 8 requests, suggesting that the worker’s resources are saturated. In our distributed tests, increasing the number of workers provides little benefit until the dataset reaches at least 30 GB (see fig. 4). This behavior arises from Qdrant’s query execution model: the client submits a query to one of the workers, which broadcasts it to the others. Each worker then searches its local shards and returns partial results to the worker first contacted by the client, which sends the final response back. Although this approach parallelizes the search computation, it also introduces communication overhead across the workers. For smaller datasets, this overhead outweighs the gains from horizontal sharding; only once the dataset size exceeds 30 GB does the parallelization begin to deliver a speedup, reducing runtime by a maximum of 3.57×. Notably, increasing the cluster size beyond four provides only marginal improvements, suggesting that the reduction in runtime due to parallelization may be overshadowed by the cost of interworker communication. **Our results suggest that further improvement could be obtained if the cluster could adaptively scale based on the size of the data.**

4 Conclusion

This work presents an initial evaluation of the distributed vector database system, Qdrant, in an HPC environment with up to 32 workers. We evaluate a realistic end-to-end biology workload, including embedding generation, data insertion, index-building, and query runtime. We release our embedding and query dataset for future use, and we provide the following initial insights based on our experience:

- Embedding generation runtime is dominated by model inference.

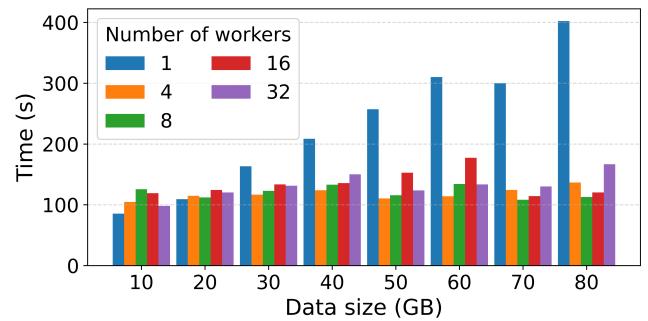


Figure 5: Query time versus dataset size for varying numbers of Qdrant workers.

- The conversion of data into Qdrant batch objects is CPU-bound and often slower than the insertion RPC, making multiprocessing a better choice than asyncio.
- Index-building is a CPU-intensive workload, saturating a compute node’s CPU while utilizing only a single worker. Offloading index-building to the GPUs may increase the benefit of utilizing multiple workers per compute node.
- Increasing the number of workers yielded only limited reductions in query runtime for our 80 GB dataset. Additional techniques may be required to fully leverage multiworker parallelism on smaller datasets.

In this study we did not focus on runtime variability or reproducibility. Future work could investigate the performance variability. We also evaluated only CPU-based index construction; a comparison against the GPU implementation is warranted in future work. Moreover, our evaluation focused on a single system; a comprehensive, multisystem study of distributed vector databases on different HPC platforms is needed to fully characterize the design space.⁶

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