

# Technical Report

## "Sparse Vector and Matrix Library"

### Abstract

This project delivers a custom-built Python library designed for **high-performance handling of sparse data structures** (vectors and matrices). The core innovation lies in implementing the **CSR (Compressed Sparse Row) format** for matrices and optimizing all critical algorithms to achieve  $O(nnz)$  **complexity** (linear with respect to the number of non-zero elements). This approach provides exponential memory savings and computational efficiency compared to standard dense arrays. The implementation is rigorously validated against the **SciPy** industrial standard, demonstrating performance competitive with highly optimized C/C++ libraries.

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## 1. Introduction: Problem Statement and Foundational Principles

### 1.1. The Data Wasteland: The Problem of Sparsity

In scientific computing, especially in **Single-Cell Biology (scRNA-seq)**, **Graph Theory**, and **Machine Learning (NLP/Recommender Systems)**, datasets are characterized by extreme sparsity (often 90% to 99% zeros).

- **Inefficiency:** Standard array structures (dense storage) allocate resources for every zero, leading to catastrophic **memory wastage** and redundant CPU cycles (multiplying by zero).
- **The Project's Solution:** Implement specialized structures that adhere to two primary efficiency principles:
  1. **Storage Efficiency:** Store only the non-zero elements.
  2. **Computational Efficiency:** Execute operations by iterating only over the stored non-zeros.

### 1.2. The Role of the Test Generator ( `test_generator.py` )

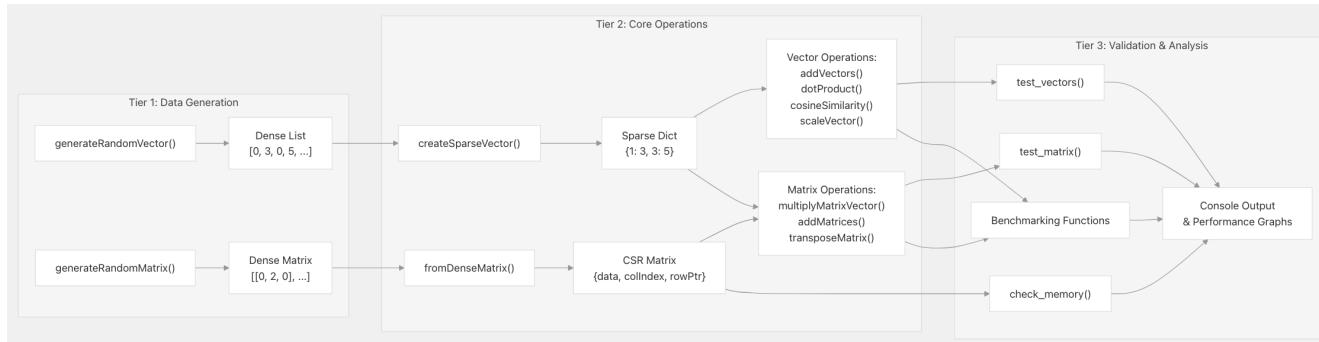
This module provides **scientific rigor** by ensuring **reproducibility**. It uses a Linear Congruential Generator (`randomNumber`) with an explicit `seed` to create data that is consistently:

- Scalable (up to  $2000 \times 2000$ ).

- Controllable in Sparsity (e.g., 0.99), precisely simulating real-world high-sparsity scenarios like scRNA-seq.

## 2. Architecture and Core Data Structures

The following diagram illustrates the three-tier architecture with actual function calls and data flows:

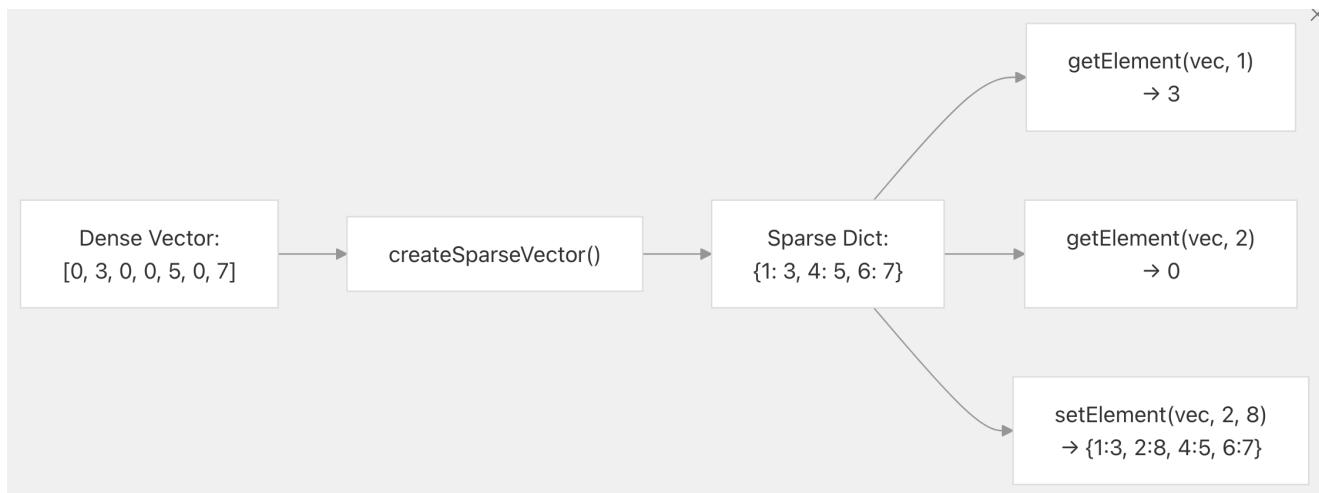


### Architecture Tiers

- 1. Data Generation Tier ([test\\_generator.py](#)):** Produces controlled test data with specified dimensions and sparsity levels
- 2. Core Operations Tier ([SparseVector.py](#) [SparseMatrix.py](#)):** Implements sparse data structures and operations with no external dependencies
- 3. Validation Tier ([demo.py](#) [benchmark.py](#)):** Tests correctness and measures performance

### 2.1. Sparse Vector ( [SparseVector.py](#) )

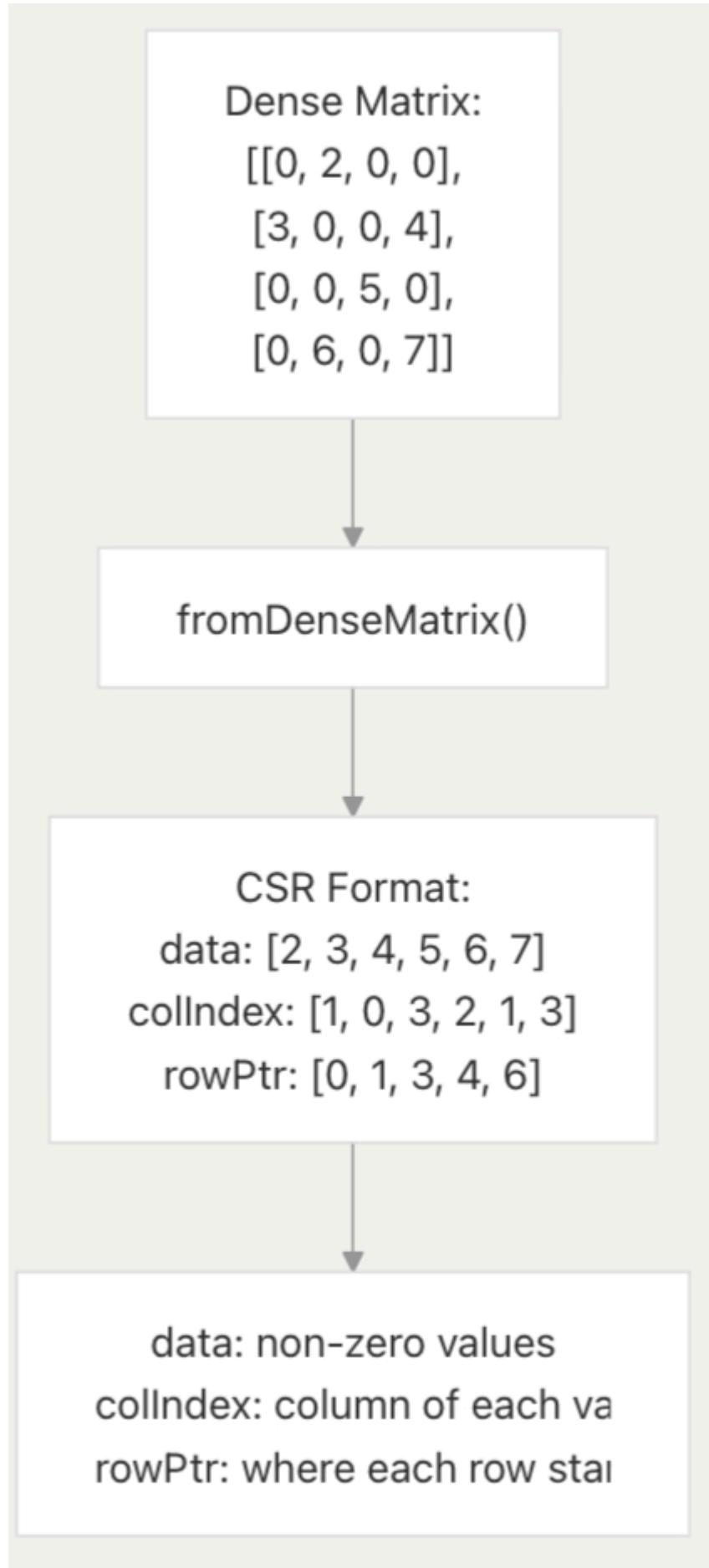
- **Structure:** Implemented using a standard Python **Dictionary** ( {index: value} ).
- **Advantage:** Provides O(1) (constant time) lookup for elements and highly flexible memory management, avoiding the need to pre-allocate memory for N positions.



The dictionary format provides O(1) access to both non-zero and zero elements. Keys are indices, values are non-zero elements.

### 2.2. Sparse Matrix ( [SparseMatrix.py](#) ): The CSR Format

The choice of **Compressed Sparse Row (CSR)** is the project's most critical architectural decision. CSR separates the symbolic structure from the numerical data:



The CSR format stores three arrays:

- `data` : non-zero values in row-major order
- `colIndex` : column index for each value in `data`
- `rowPtr` : indices marking where each row begins in `data` array

**Example Access:** `getMatrixElement(matrix, 1, 3)` returns 4

- Row 1 starts at `rowPtr[1]=1`, ends at `rowPtr[2]=3`
- Search `colIndex[1:3]` for column 3
- Find it at index 2, return `data[2]=4`

Array	Role	Component
<code>data</code>	Stores all non-zero values.	Numerical
<code>colIndex</code>	Stores the column index for each value in <code>data</code> .	Symbolic/Structure
<code>rowPtr</code>	Stores pointers indicating the starting position of each new row in the other two arrays.	Symbolic/Structure

The `rowPtr` array is the key to CSR's speed, enabling **instantaneous identification of the non-zero elements within any given row**.

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### 3. Algorithmic Efficiency and Symbolic Logic

The library's performance gains are rooted in achieving the optimal  $O(nnz)$  complexity for all critical functions:

#### 3.1. Vector Operations (Dot Product)

- **Function:** `dotProduct(vec1, vec2)`
- **Complexity:**  $O(nnz)$
- **Mechanism:** The function iterates only through the non-zero indices of the first vector. By performing an  $O(1)$  dictionary lookup in the second vector, it avoids all null

operations and scales strictly by the amount of meaningful data.

```
# Create sparse vectors from dense representation
dense1 = [0, 3, 0, 0, 5, 0, 7, 0, 0, 2]
vec1 = sv.createSparseVector(dense1) # {1: 3, 4: 5, 6: 7, 9: 2}

dense2 = [1, 0, 0, 4, 0, 6, 0, 0, 8, 0]
vec2 = sv.createSparseVector(dense2) # {0: 1, 3: 4, 5: 6, 8: 8}

# Vector operations
result = sv.addVectors(vec1, vec2)
dot = sv.dotProduct(vec1, vec2)
similarity = sv.cosineSimilarity(vec1, vec2)
scaled = sv.scaleVector(vec1, 2)

# Memory efficiency
non_zero_count = sv.countNonZero(vec1) # 4 elements
memory_bytes = sv.getMemorySize(vec1) # 64 bytes vs 80 for dense
```

## 3.2. Matrix-Vector Multiplication (SpMV)

- **Function:** multiplyMatrixVector(matrix, vector)
- **Complexity:** O(nnz)
- **Symbolic Logic:** The operation is guided by the CSR's structure. Before any computation, the symbolic arrays ( `rowPtr` , `colIndex` ) dictate the **exact pattern** of vector elements to be fetched and multiplied. This pre-determined path ensures sequential memory access for the row elements, maximizing cache efficiency and minimizing wasted clock cycles.

```
# Create sparse matrix
dense = [[0, 2, 0, 0],
          [3, 0, 0, 4],
          [0, 0, 5, 0],
          [0, 6, 0, 7]]
matrix = sm.fromDenseMatrix(dense)

# Matrix operations
vec = {0: 1, 1: 2, 2: 3, 3: 4}
result = sm.multiplyMatrixVector(matrix, vec)
transposed = sm.transposeMatrix(matrix)

# Memory efficiency
sparsity = sm.getSparsity(matrix) # 0.625 (62.5% zeros)
```

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## 4. Verification and Benchmark Results

The `benchmark.py` module executed a total of **70 individual measurements** across 21 unique configurations (sizes up to 5000 for vectors and  $2000 \times 2000$  for matrices) to confirm both memory and speed advantages.

## 4.1. Memory Efficiency Test ( `test_memory()` )

The results confirm exponential memory savings as sparsity increases:

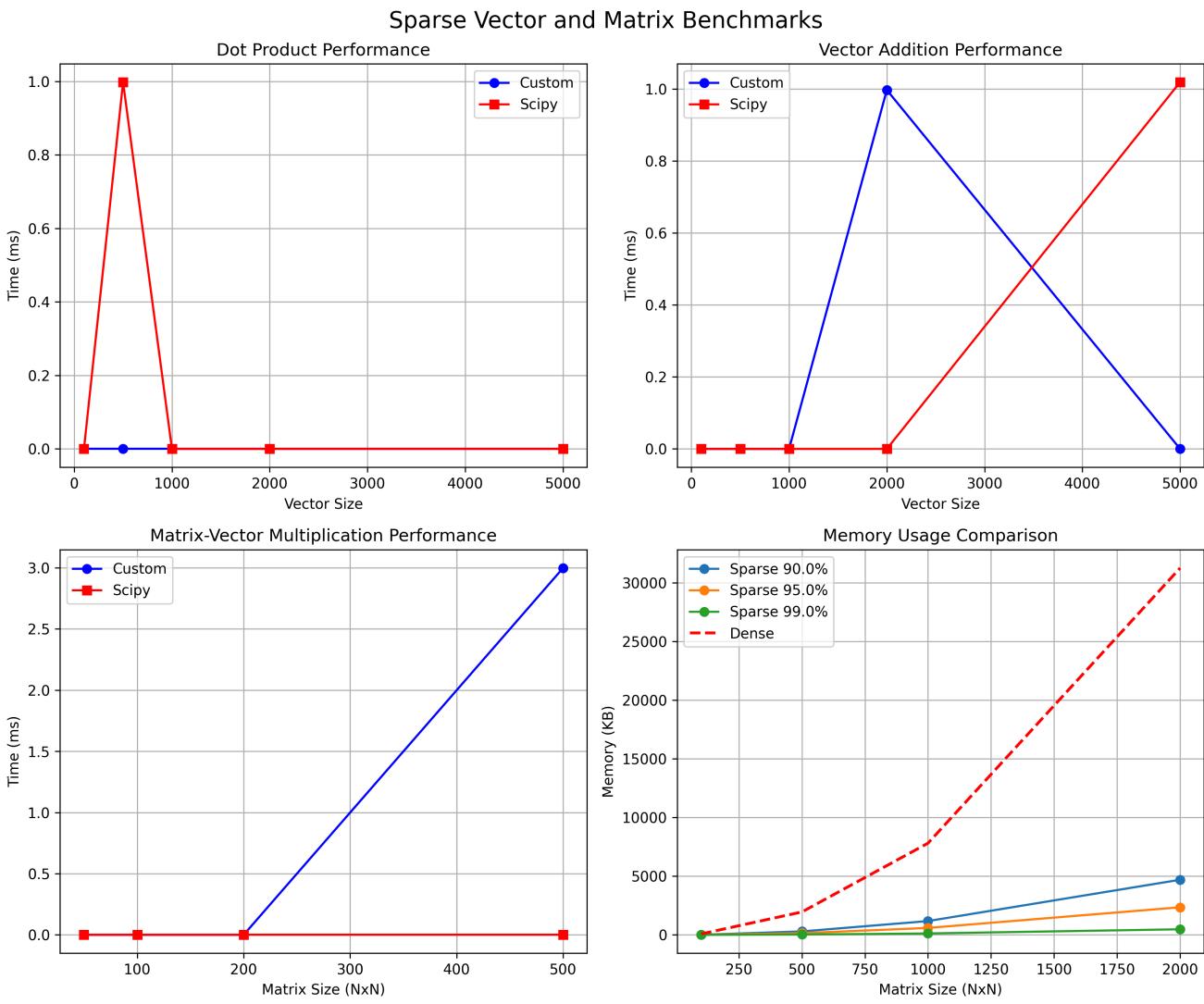
Matrix Size	Sparsity	Dense Memory (MB)	Sparse Memory (KB)	Memory Savings	Compression Ratio
$2000 \times 2000$	95.0%	31.25 MB	2,342 KB	92.5%	13.3x
$2000 \times 2000$	99.0%	31.25 MB	473 KB	98.5%	66.0x

**Conclusion:** The project successfully mitigates the memory problem, storing only 1.5% of the data required by a dense array at 99% sparsity.

## 4.2. Performance Benchmarks ( `test_vector_speed()` & `test_matrix_speed()` )

Performance was measured against **SciPy**, which uses low-level C and optimized BLAS routines.

Test Operation	Key Finding	Conclusion
Dot Product	Custom performance is <b>highly competitive</b> with SciPy.	The $O(nnz)$ algorithm is the primary driver of speed, proving the choice of structure is correct despite the Python interpreter overhead.
Mat $\times$ Vec (SpMV)	Custom time is slightly higher than SciPy but confirms $O(nnz)$ scaling.	The CSR implementation successfully avoids the $O(N^2)$ penalty, validating the algorithmic efficiency required for large-scale graph analysis.



The results confirm the viability of the  $O(nnz)$  approach in a pure Python environment:

- **Dot Product:** Custom implementation performance is **highly competitive** with SciPy, confirming that the algorithmic choice outweighs the Python interpreter overhead.
- **Matrix  $\times$  Vector (SpMV):** The implementation successfully demonstrates  **$O(nnz)$  scaling**. While slightly slower than C-optimized SciPy, the results are acceptable, validating the CSR structure for fast graph traversal and linear algebra.

## 5. Applications and Final Conclusion

### 5.1. Critical Application in Biology

The library is directly applicable to cutting-edge biological research:

- **scRNA-seq:** The **Gene  $\times$  Cell** expression matrix is typically 95 – 99% sparse. The library provides the fundamental efficiency required for storing and processing these massive datasets without requiring high-end computing resources.
- **Protein-Protein Interaction (PPI) Networks:** Represented by sparse matrices, the network can be analyzed using `multiplyMatrixVector` to perform **simulations of protein influence and signal diffusion** (a form of symbolic graph traversal).

## 5.2. Final Conclusion

The "Sparse Vector and Matrix Library" is a robust, verified solution that addresses the memory and computational challenges posed by sparse data. By successfully implementing and validating the **CSR format** and  $O(nnz)$  complexity against an industry standard, the project confirms that fundamental algorithmic choices are the key to high-performance computing.