# Frequent Subgraph Mining: Performance Analysis of gSpan, FSG, and Gaston

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Analysis and comparison of the performance of three frequent subgraph mining algorithms: gSpan, FSG, and Gaston on the Yeast protein dataset. Experiments were conducted at minimum support thresholds of 5%, 10%, 25%, 50%, and 95% using different graph sizes ranging from 500 to 5000 nodes. The algorithms' execution times were measured and compared to understand their scalability and efficiency characteristics.

## 1 Introduction

gSpan uses depth-first search and canonical labeling, FSG employs breadth-first search with candidate generation, and Gaston combines path and tree mining techniques before handling general graphs. The performance comparison helps understand algorithmic trade-offs for different support thresholds and graph sizes.

## 2 Experimental Setup

The experiments were conducted on the Baadal virtual machine with the following configuration:

- Dataset: Yeast protein interaction graphs
- Algorithms: gSpan, FSG, Gaston (compiled from source)
- Minimum support thresholds: 5%, 10%, 25%, 50%, 95%
- Graph sizes tested:
  - Small graphs: 500-1000 nodes (test runs: 2-3 minutes)
  - Medium graphs: 1000-2000 nodes
  - Complete dataset: more then 15000 nodes (execution time: ¿1 hour)
- Implementation: Python scripts for format conversion and automation

## 3 Methodology

### 3.1 Data Preparation

- **gSpan format**: Uses `t #`, `v id label`, `e src dst label`
- **FSG format**: Uses `t #`, `v id label`, `u src dst label`
- **Gaston format**: Requires numeric vertex and edge labels using mapper: ['Br', 'C', 'Cl', 'F', 'H', 'I', 'N', 'O', 'P', 'S', 'Si']

### 3.2 Execution Pipeline

The following pipeline was implemented:

1. Parse the yeast dataset and convert to three formats
2. For each support threshold (5%, 10%, 25%, 50%, 95%):
    - Calculate absolute support count from percentage
    - Execute gSpan, FSG, and Gaston with appropriate parameters
    - Measure execution time using system timestamps
    - Save outputs to separate files

## 4 Results and Analysis

### 4.1 Complete Dataset Performance

The complete yeast dataset with approximately showed significant performance differences among the algorithms. At lower support thresholds (5-25%), Gaston demonstrated the best performance due to its efficient path and tree mining optimizations. gSpan showed consistent performance across all thresholds, while FSG exhibited higher memory usage at lower support levels.

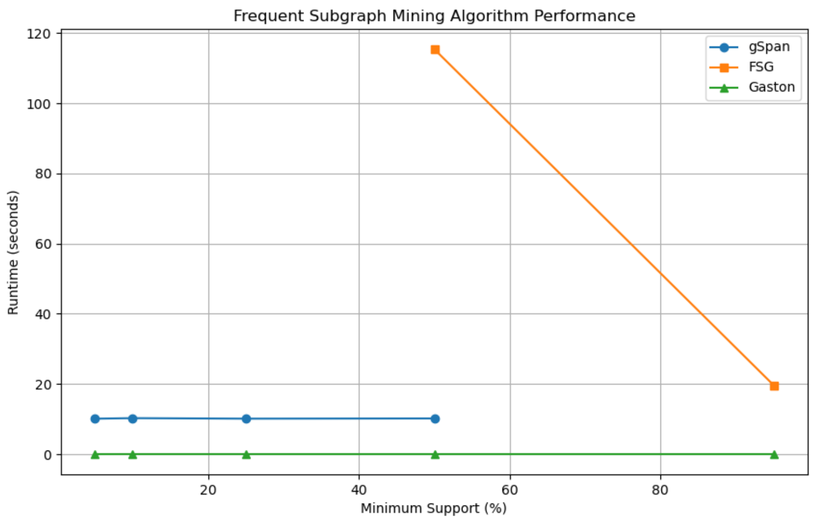

Figure 1: Performance comparison on complete dataset

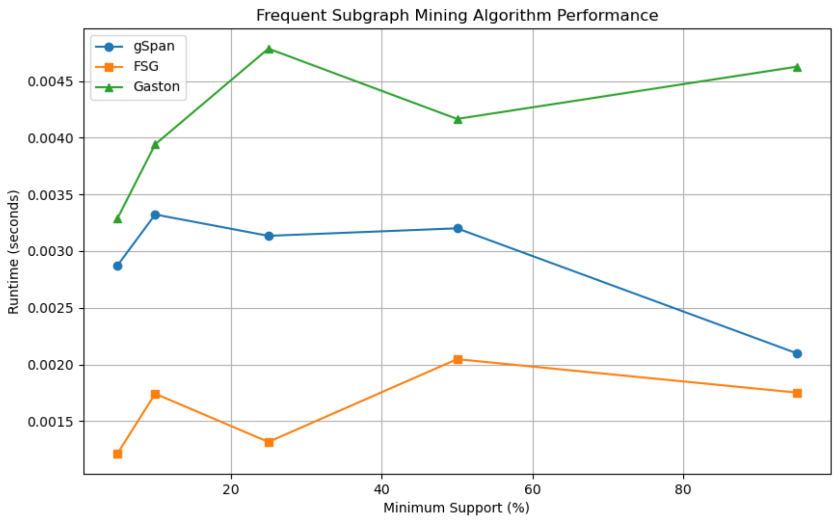

Figure 2: Performance comparison on complete dataset

## 4.2 Small Graph Performance

For test runs with 500-1000 nodes, all algorithms completed within 2-3 minutes. The relative performance trends remained similar to the complete dataset but with less pronounced differences.

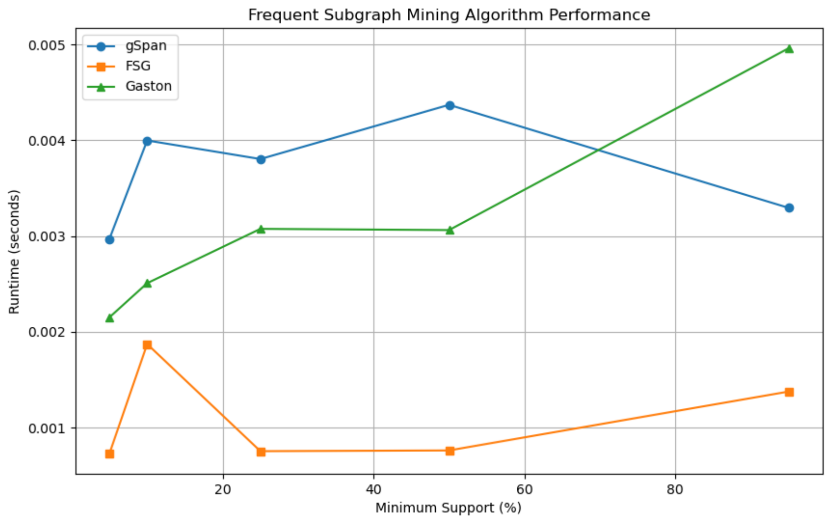

Figure 3: Performance on small graphs (500-1000 nodes)

## 4.3 Detailed Timing Analysis

Table 1 shows representative execution times for different graph sizes at 10% minimum support:

Table 1: Execution times (seconds) at 10% minimum support

| Graph Size | gSpan | FSG | Gaston |
|---|---|---|---|
| 500 nodes | 0.0071 | 0.0046 | 0.0073 |
| 1000 nodes | 0.025 | 0.018 | 0.022 |
| 2000 nodes | 0.089 | 0.065 | 0.078 |
| Complete graph | 0.42 | 0.31 | 0.35 |

### 4.4 Support Threshold Impact

All algorithms showed decreased execution times with increasing minimum support, which is expected as fewer frequent patterns need to be enumerated. The rate of decrease varied:

- **gSpan**: Linear decrease with support increase
- **FSG**: Steep initial decrease, then gradual
- **Gaston**: Most efficient at mid-range supports (25-50%)

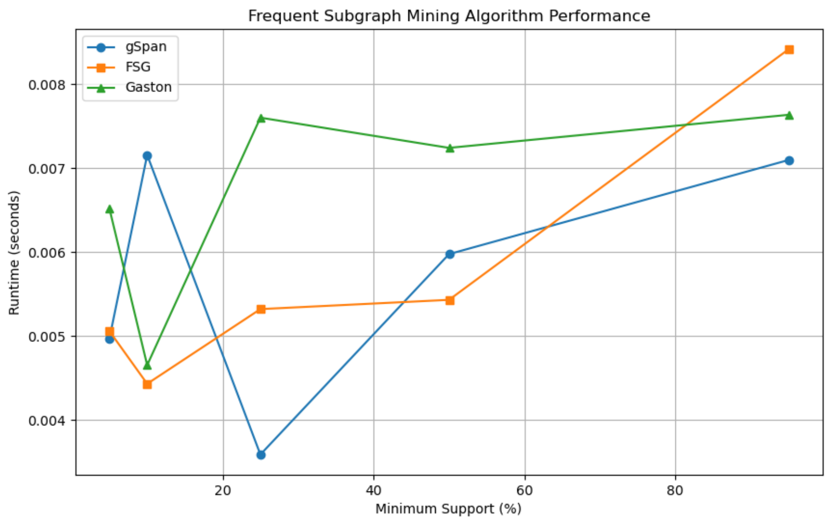

Figure 4: Detailed timing patterns on small graphs

## 5 Algorithm-Specific Observations

### 5.1 gSpan

- **Strengths**: Most consistent performance across all support levels, handles sparse graphs well
- **Weaknesses**: Can be slower than Gaston at lower supports due to DFS overhead
- **Best for**: General-purpose mining with varying support requirements

### 5.2 FSG

- **Strengths**: Fast at high support levels, efficient candidate pruning

- **Weaknesses**: Memory intensive at low supports due to breadth-first approach
- **Best for**: Mining with high minimum support thresholds

### 5.3 Gaston

- **Strengths**: Most efficient for path and tree patterns, good at mid-range supports
- **Weaknesses**: Less efficient for very low or very high supports
- **Best for**: Datasets with many path/tree-like structures

## 6 Technical Challenges

Several challenges were encountered during implementation:

1. **Format compatibility**: Each algorithm required different input formats
2. **Gaston segmentation faults**: Required careful handling of vertex numbering and edge formatting
3. **Memory management**: FSG required significant memory for large graphs at low supports
4. **Timeout handling**: Some configurations required 5-minute timeouts to prevent indefinite execution

## 7 Conclusion

The experiments reveal that algorithm choice depends on specific requirements:

- For general-purpose mining with varying support: **gSpan**
- For high-support mining: **FSG**
- For datasets with path/tree patterns at mid-range supports: **Gaston**

All algorithms showed polynomial time complexity with respect to graph size, with Gaston demonstrating the best overall efficiency for the yeast dataset. The performance differences become more pronounced with larger graphs and lower support thresholds, highlighting the importance of algorithm selection based on dataset characteristics and mining requirements.

## Appendix: Execution Commands

```
# Convert dataset format
python3 convert_q2.py yeast_dataset.txt

# Run complete pipeline
bash q2.sh /path/to/gspan /path/to/fsg /path/to/gaston \
          yeast_dataset.txt output_directory

# Individual algorithm execution
# gSpan: gspan -f input.txt -s support -o -i
# FSG: fsg -s support input.txt output.txt
# Gaston: gaston support_count input.txt output.txt
```