

Report on Max Clique as a Lower Bound for Graph Coloring

Jenik Gajera

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The following report provides a detailed reasoning for why the **maximum clique size** ($\omega(G)$) serves as a theoretical **lower bound** for the **graph chromatic number** ($\chi(G)$), along with an analysis of the provided experimental results.

The analysis incorporates both the **DIMACS benchmark graphs** and a selection of **generated graphs**. Data points where the clique size was not computed (e.g., "TIMEOUT") were excluded, resulting in an analysis set of **67 graphs** with both a computed $\omega(G)$ and a known $\chi(G)$.

1 Theoretical Reasoning: Maximum Clique as a Lower Bound

The principle that the maximum clique size provides a lower bound for the graph chromatic number is a fundamental theorem in graph theory.

1.1 Definition of Terms

- Clique:** A subset of vertices in a graph G such that every two distinct vertices in the subset are adjacent.
- Maximum Clique Size ($\omega(G)$):** The number of vertices in the largest clique in graph G .
- Chromatic Number ($\chi(G)$):** The minimum number of colors required for a valid graph coloring.

1.2 The Argument for the Lower Bound

For any clique of size k in G , all vertices must have different colors in any proper coloring. Thus:

- Every vertex in a clique is adjacent to all others.
- All $\omega(G)$ vertices in the maximum clique require $\omega(G)$ unique colors.

Therefore,

$$\omega(G) \leq \chi(G)$$

2 Data Analysis and Findings

The experimental results validate the theoretical lower bound across all analyzed graphs. The detailed comparison is available in the file `clique_coloring_analysis.csv`.

2.1 Overall Comparison

Table 1: Overall Comparison of $\omega(G)$ and $\chi(G)$

Metric	Value	Interpretation
Lower Bound Validity ($\omega(G) \leq \chi(G)$)	100.00% (67/67)	Bound holds for all graphs.
Graphs with Tight Bound ($\omega(G) = \chi(G)$)	73.13% (49/67)	Clique exactly predicts $\chi(G)$ for most graphs.
Average Difference ($\chi(G) - \omega(G)$)	1.69	Chromatic number is generally close to the lower bound.

Table 2: Comparison by Graph Type

Graph Type	Count	$\omega(G) = \chi(G)$	Count	Avg. Difference
LEI	12	12		0.00
REG	14	14		0.00
SCH	1	1		0.00
SGB	24	20		0.17
MYC	5	0		4.00
DSJ	8	2		6.13
CUL	3	0		13.33

2.2 Analysis by Graph Type

Observations:

- **Perfect-Graph-Like Families:** LEI, REG, SCH have $\omega(G) = \chi(G)$ for all instances.
- **Near-Perfect:** SGB graphs show very small deviations.
- **Hard Instances:** CUL, DSJ, MYC graphs have large gaps between $\omega(G)$ and $\chi(G)$, consistent with their construction.

3 Graph Type Descriptions and Rationale

Table 3: Graph Family Descriptions and Interpretation of Analysis Results

Abbrev.	Graph Type Name	Description	Rationale for Analysis Result
LEI	Leighton Graphs	Graphs such as <code>le450_K</code> , where K is both clique and chromatic number.	Exhibited 0.00 avg. difference; these are perfect graphs with $\omega(G) = \chi(G)$.
REG	Register Allocation Graphs	Derived from compiler register allocation problems.	Also showed 0.00 avg. difference; clique exactly predicts coloring.
SCH	Scheduling Graphs	From timetable/course scheduling problems.	Single instance showed perfect matching.
SGB	Stanford GraphBase	Includes book graphs and queen graphs.	Very small avg. gap (0.17); clique is an excellent predictor.
MYC	Mycielski Graphs	Triangle-free but high chromatic number.	Large avg. gap (4.00), as intended by Mycielski construction.
DSJ	Johnson Random Graphs	Random graphs from Johnson et al. (DSJC).	Large avg. gap (6.13); randomness increases coloring difficulty.
CUL	Culberson Flat Graphs	Constructed by partitioning vertices into K classes.	Largest avg. gap (13.33); clique size underestimates $\chi(G)$ heavily.

4 Conclusion

The experiments on DIMACS benchmark graphs and generated graphs confirm the theoretical inequality:

$$\omega(G) \leq \chi(G)$$

for every instance. In many graph families, especially perfect-graph-like ones (LEI, REG, SCH), the clique number exactly matches the chromatic number. In contrast, hard graph families (CUL, DSJ, MYC) show significant gaps, reflecting deeper structural constraints not captured by the maximum clique alone.