

Enhancing the Performance of Genetic Algorithms in Combinatorial Optimization of Large and Difficult Problems

Using Variable Adaptive Mutation Rates Controlled by 'Inbreeding'

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ABSTRACT

Blah blah blah, here is our abstract.

Keywords

Genetic Algorithms, Combinatorial Optimization, N Queens Problem, Variable Mutation

1. INTRODUCTION

- Model the intro similarly to how we did the report for AI
- Summary of the problem explain the challenges of larger N-Queens problems, provide a table showing how quickly the number of solutions grows, there is no known method of determining the exact number of solutions.
- Based on the complexity of the problem explain how the overhead of using a brute-force approach is infeasible for larger N Queens and the justification for stochastic methods.
- Emphasize that our application of the problem is finding distinct solutions, since this is much harder than just finding solutions (many of which may be duplicates in other random stochastic methods).
- The motive for variable mutation -> We were not able initially (without using reflection & rotation like we are now) to get all 92 solutions to 8 queens (impossible with fixed mutation to solve in a reasonable amount of time)
- > Started looking at biology, were inspired by the fact that nature has a natural ordering to prevent inbreeding within organisms (e.g. purebred dogs often have more health problems, easy citation!)

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-> Attempted to come up with a way to apply the negative affects of inbreeding that occur in nature to solve our GA problem

-> Our var. mutation solution worked exceptionally well, solved all 92 solutions nearly instantaneously, motivated us to pursue the implications further.

The *proceedings* are the records of a conference. ACM seeks to give these conference by-products a uniform, high-quality appearance. To do this, ACM has some rigid requirements for the format of the proceedings documents: there is a specified format (balanced double columns), a specified set of fonts (Arial or Helvetica and Times Roman) in certain specified sizes (for instance, 9 point for body copy), a specified live area (18 × 23.5 cm [7" × 9.25"]) centered on the page, specified size of margins (1.9 cm [0.75"]) top, (2.54 cm [1"]) bottom and (1.9 cm [.75"]) left and right; specified column width (8.45 cm [3.33"]) and gutter size (.83 cm [.33"]).

The good news is, with only a handful of manual settings¹, the L^AT_EX document class file handles all of this for you.

The remainder of this document is concerned with showing, in the context of an "actual" document, the L^AT_EX commands specifically available for denoting the structure of a proceedings paper, rather than with giving rigorous descriptions or explanations of such commands.

1.1 Background and Problem Domain

Typically, the body of a paper is organized into a hierarchical structure, with numbered or unnumbered headings for sections, subsections, sub-subsections, and even smaller sections. The command `\section` that precedes this paragraph is part of such a hierarchy.² L^AT_EX handles the numbering and placement of these headings for you, when you

¹Two of these, the `\numberofauthors` and `\alignauthor` commands, you have already used; another, `\balancecolumns`, will be used in your very last run of L^AT_EX to ensure balanced column heights on the last page.

²This is the second footnote. It starts a series of three footnotes that add nothing informational, but just give an idea of how footnotes work and look. It is a wordy one, just so you see how a longish one plays out.

use the appropriate heading commands around the titles of the headings. If you want a sub-subsection or smaller part to be unnumbered in your output, simply append an asterisk to the command name. Examples of both numbered and unnumbered headings will appear throughout the balance of this sample document.

1.1.1 The N-Queens Puzzle

Because the entire article is contained in the **document** environment, you can indicate the start of a new paragraph with a blank line in your input file; that is why this sentence forms a separate paragraph.

1.2 Related Work

We have already seen several typeface changes in this sample. You can indicate italicized words or phrases in your text with the command `\textit`; emboldening with the command `\textbf` and typewriter-style (for instance, for computer code) with `\texttt`. But remember, you do not have to indicate typestyle changes when such changes are part of the *structural* elements of your article; for instance, the heading of this subsection will be in a sans serif³ typeface, but that is handled by the document class file. Take care with the use of⁴ the curly braces in typeface changes; they mark the beginning and end of the text that is to be in the different typeface.

You can use whatever symbols, accented characters, or non-English characters you need anywhere in your document; you can find a complete list of what is available in the *L^AT_EX User's Guide*[?].

2. OUR APPROACH

- Describe the variable mutation rate algorithm and the two parameters that it has in comparison to fixed mutation's one param, (step size for changing the mutation rate and the inbreeding threshold).

2.1 Applying Variable Mutation Rates

- For explaining the variable mutation rate there is no need for a formal algorithm essentially it boils down to the following:

- For each generation evaluate the population chromosome similarity (see below for population chromosome similarity algorithm)

- If the population chromosome similarity is less than the threshold increase the mutation rate by the step size. If the similarity is greater than the threshold decrease the mutation rate by the step size. This results in the mutation rate adjusting up or down such that the population chromosome similarity approaches an equilibrium near the inbreeding threshold.

A formula that appears in the running text is called an inline or in-text formula. It is produced by the **math** environment, which can be invoked with the usual `\begin. . . \end` construction or with the short form `\$. . . \$`. You can use any of the symbols and structures, from α to ω , available in L^AT_EX[?]; this section will simply show a few examples of in-text equations in context. Notice how this equation:

³A third footnote, here. Let's make this a rather short one to see how it looks.

⁴A fourth, and last, footnote.

$\lim_{n \rightarrow \infty} x = 0$, set here in in-line math style, looks slightly different when set in display style. (See next section).

2.1.1 Chromosome Similarity Algorithm

- For explaining the chromosome similarity algorithm (which is a little more complicated to avoid the naive $O(n!)$ solution, instead it is now linear complexity). Even though in terms of theoretical big-O complexity it is constant (since it's just based on the population size which is constant) it is worthwhile mentioning that from our empirical evidence using profiling of the code using the naive $O(n!)$ solution has a significant impact for larger population sizes (so much so that it caused a significant degrade in performance motivating us to profile the code and improve the original algorithm)

- I will write the formal algorithm in latex using the latex algorithm extension <http://en.wikibooks.org/wiki/LaTeX/Algorithms>

Again, in either environment, you can use any of the symbols and structures available in L^AT_EX; this section will just give a couple of examples of display equations in context. First, consider the equation, shown as an inline equation above:

$$\lim_{n \rightarrow \infty} x = 0 \quad (1)$$

Notice how it is formatted somewhat differently in the **displaymath** environment.

2.2 Implementation

- An overview of our GA implementation so that someone wishing to replicate our results knows how we implemented our solution.

- Could potentially provide a URL to the source code implementation on github

- Describe the chromosome design, the ordering of each gene of the chromosome represents the horizontal position of each queen on the board and the corresponding vertical position of the queen is stored in the gene of the chromosome.

- > I think it would be worthwhile to have a very small diagram highlighting this

- Fitness function, I can write the formal algorithm for this, each pair of queens that have a vertical or diagonal collision is recorded as a value of 2 (one collision from the perspective of each queen). This number is then represented as a fraction over 1 such that a chromosome with a larger number of collisions will have a much lower fitness value.

- If no collisions occur the default value is 1 resulting in a fitness of $(1/1 = 1)$ which is a solution to the problem.

- For queens with multiple collisions each pair of queens will be recorded as 2 collisions, in the event that there are three pairs of queens with collisions, one pair with a vertical collision, one with a diagonal, and one with a separate diagonal collision the fitness value would be $(1 / 6)$.

- In the event where there are multiple types of collisions (say two pairs of queens each with vertical collisions, and one with a horizontal collision) the fitness value would be $(1 / 8)$, for a higher number of collisions this often happens making the fitness value even lower than just a multiple of 2 x pairs of collisions.

- > Might be helpful to give a diagram

- > Due to the ordering of the queens in the chromosome there can only be vertical or diagonal collisions (since two queens can never be on the same row).

- Roulette wheel selection method, by generating a ran-

dom floating point number and selecting a chromosome value where the random number lies within the bounds. The range of random values that can be chosen changes based on the maximum upper and lower bounds of the sum of the fitness of the chromosomes in the population.

- Each of the ranges of values that a particular chromosome can have is weighted based on the fitness of the chromosome. For example in a population with 4 chromosomes two of which are solutions (fitness 1) and two with a single pair of collisions (fitness $1/2 = 0.5$) the ranges of values for each chromosome would be as follows:

[0, 1), [1, 2), [2, 2.5), [2.5, 3), and the bounds of the random floating point value generated for the roulette wheel selection would be [0, 3).

- Crossover operation (70% chance), cloning (30% chance), (cite paper justifying why we used these values, they are often recommended/used values)

- Background mutation operation, applied to chromosomes, this is variable rather than a traditional fixed value, e.g. a 5% value results in a 5% chance of mutation being applied to chromosomes.

- Mutation operator changes ONE of the genes of the chromosome randomly, which results in changing the the y coordinate of a random queen in the chromosome to a random value within the range of possible y values.

- If a chromosome of the current population has a fitness value of 1 it is compared to the list of previous solutions to see if it is unique. If the solution is unique the rotation (rotating the solution an additional three times) and reflection (performing reflection on the solution) followed by three additional rotations operations are applied to find a total of 8 solutions. Each solution found after rotation and reflection is compared to the list of previous solutions to verify that it is a unique solution.

-> We do not keep duplicate solutions, this is important since someone may think that out of the 1000's of solutions we found many of them are just duplicates, when in fact they are all DISTINCT solutions.

- The current population is then replaced with the new population that was created by applying the crossover, cloning, and mutation operations.

2.3 Methodology

- Implementation in Java
- Experiments were conducted on the HPC facilities provided (SHARCNET)

- describe the study and control (diff. fixed mutation rates, list them all, vs. variable mutation rate with a fixed inbreeding threshold of 15%), this had 1 fixed param (inbreeding threshold)

-> This should probably be put in a table.

- N queens problem sizes used: For 8 - 16 queens used each n queens size, for 16 - 26 used each even sized N queens problem, lastly a test using 32 queens.

- Number of generations for each N queens problem (10 million generations for all except 32 queens), 50 million generations were used for 32 queens given the increased complexity of the problem.

- sample sizes (30, 15, 10)

-> I will give you a table with each n queens problem, the sample sizes used for each and the number of generations, this would reduce a lot of text needed to explain the items.

-> justify why the sample sizes were reduced for larger

problems given the computational limitations of SHARCNET (max 256 jobs, 7 days CPU time, regardless and your job would be killed)

- describe the data collected, explain how each of the attributes such as population fitness, similarity are calculated based on the mean of the population for 1000 generations at a time (mean of means), rather than the mean of each population for each generation (TOO MUCH DATA!)

Now, we'll enter an unnumbered equation:

$$\sum_{i=0}^{\infty} x + 1$$

and follow it with another numbered equation:

$$\sum_{i=0}^{\infty} x_i = \int_0^{\pi+2} f \quad (2)$$

just to demonstrate L^AT_EX's able handling of numbering.

2.4 Why Not Fixed Mutation?

Citations to articles [?, ?, ?, ?], conference proceedings [?] or books [?, ?] listed in the Bibliography section of your article will occur throughout the text of your article. You should use BibTeX to automatically produce this bibliography; you simply need to insert one of several citation commands with a key of the item cited in the proper location in the .tex file [?]. The key is a short reference you invent to uniquely identify each work; in this sample document, the key is the first author's surname and a word from the title. This identifying key is included with each item in the .bib file for your article.

- cite specific results and why we think they are important, what is the significance of them and how they support our results/hypothesis that in the case of N Queens var. mutation is better than fixed.

- cite the result showing the best fixed mutation vs. the variable mutation for each N-queens problem, try and use both the figure and the table, the table has some additional interesting information which cannot be conveyed in the image alone.

- cite interesting results of the fat boxplots in the range of chromosome similarity for the optimal fixed mutation rates, use the "person stepping" analogy and how that certain fixed mutation rates had the widest range in chromosome similarity allowing it to hone in on solutions faster.

- Try and incorporate one of the scatter plots as well that show very interesting results and see if you can use it to compare/contrast the results of the following plots

- variable mutation rate scatter plot - variable mutation rate similarity scatter plot - best fixed mutation rate similarity scatter plot

The details of the construction of the .bib file are beyond the scope of this sample document, but more information can be found in the *Author's Guide*, and exhaustive details in the *L^AT_EX User's Guide*[?].

This article shows only the plainest form of the citation command, using \cite. This is what is stipulated in the SIGS style specifications. No other citation format is endorsed or supported.

3. CONCLUSIONS AND FURTHER RESEARCH

- Wait until the rest of the paper & we have more feedback before writing the conclusions.

Table 1: Frequency of Special Characters

Non-English or Math	Frequency	Comments
\emptyset	1 in 1,000	For Swedish names
π	1 in 5	Common in math
\$	4 in 5	Used in business
Ψ_1^2	1 in 40,000	Unexplained usage

- Further research into adjusting the inbreeding threshold, for the purpose of the research a constant inbreeding threshold of 15% was used, however further research could be done in testing different thresholds.

- Comparing the results of variable mutation with fixed mutation using other types of combinatorial/optimization problems such as TSP, constraint satisfaction problem (CSP), etc.

- Variable population size based on the amount of inbreeding (if you have a lot of inbreeding in nature the organisms will have higher mutation rate and deformities, the population will shrink)

- Having the mutation operator affect more than one gene if it goes > 100%?

Because tables cannot be split across pages, the best placement for them is typically the top of the page nearest their initial cite. To ensure this proper “floating” placement of tables, use the environment **table** to enclose the table’s contents and the table caption. The contents of the table itself must go in the **tabular** environment, to be aligned properly in rows and columns, with the desired horizontal and vertical rules. Again, detailed instructions on **tabular** material is found in the *LaTeX User’s Guide*.

Immediately following this sentence is the point at which Table 1 is included in the input file; compare the placement of the table here with the table in the printed dvi output of this document.

To set a wider table, which takes up the whole width of the page’s live area, use the environment **table*** to enclose the table’s contents and the table caption. As with a single-column table, this wide table will “float” to a location deemed more desirable. Immediately following this sentence is the point at which Table 2 is included in the input file; again, it is instructive to compare the placement of the table here with the table in the printed dvi output of this document.

3.1 Figures

Like tables, figures cannot be split across pages; the best placement for them is typically the top or the bottom of the page nearest their initial cite. To ensure this proper “floating” placement of figures, use the environment **figure** to enclose the figure and its caption.

This sample document contains examples of **.eps** and **.ps** files to be displayable with LaTeX. More details on each of these is found in the *Author’s Guide*.

As was the case with tables, you may want a figure that spans two columns. To do this, and still to ensure proper “floating” placement of tables, use the environment **figure*** to enclose the figure and its caption. and don’t forget to end the environment with **figure***, not **figure**!

Note that either **.ps** or **.eps** formats are used; use the



Figure 1: A sample black and white graphic (.eps format).



Figure 2: A sample black and white graphic (.eps format) that has been resized with the epsfig command.

`\epsfig` or `\psfig` commands as appropriate for the different file types.

3.2 Theorem-like Constructs

Other common constructs that may occur in your article are the forms for logical constructs like theorems, axioms, corollaries and proofs. There are two forms, one produced by the command `\newtheorem` and the other by the command `\newdef`; perhaps the clearest and easiest way to distinguish them is to compare the two in the output of this sample document:

This uses the **theorem** environment, created by the `\newtheorem` command:

THEOREM 1. *Let f be continuous on $[a, b]$. If G is an antiderivative for f on $[a, b]$, then*

$$\int_a^b f(t)dt = G(b) - G(a).$$

The other uses the **definition** environment, created by the `\newdef` command:

Definition 1. *If z is irrational, then by e^z we mean the unique number which has logarithm z :*

$$\log e^z = z$$

Two lists of constructs that use one of these forms is given in the *Author’s Guidelines*.

There is one other similar construct environment, which is already set up for you; i.e. you must *not* use a `\newdef` command to create it: the **proof** environment. Here is an example of its use:

PROOF. Suppose on the contrary there exists a real number L such that

$$\lim_{x \rightarrow \infty} \frac{f(x)}{g(x)} = L.$$

Then

$$l = \lim_{x \rightarrow c} f(x) = \lim_{x \rightarrow c} \left[gx \cdot \frac{f(x)}{g(x)} \right] = \lim_{x \rightarrow c} g(x) \cdot \lim_{x \rightarrow c} \frac{f(x)}{g(x)} = 0 \cdot L = 0,$$

which contradicts our assumption that $l \neq 0$. \square

Table 2: Some Typical Commands

Command	A Number	Comments
<code>\alignauthor</code>	100	Author alignment
<code>\numberofauthors</code>	200	Author enumeration
<code>\table</code>	300	For tables
<code>\table*</code>	400	For wider tables

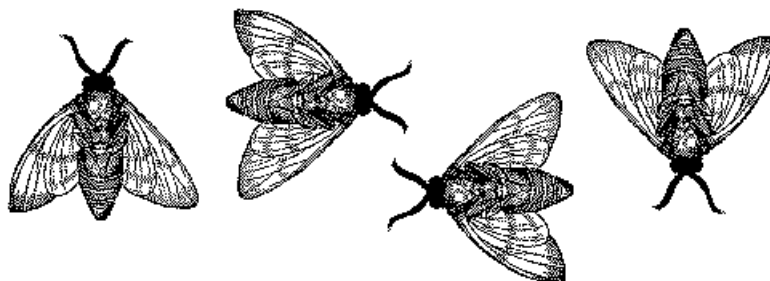


Figure 3: A sample black and white graphic (.eps format) that needs to span two columns of text.

Complete rules about using these environments and using the two different creation commands are in the *Author's Guide*; please consult it for more detailed instructions. If you need to use another construct, not listed therein, which you want to have the same formatting as the Theorem or the Definition[?] shown above, use the `\newtheorem` or the `\newdef` command, respectively, to create it.

A Caveat for the T_EX Expert

Because you have just been given permission to use the `\newdef` command to create a new form, you might think you can use T_EX's `\def` to create a new command: *Please refrain from doing this!* Remember that your L^AT_EX source code is primarily intended to create camera-ready copy, but may be converted to other forms – e.g. HTML. If you inadvertently omit some or all of the `\defs` recompilation will be, to say the least, problematic.

4. CONCLUSIONS

This paragraph will end the body of this sample document. Remember that you might still have Acknowledgments or Appendices; brief samples of these follow. There is still the Bibliography to deal with; and we will make a disclaimer about that here: with the exception of the reference to the L^AT_EX book, the citations in this paper are to articles which have nothing to do with the present subject and are used as examples only.

5. ACKNOWLEDGMENTS

This section is optional; it is a location for you to acknowledge grants, funding, editing assistance and what have you. In the present case, for example, the authors would like to thank Gerald Murray of ACM for his help in codifying this *Author's Guide* and the `.cls` and `.tex` files that it describes.

6. REFERENCES

- [1] M. Bowman, S. K. Debray, and L. L. Peterson. Reasoning about naming systems. *ACM Trans. Program. Lang. Syst.*, 15(5):795–825, November 1993.

- [2] J. Braams. Babel, a multilingual style-option system for use with latex's standard document styles. *TUGboat*, 12(2):291–301, June 1991.
- [3] M. Clark. Post congress tristesse. In *TeX90 Conference Proceedings*, pages 84–89. TeX Users Group, March 1991.
- [4] M. Herlihy. A methodology for implementing highly concurrent data objects. *ACM Trans. Program. Lang. Syst.*, 15(5):745–770, November 1993.
- [5] L. Lamport. *LaTeX User's Guide and Document Reference Manual*. Addison-Wesley Publishing Company, Reading, Massachusetts, 1986.
- [6] S. Salas and E. Hille. *Calculus: One and Several Variable*. John Wiley and Sons, New York, 1978.

APPENDIX

A. HEADINGS IN APPENDICES

The rules about hierarchical headings discussed above for the body of the article are different in the appendices. In the `appendix` environment, the command `section` is used to indicate the start of each Appendix, with alphabetic order designation (i.e. the first is A, the second B, etc.) and a title (if you include one). So, if you need hierarchical structure *within* an Appendix, start with `subsection` as the highest level. Here is an outline of the body of this document in Appendix-appropriate form:

A.1 Introduction

A.2 The Body of the Paper

A.2.1 Type Changes and Special Characters

A.2.2 Math Equations

Inline (In-text) Equations.

Display Equations.

A.2.3 Citations

A.2.4 Tables

A.2.5 Figures

A.2.6 Theorem-like Constructs

A Caveat for the T_EX Expert

A.3 Conclusions

A.4 Acknowledgments

A.5 Additional Authors

This section is inserted by L^AT_EX; you do not insert it. You just add the names and information in the `\additionalauthors` command at the start of the document.

A.6 References

Generated by bibtex from your .bib file. Run latex, then bibtex, then latex twice (to resolve references) to create the .bbl file. Insert that .bbl file into the .tex source file and comment out the command `\thebibliography`.

B. MORE HELP FOR THE HARDY

The sig-alternate.cls file itself is chock-full of succinct and helpful comments. If you consider yourself a moderately experienced to expert user of L^AT_EX, you may find reading it useful but please remember not to change it.