Writing the Research Report

The research report demonstrates your ability to write a **summary** of your project using a standard scientific style of reporting. It requires that you select only what is important and state that in a clear and concise way. It is a **report** about what you did, **not a detailed record** of what you did.

Research Report Requirements:

1. The first line of your report should be your project title.

2. The second line should be your name(s) and school.

3. The report format will depend on the type of project (Experiment, Innovation or Study). The below chart indicates acceptable formats based on your project type.

4. Make sure the format and your writing is clear and concise, with correct spelling and grammar. Use either Times New Roman or Arial fonts, size 12, and 1.5 line spacing.

5. Do not include raw data, detailed observations or any appendices in your report. The research report is a brief summary and should not include these main materials.

6. Limit your report to 500 words or less. Anything over this word limit will not be considered.

7. Your report must be written in your own words — no copy and paste! You must also provide a list of resources/references you used while working on your project.

8. Your project may be incomplete at this point. Students are permitted to continue to work on their projects up to April 4th. If your project is incomplete, you must also include in your report a description of future plans for your project (how you will continue/complete it).

Acceptable Formats for Your Research Report:

Experiment	Innovation	Study
Background (and/or Hypothesis)	Introduction & Background	Background & Problem
Purpose	Purpose	Purpose or Thesis
Procedure	Design Criteria	Evidence or Supporting Data
Results	Procedure or Methodology	Results
Discussion	Results	Discussion
Conclusions	Conclusions & Recommendations	Conclusions
Acknowledgements	Acknowledgements	Acknowledgements

Explanatory Notes:

<table>
<tr><th>Experiment</th><th>Innovation</th><th>Study</th></tr>
<tr><td colspan="3">The Background, Introduction & Background, and Background & Problem sections are intended to describe information that explains why the project was done. It is not meant to be a discussion of what could be, or ideas of why something is the way it is.</td></tr>
<tr><td colspan="3">The Purpose and Purpose or Thesis sections are to describe the more specific objectives of the project.</td></tr>
<tr><td></td><td>The Design Criteria describes in some detail how one would know if the innovation is successful.</td><td>The Evidence of Supporting Data summarizes sources and information brought together to support the Purpose or Thesis.</td></tr>
<tr><td colspan="2">The Procedure and Procedure or Methodology must be a very brief outline of the materials and methods used in the experiment or development work on the innovation, not a detailed accounting.</td><td></td></tr>
<tr><td colspan="3">The Results sections summarize what you found and show how that relates to the purpose. A brief discussion of the limitations, or suggestions for further research, may be included for experiments.</td></tr>
<tr><td colspan="3">The Discussion section is where you interpret the results and limitations of your project.</td></tr>
<tr><td colspan="3">The Conclusions & Recommendations and Conclusion sections briefly answer the problem posed in the Purpose and Purpose or Thesis sections.</td></tr>
<tr><td colspan="3">In the Acknowledgments paragraph, recognition should be given to all who provided significant assistance to the researcher in development of the project, in the form of guidance, materials, or facilities. The judges may use this information when formulating questions for the interview with you and when deliberating on the quality of your work. This section of the report will not be marked.</td></tr>
</table>

Below are report samples to give you a start.

Sample - Experiment

Testing for Antibiotic Resistance
<name> <school>

Background and Purpose
The development of antibiotic resistance among pathogenic bacteria is a growing concern in medicine and food production. As antibiotics are used more frequently, bacterial colonies with antibiotic resistance become more prominent. As a result, it is becoming increasingly important to determine how frequently the use of an antibiotic results in the growth of resistant strains. As such, I designed this experiment with the goal of determining how often certain antibiotics produce bacterial colonies with resistance to those antibiotics. The four antibiotics used were kanamycin, tetracycline, chloramphenicol, and ampicillin. All four are frequently used in medicine and other industries, and data from the experiment will help to determine which are the most likely to generate resistant bacteria when used in uncontrolled environments, like the human body. This knowledge can be used to limit the propagation of antibiotic-resistant bacterial colonies in the wild.

Procedure
First, I exposed four plates of *Escherichia coli* bacteria to a low concentration of one antibiotic using paper disks. I accomplished this by growing a lawn of *E. coli* on each plate, then adding a disk of filter paper that had been soaked in a diluted antibiotic solution. I placed the plates in an incubator at 37 degrees Celsius for 8 hours to allow growth to occur. I then harvested colonies from inside zones of inhibition created by the antibiotic disks and incubated them for 8 hours under the same conditions described above. Finally, I placed the harvested colonies in a test tube containing a higher concentration of the antibiotic than the one to which they were originally exposed. Simultaneously, I exposed a control group of regular *E. coli* to each of the four high concentration antibiotics in the same way. After 24 hours, I measured the density of bacteria in each test tube using a spectrometer.

Results and Conclusions
The results of the experiment have not yet been finalized, but the goal is to determine which antibiotics are most likely to produce resistant bacterial colonies. These data will be applicable in medicine, where it is preferable to use antibiotics that produce fewer resistant colonies so that the antibiotic will remain effective over time. For example, if the resistant bacteria that grow in the inhibition range of tetracycline were highly resistant to high concentrations of the antibiotic, it would suggest that future use of tetracycline in uncontrolled environments could risk releasing resistant bacteria into the wild.

Acknowledgements
I would like to acknowledge <name> for granting me access to the University of Waterloo Applied Mathematics Biology Lab and its equipment so I could complete the experiment. Thanks also to <teacher> for answering questions and addressing concerns I had while planning the project.

Sample - Innovation

A Novel Algorithm for Identifying Sequence Motifs

<name> <school>

Introduction and Background

DNA (deoxyribonucleic acid) consists of monomers (nucleotides) with three key components: a sugar, a phosphate group, and a nitrogenous base (adenine, cytosine, guanine, or thymine). DNA is the hereditary material in all forms of life. It carries genetic instructions used for growth, development, and reproduction. Motifs are short sequence patterns that represent the fundamental units of biological function, and they can encode protein, or facilitate DNA and RNA interactions, as well as catalytic functions. They are found in both the coding and non-coding parts of the genome. Motifs allow for the identification of genes that contribute to specific functions of an organism. Motif discovery involves the identifying of motifs within sequences through experimental or computational means. Finding these motifs experimentally is very expensive in terms of time and resources, which is why many algorithms have been developed to identify motifs through computational means.

Purpose

The purpose of this project is to develop a novel algorithm that will attempt to solve the problem of finding DNA sequence motifs in an original way to increase the efficiency and accuracy of motif discovery.

Design Criteria

A successful algorithm is one that can accurately identify motifs within known sequences, i.e. the motifs have already been experimentally determined. The algorithm should identify these motifs faster than current algorithms such as the MEME (Multiple Expectation-maximization for Motif Elicitation) or GLAM2 (Gapped local alignment of motifs).

Procedure

The first step in this project was to read the large data files containing sequences into a nice data structure for manipulating in Python. After reading the data, from files in FASTA format, into Python, I explored different algorithms to identify the most prominent motifs. I recorded the number of times a k-mer (sequence of length k) appeared in the set of sequences and used it as the primary value for ranking motifs. However, it became apparent that analyzing only one sequence for motifs was not returning accurate motifs. Next, I randomly shuffled the data set obtained from a cell to create another data set. Then, I was able to compare these two sets of sequences to determine which motifs were unique to the original sequence by using the ratio of the frequencies of the motifs in the two different sequences. After this, I calculated the p-value (using the binomial test) to test the statistical significance of motif occurrences and rank motifs more accurately.

Results

When analyzing the PITX1 (paired-like homeodomain 1) sequences, which were obtained experimentally, the target motif was the “GGATTA” binding motif. I found it to be prominent but not the top ranked motif. However, I found many variants of the “CAGCTG” motif to have very high rankings. When I further researched the cause of this abnormality, I discovered that the “CAGCTG” motif is an E-box (enhancer-box) DNA response element that acts as a protein-binding site. Previous studies have experimentally confirmed that the E-box and PITX1 motifs co-occur due to protein-protein interactions between the proteins encoded by the genes containing these motifs.

Conclusion

In conclusion, I successfully created a newly designed algorithm for DNA motif discovery that was relatively fast when compared to more complex algorithms such as MEME, since analyzing data sets of over 10,000 sequences took around five minutes. Such a method of DNA motif discovery could help find new motifs and connect them to their biological function.

Acknowledgements

I would like to acknowledge my mentor, <name>, for his support and help throughout the making of this project.

SAMPLE - STUDY

The Cure for Diabetes

<name> <school>

Background and Problem

Diabetes mellitus is an autoimmune disease that affects millions of individuals. It is a chronic disease where the body cannot produce insulin, or cannot use the insulin it produces. Insulin is a hormone produced by the pancreas, controlling the amount of sugar in the blood. It is crucial to maintaining proper health, which is why diabetes can be fatal. Without insulin, the body cannot turn sugar into usable energy, and individuals experience high blood sugars, which cause damage to organs, blood vessels, and nerves. There are two types of diabetes: Type 1 and Type 2. Type 1 (juvenile onset/insulin-dependent) diabetes typically occurs in children, and it is due to the complete lack of insulin production. On the other hand, Type 2 (adult onset/insulin independent) diabetes can occur in the instance of obesity or in late adulthood. It is due to the resistance to insulin, and the pancreas gradually makes less and less insulin as the disease gets worse.

Purpose/Thesis

The purpose of this study is to explore current research into a cure for diabetes mellitus and to draw our own conclusions or predictions for future advancements.

Evidence and Supporting Data

There are numerous ongoing studies and advancements regarding the cure for diabetes. Firstly, medical researchers are exploring the use of immunology in efforts to find a cure. They are trying to find a way to transplant islet cells that produce insulin without having the body's immune system destroy them. Additionally, the use of engineering embryonic or adult stem cells to regenerate islet cells is an optimistic approach to finding a cure, assuming that most Type 1 diabetics still have some islet cells left to regenerate.

Conclusion

Overall, diabetes is a severe disease where insulin is no longer produced, but there is an ample amount of cutting edge research in an effort to find a cure. The future of diabetes lies in the hands of immunology and stem cell research.

Acknowledgements

Special thanks to <name> MD at the Hospital for Sick Children for answering our questions regarding Diabetes, and for educating us about her past and current research on the disease.