Illnesses of high mortality rate such as breast cancer elicit questions related to the patient’s time left to live. The common methods used to arrive at an estimate include comparing the patient’s health condition to previous medical records and treatments, referral to statistically-computed survival rates based from historical records, or consulting another breast cancer expert. The application of data mining on medical records to create predictive models for cancer survivability has been proven to hold significant accuracy by numerous scientific and applied researches throughout the years. Agrawal et al.’s “Lung Cancer Outcome Calculator” provides a framework for developing a predicted survival calculator for different cancers based on a patient’s health condition. This research aims to develop the Breast Cancer Outcome - Survival Online Measurement Calculator (BOSOM Calculator), an online application that takes a patient’s clinical cancer data to give a predicted cancer survival based on a dataset from the Surveillance, Epidemiology, and End Results Program (SEER).
Prediction of Polyketide product from Module Organization of Enzymes Using Cumulative Tanimoto Fragment Scores

Polyketide is a major class of natural products possessing several pharmacological properties. Performing wet laboratory experiments to discover a functional polyketide is costly and difficult because of its trial-and-error nature. However, the analogous biosynthesis of these metabolites to fatty acids makes the resulting compound predictable. Through the use of information technology, a stand-alone computational tool -Predyketide - is created to observe the resulting structure per elongation, and to allow prediction and visualization of the most possible natural product compound. The list of all known building blocks (starter and extender) used in the system is gathered from ASMPKS, another polyketide-related system. With these functionalities, this application can help in the discovery of new drugs requiring lesser time and effort.
Visualization of Multivariate Health Data Using Self-Organizing Maps

Data that are multivariate in nature is a type of data that may contain subtle patterns. However, it is considered to be an obstacle in research most of the time since classical statistics may find it encumbering to analyze. However, computational statistics, a collaboration between computer science and statistics, offers a suite of algorithms that may be used to surpass obstacles such as this. The Self-Organizing Map and Data Visualization are examples of these. The Self-Organizing Map is an artificial neural network that employs a process to reduce multidimensional data into a low-dimensional representation while Data Visualization is a process that aims to give the human brain a visual representation of knowledge about certain data. SOM Visualize is a software that makes use of both processes. The tool enables users to input data and visualize several patterns such as clusters, associations, as well as a geographical representation that exist in the data. It may give several hypotheses that may be confirmed through other statistical tests and SOM Visualize has therefore enabled the possibility of analysis of multivariate data.
Many topics in Automata and Languages Theory including context-free languages involve tedious tasks that are prone to error when done manually. Conventional instructional methods have many drawbacks when used to teach the numerous dynamic processes found in computer science. Interactive software provides one possible solution to these limitations of traditional teaching and learning resources. One of these is CMAN: Context-free Grammar Manipulator, an interactive pedagogical tool to construct grammars, convert it to normal forms and view its corresponding Pushdown Automaton. It can also test a string for membership using Cocke-Younger-Kasami algorithm then get its leftmost and rightmost derivation. It also provides an interactive graphical environment for parse tree construction. Lectures and assessment examination is also provided for users quick reference.
“A metabolic pathway within an organism is a series of enzymatic reactions consuming certain metabolites and producing others. These metabolites do not only play a part in one metabolic pathway but is integrated in others as well thus forming a complex network of reactions” [2]. A vast knowledge in both biochemistry and cell physiology is needed in the projection and analysis of this complex network of reactions.

Due to the difficulty of understanding and analyzing these pathways, illustrations and graphical representations of the composition of the pathways are needed.

The development of the Generic Pathway Generator (GPG) which generates different metabolic pathways helps the users to visualize and understand the relationship of the different enzymes and factors that affect the end products of the different pathways. The results generated by the system can be used to analyze the characteristics of the different organisms that resulted because of the factors in the pathways and the alteration of the different enzymes, genes and other inputs.

The development of this pathway website can help the different researchers compile their studies (experiments and projects) and generate pathways based on them. The automation of compilation of their studies can enable users to easily update their experiments and projects. GPG also enables users to easily connect the different pathway studies and see the resulting pathway.