Mathematically Modeling Genetic Amplification

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The goal of this project was to form a mathematical model of genetic amplification. Unlike previous attempts this equation was based off of actual data, thereby greatly reducing the percent error, and correlates messenger-ribonucleic acid (mRNA) concentration to rate of protein synthesis. For this equation, due to time constraints, only 8 proteins, and their respective mRNA's were analyzed. In order to gather the mRNA concentration, real time quantitative polymerase chain reactions (qPCR) was utilized. Next, the amount of protein was determined by using a procedure known as the Western Blot and pixel intensity and standards were utilized to determine the rate of protein synthesis. The data from both the Western Blot and the qPCR were combined to form points (Western Blot, qPCR) and using Wolfram Mathematica curve fitting was utilized to format the optimal equation. After testing transcendental functions, higher order polynomial functions, as well as trigonometric functions, the final equation was determined to be: 129.24119688766737""+34.3200375114914ⅇ^x-231.86585152919x+256.1916986069598x^2+691.2290355371973x^3+580.6315701337923x^4-405.37877925005387x^5-2511.485702371964x^6-5782.961733730821x^7-9744.5595050334x^8-12732.166758443494x^9-10592.529333380615x^10+5759.663668443907x^11+54822.54623825022x^12+172578.7242743045x^13 Using this equation and the method for the production of this equation disorders and diseases such as obesity and cancer may be diagnosed at an earlier stage.