A Universal DNA Computing Method

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With the significant advantages in solving NP-complete problems, DNA computing is considered a promising computational method. This project presented a novel DNA universal computing method and constructed a feasible calculation model out of single strands by adopting special coding rules and unique calculation logic. Our method can be broken down into three parts. First is using DNA to represent what to compute. We used the sequence of DNA single-strands to map numbers in calculation according to coding rules we built. Then is to determine how to compute with DNA. For this part, we used group theory in mathematics to establish our computing rules. The third part is to extract the outputs from DNA solution. We used complex coding and improved biological techniques to help accomplish the purpose. Achieving all these steps, we have successfully built a universal DNA computing method. Using simple biological structures, we could successfully construct our model with improved efficiency without the need of using enzymes. Our model is capable of doing serial operation, parallel operation and asynchronous operation at the same time. So within large scale computing problems, it has shown merits comparing with conventional electronic computers. To conclude, as being proved through both theoretical and experimental ways, our model has a possibility to be a future way of building supercomputers with DNA.

Awards Won: