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In order to optimize a gene in terms of mRNA binding energy, the algorithm was developed utilizing both mRNA prediction and codon optimization modules. At the code level, an original sequence is continuously modified until its Gibbs free energy is in a specific range given by minimum or maximum Gibbs free energy where the modification refers to synonymous substitution. With regard to the modification strategy, the simplest approach is that the number of mutations is gradually increased one by one when the calculated Gibbs free energy is out of range. Meanwhile, the base module was

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also used to develop more complicated modules. For example, a binding energy profile of a long test sequence can be optimized by repeatedly applying the base algorithm to all local sequences with a moving window method. In this way, all local mRNA structures can be optimized while minimizing the number of base changes. Similarly, a user can increase or decrease binding energy at specific locations in a sequence. Visual Gene Developer has a specialized window for mRNA optimization for a typical user and provides related class functions for a module developer. An online programming environment for you to learn programming . Even with an account, you can still visit the site even without an account. You can find a free workspace , the place that you will be able to explore to learn how to code. [cran.r-project.org](http://cran.r-project.org)[install.r-project.org](http://install.r-project.org)[stall.github.io](http://stall.github.io)[download.r-project.org](http://download.r-project.org)[r-project.org](http://r-project.org)[sourceforge.net](http://sourceforge.net)[github.com](http://github.com)[codecode.org](http://codecode.org)[codecamp.com](http://codecamp.com)[educators.r-project.org](http://educators.r-project.org)[sourceforge.net](http://sourceforge.net)[khanacademy.org](http://khanacademy.org)[baylorbros.com](http://baylorbros.com)[github.com](http://github.com)[baylorbros.com](http://baylorbros.com)

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