Protein Synthesis Algorithm and a New Metaphor for Selecting Optimum Tools*

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With assistance from DNA, mRNA, tRNA, RNA polymerase and aminoacyl-tRNA synthetase, biological systems synthesize amino acids in a particular sequence to produce a specific protein for a particular activity. On the other hand, using the parameters of some physical objects, such as, namely, parts design, machine tools, cutting tools and their machinability data, optimum tool selection for machining a particular part is accomplished. Analogizing the optimum tool selection process to the protein synthesis process, the above-mentioned objects were organized using the Protein Synthesis Algorithm derived from the protein synthesis mechanism. Unlike other related methods, this new method uses only a single database and avoids complex simulations. From an experiment in which the Protein Synthesis Algorithm was applied to turning tool selection, the claimed lucidity and straightforwardness of this method was confirmed.

Key Words: Biological System, Artificial System, Protein Synthesis, Metaphor, Tool Selection

1. Introduction

The testified methodologies for selecting tools and cutting conditions are quite diversified⁽¹⁾⁻⁽⁵⁾, but observations have ensured⁽⁶⁾ that the information sources for all these methodologies are constant and can be distinguished by some independent physical objects, namely, parts design, machine tools, cutting tools and their machinability data. Thus, fundamentally, synthesis operations are implicitly carried out among the dominant parameters of the above-mentioned objects to produce meaningful information with respect to the data.

Synthesis is the key with which all biological systems are performed with the highest degree of order and flexibility. The functions of biological systems are controlled and stimulated by enzymes which are proteins that are polymers of amino acids. A mechanism known as the protein synthesis mechanism

is incorporated to bond the amino acids with assistance from several independent molecules, whenever an enzyme is required. The "synthesis" idea provides a concept for manufacturing engineers who seek more friendly and lucid technique to help in crucial decision-making, such as in manufacturing, tool and cutting condition selection. Based on this idea we concentrate on mimicking the idea of protein synthesis in an algorithm form. Then, using the developed algorithm, the optimum tool selection aspects are elaborated in accordance with the new idea of "synthesis".

Notation

$a_{pmax}, a_{pr}, a_{pro}$: maximum, real, optimum depths of cut (mm)
 C_a, C_p : cutting allowance, position (mm)
 f_{max}, f_r, f_{ro} : maximum, real, optimum feed rates (mm/rev)
 F_{max}, F', F_s, F_r : maximum, torque-based, safe, real cutting forces (N)
 j_m, j_{mr} : given, real job material groups
 l : cutting edge length (mm)
 m_i : machining information

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- mt_s : machine tool specifications
 N_R : RPM ranges (rev/min)
 P_{max}, P_r : maximum, real cutting powers (kW)
 Q_r : productivity (cm³/min)
 r_ϵ : cutting tool nose radius (mm)
 s_l : slenderness ratio
 t_m, t_{mr}, t_{mro} : given, real, optimum tool material groups
 T_{max} : maximum torque at rated spindle speed (kg·m)
 $t_{ool}, t_{ool,opt}$: given, optimum cutting tool specifications
 V_R, V_r : range, real cutting velocities (m/min)
 Δ, Ω : parameters set from cutting tools
 $f, f_{opt}, f_{opt,p}$: given, optimum, productive machinability data
 μ : parameters set from feature and machine tool
 Σ : parameters set from feature, machine tool and cutting tool

2. Biological Protein Synthesis Mechanism

Molecules, such as DNA, free bases of DNA, *t*RNA, amino acid, RNA polymerase and aminoacyl-*t*RNA synthetase, are essential for protein synthesis. The whole synthesis mechanism is divided into two distinct processes defined as DNA transcription and RNA translation. Figure 1 illustrates these processes and the associated independent molecules.

As shown in Fig. 1, DNA transcription generates a copy of a particular region of DNA (gene) using a special enzyme, RNA polymerase (ENZ_m). The copied molecule is called messenger RNA (*mRNA*). Three base-pairs inside *mRNA*, AUG, GCA, etc., are

called codons⁽⁷⁾. Each codon codes a particular amino acid. There exist only 20 types of amino acids, so there should be at least 20 types of codons. In fact, there are 64 possible codons for the 20 types of amino acids. Therefore, one amino acid can be coded by more than one codon.

Since there are no chemical affinities among codons and amino acids, another process, called RNA translation, gathers amino acids accordingly, assisted by transfer RNA⁽⁸⁾ (*t*RNA) and aminoacyl-*t*RNA synthetase⁽⁹⁾ (ENZ_t). *t*RNA acts as an adaptor between a codon and an amino acid. It has the ability to physically carry an amino acid and also to communicate with a codon using its anticodon which is complementary base-pair of the codon present in *t*RNA. Therefore, one *t*RNA is designed to carry one definite type of amino acid dictated by its anticodon. As discussed earlier, one amino acid has several codons; in the same way, there is more than one *t*RNA to convey one type of amino acid. Thus, the accuracy of protein synthesis depends crucially on the mechanism which links each amino acid to its decorous *t*RNA molecule or molecules. This mechanism is controlled by the ENZ_t enzyme. The ENZ_t matches the correct amino acid to the corresponding *t*RNA and produces a *t*RNA-amino acid compound. When this compound approaches its correct codon, the codon is bonded to the anticodon of the same compound. At that precise moment the compound releases the bonded amino acid to the growing protein chain. In Fig. 1, this process, codon-anticodon-amino acid translation, is illustrated, revealing the instant when a codon, UUC, is translation by its anticodon, AAG, and right amino acid, Phe (shown by a square).

3. Protein Synthesis Algorithm

Protein synthesis is an information processing technique. First it recognizes some independent molecules, DNA, *t*RNA, amino acids, ENZ_m, ENZ_t, and then it generates *mRNA* as a summation of codons from one part of DNA (gene). Consequently, information from a single codon is used to select an optimum anticodon (*t*RNA) with the help of ENZ_t. Finally, using the selected anticodon, an amino acid is singled out.

Based on the above principle, an algorithm called Protein Synthesis Algorithm is developed which is shown in Fig. 2.

Referring to Fig. 2, the DNA concept serves as an information bank in which the system input is stored. On the reverse side, the protein provides a facility to represent the system output. The amino acids provide a reservoir for output elements. The gene is merely a part of the input that has direct relation to the

Fig. 1 Biological protein synthesis mechanism

Fig. 2 Protein synthesis algorithm

phenomenon dictated by an input-output pair. The $ENZm$ plays the role of the pattern recognizer of the gene and also produces a modified information code from the gene as $mRNA$. The codon is part of a modified information and is competent enough to collect one output element. Anticodons are interpreted as the adaptor information that is required to relate input and output. The sources of adaptor information are the $tRNAs$. The $ENZt$ is nothing but a dynamic selection criterion of an adaptor information for a given copied pattern and set of output elements.

The working principle of Protein Synthesis Algorithm is self-explanatory in Fig. 2. First of all, from the input information some patterns (meaningful information with respect to output) are scrutinized with the help of the predefined patterns. Then the dynamic selection criterion is initialized by synthesizing information from two different directions, one being the first copied pattern and the other is the available output elements of that pattern. Subsequently, the dynamic selection criterion interacts with the sources of adaptor informations and the best suited adaptor information is evaluated. Then the selected adaptor information is used to obtain the most appropriate output element. This process is repeated until the last copied pattern is used and the selected output elements appear as system output. This working principle will be understood better after applying the following model.

Fig. 3 Kinetic and kinematic limits of machining operations

4. General Tool Selection System Using Protein Synthesis Algorithm

During any machining operation, the relative motion between a cutting tool and a job, maintained by the corresponding machine tool, creates a certain kinetic and kinematic situation. However, the machining information (m_i) derived from the parts design, the machine tool specifications (mt_s) and some cutting tool parameters (t_{ool}) directly influence the safe kinetic and kinematic limits of machining operation, as illustrated in Fig. 3 by the dotted line. Specifically, these m_i , mt_s and t_{ool} are composed of the parameter sets

$$m_i = \{j_m, c_a, c_p, s_l\} \quad (1)$$

$$mt_s = \{P_{\max}, T_{\max}, F_{\max}(s_l)^{(10)}, N_R\} \quad (2)$$

$$t_{ool} = \{t_m, r_e, l\}. \quad (3)$$

Machining data analysis⁽¹⁰⁾ has confirmed that unlike other parameters of mt_s , $F_{\max}$ is a variable of the overhang or approximately a function of the slenderness ratio (s_l).

On the other hand, every single set of machinability data of cutting tools represents a real kinetic and kinematic situation, dominated by particular set of cutting conditions, which is represented by a continuous line in Fig. 3. In general, the kinetic and kinematic situation of a single set of machinability data is denoted by f :

$$f = \{j_{mr}, t_{mr}, a_{pr}, f_r, V_r, P_r, F_r, Q_r\}. \quad (4)$$

Thus, the kinetic and kinematic situations represented by f and some equivalent situations of f , derived from m_i , mt_s and t_{ool} , can be brought together to calculate the most productive and safe f and the corresponding optimum tool.

Based on the above principle, idea of synthesis hidden inside the designed Protein Synthesis Algorithm is used to sketch paths among physical items in

Fig. 3. Figure 4 shows the modeling method and Table 1 summarizes the metaphorical meaning of the molecules involved in the protein synthesis mechanism in terms of general and tool selection system.

According to the designed method in Fig. 4, the whole information process is divided into two parts: part design transcription and machining information translation.

First, the designed method collects machining information from the given part design. Then it initializes the safe kinetic and kinematic limits (which act as dynamic selection criterion) using the machine tool specifications. Then it synthesizes the information from two directions (one from the machining

Table 1 Metaphorical meaning of protein synthesis items in terms of general and tool selection system

biological system	general system	tool selection system
DNA	input	product-blank
ENZ _m	pattern recognition	machining feature
Codon	useful part of input	machining information
mRNA	summation of useful parts	sum of machining information
ENZ _t	dynamic selection criterion	kinetic, kinematic limits
tRNA	source of adaptor information	machinability data of tool
anticodon	adaptor information	$t_m^{\#}, a_p^{\#}, f^{\#}$
amino acid	output element	a tool
protein	output	selected tools set

t_m = tool material, a_p = depth of cut, f = feed rate

Fig. 4 Tool selection system using protein synthesis algorithm

information and the other from cutting tools), one at a time, until it (mt_s) transforms into an equivalent structure of f . After this, the synthesized information interacts with the machinability data to determine the most productive and safe f . Consequently, the parameters, tool material, depth of cut and feed rate, within the selected f , appear as adaptor information because these parameters have a direct relation to the cutting tool specification (t_{ool}). Lastly, using the selected adaptor information, the optimum tool is singled out.

4.1 Part design transcription

The principle of this process is self-explanatory in Fig. 4. The purpose of this process is to collect machining information (m_i) from every machining feature of a given part design. In the first step, the parts design (product and blank) is recognized and then, using predetermined machining features as the pattern recognizer, the given parts design is separated into features. Finally, the machining information for every copied feature is stored in the format of m_i . However, the values of the parameters of m_i depend on the geometric nature of the feature, or in other words, on the machining operation (turning, drilling, milling, etc.).

4.2 Machining information translation

According to Fig. 4, the machining information process corresponds to step 4 to step 12. Significantly, this process has two motives, one is to find adaptor information by selecting the most productive and safe machinability data and the other is to determine the optimum tool using the selected adaptor information. Figure 5 explains this process in more detail than in Fig. 4.

To calculate the required adaptor information, the system carried out some synthesis operations involving the parameter sets m_i , t_{ool} and mt_s . The first synthesis between m_i and mt_s produces μ , where

$$\mu = \{j_m, c_a, V_R, P_{max}, F_{max,r}\}. \quad (5)$$

The determination process of $F_{max,r}$ and V_R is illustrated in Fig. 5.

Meanwhile, standard practices⁽²⁾ indicate that the maximum depth of cut and feed rate achievable by a tool are $a_{pmax} \approx 0.5 \cdot l$ and $f_{max} \approx 0.8 \cdot v_c$. Utilizing these guidelines, two other functions, Δ and Ω , can be generated from every single given cutting tool (t_{ool}). Thus,

$$\Delta = \{a_{pmax}, f_{max}, t_m\} \quad (6)$$

$$\Omega = \{f_{max}, t_m\}. \quad (7)$$

However, if μ and Ω are just being synthesized, then the result (denoted as Σ) becomes similar in content to f where

$$\Sigma = \mu + \Omega \quad (8)$$

$$\text{or, } \Sigma = \{j_m, t_m, c_a, f_{max}, V_R, P_{max}, F_{max,r}\}. \quad (8.a)$$

Physically, Σ s are nothing but the safest kinetic

and kinematic limits shown in Fig. 3. Therefore, the most productive (Q_r is maximum) machinability data set under the constraints of Σ is the optimum machinability data set or f_{opt} . Thus,

$$f = f_{opt} \text{ given: Rule 1} \quad (9)$$

where

Rule 1 :: maximize Q_r while

$$j_m = j_{mr} \text{ \& } t_m = t_{mr} \text{ \& }$$

$$c_a \geq a_{pr} \text{ \& } f_{max} \geq f_r \text{ \& } V_r \text{ is within } V_R \text{ \& }$$

$$P_{max} > P_r \text{ \& } F_{max,r} > F_r.$$

There are several f_{opt} that depend on the number of Σ . From them only one f_{opt} , denoted as $f_{opt,Qmax}$ (see Fig. 5) can be selected again by the same governing parameter, Q_r , the productivity. Meanwhile, it is clear from Δ and t_{ool} that the depth of cut, feed rate and tool material are the three parameters which are

directly related to f and t_{ool} . Thus, these three parameters inside $f_{opt,Qmax}$ are the required adaptor information, a_i . That is,

$$a_i = f_{opt,Qmax}(t_{mro}, a_{pro}, f_{ro}). \quad (10)$$

The tool whose corresponding Δ has the same material as t_{mro} and also holds the equal or the smallest dimension beyond a_{pro} and f_{ro} , is the desired optimum tool, that is,

$$t_{ool} = t_{ool,opt} \text{ given: Rule 2} \quad (11)$$

where

Rule 2 :: minimize $a_{pmax} \cdot f_{max}$

$$\text{while } t_{mro} = t_m \text{ \& } a_{pro} \leq a_{pmax} \text{ \& } f_{ro} \leq f_{max}.$$

The preceding loop continues until the last machining information is translated and finally, the selected optimum tool list is displayed as output.

Fig. 5 Machining information translation process

Fig. 6 The given part design

Fig. 7 Machining information translation for m_{i1}

5. Example Problem

For a better understanding of the developed method, a numerical example is presented, considering only the case of turning because it has the highest

number of potential tools.

The part to be machine is shown in Fig. 6. Referring to this figure, in the turning feature c_a is $0.5(D_{\max} - D_{\min}) = x_2 - x_1$, c_p is $D_{\max} = 2 \cdot x_2$ and s_1 is $L/D_{\min} = z_1/x_1$.

Therefore, there are two m_i , m_{i1} and m_{i2} , for the given parts design. Calculation confirmed that m_{i1} is $\{1, 4, 100, 2.71\}$ and m_{i2} is $\{1, 2, 92, 2.84\}$.

For this example, a machine tool with $mt_s = \{P_{\max} = 25 \text{ kW}, T_{\max} = 40 \text{ kg.m}, F_{\max} = (25 \text{ kN}(0 \leq s_l \leq 1.5), 10 \text{ kN}(1.6 \leq s_l \leq 3.0), 5 \text{ kN}(s_l > 3.1))$ and $N_R = 30 \sim 3000\}$ are considered.

Figure 7 represents the specifications of the available cutting tools. Since the cutting tools are from the maker, SECO, the machinability data have been collected from SECO's machinability data book⁽¹¹⁾, and a cross section of the related data is given.

In fact, SECO has supplied data up to P_r , and using the following two basic relationships, F_r and Q_r have been estimated.

$$P_r = F_r \cdot V_r \quad (12)$$

$$Q_r = a_{pr} \cdot f_r \cdot V_r \quad (13)$$

The numerical values of the parameter Σ are given in Fig. 7. With these values, a search (using Rule 2) for the optimum data produces, for m_{i1} , $f_{opt, Qmax}$ of $(1, 1, 3, 0.65, 330, 23, 4142, 644)$, and for the corresponding adaptor information a_{i1} of $(1, 3, 0.65)$.

Applying Rule 2 (with numerical value belong to a_{i1}) the tools in Fig. 7 suggest that the optimum tool for m_{i1} is $t_{ool, opt} = \text{TN--08 04 08--TP15}$. Exactly in the synonymous manner, the second optimum tool needed for m_{i2} can be determined.

This example reveals some unique contributions of the Protein Synthesis Algorithm to tool selection. It only needs one database instead of multiple databases that are often required in other related methods. Furthermore, each single set of data has been considered as an independent piece of information. This ensures complete avoidance of empirical equation that are usually needed to handle data. Moreover, in the proposed method, the given information of a machining operation (part design, cutting tools and machine tools) and the machinability data have been organized separately. All these aspects have resulted in an extremely flexible and adaptive tool selection system.

6. Conclusion

For the purpose of cutting tool selection, we have pointed out the relationship among some objects, namely, parts design, machine tools, cutting tools and machinability data, with the aid of an algorithm called the Protein Synthesis Algorithm which was derived from the biological protein synthesis mechanism.

Both the generation of synthesized information from some recognized physical objects and the interaction of this information with some given data are the most significant characteristics and advantages of this algorithm. However, the predominant contribution and portrayal of individual objects, noted above, in the selection criterion of optimum cutting tools or cutting conditions, is transparent and straightforward when using parameter set Σ .

The metaphorical meaning, summarized in Table 1, of the biological molecules that are involved in the protein synthesis mechanism could aid other system engineers to comprehend their problems in the manner of "synthesis".

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