

Integration of Genetic Programming and TABU Search Mechanism for Automatic Detection of Magnetic Resonance Imaging in Cervical Spondylosis

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ABSTRACT

Cervical spondylosis is a kind of degenerative disease which not only occurs in elder patients. The age distribution of patients is unfortunately decreasing gradually. Magnetic Resonance Imaging (MRI) is the best tool to confirm the cervical spondylosis severity but it requires radiologist to spend a lot of time for image check and interpretation. In this study, we proposed a prediction model to evaluate the cervical spine condition of patients by using MRI data. Furthermore, to ensure the computing efficiency of the proposed model, we adopted a heuristic programming, genetic programming (GP), to build the core of refereeing engine by combining the TABU search (TS) with the evolutionary GP. Finally, to validate the accuracy of the proposed model, we implemented experiments and compared our prediction results with radiologist's diagnosis to the same MRI image. The experiment found that using clinical indicators to optimize the TABU list in GP+TABU got better fitness than the other two methods and the accuracy rate of our proposed model can achieve 88% on average. We expected the proposed model can help radiologists reduce the interpretation effort and improve the relationship between doctors and patients.

KEYWORDS

Cervical Spondylosis, MRI, Genetic Programming, TABU Search, Automatic Detection.

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I. INTRODUCTION

CERVICAL spondylosis is a kind of degenerative disease which widely occurs in middle and old aged patients [1]. Besides aging issue, it may be also caused by the structural change of the cervical discs and vertebrae or spinal injury. Cervical spondylosis is a typical change in the cervical spine aging process, and is the most common reason for degenerative changes with the spinal column [2]. The bony structures of the vertebral bodies, known as osteophytes or spurs, also grow with age, which can cause compression of the spinal cord and stenosis of neuroforamina. According to statistics, more than 85% of people above 60 years old are affected by cervical spondylosis. Patients

with cervical spondylosis might have symptoms including soreness, pain in the neck and shoulders, numbness, sensory change, weakness or muscular atrophy of the upper limbs as well as unstable gait caused by involvement of the lower limbs.

In addition, according to the interview results with radiologists, the cause of cervical spondylosis is also closely related to a person's lifestyle, work, and poor posture. For illustration, long-term continuous use of electronic devices in an inappropriate posture may lead to cervical spine disease, causing neck pain or muscle fatigue. The prevalence of cervical spondylosis is even higher among those who have to use computers and those who have to flex their necks for a long time [3]. The viewpoint is consist with the reported statistics that indicated the excessive use of electronic products has increased the number of patients with cervical disease [4]. Therefore, in the recent decades, cervical spondylosis not only occurs in the elderly but also develops widely in the younger population. The age distribution of cervical spondylosis patients is much lower than before. Unfortunately,

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according to a report published by eMarketer, the penetration rate of the electronic devices in Taiwan is the highest in the world(73.4%), followed by Singapore (71.8%) and Korea (70.4%) [5][6]. What is known as “smartphone zombie” or “Smombie” has accelerated the cervical spondylosis in all age groups. Smombie-related cervical spondylosis has become a new worldwide disease that threatens the human beings [7]. Therefore, how to efficiently diagnose cervical spondylosis is becoming an important issue.

The human cervical spine consists of many different structures with many nerve endings evenly distributing on it that makes cervical spine a very complex structure. Diagnosis of cervical spondylosis could be achieved by four different imaging tools, including X-rays, computed tomography (CT), myelography, and magnetic resonance imaging (MRI). Among all of them, MRI is most preferred for its noninvasiveness, high soft tissue contrast, high resolution, and free of radiation exposure. It is capable of clearly distinguishing the vertebrae, disc, cerebral spinal fluid (CSF), spinal cord, and fat so that it outperforms all other aforementioned imaging tools in diagnosing cervical spondylopathy. In addition, MRI is able to detect the edema and ischemic change of the spinal cord, which helps determine the severity of spinal cord injury. Comparing to other tools mentioned above, as MRI used for the cervical spondylosis diagnosis, a false positive error (we regarded cervical spondylosis as positive which the patients are more concerned about) is more harmless than a false negative error [8].

However, in spite of all the merits, the MRI takes radiologists (or experts from other fields) a lot of time for MRI image check and interpretation. While pursuing more detailed medical information (such as advanced imaging techniques, videos, and laboratory data), the data amount increases accordingly. That is definitely a big burden for radiologists and might further increase the risk of misinterpretation due to physician’s fatigue. Moreover, the shortage of medical manpower remains a problem, and training a medical expert takes rather a long time. Even not for cervical spondylosis diagnosis, the medical experts (such as clinicians and medical examiners) need more assistance for such image tool usage. We believe information technology (IT), including machine learning or data analytics prediction, can help solve the problems. For illustration, there is a research that refers improving radiologists’ performance by using artificial intelligence system [9].

Also, Lin uses deep learning for automated contouring of primary tumor volumes of nasopharyngeal carcinoma MRI. It has a positive impact on tumor control and patient survival [10]. Using IT technology to help MRI interpretation is feasible.

In the past, most researches used image recognition [11][12] or feature extraction [13][14] for MRI images process. Although the MRI technology for image recognition can achieve a good accuracy rate, the detection method is like a black box and it is difficult to interpret. Therefore, how to assist clinic select appropriate feature from MRI via algorithms is an important issue.

In the literature, meta-heuristic algorithms and neural networks are used to solve decision problems, some heuristic algorithms can find good solutions, but they take more time [15]. In this research, we need to establish a flexible feature selection model based on a variety of features of cervical spine data. The model is expected to identify appropriate feature accurately and implement quickly. Therefore, Genetic Programming should be a good candidate [16], and TABU can be added to accelerate the algorithm.

In this study, we proposed a prediction model to evaluate the cervical spine condition of patients by using MRI data. The prediction model provides radiologists and neuroradiologists with prediction results of patients’ cervical spondylosis severity for their diagnosis reference. Furthermore, to ensure the computing efficiency of the

proposed model, we adopted a heuristic programming known as genetic programming (GP) to build the core of refereeing engine. Additionally, to guarantee the output of optimal solution, we used referencing search algorithm [16]-[19] by combining the TABU search (TS) with the evolutionary GP. Finally, to validate the accuracy of the proposed model, we implemented experiments via using actual MRI image and compared our prediction results with radiologists’ diagnosis to the same MRI image. We expected the proposed model can help radiologists reduce the interpretation effort and improve the relationship between doctors and patients.

II. THE CONCEPTUAL ARCHITECTURE AND DIAGNOSIS PROCESS OF THE PREDICTION MODEL

As indicated in the report from the National Research Council (NRC) of the United States in 2011, a successful medical analyzing system should contain two components, First, appropriate strategies are used to design and collect disease-relevant information from patients. Second, the data analytics methodologies are used to establish a practical architecture for data analysis. The clinician can then take new patients’ data to test and verify such architecture [20]. To establish a prediction model for cervical spondylosis diagnosis based on the concept above, the proposed framework integrated abundant information, which was generated by disease-related inspection mechanism, and established a flexibly and comprehensively intelligent assistant model.

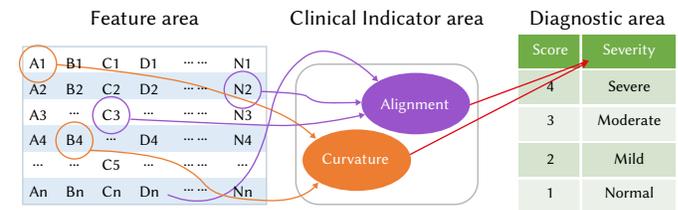


Fig. 1. The conceptual architecture of proposed predicted model.

As shown in Fig. 1, the predicted model is divided into three parts: the feature area, the clinical indicator area and the diagnostic area. In detail, the feature area collects data of the cervical magnetic resonance imaging which is measured by K-PACS. To measure the cervical spondylosis diagnosis, we adopted three indicators, including alignment, curvature and the aggregative diagnostic result which contains four severity levels. Finally, the diagnostic area reports the severity score as a reference for the doctor, enabling medical experts and patient to understand the diagnosis of cervical spondylosis. The severity score, ranging from 1 to 4, stands for the normal, mild, moderate and severe level of cervical spondylosis. To validate the proposed model, we cooperated with neuroradiologists and collected patients’ MRIs of cervical spine with relative diagnosis results. The cervical vertebrae features required for the prediction model were measured under the guidance of the neuroradiologists. Then, these features were regarded as labels (named alignments, curvature, and severity) to establish and train the predictive model of cervical spondylosis. After training, the prediction model was applied to the test dataset and the accuracy with the diagnosis result of clinic was compared. The analytics process is detailed below.

A. The Analytics Process of the Proposed Prediction Model

To optimize the prediction performance, the proposed model integrated the TABU search algorithm with genetic programming (GP) to establish a prediction model. The analytics process is shown in Fig. 2.

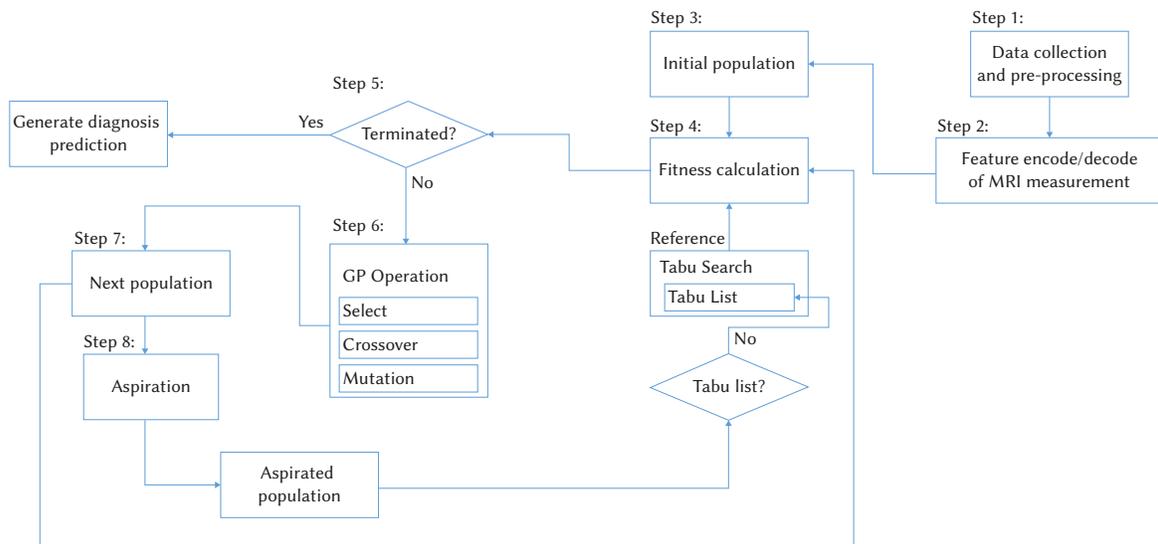


Fig. 2. Analytics process of the proposed prediction model.

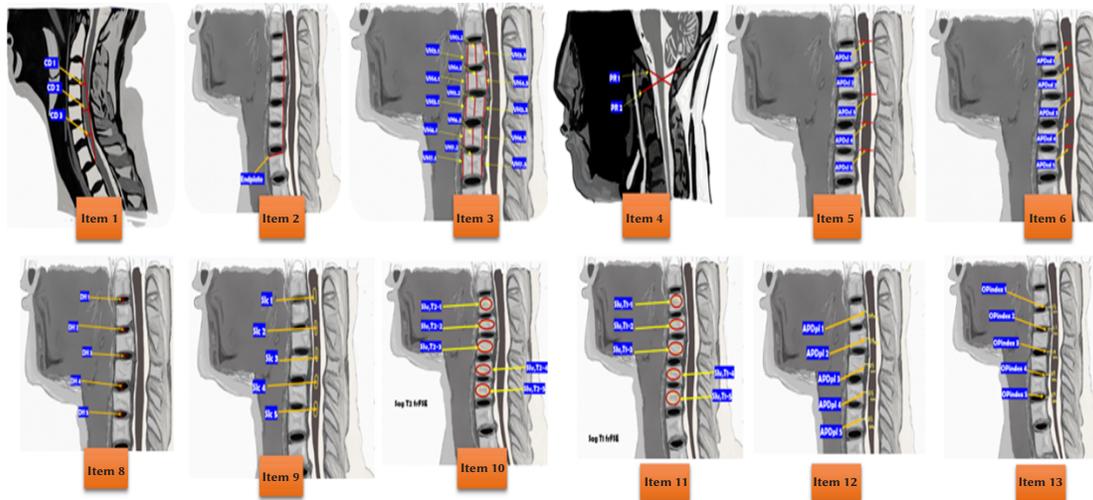


Fig. 3. Operational definition of features.

The analytics process consists of four sub-procedures, including data collection and pre-processing (step 1 in section II.B), feature encoding/decoding (step 2 in section II.C), integrating prediction model of GP (step 3 to step 6 in section II.D), with TABU search to optimize prediction result (step 6 to step 8 in section II.E). Moreover, we will further explain step 3 initial population in Fig. 7 and Fig. 8 and explain the GP process in Fig. 9. The sub-procedures are detailed from section II.B to II.E.

B. Data Collection and Pre-processing

The image data of MRI was collected from the patients' original cervical vertebrae MRIs, which were generated at the division of Magnetic Resonance Imaging in the Tri-Service General Hospital, as shown in Fig. 3 for demonstration. With high-resolution images, MRI enables radiologists to accurately diagnose cervical spine diseases and determine the extent of cervical cord damage. We adopted sagittal fast spin echo T2-weighted image and sagittal fast spin echo T1-weighted image mode to measure the cervical spine features. The images need to be clearly identified as the appropriate research data by the contours of the cervical spine. The cervical vertebrae consist of seven segments called C1 to C7. However, the atlas' shape of C1 is different from others',

which have no body and are fused with the C2. Therefore, according to the suggestions from clinicians and radiologists, the measurement of cervical spine in the present study is based on C2 to C7.

In order to clearly identify the appropriate research data by the contours of the cervical spine, so that eliminated 6 images which were not clear or had missing part. The measurement features of the study are 67 features in 13 items. After image measurement and data processing, study had 147 cases of data for further analysis.

For data pre-processing, the first step is MRI image interpretation. By checking MRI, radiologists determine patients' cervical spine either normal or minor cervical spondylosis. Next, based on the definitions, we measured the cervical spine features for further model establishment. These features include curvature distance, vertebral body height and so on. However, the original images in the observation of the cervical spine may be hard to be interpreted (which may be caused by the poor resolution or angle) and each image may have different levels of definition as we measured. Therefore, we used the software to scale the images and selected the clearest MRI pictures according to the measure definition, making the collected data more accurate. The description and encoding/decoding of each feature are discussed in section II.C.

C. Feature Encoding/Decoding of MRI Measurement

To achieve higher accuracy prediction model, we collected a large number of cervical MRI images from the patients and used cervical anatomical position as the baseline when measuring. We adopted the software K-PACS to measure 67 features and then divided these features into 13 items according to their class as shown in Table I. The ways of measurement and each item’s operational definition are also displayed in Table I and Fig. 3 respectively. In Table I, we could find a huge amount of information which clinicians should read, understand, make diagnosis with, and explain to patients’ and their family members. Usually, to ensure the diagnosis accuracy, clinicians have to spend a lot of time dealing with this huge MRI information. Therefore, they tend to have limited time to communicate with their patients. To improve the doctor-patient relationship, clinicians need more support and assistance, such as a prediction model, to help them interpret MRI information.

TABLE I. THE DESCRIPTION AND ENCODE/DECODE OF FEATURES OF MRI MEASUREMENT

Item	Description	Encode as	Shown in Fig. 3
Item 1	Curvature distance of cervical vertebrae	CD1, CD2, CD3	(a)
Item 2	Anteroposterior diameter of superior endplate of cervical vertebrae	Endplate	(b)
Item 3	Vertebrae height	VH3.1-3 · VH4.1-3 · VH5.1-3 · VH6.1-3 · VH7.1-3	(c)
Item 4	Power ratio (The distance of cranial basis to posterior arch / The distance of occiput posterior to anterior arch)	PR1, PR2, PR3	(d)
Item 5	Antero posterior diameter of cervical canal	APDcl1-5	(e)
Item 6	Antero posterior diameter of cervical cord	APDcd1-5	(f)
Item 7	Item 5(APDcl) / Item 6(APDcd)	APDd1-5	(g)
Item 8	Disk height	DH1-5	(h)
Item 9	Singal intensity of cervical cord	SI1-5	(i)
Item 10	Sagittal fast spin echo T2-weighted image (vetebra signal intensity)	SIvT2-1~SLVT2-5	(j)
Item 11	Sagittal fast spin echo T1-weighted image (vetebra signal intensity)	SIvT1-1~SLVT1-5	(k)
Item 12	Anteoposterior diameter of posterior longitudinal ligment	APDpl1-5	(l)
Item 13	Posterior disk herniation index	OPindex1-5	-

Additionally, for solution encoding, in this study, we adopted genetic programming (GP) as our heuristic search methodology. In the calculation process of GP, it evolves a more appropriate solution via each generation convergence. GP presented the solution as a “tree” structure, as shown in Fig. 4. Each tree represents a predictive solution from the prediction model that represents a diagnosis path for the cervical spondylosis prediction. The tree structure has three parts: the roots (e.g., X in Fig. 4), the stems (e.g., -, /, +, or Exp in Fig. 4), and the leaves (e.g., parameters, the cervical vertebrae feature in Table

I). This encoding approach is like gene sequencing that produced the best tree of prediction model after several generations of successive evolutionary processes.

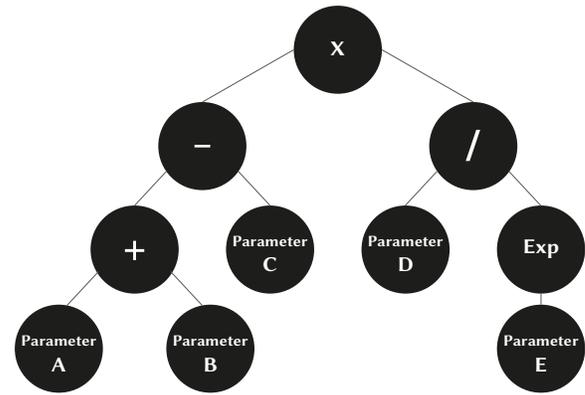


Fig. 4. The tree structure of genetic programming.

Finally, for the solution encoding and decoding, the GP method used LISP language to express the binary tree structure. As shown in Fig. 5, the tree’s encoding was presented as. root : C ; left : A / C,H / 1,4,40 / ; right : E / F,C / 32,27,33 /. The tree’s decoding was presented as ((1,4,C)(40,H)A)((32,F)(27,33,C)E)C. This decode way is also called postfix.

Encode:
 root: C
 left: A / C, H / 1, 4, 40 /
 right: E / F, C / 32, 27, 33 /

Decode(Postfix):
 ((1, 4, C)(40, H) A)
 ((32, F) (27,33, C) E) C

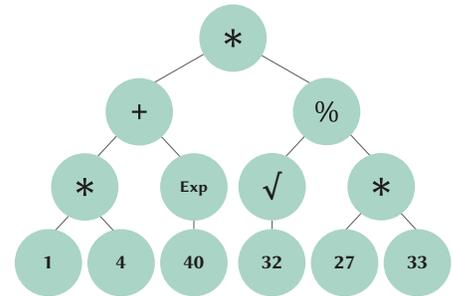


Fig. 5. The tree encoding and decoding schematic diagram.

D. Establish GP-based Forecasting Model

To ensure high accuracy of GP-based prediction model, we set the initial populations and then selected the tree with high fitness to multiply through the crossover and mutation. We repeated above process until reaching the terminal condition. Furthermore, we added TABU Search (TS) restriction and reward mechanism such as TABU list, candidate list and aspiration criterion in the process. Each node in the tree represents the terminal node (the related features of cervical magnetic resonance imaging), shown in Fig. 6A, and the function node, shown in Fig. 6B.

As the collected cervical features input, at first, the initial population was generated as a tree structure randomly. An operator (as A-E shown in Fig. 5.B) was chosen as the root node. The tree was generated from top (the roots) to bottom and left to right. Besides the operator node F to node I, for the function nod from operator code A to the operator code E, we needed two child nodes from terminal node as shown in Fig. 5A. As the depth of the tree reached the threshold from top to the bottom, it took any variable or constant from the terminal node collection (in this study it was the cervical vertebrae feature) to end the tree’s expansion. The process of building the initial population is shown as Fig. 7 and the tree-expansion algorithm is shown in Fig. 8.

Parameter	Code	Operator	Code								
CD1	1	VH6.3	16	APDcd4	31	Slc4	47	APDpl4	62	+	A
CD2	2	VH7.1	17	APDcd5	32	Slc5	48	APDpl5	63	-	B
CD3	3	VH7.2	18	APDd1	34	Slv,T2-1	49	OPindex1	64	*	C
Endplate	4	VH7.3	19	APDd2	35	Slv,T2-2	50	OPindex2	64	/	D
VH3.1	5	PR1	20	APDd3	36	Slv,T2-3	51	OPindex3	65	%	E
VH3.2	6	PR2	21	APDd4	37	Slv,T2-4	52	OPindex4	66	√	F
VH3.3	7	PR3	22	APDd5	38	Slv,T2-5	53	OPindex5	67	%100	G
VH4.1	8	APDcl1	23	DH1	39	Slv,T1-1	54			Exp	H
VH4.2	9	APDcl2	24	DH2	40	Slv,T1-2	55			1/x	I
VH4.3	10	APDcl3	25	DH3	41	Slv,T1-3	56				
VH5.1	11	APDcl4	26	DH4	42	Slv,T1-4	57				
VH5.2	12	APDcl5	27	DH5	43	Slv,T1-5	58				
VH5.3	13	APDcd1	28	Slc1	44	APDpl1	59				
VH6.1	14	APDcd2	29	Slc2	45	APDpl2	60				
VH6.2	15	APDcd3	30	Slc3	46	APDpl3	61				

Fig. 6. (A) terminal node and (B) function node for GP tree structure.

```

1 Environment parameters {
2   Input train_data (patient, diagnosis from doctor)
3   init GP operators_set
4   Set GP parameters (random level, mutation rate, crossover
   rate, population size...)
5 }
6 For (i ≤ population size) {
7   Set tree root;
8   Left-Tree=Creat-Sub-Tree(Tree-Level-1);
9   Right-Tree=Creat-Sub-Tree(Tree-Level-1);
10 }

```

Fig. 7. The process of building the initial population.

```

1 Create-Sub-Tree (int Tree-Level) {
2   set parameters (random level, operator)
3   if (i<level) {
4     newtree add operator as node
5     determine number of child node by operator type }
6   else if (i=level) {
7     newtree add cervical vertebrae feature as node }
8   output newtree }

```

Fig. 8. The process of GP-tree expansion.

1. Fitness Function Mechanism

To ensure the calculation efficiency as dealing with large amount of MRI data, the fitness function compare the physician’s diagnosis results with prediction results. The value X_n was calculated by the model (which represents the prediction result of the n th patient) and was compared with the physician-diagnosed value Y_n (which represents the diagnosis result by physician of the n th patient), where n is the total patients. The prediction model regarded the comparison gap as fitness value for next generation reevaluation reference. When the absolute value, resulting from X_n minus Y_n , was equal to 0, the fit pulsed 1 that we try to reverse gap to fitness value. Finally, we counted the fit, divided it by n , and took the percentage as the fitness value of population. The formula is shown as follows:

$$fit(n) = |X_n - Y_n| \quad \text{if } |X_n - Y_n| = 0, \quad fit + 1 \quad \text{else } fit + 0 \quad (1)$$

$$Fitness = \frac{\sum^n fit(n)}{n} \times 100 \quad (2)$$

The survival probability of individual population depended on the fitness value which was obtained by the fitness function. Therefore, according to the value of the fitness function, the higher fitness value represents, the better accuracy rate that compare with physician-diagnosed results. The correct rate was an important reference to create the next population of generation.

2. Genetic Programming Evaluation Process

GP evaluation required several kinds of parameters, including the population size, crossover rate, mutation rate and evolutionary generation, etc. The purpose of evolution was to produce a new and better solution. Thus, calculating the fitness value kept the quality of the parent generation for the next generation of evolution, and was expected to produce excellent final generation. After the fitness and diversity of the parental groups were determined, we started on the computing operations of evolution, which includes three stages: select, crossover and mutation. This evaluation process was repeated until a termination condition was reached. The detail of each stage describe as follow:

- *Select*: The purpose of this stage is survival probability of the fittest, through picking the parents with the highest fitness as elitism to stay until next generation and allow them to generate offspring with higher probability.
- *Crossover*: The purpose of this stage is increase populations diversity. A probability is generated randomly and compare to the crossover rate. As the probability is bigger than crossover rate, two selected parents’ tree from population were exchanged their gene to generate two offspring as new children.
- *Mutation*: The purpose of this stage is to prevent the final solution falling into local optimization. Similar to crossover, a probability is generated randomly and compare to the mutation rate. As the probability is bigger than mutation rate, one the selected function node from the population changed the operator as a new child.

In the beginning, we sorted individual tree within population according to their fitness value from upper to lower. Using the elitism method, we reserved top 50% of these trees to survive directly in the next generation. Similar to elitism methodology, it can ensure optimization solution survival with higher probability and keep next population with certain steadily. Then, for the crossover operation, we put the selected trees into pairs. Each pair had a chance (according to mutation rate) of exchange in order to increase the evolution diversity. Crossover operator randomly selected the sub-tree to exchange (left to left, left to right, right to left and right to right) and generate new

children. Finally, similar to crossover operator, the mutation operator prevents the experiment from getting the locally optimal solution. There are two ways for mutation operation, which are node mutation and structural mutation. After the mutation, we put the evaluated tree into next generation and randomly created new tree to fulfill the size of the population which became a new generation. This evolution operation was repeated until it reached the termination condition.

3. Termination Criterion

The termination condition of this study is to reach the threshold of evolutionary generations. According to related research set 200 generations as threshold, we also found that setting more generations didn't improve accuracy, while setting less generations caused the lack of ethnic diversity. Therefore, this study observed the effect of the evolution of different populations within 200 generations. We selected the better results of the number of populations and checked the stability of different number of generations according to each number of generations after repeating ten times of experiments. After that, we unified different generations convergence effect to set the threshold for the termination of the evolution as 150 generations.

E. TS Mechanism

Genetic programming was a kind of randomly search so it didn't guarantee that the optimal solution can be obtained. For that reason, this study added TABU search as the auxiliary heuristic rule. The features of the previous generation were recorded in order to avoid making the result fall into local optimal solution. There were two ways to record. One was the short-term memory (TABU list); another was long-term memory (Candidate list). The operation of the TABU mechanism is shown in Fig. 9.

```

1 GeneticProgramming {
2   set parameter t as terminal condition
3   while (t < terminal iteration) {
4     select tree from long term memory as new tree
5     calculate fitness of new tree |
6     do Tabu record {
7       Record the poor adaptability of the features (short memory)
7       Record the first optimal solution of 10 generations (long memory)
8     }
9     evolution(select · crossover · mutation)
10    Tabu list update by the relevant principles of disruption
11    t = t+1
12    Keep Tabu steps updating short and long memory
13    until reached the terminal condition
14  }

```

Fig. 9. The operation of the TABU mechanism.

In a certain number of generations prohibited these populations been choosing in order to increase the diversity of evolution. TABU list had aspiration criterion to prevent the real superior solution from been prohibited. In addition, the long-term memory through establishing the candidate list to help generate a better new generation, using a more efficient way conducted a global search.

III. EXPERIMENTS DESIGN AND RESULTS ANALYSIS

We adopted Visual C # to implement GP combined with TABU search were applied in this study. The cervical spine features with the relevant operator produced hundreds of tree-like models of each population. Repeating the evolutionary mechanism (selection,

crossover, mutation) was conducted to seek the optimal solution that similar to clinical judgment. The TABU search method prevented GP from falling into the local best solution situation. Through the move, TABU lists and candidate lists increased the diversity of ethnic groups and strengthened the global search. Finally, the perdition model was summed up to assist neuroradiologists to diagnose in the future.

A. Experiment Parameters Setting

To validate the proposed model, the cervical spine MRIs were collected from Tri-Service General Hospital. At first, we selected 153 MRI cases of cervical spine disease and measure all features under the supervision of an neuroradiology's. However, it was necessary to use the Sagittal fast spin echo T2-weighted image and Sagittal fast spin echo T1-weighted image for measurement so that eliminated 6 images which were not clear or had missing part. After image measurement and data processing, we got 147 cases of data for analysis. We using picture archiving and communication system, for each patient, 67 features in 13 items were screenshots and stored under neuroradiologist examination and correction. Furthermore, the third party (medical students) checked the measurement and confirmed the correctness.

Based on the proposed model shown in Fig. 2, the GP method was combined with TS method. By testing relevant parameter combination, including: suitable size of the populations, generations, evolution-related parameters, TS related conditions, we design two experiment series, including: evolutionary parameters combination testing (marked as experiment 1 in section 3.2) and proposed model validation (marked as experiment 2 in section 3.3).

B. Experiment 1: Evolutionary Parameters Combination Testing

We reference previous GP researches to set evolution parameters below. These parameters including: tree layers, select rate, crossover rate and mutation rate were set to 3-5, 0.5, 0.5 and 0.1 accordingly The terminal node and function node were list in Fig. 5.

Furthermore, to find out feasible population size, we tested four population size scale, such as: 50, 100, 150 and 200 as sub-experiment. Each sub-experiment was repeated for 20 generations. The average fitness value and standard deviation for each sub-experiment were shown in Fig. 10. According to these sub-experiments, we found that the highest average of the fitness value occurred when the population size was 150. And its standard deviation was also lower than the other population size which represented the evolution of P150 was stable. Therefore, we set the 150 as populations size for the following experiments. Finally, for the last parameter, generation, the maximum of 200 evolutionary generations was set. These parameters were further used for the proposed model validation in experiment 2.

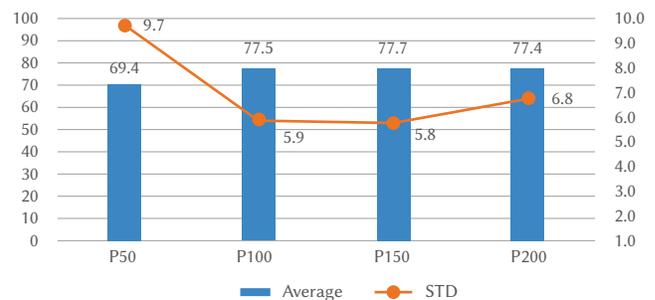


Fig. 10. The result of experienced four sizes of population.

C. Experiment 2: Cervical Curvature and Cervical Alignment Test Results

According to the proposed model in Fig. 2, we conducted a two-stage experiment. In Stage 1, we used GP method combined with TS

to predict the degree of curvature of the clinical indicators and the degree of alignment. In Stage 2, we put the relevant features in the clinical indicators into the TS mechanism and check the convergence performance that improved by TS mechanism.

We compared the genetic planning method (GP), genetic programming method combined with TABU search method (GP + TABU) and used clinical indicators to optimize the TABU list in GP+TABU (GP + TABU + Refined_list). We compare these three experimental methods via ten tests. The cervical spine severity data was divided into training set and test set. We took 70% of the data as a training set, the remaining 30% for the test set. The experimental results were summarized in Table II. The experiment found that using clinical indicators to optimize the TABU list in GP+TABU got better fitness than the other two methods that the accuracy rate of our proposed model can achieve 88% on average.

TABLE II. EXPERIMENTAL RESULTS

Test times	Method	GP	GP+TABU	GP+TABU +Refined_list
1		79%	83%	88%
2		73%	89%	89%
3		74%	89%	88%
4		87%	82%	90%
5		87%	77%	89%
6		81%	81%	88%
7		80%	74%	86%
8		73%	76%	89%
9		71%	80%	86%
10		89%	79%	89%

Furthermore, from 67 features, we intended to find out import cervical vertebrae for diagnosis reference. According to the experimental results, we summarized the features of item statistical results as shown in Fig. 11. We found top 3 features were vertebral height, vertebral signal intensity (Sagittal fast spin echo T2-weighted image) and vertebral signal intensity (Sagittal fast spin echo T1-weighted image), showing a significant effect for determining the severity of the cervical vertebrae. Also, we found the indexes of both cervical vertebrae's curvature distance and anteroposterior diameter of posterior longitudinal ligament were 0. This represented that the two items for the diagnosis of patients with cervical spine severity had lower impact. For clinician reference, these important feature indexes may reveal more clues for future diagnosis process.

Experiment of the severity of cervical vertebrae

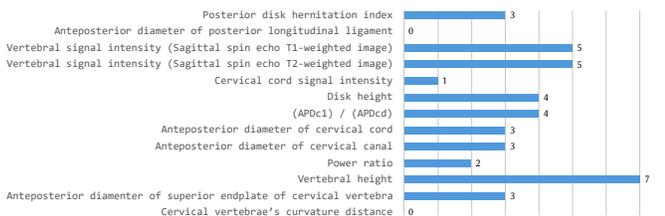


Fig. 11. The statistical results of features in experimental prediction model.

IV. CONCLUSIONS

Cervical spondylosis is a kind of degenerative disease which not only occurs in elder patients. According to previous researches, the prevalence of cervical spondylosis is even higher in those who have to

use computers and those who have to flex their necks for a long time. The age distribution of cervical spondylosis patients is decreasing year by year. For now, MRI is the best tool to confirm the cervical spondylosis severity, despite of the fact of taking radiologists a lot of time for image check and interpretation.

In this study, we proposed a prediction model to evaluate the cervical spine condition of patients by using MRI data. Furthermore, to ensure the computing efficiency of the proposed model, we adopted a heuristic programming, genetic programming (GP), to build the core of refereeing engine and combined the TABU search (TS) with the evolutionary GP. Finally, to validate the accuracy of the proposed model, we implemented experiments and compared our prediction results with radiologists' diagnosis on MRI image. The experiment found that using clinical indicators to optimize the TABU list in GP+TABU would have better fitness than the other two methods and the accuracy rate of our proposed model can achieve 88% on average.

Furthermore, from 67 features, we found out import cervical vertebrae for diagnosis reference. We expected the proposed model can help radiologists reduce the interpretation effort and improve the relationship between doctors and patients. More case studies and model production can be our future works.

For future works, the production of the model could combine with some novel models for example Recurrent Neural Networks (RNN). RNN greatly relies on features and knowledge extracted from tasks [21], and its selections are motivated by what it has learned from the past or focus on the multi-target model [22] to predict. On the other hand, future works could also implement this feature extraction algorithm on medical CT images [23].

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