A Comparison of Linear Genetic Programming and Neural Networks in Medical Data Mining

Markus Brameier Wolfgang Banzhaf

Fachbereich Informatik

Universität Dortmund

44221 Dortmund, GERMANY

email: brameier,banzhaf@LS11.cs.uni-dortmund.de

Abstract

We introduce a new form of linear genetic programming. Two methods of acceleration of our GP approach are discussed: (1) an efficient algorithm that eliminates intron code; (2) a demetic approach to virtually parallelize the system on a single processor. Acceleration of runtime is especially important when operating with complex datasets as they are occuring in real-world applications. We compare GP performance on medical classification problems from a benchmark data base with results obtained by neural networks. Our results show that genetic programming performs comparable in classification and generalization.

1 Introduction

Genetic programming (GP) has been formulated originally as an evolutionary method for breeding programs using expressions from the functional programming language LISP [15]. We employ a new variant of linear GP that uses sequences of instructions of an imperative programming language. More specifically, the method operates on genetic programs which are represented as linear sequences of C instructions. One strength of our LGP system is that non-effective code, called introns, i.e., dispensible instructions that do not affect program behavior, can be removed before a genetic program is executed during fitness calculation. This does not cause any changes to the individuals in the population during evolution or in behavior but results in an enormous acceleration in execution speed.

Introns are also found in biological genomes, where they appear in DNA of eucaryotic cells. It is interesting to realize that these natural introns are removed, too, before proteins are synthesized. While eliminating introns reduces total runtime, a demetic population has been employed to decrease the training time further, even on a serial machine.

Genetic programming and artificial neural networks (NN) can be seen as alternative techniques for the same tasks, like e.g. classification and approximation problems. In the analysis of medical data neural networks have become an alternative to classical statistical methods in recent years. Ripley and Ripley [23] have reviewed several NN techniques in medicine including methods for diagnosis and prognosis tasks, especially survival analysis. Most applications of neural networks in medicine refer to classification tasks. A comprehensive list of medical applications of neural networks can be found in [4].

In contrast to neural networks, genetic programming has not been used very extensively for medical applications to date. Gray et al. [11] report from an early application of GP in cancer diagnosis where the results had been found to be better than with a neural network. In [16] a grammar-based GP variant is used for knowledge extraction from medical databases. Rules for the diagnosis have been derived from the program tree that uncover relationships among data attributes. The outcomes of different types of classifiers, including neural networks and genetic programs, are combined in [25]. This strategy results in an improved prediction of thyroid normal and thyroid carcinoma classes.

In the present paper genetic programming is applied to medical data widely tested in the machine learning community. More specifically, our linear variant of GP is tested on six diagnosis problems that have been taken from the Proben1 benchmark set of real-world problems [21]. The main objective here is to show that for these problems genetic programming is able to achieve classification rates and generalization performance quite similar to neural networks. The application further demonstrates the ability of genetic programming in data mining, where general descriptions of information are to be found in large real-world databases. For supervised learning tasks this normally means to create predictive models, i.e., classifiers or approximators, that generalize from a set of learned data to a set of unknown data.

The paper is organized as follows: In Section 2 the genetic programming paradigm in general and linear GP in particular are introduced. We further present an efficient algorithm that removes non-effective code from linear genetic programs prior to execution. A detailed description of the medical data we have used can be found in Section 3. The setup of all experiments is described in Section 4 while Section 5 presents results concerning intron elimination, classification ability and training time. Finally we discuss some prospects for future research.

2 Genetic Programming

Evolutionary algorithms (EA) mimic aspects of natural evolution to optimize a solution towards a defined goal. Following Darwin's principle of natural selection differential fitness advantages are exploited in a population to lead to better solutions. Different research subfields of evolutionary algorithms have emerged, such as *genetic algorithms* [12], *evolution strategies* [24], and *evolutionary programming* [8]. In recent years these methods have been applied successfully to a wide spectrum of problem domains, especially in optimization. A general evolutionary algorithm can be summarized as follows:

Algorithm 1 (Evolutionary Algorithm):

1. Randomly initialize a population of individual solutions.
2. Randomly select individuals from the population and compare them with respect to their fitness. The *fitness* measure defines the problem the algorithm is expected to solve.
3. Modify fitter individuals using some or all of the following variation operations:
    - *Reproduction.* Copy an individual without change.
    - *Recombination.* Exchange substructures between two individuals.
    - *Mutation.* Exchange a single unit in an individual at a random position.
4. If the termination criterion is not reached, $\rightarrow$ 2.

5. Stop. The best individual represents the best solution found.

A comparatively young and growing research area in the context of evolutionary algorithms is *genetic programming* that uses computer programs as individuals. In early work Friedberg [9, 10] attempted to solve simple problems by teaching a computer to write computer programs. Due to his choice of search strategy, however, he failed. Based on the success of EAs in the 1980s, Cramer applied an evolutionary algorithm to computer programs. Programs were already represented as variable-length tree structures in his TB language [7]. It was then with the seminal work of Koza [14, 15] that the field of genetic programming really took off.

In GP the individual programs map given input-output examples, called *fitness cases*, while their fitness depends on the mapping error. The inner nodes of the program trees are functions and the leafs are *terminals* that mean input variables or constants. The operators applied to generate individual variants, i.e., recombination and mutation, must guarantee that no syntactically incorrect programs are allowed to be generated during evolution (*syntactic closure*). Figure 1 illustrates the recombination operation in a *tree-based* GP system.

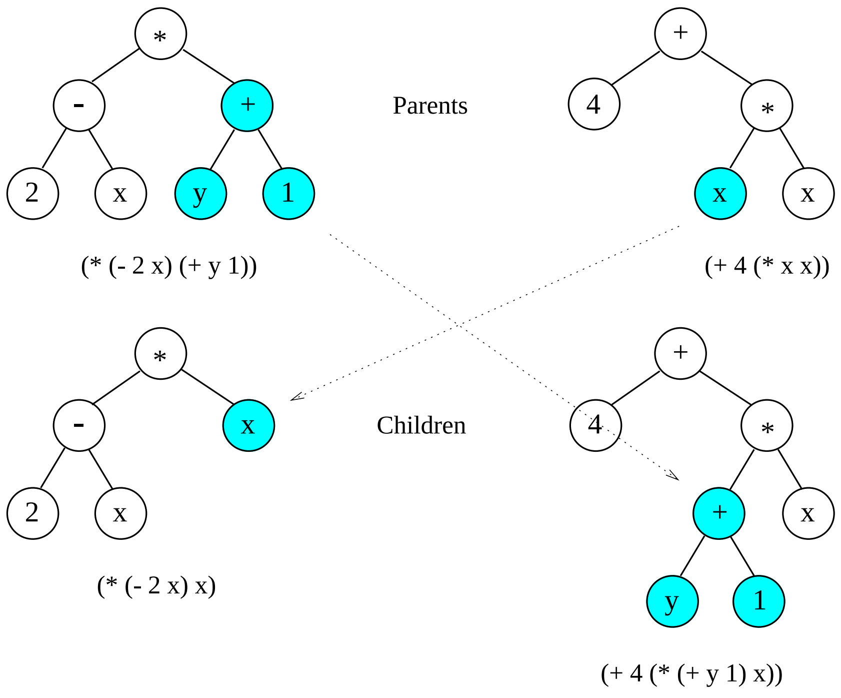

Figure 1: Crossover in tree-based GP. Subtrees in parents are selected and exchanged.

In recent years, the scope of genetic programming has expanded considerably and now includes evolution of linear and graph representations of programs as well, in addition to tree representations [3]. A strong motivation for investigating different program representations in GP is that for each representation form as well as for different learning methods in general there exist problem domains that are more suitable than others.

2.1 Linear Genetic Programming

In the experiments described below we use *linear* GP, a genetic programming approach with a linear representation of individuals. Its main characteristic in comparison to tree-based GP is that expressions of a functional programming language (like LISP) are substituted by programs of an imperative language (like C).

The use of linear bit sequences in GP again goes back to Cramer and his JB language [7]. Cramer later discarded his approach in favor of a tree representation. A more general linear approach was introduced by Banzhaf [2]. Nordin's idea of using machine code for evolution was the most radical "down-to-bones" approach [17] in this context. It was subsequently expanded [18] and led to the AIMGP (*Automatic Induction of Machine code by Genetic Programming*) system [20, 3]. In AIMGP, individuals are manipulated directly as binary machine code in memory and are executed directly without passing an interpreter during fitness calculation. This results in a significant speedup compared to interpreting systems. Due to their dependence on specific processor architectures, however, AIMGP systems are restricted in portability.

Our LGP system implements another variant of linear genetic programming. An individual program is represented as a variable-length string composed of simple C instructions. An excerpt of a linear genetic program is given below.

```
void ind(v)
  double v[8];
{
  ...

  v[0] = v[5] + 73;
  v[7] = v[0] - 59;          (I)
  if (v[1] > 0)
  if (v[5] > 21)
    v[4] = v[2] * v[1];
  v[2] = v[5] + v[4];        (I)
  v[6] = v[0] * 25;
  v[6] = v[4] - 4;
  v[1] = sin(v[6]);
  if (v[0] > v[1])         (I)
    v[3] = v[5] * v[5];    (I)
  v[7] = v[6] * 2;
  v[5] = v[7] + 115;       (I)
  if (v[1] <= v[6])
    v[1] = sin(v[7]);
}
```

The *instruction set* (or *function set*) of the system is composed of arithmetic operations, conditional branches and function calls. The general notation of each *instruction type* listed in Table 1 shows that — except for the branches — all instructions implicitly include an assignment to a variable v_i (*destination variable*). This facilitates the use of multiple program outputs in linear GP while in tree-based GP those side-effects need to be incorporated explicitly.

Instruction Type	General notation	
Arithmetic operation	$v_i := v_j \ op \ v_k \| c$	$op \in \{+, -, *, /\}$
Conditional branch	$if \ (v_i \ cmp \ v_k \| c)$	$cmp \in \{>, \leq\}$
Function call	$v_i := f(v_j)$	$f \in \{sin, cos, sqrt, exp, log\}$

Table 1: Instructions in LGP.

Instructions either operate on two variables (*operand variables*) or on one variable and one integer constant c. At the beginning of program execution these variables hold the program inputs and at the end the program output(s). Variables and constants form the "terminal set" of linear GP. Each instruction is encoded into a four-dimensional vector which hold the instruction identifier, indices of all participating variables and a constant value (optionally). For instance, $v_i := v_j + c$ is represented as $(id(+), i, j, c)$. Since each vector component uses one byte of memory only the maximum number of variables is restricted to 256 and constants range from 0 to 255 at maximum. This representation allows an efficient recombination of the programs as well as an efficient interpretation.

Partially defined operations and functions are protected by returning a constant value (here 1) for all undefined inputs. Sequences of branches are interpreted as *nested branches* like in C which allows complex conditions to be evolved. If the condition of a branch or nested branch is false only one instruction is skipped, namely the next non-branch in the program. This treatment of conditionals has enough expressive power because leaving out or executing a single instruction can deactivate much of the preceding effective code or reactivate preceding non-effective code respectively (see Section 2.2).

The evolutionary algorithm of our GP system applies *tournament selection* and puts the lowest selection pressure on the individuals by allowing only two individuals to participate in a tournament. The loser of each tournament is replaced by a copy of the winner. In such a *steady state* EA the population size is always constant and determines the number of individuals created in one *generation*.

Figure 2 illustrates the *two-point string crossover* used in LGP for recombining two tournament winners. A segment of random position and random length is selected in each of the two parents and exchanged. If one of the resulting children would exceed the maximum length crossover is aborted and restarted with exchanging equally sized segments.

The crossover points only occur *between* instructions. *Inside* instructions the *mutation* operation randomly replaces either the instruction identifier, a variable or the constant (if existent) by equivalents from valid ranges. Constants are modified through a certain standard deviation (*mutation step size*) from the current value. Exchanging a variable, however, can have an enormous effect on the program flow which might be the reason why in linear GP high mutation rates have been experienced to produce better results.

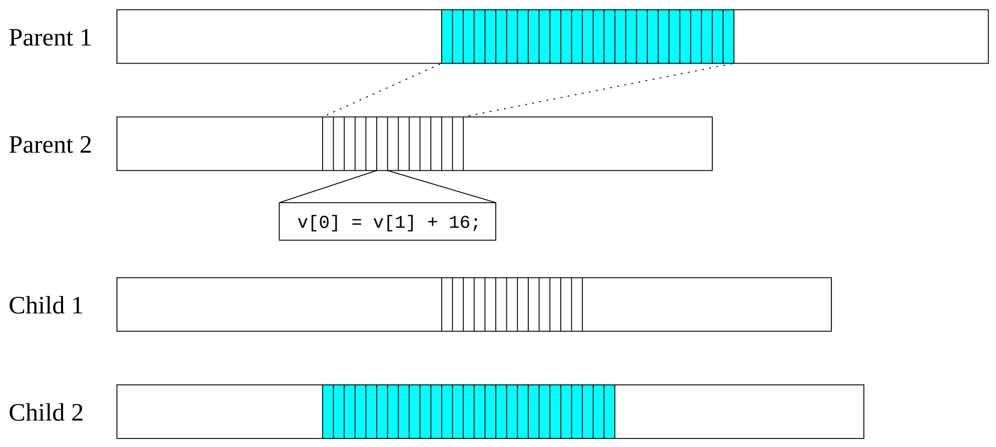

Figure 2: Crossover in linear GP. Continuous sequences of instructions are selected and exchanged between parents.

In genetic programming the maximum size of program is usually restricted to prevent programs from growing without bound. In our linear GP system the maximum number of instructions allowed per program has been set to 256. For all tested problems this configuration has been experienced to be a sufficient maximum length. Nevertheless, individual programs of maximum length can still vary in size of their effective code (*effective length*, see Section 2.2). Since each instruction is encoded into four bytes of memory an individual holds at most 1KB of memory. That makes the system quite memory efficient as well.

2.2 Removing Introns at Runtime

In nature *introns* denote DNA segments in genes with information that is not expressed in proteins. The existence of introns in eucaryotic genomes may be explained in different ways: (i) Since the information for one gene is often located on different *exons* (gene parts that are expressed) introns may help to reduce the number of destructive recombinations between chromosomes by simply reducing the probability that the recombination points will fall within an exon region [28]. In this way complete protein segments encoded by specific exons are more frequently mixed than interrupted during evolution. (ii) Perhaps even more important for understanding the evolution of higher organisms is the realization that new genetic material can be "tested" while retaining a copy of the original information in intron code.

After the DNA is copied the introns are removed from the resulting *messenger*-RNA that actually participates in gene expression, i.e., protein biosynthesis. A biological reason for the removal of introns might be that genes are more efficiently translated during protein biosynthesis in this way. Without being in conflict with ancient information held in introns, this might have an advantage, presumably through decoupling of DNA size from direct evolutionary pressure.

In analogy, an *intron* in a genetic program is defined as a program part without any influence on the calculation of the output(s) for all possible inputs. Other intron definitions common in genetic programming postulate this to be true only for the fitness cases [3, 19]. Introns in GP play a similar role as introns in nature in that they act as redundant code segments that protect advantageous building-blocks from being destroyed by crossover. Further, they also contribute to the preservation of the diversity of the population by retaining genetic material from direct evolutionary pressure.

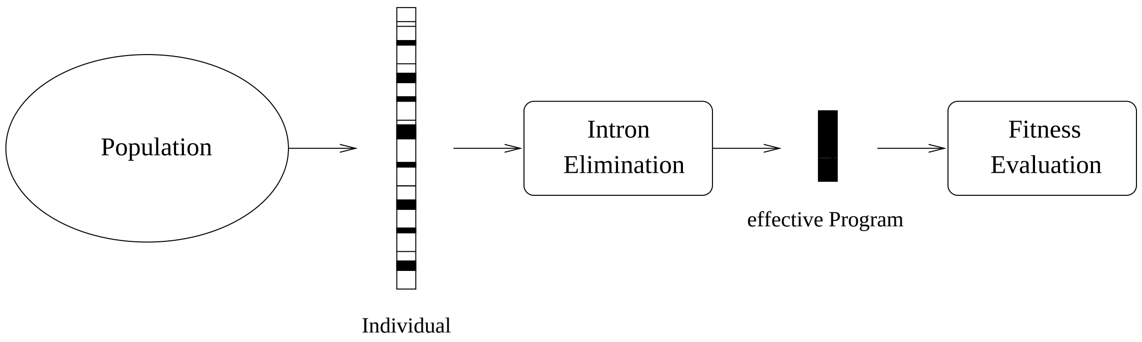

Figure 3: Elimination of intron code (white) in LGP. Only effective code (black) is copied to the execution buffer.

Two types of introns can be distinguished in linear GP. *Structural introns* denote single *non-effective* instructions that emerge from manipulating variables which are *not used* for the calculation of the outputs at that program position. In contrast to that, a *semantical intron* is an instruction or a sequence of instructions that manipulate relevant variables where the state of the variables remains constant. Three rather simple examples of semantical introns are:

(1)
```
v[0] = v[0] + 0;
```

(2)
```
v[0] = v[1] + 1;
v[0] = v[1] - 1;
```

(3)
```
if (v[0] > v[0])
v[i] = v[j] + c;
```

Example (3) is a special case because the operation is *not executed* at all due to the condition of the branch which is never fulfilled. Since it is much easier for the GP system to implement structural introns, the rate of semantical introns in linear genetic programs is usually low. In the following the term "intron" always denotes a structural intron.

The program structure in linear GP allows introns to be detected and eliminated much easier than in tree-based GP. In LGP all non-effective instructions are removed from a genetic program before evaluating fitness cases. This is done by copying all *effective* instructions to a temporary program buffer. This action does not affect the representation of the individuals in the population (see Figure 3). Thus, the important property of the non-effective code to protect the information holding code from being disrupted is preserved. In analogy to the elimination of introns in nature, the linear genetic code is interpreted more efficiently. Because of this analogy the term "intron" might be more justified here than in tree-based GP.

The following algorithm detects all structural introns in a linear genetic program. Note that whether a branch is an intron or not only depends on the status of the operation that directly follows. In the example program from Section 2.1 all instructions marked with an `(I)` are introns provided that the program outputs are stored in `v[0]` and `v[1]`.

Algorithm 2 (Intron detection):

1. Let the set V always contain all program variables which have an influence on the final program output

at the current position.

$V := \{ v_i \mid v_i \text{ is output variable } \}$

Start at the last program instruction and move backwards.

2. Mark the next operation with *destination* variable $v_i \in V$.

   If such an instruction is not found, $\rightarrow$ 5.

3. If the operation directly follows a branch or a sequence of branches mark these instructions, too, else remove v_i from V.

4. Insert the *operand* variables of new marked instructions in V if not already contained. $\rightarrow$ 2.

5. Stop. All *non-marked* instructions are introns.

All *marked* instructions are copied to form the *effective program.* The algorithm needs linear runtime $O(n)$ at worst where n is the maximum length of the genetic program. Actually, detecting and removing the non-effective code from a program only requires about the same time as calculating one fitness case. The more fitness cases are calculated the more this computational overhead will pay off.

By ignoring non-effective instructions during fitness evaluation a large amount of computation time can be saved. A good estimate of the overall acceleration in runtime is the factor

$$\alpha_{acc} = \frac{1}{1 - p_{intron}} \tag{1}$$

where p_{intron} denotes the average intron percentage of a genetic program and $1 - p_{intron}$ the respective percentage of effective code. The intron percentage of all individuals is computed by this algorithm and can be put to further use, e.g. for statistical analysis.

Linear GP programs can be transformed into functional expressions by a successive replacement of variables starting with the last effective instruction. It is obvious that such a tree would grow exponentially with effective program length and could become extremely large. These trees normally contain many identical subtrees, since the more they grow the more instances of a variable are likely to be replaced by the next assignment. This might give an indication of what we believe is the expressive power of a linear representation.

3 The Medical Datasets

In this contribution genetic programming is applied to six medical problems. Table 2 gives a brief description of the diagnosis problems and the diseases that are to be predicted. Medical diagnosis problems always describe classification tasks which are much more frequent in medicine than approximation problems.

Problem	Diagnosis task
cancer	benign or malignant breast tumor
diabetes	diabetes positive or negative
gene	intron-exon, exon-intron or no boundary in DNA sequence
heart	diameter of a heart vessel is reduced by more than 50% or not
horse	horse with a colic will die, survive or must be killed
thyroid	thyroid hyperfunction, hypofunction or normal function

Table 2: Medical diagnosis tasks of PROBEN1 benchmark datasets.

The datasets have been taken unchanged from an existing collection of real-world benchmark problems, PROBEN1 [21], that has been established originally for neural networks. The results obtained with one of the fastest learning algorithms for feed-forward neural networks (RPROP) accompany the PROBEN1 benchmark set to serve as a direct comparison with other methods. Comparability and reproducibility of the results are facilitated by careful documentation of the experiments. Following the benchmarking idea the results for neural networks have been adopted completely from [21]. But most results have been verified by test simulations. The main objective of the project was to realize a fair comparison between genetic programming and neural networks in medical classification and diagnosis. We will show that for all problems discussed the performance of GP in generalization comes very close to or is even better than the results documented for neural networks in [21].

All PROBEN1 datasets originate from the *UCI Machine Learning Repository* [5]. They are organized as a sequence of independent sample vectors divided into input and output values. For better comparability of results, the representation of the original (raw) datasets has been preprocessed in [21]. Values have been normalized, recoded and completed. All inputs are restricted to the continuous range [0,1] except for the gene dataset which holds -1 or $+1$ only. For the outputs a binary *1-of-m encoding* is used where each bit represents one of the m possible output classes of the problem definition. Only the correct output class carries a "1" while all others carry "0". It is characteristic for medical data that they suffer from unknown attributes. In PROBEN1 most of the UCI datasets with missing inputs have been completed by 0 (30% in case of the horse dataset).

Table 3 gives an overview of the specific complexity of each problem expressed in the number of attributes, divided into continuous and discrete inputs, plus output classes and number of samples. Note that some attributes have been encoded into more than one input value.

Problem	Attributes	Inputs		Classes	Samples
		continuous	*discrete*		
cancer	9	9	0	2	699
diabetes	8	8	0	2	690
gene	60	0	120	3	3175
heart	13	6	29	2	303
horse	20	14	44	3	364
thyroid	21	6	15	3	7200

Table 3: Problem complexity of PROBEN1 medical datasets.

4 Experimental Setup

4.1 Genetic Programming

For each dataset an experiment with 30 runs has been performed with LGP. Runs differ only in their choice of a random seed. Table 4 lists the common parameter settings used for all problems.

Parameter	Setting
Population size	5000
Number of demes	10
Migration rate	5%
Classification error weight in fitness	1.0
Maximum number of generations	250
Crossover probability	90%
Mutation probability	90%
Maximum mutation step size for constants	± 5
Maximum program size	256 instructions
Initial maximum program size	25 instructions
Function set	$\{+, -, *, /, sin, exp, if >, if \leq\}$
Terminal set	$\{0, .., 255\} \cup \{v_0, .., v_{k-1}\}$ (k inputs)
Random seed	system time

Table 4: Parameter settings for LGP.

For benchmarking, the partitioning of the datasets was adopted from PROBEN1. The *training set* always included the first 50% of the samples from the dataset, the next 25% were defined as the *validation set* and the last 25% were the *test set*. In PROBEN1 three different compositions of each dataset were prepared, each with a different order of samples. This should increase the confidence that results are independent of the particular distribution into training, validation and test set.

The fitness of an individual program is always computed using the complete training set. After each generation, generalization performance is checked by calculating the error of the best-so-far individual using the validation set in order to check its ability *during* training. The test set is used only for the individual with minimum validation error *after* training.

Throughout this paper, *fitness* $F(p)$ of an individual program p has two parts, the *mean square error* (MSE) and the *classification error* (CE). The MSE is calculated using the squared difference between the predicted output o_{ij}^{pred} and the desired output o_{ij}^{des} for all n training samples and m outputs. The *mean classification error* (MCE) is computed as the average number of incorrectly classified examples:

$$F(p) = \frac{1}{n \cdot m} \sum_{i=1}^{n} \sum_{j=1}^{m} (o_{ij}^{pred} - o_{ij}^{des})^2 + \frac{w}{n} CE = MSE + w \cdot MCE \tag{2}$$

The mean CE is weighted by a parameter w (see Table 4). In this way, the classification performance of a program determines selection directly. The MSE allows an additional continuous fitness improvements.

For fair comparison, the *winner-takes-all* classification method has been adopted from [21]. Each output class corresponds to exactly one program output. The class with the highest output value designates the response according to the 1-of-m output representation introduced in Section 3.

Since only classification problems are dealt with in this contribution the *test classification error* characterizing the generalization performance and the generation in which the individual with the minimum validation error appeared (*effective training time*) are the quantities of main interests.

4.1.1 Population Structure

In evolutionary algorithms the population of individual solutions may be subdivided into multiple subpopulations. Migration of individuals among the subpopulations causes evolution to occur in the population as a whole. Wright first described this mechanism as the *island model* in biology [29] and reasoned that in semi-isolated subpopulations, called *demes*, evolution progresses faster than in a single population of equal size. This inherent acceleration of evolution by demes could be confirmed for EAs [27] and for GP in particular [26, 1]. One reason for this acceleration may be that genetic diversity is preserved better in multiple demes with restricted migration. Diversity in turn influences the probability that the evolutionary search hits a local minimum. A local minimum in one deme might be overcome by other demes with better search direction. A nearly linear acceleration can be achieved in evolutionary algorithms if demes are run in parallel on multi-processor architectures [1, 6].

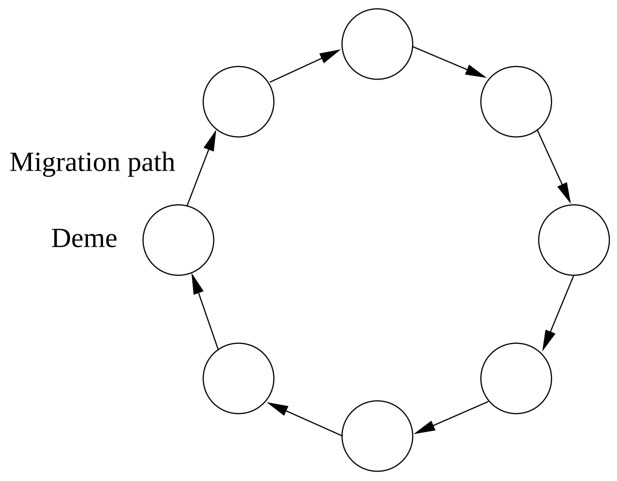

Figure 4: Stepping stone model of directed migration on a ring of demes.

A special form of the island model, the *stepping stone model* [13], assumes that migration of individuals is only possible between certain adjacent demes which are organized as graphs with fixed connecting links. Individuals can reach remote populations only after passing through these neighbors. In this way, the possibility that there will be an exchange of individuals between two demes depends on their distance in the graph topology. Common topologies are ring or matrix structures.

In our experiments, the population is subdivided into 10 demes each holding 500 individuals. This partitioning has been found to be sufficient for investigating the effect of multiple demes. The demes are connected by a directed ring of migration links by which every deme has exactly one successor (see Figure 4). After each generation a certain percentage of best individuals from each deme, determined by the *migration rate*, emigrates into the successor deme thereby replacing the worst individuals. By reproducing locally best solutions into several demes of the population, learning may accelerate because these individuals might further develop simultaneously in different demes. Care has to be taken, however, against premature loss of diversity caused by a faster proliferation of best individuals in the population. Specifically if the migration between demes is not restricted to certain migration paths or occurs too frequently, this might happen. Therefore, migration between demes has been organized in a ring topology here with a modest migration rate of about 5 percent.

4.2 Neural Networks

Experimental results in [21] have been achieved using standard multi-layer perceptrons (MLPs) with fully connected layers. Different numbers of hidden units and hidden layers (one or two) had been tried before arriving at the best network architecture for each dataset. The training method was RPROP learning [22], a fast and robust backpropagation variant. For further information on the RPROP parameter settings and the special network architectures the reader may consult [21].

The generalization performance on the test set was computed for the state of the network with minimum validation error during training. The number of *epochs*, i.e., the number of times the training samples were presented to the network, until this state was reached measures the *effective training time* of the network.

5 Results and Comparison

5.1 Intron Rate

Problem	Introns (%)		Effective Code (%)		Branches (%)		Speedup
	average	*stddev*	*average*	*stddev*	*average*	*stddev*	
cancer	65.45	2.79	34.55	2.79	23.19	0.85	2.9
diabetes	74.50	0.62	25.50	0.62	—	—	3.9
gene	90.49	1.07	9.51	1.07	21.74	0.73	10.5
heart	88.17	0.91	11.83	0.91	—	—	8.5
horse	90.82	0.42	9.18	0.42	—	—	10.9
thyroid	72.24	1.83	27.76	1.83	20.12	0.77	3.6

Table 5: Percentage of introns, effective code and branches per run with speedup factors for removing introns before program execution. There are notable differences between problems.

Table 5 shows the average percentage of non-effective code and effective code per run (in percent of the absolute program length) as well as the resulting acceleration (using Equation 1) for the medical problems under consideration. Regularly, an intron rate of **80%** has been observed which corresponds to an average decrease in *runtime* by intron elimination of about a factor **5**. This speedup is of practical significance especially when operating with large datasets as they occur in medicine. A further benefit of removing non-effective code is that the higher *processing speed* of the genetic programs would make them more efficient in time-critical problem environments. We emphasize again that the elimination of introns as described in Section 2.2 cannot have any influence on the fitness or classification performance of a program.

From Table 5 it can also be observed that the percentages strongly vary with the problem. The differences in results between the three datasets tested for each problem were found to be only tiny and are, therefore, not specified here. The standard deviation of runs has proven to be amazingly small by comparison.

For some problems, including diabetes, heart, and horse, the best classification results (see below) have been produced without conditional branches. This might be due to the fact that if branches are not necessary for a good solution they would promote rather specialized solutions. Other problems, especially gene, have worked considerably better with branches. Except for branch instructions, all problems have been tried with the same function set and system configuration.

Compared to other operations and function calls branches are very cheap in execution time. Additional computation is saved with branches because not all (conditional) operations of a program are executed for each training sample. The average percentage of branches in a linear genetic program is given in Table 5 for the benchmark problems solved with branches. In general, the calculation of the relative speedup factors relies on the assumption that different instructions of the instruction set are homogeneously distributed in the population — including both non-effective code and effective code of the programs.

5.2 Generalization Performance

Table 6 shows the classification error rates obtained with genetic programming (GP) and neural networks (NN), respectively, for the medical datasets discussed in Section 3. Best and average classification error (CE) of all GP runs are documented on the validation and test set for each medical dataset, together with the standard deviation. A comparison with the test classification error of neural networks (reprinted from [21]) is most interesting. For that purpose the difference Δ between the average test errors of NN and GP is printed in percent. Unfortunately, the classification results on the validation set and the results of the best runs are not specified in [21].

	GP						NN		
Problem	Validation CE (%)			Test CE (%)			Test CE (%)		Δ (%)
	best	*average*	*stddev*	*best*	***average***	*stddev*	***average***	*stddev*	
cancer1	1.71	2.45	0.34	0.57	2.18	0.59	1.38	0.49	-36.70
cancer2	0.57	1.39	0.40	4.02	5.72	0.66	4.77	0.94	-16.61
cancer3	1.71	2.62	0.45	3.45	4.93	0.65	3.70	0.52	-24.95
diabetes1	20.31	22.19	1.09	21.35	23.96	1.42	24.10	1.91	+0.58
diabetes2	21.35	23.21	1.33	25.00	27.85	1.49	26.42	2.26	-5.14
diabetes3	25.52	26.69	0.65	19.27	23.09	1.27	22.59	2.23	-2.17
gene1	7.81	11.16	2.30	9.21	12.97	2.24	16.67	3.75	+22.20
gene2	9.07	12.93	2.30	8.45	11.95	2.15	18.41	6.93	+35.09
gene3	7.18	10.77	2.11	10.09	13.84	2.09	21.82	7.53	+36.57
heart1	7.89	10.53	2.38	18.67	21.12	2.02	20.82	1.47	-1.42
heart2	14.47	18.58	2.39	1.33	7.31	3.31	5.13	1.63	-29.82
heart3	15.79	18.81	1.47	10.67	13.98	2.03	15.40	3.20	+9.22
horse1	28.57	32.40	2.22	23.08	30.55	2.24	29.19	2.62	-4.45
horse2	29.67	34.30	2.65	31.87	36.12	1.95	35.86	2.46	-0.72
horse3	27.47	32.65	1.94	31.87	35.44	1.77	34.16	2.32	-3.61
thyroid1	0.83	1.31	0.34	1.28	1.91	0.42	2.38	0.35	+19.75
thyroid2	1.11	1.62	0.31	1.44	2.31	0.39	1.91	0.24	-17.32
thyroid3	0.89	1.47	0.23	0.89	1.88	0.36	2.27	0.32	+17.18

Table 6: Classification error rates of GP and NN for PROBEN1 medical datasets. NN data taken from [21]. Difference Δ in percent from baseline average NN results. Positive Δs indicate improved GP results over NN.

Our results demonstrate that linear genetic programming is able to reach a generalization performance quite similar to multi-layer perceptrons using RPROP learning. The small number of runs performed for each dataset may, however, give an order of magnitude comparison only. In addition, the results for GP are not expected to rank among the best, since parameter settings have not been adjusted to each benchmark problem. This has deliberately not been carried out in order to show that even a common choice of the GP parameters can produce reasonable results. In contrast, the NN architecture applied in [21] has been adapted specifically for each dataset. Finally, the PROBEN1 datasets — especially the coding of input and output values (see Section 3) — are prepared for being advantageous to neural networks but not necessarily to GP approaches.

Notably for the gene problem the test classification error (average and standard deviation) has been found to be much better with GP. This is another indication that GP is able to handle a very high number of input dimensions efficiently (see Table 3). On the other hand, cancer turned out to be considerably more difficult for GP than for NN judged by the percentage difference in average test error.

Looking closer, classification results for the three different datasets of each problem show that the difficulty of a problem may change significantly with the distribution of data into training, validation and test set. Especially the test error differs with the data distribution. For instance, the test error is much smaller for dataset heart2 than for heart1. For some datasets the training, validation and test sets cover the data space differently. As a result a strong difference between validation and test error might occur, as in the cancer and heart examples discussed.

5.3 Training Time

	GP		NN	
Problem	effective Generations		effective Epochs	
	average	*stddev*	*average*	*stddev*
cancer1	26	24	95	115
cancer2	26	25	44	28
cancer3	17	11	41	17
diabetes1	23	14	117	83
diabetes2	28	25	70	26
diabetes3	21	15	164	85
gene1	77	21	101	53
gene2	90	20	250	255
gene3	86	14	199	163
heart1	17	14	30	9
heart2	20	14	18	9
heart3	21	18	11	5
horse1	18	16	13	3
horse2	19	16	18	6
horse3	15	14	14	5
thyroid1	55	18	341	280
thyroid2	64	15	388	246
thyroid3	51	14	298	223

Table 7: Effective training time of GP and NN (rounded).

The *effective training time* specifies the number of (*effective*) generations or epochs, respectively, until the minimum validation error occured. One can deduce from Tables 3 and 7 that more complex problems cause more difficulty for GP and NN and thus a longer effective training time. A comparison between generations and epochs is, admittedly, rather difficult, but it is interesting to observe that effective training time for GP shows lower variation than for NN.

An important further result of our GP experiments is that effective training time can be reduced considerably by using demes (as described in Section 4), without leading to a decrease in generalization performance. A comparable series of runs without demes but with the same population size has been performed for the first dataset of each problem. The average classification rates documented in Table 8 differ only slightly from the results obtained with a demetic population (see Table 6).

	GP without Demes					
Problem	Validation CE (%)			Test CE (%)		
	best	*average*	*stddev*	*best*	*average*	*stddev*
cancer1	1.14	2.05	0.50	1.15	2.85	1.22
diabetes1	19.27	21.43	0.72	20.31	24.39	1.75
gene1	7.68	11.03	2.99	8.95	12.56	3.09
heart1	7.89	11.01	3.00	18.67	22.27	2.94
horse1	26.37	32.40	1.92	21.98	30.73	3.51
thyroid1	0.72	1.27	0.43	1.22	1.96	0.54

Table 8: Classification error rates of GP without demes. Average results similar to results with demes (see Table 6).

	GP *with* Demes		GP *without* Demes		
Problem	effective Generations		effective Generations		Speedup
	average	*stddev*	*average*	*stddev*	
cancer1	26	24	62	67	2.4
diabetes1	23	14	62	53	2.7
gene1	77	21	207	42	2.7
heart1	17	14	68	75	4.0
horse1	18	16	59	63	3.3
thyroid1	55	18	200	36	3.6

Table 9: Effective training time of GP with and without demes. Significant acceleration with demes.

Table 9 compares the effective training time using a panmictic (non-demetic) population with the respective results from Table 7 after the same maximum number of 250 generations. On average, the number of effective generations is reduced by a factor of about **3** when using demes. Thus, a significantly faster convergence of the runs is achieved with a demetic approach. This acceleration may be due to the elitist migration strategy applied here.

5.4 Further Comparison

Reducing the (*relative*) training time on a generational basis affects the *absolute* training time, too, since runs may be stopped earlier. Comparing the absolute runtime in genetic programming and neural networks the fast NN learning algorithm has been found to be superior. One should keep in mind, however, that large populations have been used with the GP runs in order to guarantee sufficient diversity and a sufficient number of demes. Moreover, since we concentrated on a comparison in classification performance the configuration of our LGP system has not been optimized for runtime. If a small population size would be used intron elimination which accelerates LGP runs several times will help to relax the difference in runtime between both techniques.

In contrast to neural networks, GP is not only capable of predicting outcomes but may also provide insight into and a better understanding of the medical diagnosis by allowing an analysis of the resulting genetic programs [16]. Knowledge extraction from genetic programs is more feasible with programs that are compact in size and free from redundant information. Thus the elimination of non-effective code in our linear GP system serves another purpose in generating more intelligible results than NN.

6 Discussion and Future Work

We have reported on linear genetic programming applied to a number of medical classification tasks. All datasets originate from a set of real-world benchmark problems established for neural networks [21]. For genetic programming there is still a lack of a *standard set* of benchmark problems. Such a set would give researchers the opportunity for a better comparability of their published methods and results. An appropriate benchmark set should be composed of real-world datasets taken from real problem domains as well as artificial problems where the characteristics of the data are exactly known.

But a set of benchmark problems is not enough to guarantee comparability and reproducibility of results. A single parameter that is not published or an ambiguous description can make an experiment irreproducible and may lead to erratic results. In many published contributions either comparisons with other methods were not given at all or experiments with the methods compared to had to be reimplemented first. In order to make a direct comparison of published results easier a set of *benchmarking conventions* has to be defined, along with the benchmark problems. These conventions should describe standard ways of setting up and documenting an experiment, as well as measuring and documenting the results. A step in this direction has been taken by Prechelt for neural networks [21].

We have presented an efficient algorithm for the detection of non-effective instructions in linear genetic programs. The elimination of these introns before fitness evaluations results in a significant decrease in runtime. In addition, the number of relevant generations of the evolutionary algorithm was reduced by using a demetic population in tandem with an elitist migration strategy. Increasing the runtime performance of genetic programming with these techniques is especially important when operating with large datasets from real-world domains like medicine.

By using demes in genetic programming we observed that the best generalization on the validation set is reached long before the final generation. Wasted training time can be saved if runs are stopped earlier. Appropriate *stopping rules* that monitor the progress in fitness and generalization over a period of generations need to be defined, though.

Information about the effective size of the genetic programs could be used for *parsimony pressure*. In contrast to punishing absolute size this would not counteract intron growth. Rather, introns may fulfill their function as a protection device against destructive crossover operations, while programs with short effective code still would be favoured by evolution.

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