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**Evolutionary optimization of machine
learning workflows**

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Dedication.

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Contents

Introduction	2
1 Preliminaries	3
1.1 Machine learning	3
1.1.1 Model ensembles	4
1.2 Metalearning	4
1.3 Evolutionary computing	5
1.3.1 Multi-objective optimization	6
1.4 Genetic programming	6
1.4.1 Tree-based genetic programming	6
1.4.2 Developmental genetic programming	7
1.5 Workflows	7
2 Related work	8
2.1 AutoML	8
2.2 TPOT	8
3 Our solution	9
Conclusion	10
Bibliography	11
List of Figures	13
List of Tables	14
List of Abbreviations	15
A Attachments	16
A.1 First Attachment	16

Introduction

1. Preliminaries

What we will talk about, theory

1.1 Machine learning

The field of machine learning encompasses a broad range of algorithms and statistical methods for data processing. In his book on machine learning, Flach provides the following general definition:

Machine learning is the systematic study of algorithms and systems that improve their knowledge or performance with experience. (Flach [2012])

The knowledge of a system is gained through learning from *experience*. This procedure is referred to as the *training* phase. In this process, the algorithm adjusts its parameters according to the nature of training data. The result of the process is a prediction function, which depends on learned parameters. By applying this function on previously unseen data, denominated as the *testing* data, we obtain the output of the algorithm. The result is then evaluated to determine the performance of the method. (Bishop [2006]) The character of the learning process varies with different machine learning problems. There are three main classes of tasks: *supervised*, *unsupervised* and *reinforcement* learning.

In case of supervised learning, the training data is a set of labelled examples and the task is to predict labels of previously unseen data. The field is further subdivided into two groups. If the labels are elements of a finite number of discrete categories, the problem is called *classification*. The continuous case is then called *regression*.

In contrast to supervised learning, in unsupervised learning the training data is unlabelled. The key task is therefore to divide the data into groups of similar examples.

The task of reinforcement learning is to find suitable actions as to maximize a reward. The training data is typically some history of previous actions and corresponding rewards.

It is important to note that good performance on training data does not ensure just as good performance on new data. Sometimes the model performs exceptionally well on training data, but fares much worse on testing data. This behaviour is called *overfitting* and usually occurs when unnecessarily subtle details of the data are learned. The opposite concept is called *generalisation*, which is the ability to perform well on different types of testing data.

A related term is the so-called ‘*bias-variance dilemma*’. A low-complexity model will not overfit, but a lot of errors will be made, thus introducing a certain bias from the correct output. On the other hand, by increasing the number of model parameters, it will highly depend on training data. Then, with small changes in data there will be a high variance in output. A balance can rarely be achieved in practice, hence it is often necessary to choose the side which is less harmful to the task. (Flach [2012, p. 93–94])

1.1.1 Model ensembles

Model ensembles are powerful learning techniques that combine simpler models to achieve better results.

The rationale behind ensembles is also of theoretical character, namely from statistics and from computational learning theory. In statistics, a general idea is to average measurements to get more stable and reliable results. Here, the models are trained on data samples or feature subsets and the results are then combined into a final hypothesis.

The computational learning theory defines the term *learnability*, which describes whether a concept language can be reliably learnt. A concept is defined as a logical expression which describes a set of instances. A hypothesis space is then the space of possible concepts.

Having a model M and a concept language C , C is (strongly) *PAC-learnable* by M if the model outputs most of the time a hypothesis with a very small error. The model is not required to be correct every time, as the set of chosen instances described by the language might be atypical or not representative enough. We can also define the *weak learnability* of C by M where M outputs a hypothesis which is slightly better than random guessing (i.e. success rate over 0.5). A more detailed elaboration is beyond the scope of this work and can be found in books of [Flach, 2012] and [Mitchell, 1997].

The assumption of strong learnability may appear to be quite strong, as the model must output a correct hypothesis on almost all example sets. However, Shapire proved that a model is weakly learnable if and only if it is PAC-learnable. Schapire [1990]

1.2 Metalearning

When using machine learning in practice, it is not always evident which model is suitable for a particular problem. Moreover, there is a vast number of model and parameter combinations to choose from, not to mention model ensembles. The metalearning, also known as ‘learning to learn’, aims to solve these problems by automatizing the process of model selection. As a new field, it offers numerous concepts, from full automation of the process to model recommendation.

Just as the traditional learning — here referred to as *base-learning* — metalearning improves with experience. The difference lies in the learning process. While base-learning comprises of a single run on a specific task, metalearning may include several runs or many different tasks.

In the research area of model recommendation, the training data is most frequently a history of previous runs. A suitable model is then chosen by examining which models were successful on similar tasks. As the problem data may differ significantly, the task cannot be usually compared directly. Therefore, we need to accumulate some kind of *metaknowledge* which can be extracted from substantially different data.

Describe meta-data, meta-features, EVA approach.

1.3 Evolutionary computing

Evolutionary computing is a heuristic method of optimization inspired by Charles Darwin’s theory of *natural selection*. Darwin [1859] In a population, individuals with the best characteristics are most likely to reproduce, thus passing the traits to the offspring. As the evolution is repeated over several generations, the most advantageous traits predominate. This phenomenon is also called ‘survival of the fittest’.

In an evolutionary algorithm, the goal is to find the “best” solution to the given problem. The term ‘population’ refers to a set of solutions encoded as chromosomes which represent the defining features of a particular solution. The ‘natural selection’ can be then understood as a stochastic search through the space of possible chromosome values. (Engelbrecht [2007])

As can be seen in algorithm 1, a genetic algorithm should define a suitable *selection* method, *mutation* and/or *crossover* operators and the *fitness function*. The algorithm terminates when some *stopping condition* is met. Some commonly used criteria, as listed by Engelbrecht, are for example a limit on the number of generations, a objective function threshold or termination after no improvement is observed. ([Engelbrecht, 2007])

Algorithm 1: Evolutionary algorithm

Data: population size n , stopping condition c , crossover probability p_{cx}
and mutation probability p_{mut}

Result: evolved individuals

```
 $P(0) \leftarrow$  population of size  $n$ 
while  $c$  is not met:
    for individual  $ind$ :
        compute fitness  $f(ind)$ 
    for  $i$  in  $\text{range}(n/2)$ :
         $i_1, i_2 \leftarrow$  select two individuals
        if  $p_{cx}$ :
            perform crossover
        if  $p_{mut}$ :
            perform mutation
     $P(n+1) \leftarrow$  select individuals from  $P(n)$ 

return  $P(c)$ 
```

The advantage of genetic algorithms is such that there are potentially many different solutions present in every population. With well defined selection and fitness, the algorithm performs a multi-directional search. In comparison with other directed search methods, this proves to be a more robust approach. (Michalewicz [1996], Mitchell [1997])

1.3.1 Multi-objective optimization

1.4 Genetic programming

In this section, we present a subfield of evolutionary computing — the genetic programming — where the population is a set of computer programs. The aim of this technique is to evolve programs which provide a good solution to the given problem. There are various approaches in means of how to represent the individuals and what kind of genetic operators to use. The fitness is computed by running the program and comparing the result with the desired output. Poli et al. [2008]

Mention typed GP here

1.4.1 Tree-based genetic programming

The individuals are most frequently represented in the form of *syntax trees*. Inner nodes of the tree are functions, whereas leaves are constants and variables. The initialization step is thus very important, as there are many different ways how to design trees. Also, specialized genetic operators need to be designed.

Initialization During the initialization, both functions and constants are selected from a set of possible nodes which is provided as input to the algorithm. As was mentioned, there are various methods of initialization. We will present two methods which are among the simplest and most used ones — *grow* and *full*.

In both cases, nodes are inserted to the tree up to a certain height limit. The two methods differ only in the way how nodes are selected. The *grow* method allows to select both functions and terminals before the limit is reached; afterwards, only terminals can be inserted. The *full* method restricts the selection only to functions on all levels but the last one, thus generating a full tree. Leaves are then chosen from the terminal set like in the previous approach.

The drawback of the *full* method is that all trees are very similar. On the contrary, the *grow* method generates a wide range of sizes and shapes, but the number of nodes in a tree might be too small. Because of that, a method called *ramped half-and-half* is often used in practice. It combines both of the presented methods; half of the population is generated using the *full* method, the other one via *grow* method. Also, instead of one height limit, a range of values is used to introduce more diversity.

Genetic operators The most common type of crossover is *subtree crossover* of two individuals. A random node — the crossover point — is selected in each individual independently. Then, subtrees corresponding to the points are exchanged between them.

Similarly, the most used mutation technique is *subtree mutation*. Just like in subtree crossover, a mutation point is randomly chosen. Afterwards, the corresponding subtree is entirely replaced by a new randomly generated tree.

1.4.2 Developmental genetic programming

1.5 Workflows

2. Related work

2.1 AutoML

2.2 TPOT

3. Our solution

Conclusion

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List of Algorithms

1	Evolutionary algorithm	5
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List of Figures

List of Tables

List of Abbreviations

A. Attachments

A.1 First Attachment