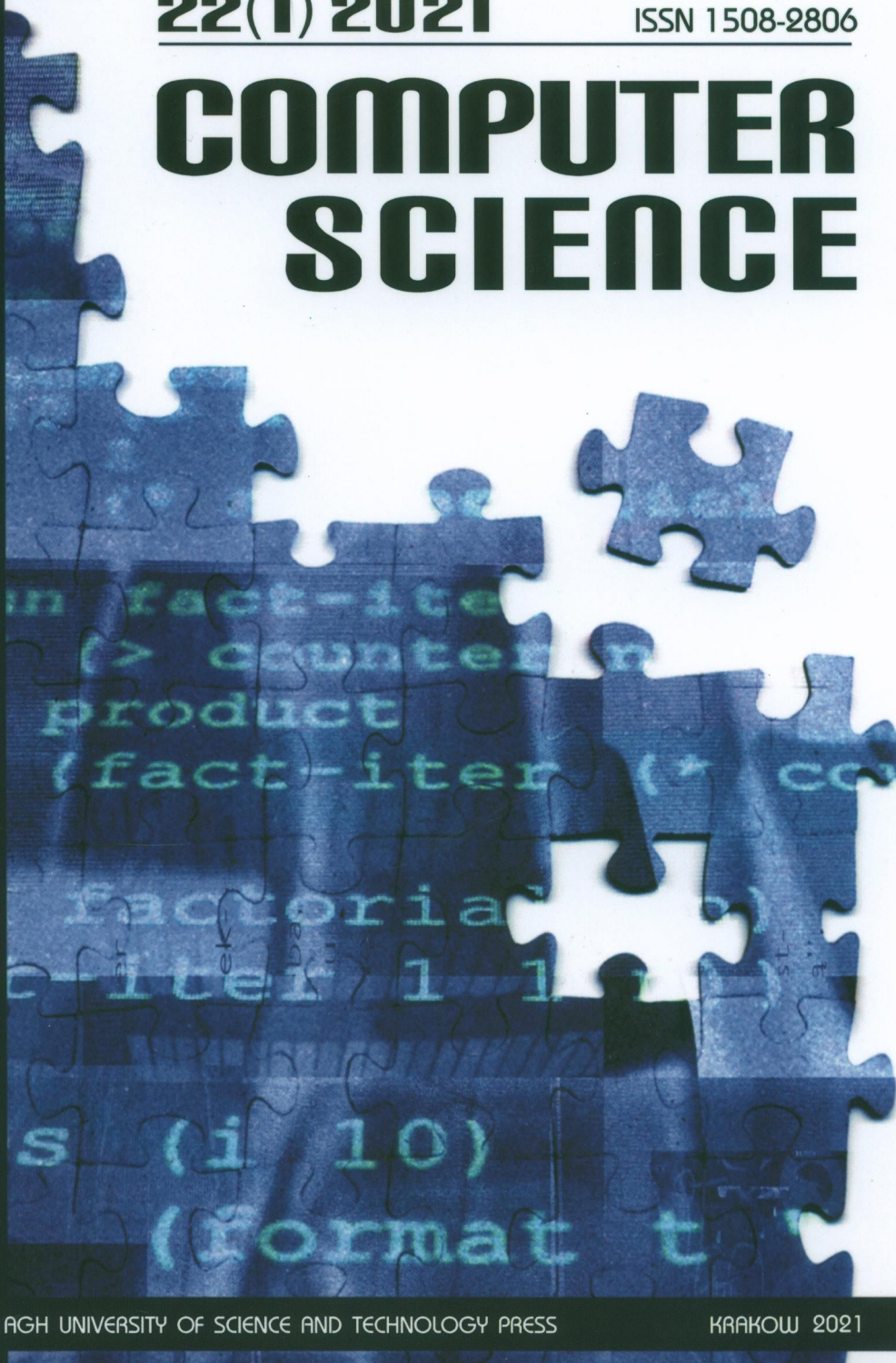


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in fact-ite  
(> counter n  
product  
(fact-iter (* co  
factorial  
t-iter 1 1  
s (i 10)  
(format t "
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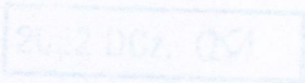
*Battulga Davaasambu, Tumnee Telmuun, Dominik Sasko,
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Abstract: Cross-project defect prediction (CPDP) shows advantages over traditional defect prediction settings. These works do not take the training and testing data of defect prediction from the same project, instead, dissimilar projects are employed. Selecting the proper training data plays an important role in success of CPDP. In this study, a novel clustering method called complexFuzzy is presented for selecting the training data of CPDP. The method reveals the most defective instances that the experimental predictors exploit in order to complete the training. To that end, a fuzzy-based membership is constructed on the data sets. Hence, overfitting (which is a crucial problem in CPDP training) is alleviated. The performance of complexFuzzy is compared to its 5 counterparts on 39 data sets by utilizing 4 classifiers. According to the obtained results, complexFuzzy is superior to other clustering methods in CPDP performance.

Keywords: cross-project defect prediction, complexFuzzy, training instance selection, fuzzy clustering

Citation: Computer Science 35(1) 2021, 3-37

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```
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(> counter n  
product  
(fact-iter (* co  
factorial  
t-iter 1 1  
s (i 10)  
(format t "
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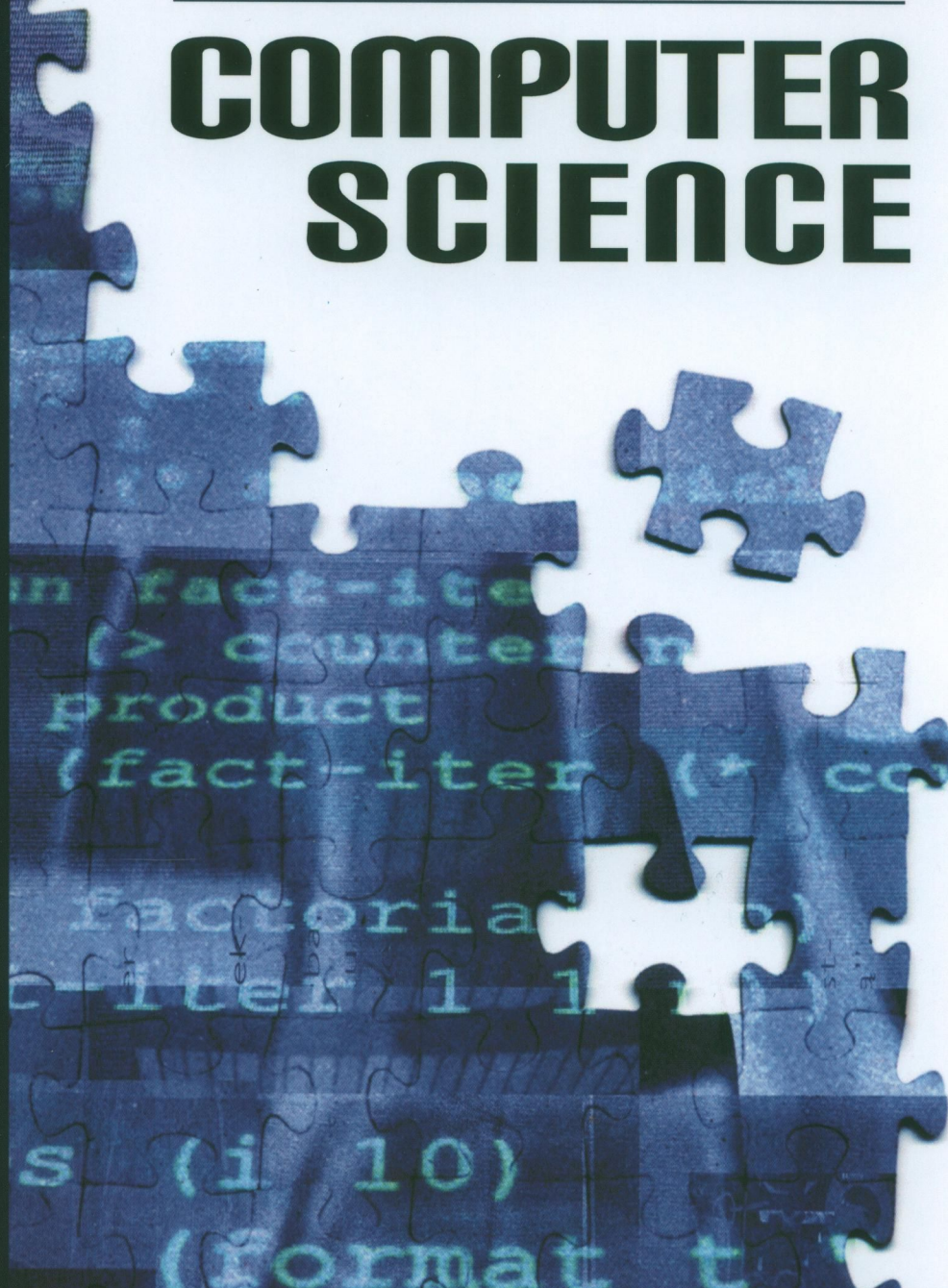
Citation: Computer Science 22(2) 2021, 167-168

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22(3) 2021

ISSN 1508-2806

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The background of the cover features a collage of blue puzzle pieces. Some pieces are assembled, while others are missing, revealing a green monospaced code. The code is a Scheme-like implementation of a factorial function using a loop and a counter.

```
in fact-iter  
(> counter n  
  product  
  (fact-iter (* co  
factorial  
t-iter 1 1  
s (i 10)  
(format t
```

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Abstract Measuring the diversity in evolutionary algorithms that work in real-world world, and it is often computationally complex, but it is feasible. However, measuring the diversity in combinatorial domains is practically impossible. Accordingly, in this paper we propose several practical and feasible diversity measurement techniques that are dedicated to aid many optimization algorithms, leveraging the fact that we can focus on a phenotype table even though an analysis of the search space is at least an NP problem where the direct outcomes of the search are expressed and can be analyzed. Besides sketching up the algorithms, we apply them to several benchmark problems and discuss their efficacy.

Keywords ant colony optimization, diversity measuring, combinatorial and evolutionary biology, metaheuristics

Citation Computers Science 22(3) 2021: 297-320

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2022.002.151