



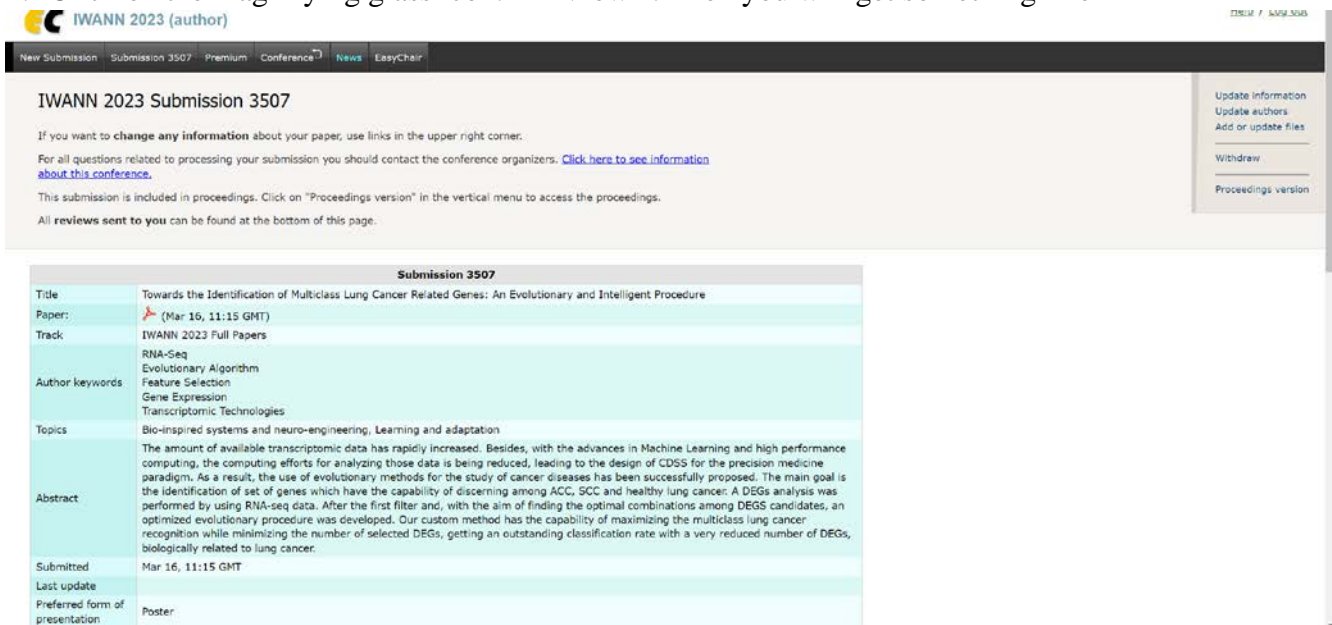
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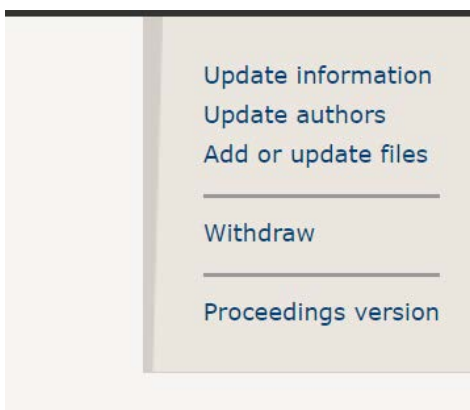
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Submission 3507

Title	Towards the Identification of Multiclass Lung Cancer Related Genes: An Evolutionary and Intelligent Procedure
Paper:	 (Mar 16, 11:15 GMT)
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Author keywords	RNA-Seq Evolutionary Algorithm Feature Selection Gene Expression Transcriptomic Technologies
Topics	Bio-inspired systems and neuro-engineering, Learning and adaptation
Abstract	The amount of available transcriptomic data has rapidly increased. Besides, with the advances in Machine Learning and high performance computing, the computing efforts for analyzing those data is being reduced, leading to the design of CDSS for the precision medicine paradigm. As a result, the use of evolutionary methods for the study of cancer diseases has been successfully proposed. The main goal is the identification of set of genes which have the capability of discerning among ACC, SCC and healthy lung cancer. A DEGs analysis was performed by using RNA-seq data. After the first filter and, with the aim of finding the optimal combinations among DEGs candidates, an optimized evolutionary procedure was developed. Our custom method has the capability of maximizing the multiclass lung cancer recognition while minimizing the number of selected DEGs, getting an outstanding classification rate with a very reduced number of DEGs, biologically related to lung cancer.
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