2020 International Joint Conference on Neural Networks

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  Title:      One-class SVM to identify candidates to reference genes based on the augment of RNA-seq data with Generative Adversarial Netwo
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  Preferred form of presentation: Any

  Abstract:
Reference genes (RG) are constitutive genes required for the maintenance of basic
cellular functions. Different high-performance technologies are used to identify
these types of genes, including RNA sequencing (RNA-seq), which allows measuring
gene expression levels in a specific tissue or an isolated cell. In this paper,
we present a new approach based on Generative Adversarial Network (GAN) and
Support Vector Machine (SVM) to identify in-silico candidates for references
gene. The proposed method is divided into two main steps. First, the GAN is used
to increase a small number of reference genes found in the public RNA-seq dataset
of Escherichia coli. Second, a one-class SVM is evaluated using some real
reference genes and synthetic ones generated by the GAN in the first step. The
results show that the proposed method has a 95% recall score in the test data.
The main contribution of the methodology proposed was to reduce the amount of
candidate reference genes to be tested in the laboratory by up 80%.

  Paper Topics:
    8c.  Bioinformatics
    2i.  Support vector machines and kernel methods
    2e.  Deep learning

  Student Paper: No

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Sincerely,
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