

*Opinion Article***Laboratory diagnosis of infectious diseases and microbes****Gil Blanco***

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DESCRIPTION

Digitalization and artificial intelligence have advanced significantly in recent years. Data-driven solutions are particularly useful in the medical field because there is a high level of automation and data uniformity. Significant developments have also been reported in clinical microbiology, but it will take time and face many regulatory and technological obstacles before they can be used on a regular basis. One of the low-hanging fruits for diagnostics scenarios is the association of genome sequences and proteomic profiles with pathogen phenotypes. Other low-hanging fruits for diagnostics scenarios are the automated analysis of images, such as microscopy slides or agar plates, and dashboards to connect and visualise microbiology data. Standardized data formats, ontologies, an interoperable IT environment with enough storage and processing power, and technical know-how to cater to the needs of microbiologists are all needed for clinical applications infectious diseases experts.

Enumerate the machine learning methods used for routine electronic health record analysis. The diversity of machine learning methods included support vector machines, logistic regression, random forests, and artificial neural networks. Ask if the time has come for machine learning in ordinary clinical microbiology practise. One significant shortcoming is the lack of critical knowledge on data processing. The data sources employed in 97 investigations were extremely varied, ranging from mass spectrometry to genomic data and microscopic images. The fact that almost 40% of studies came from low and middle-income nations highlights the opportunities that digitalization and digital biomarkers present, especially in light of falling costs and cloud-based services. To demonstrate how digital biomarkers affect pertinent outcomes, however, they must also be validated in clinical research. Reproduction and validation studies have a significant problem due to the absence of standardised data and techniques. Two well-known studies on the coronavirus disease 2019 (COVID-19) were recently

retracted due to problems with data processing. It is obvious that journals require guidelines for exchanging data and code. The FAIR guiding principles offer great direction. On Godthab, software code and tools are frequently exchanged; however the information is frequently vague or lacks explanatory code books or tutorials. The new research quality standard should include proper data and code management procedures, which will enable independent assessment of machine learning algorithms and data sets.

Microscopy for traditional Gram stains, ova and parasite preparation, and histopathology slides may be completely transformed by machine learning-based image analysis. For instance, a neural network could classify Gram stains from positive blood cultures into Gram positives/negatives and cocci/rods with astounding accuracy. It should be noted that producing high-quality photos, storing data, and analysing data may need cutting-edge infrastructure. Smartphones, however, can fill up the technological gaps. Similar to how single bacterial colonies growing on agar plates may be classed or even recognised using pattern recognition. The workflow in contemporary diagnostic laboratories is anticipated to be drastically altered by applications like automated microscopy and agar plate inspection. Similar to how biochemical tests have become essentially obsolete as a result of the use of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry for identification. Support vector machines, genetic algorithms, artificial neural networks, and fast classifiers were the most widely utilised machine learning approaches. Only four of the recognised studies validated their findings, and they had a wide range of characteristics.

As demonstrated, numerous models have forecasted various outcomes of, for instance, fatality rates and the impact of the lockdown during the COVID-19 crisis. The scientific community needs access to high-quality real-time data in machine-readable formats during public health emergencies. The infrastructure for monitoring public health must be further developed. The influence on the general population and the economy is enormous, thus models should be evaluated in a manner similar to how algorithms are in personalised medicine

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if they are used to make public health choices. There is no doubt that clinical microbiology and infectious illness are in for an exciting and difficult period. We can use the advantages

of digitization and machine learning to enhance diagnostics and patient care by starting with standards in data and code handling.