

DEEP LEARNING SYSTEM TO IMPROVE DIAGNOSTIC ACCURACY FOR REAL-TIME QUANTITATIVE POLYMERASE CHAIN REACTION DATA

Tech ID: 34196 / UC Case 2026-001-0

PATENT STATUS

Patent Pending

BRIEF DESCRIPTION

Manual interpretation of real-time quantitative PCR (RT-qPCR) data is prone to human error, noise, and variability, leading to potential misdiagnosis or test redundancies. UC Berkeley researchers have developed a novel deep learning framework that significantly improves diagnostic accuracy by fusing Long Short-Term Memory (LSTM) networks with Vision Transformers (ViT). This hybrid architecture captures both sequential fluorescence patterns and structural amplification dynamics from raw time-series data and image-based renderings. By leveraging a uniquely curated dataset of over 24,000 verified samples, the system accurately discriminates between true-positive and true-negative samples, predicts viral dilutions, and forecasts patient re-test outcomes, providing an objective tool for early triage and increased laboratory throughput.

SUGGESTED USES

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Infectious Disease Diagnostics: Enhancing the accuracy of pathogen detection in clinical laboratories for viruses such as SARS-CoV-2.

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Laboratory Workflow Automation: Reducing the need for manual curve review by experts through high-fidelity automated classification.

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Test Triage and Forecasting: Identifying samples that require re-testing or confirmation early in the diagnostic pipeline.

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High-Throughput Screening: Improving data processing speeds and reliability in large-scale public health testing programs.

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Quantitative Viral Load Analysis: Utilizing the model to predict viral dilutions for monitoring disease progression or treatment efficacy.

ADVANTAGES

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INVENTORS

» Obermeyer, Ziad

OTHER INFORMATION

CATEGORIZED AS

» **Biotechnology**

» Bioinformatics

» **Computer**

» Software

» **Medical**

» Diagnostics

» Disease: Infectious Diseases

» Screening

» **Research Tools**

» Bioinformatics

» Nucleic Acids/DNA/RNA

RELATED CASES

2026-001-0

Hybrid Multimodal Learning: The first system to combine sequential (LSTM) and structural (ViT) data extraction for superior PCR curve analysis.

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Increased Diagnostic Precision: Outperforms conventional thresholding methods by identifying subtle patterns invisible to traditional software.

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Robust Multi-Task Framework: Jointly predicts biological labels and laboratory thresholds to ensure clinical relevance and interpretability.

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Data-Driven Reliability: Grounded in a proprietary dataset of nearly 25,000 experimentally verified samples for high-confidence results.

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Predictive Forecasting: Offers unique forecasting capabilities for re-test outcomes, optimizing resource allocation in clinical settings.

RELATED MATERIALS



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