Statement of Significance:

This study presents a significant advancement in the prediction of Coccidioidomycosis (Valley Fever) incidence using state-of-the-art machine learning techniques. Our research makes several key contributions:

1. Novel Application: We introduce the first application of extended Long Short-Term Memory (xLSTM) networks to epidemiological forecasting using comprehensive meteorological data. This represents a significant step forward in leveraging advanced AI techniques for public health predictions.
2. Improved Accuracy: Our xLSTM model demonstrates a substantial improvement in predictive accuracy, achieving a 49.13% reduction in Root Mean Squared Error compared to baseline methods. This enhanced precision could significantly improve the ability to anticipate and prepare for disease outbreaks.
3. Temporal Insights: By effectively capturing long-term dependencies in meteorological data, our model provides new insights into the complex relationship between climate patterns and Coccidioidomycosis incidence. This deepens our understanding of environmental factors influencing disease spread.
4. Public Health Impact: The improved forecasting capability has direct implications for public health strategies, potentially enabling more targeted and timely interventions in endemic areas. This could lead to more efficient resource allocation and improved disease management.
5. Methodological Contribution: Our comprehensive comparison of multiple model architectures (Baseline, MLP, LSTM, xLSTM) provides valuable insights into the relative strengths of these approaches for time-series epidemiological data.
6. Interdisciplinary Approach: This work demonstrates the power of integrating machine learning techniques with epidemiological and meteorological data, setting a precedent for similar interdisciplinary approaches in other areas of public health.

By enhancing our ability to predict Coccidioidomycosis outbreaks, this research has the potential to significantly impact disease prevention and control strategies, particularly in endemic regions. Moreover, the methodologies developed here could be adapted to forecast other environmentally influenced diseases, broadening the impact of this work beyond Coccidioidomycosis.