

Forecasting Chronic Wasting Disease with a Metapopulation-SIR Informed Graph Neural Network

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Introduction

Chronic Wasting Disease (CWD) is a degenerative prion disease affecting cervids (e.g., deer, elk). Reported in 36 U.S. states (see Figure 1) and internationally (2), it attacks the nervous system. Symptoms include stumbling, tremors, drooling, and death; no cure or treatment exists (1).

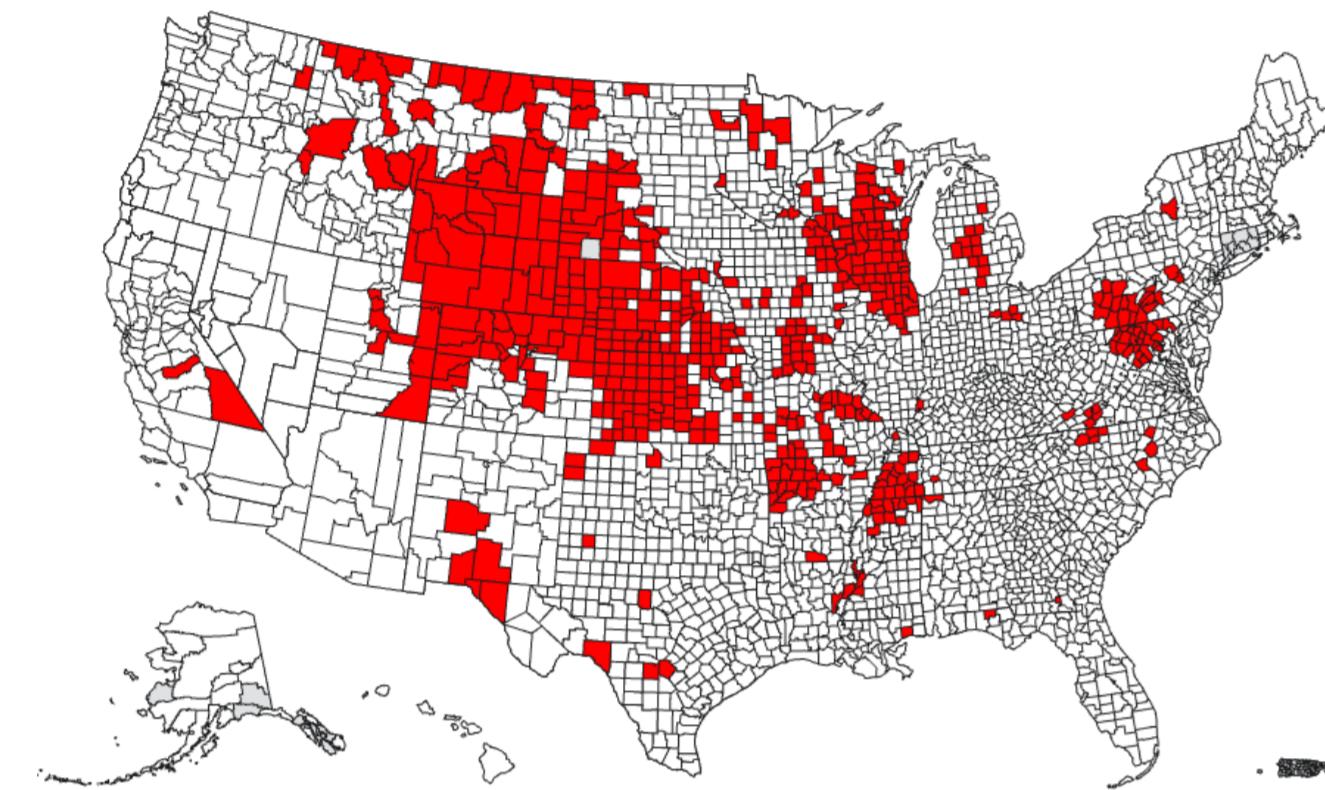


Figure 1. Counties in the United States with reported cases of CWD in wild cervids, as of April 2025. Data is based on state wildlife agencies and the United States Geological Survey (2).

In addition to the harm CWD causes to cervids, it imposes a **heavy economic burden**. A 2002 study found that CWD discovery decreased hunter participation by **5.4%** in Wisconsin (4), which impacts cervid population regulation and related industries (hospitality, dining). Furthermore, the farmed cervids industry spent **\$307,950** on CWD sampling in 2020, and the US government spent **\$284.1 million** from 2000–2021 in efforts to combat its spread (3).

Problem Definition

We seek to address the following research question: *Can the spread of Chronic Wasting Disease be accurately predicted both across and within regions over time?*

We employ a **graph neural network (GNN)**, informed by a Metapopulation-SIR model tailored to CWD infection dynamics, to predict the spread of CWD throughout different regions over time. The impact of this model is twofold: it advances epidemic forecasting through a novel integration of GNN and a domain-specific metapopulation-SIR model, and it provides governments, farmers, and hunters with a practical tool to better anticipate and mitigate the spread of CWD.

Conclusions

The proposed graph neural network trained on infection data with a Metapopulation-SIR loss term **out-performs** a classical Metapopulation-SIR ODE model and other neural network methods.

This improvement in accuracy allows for better management of CWD as high infection count areas can be targeted for management via culling, **lowering the impact on the human population**.

However, the model demonstrated an overly-aggressive spread of CWD via small infection counts in a large number of counties. This issue hinders the model's ability to be used to reliably predict the spread of the disease across regions.

For future work, one could increase the dataset size to include the missing states and aim to better handle the sparsity of the dataset. In conclusion, this work shows that a GNN coupled with Metapopulation-SIR loss terms can play a meaningful role in managing CWD and reducing its effects on both cervid and human populations.

Methodology

- Data Collection:** The dataset includes **31,636** county-level CWD infection entries spanning July 2000 – June 2021 for **1,438** counties across 16 states.
- Spatio-Temporal Graph:** The input graph contains **1,438** nodes (counties) and **8,064** unweighted edges connecting adjacent counties based on U.S. Census data (5). Each node has both *spatial* (latitude, longitude, area) and *temporal* (+/- tests, harvests, cervid facilities) features.
- Loss Function:** The loss incorporates infection count, harvest count, and SIR-based MSEs.

Model

The model is a hybrid **Graph Neural Network (GNN)** which consists of a **Graph Attention Network (GAT)** feeding into a **Gated Recurrent Unit (GRU)** network. It outputs forecasted infection and harvest counts per county, along with the best-fitting SIR parameters (β, γ). Training is guided by a hybrid loss function that incorporates the Metapopulation-SIR model.

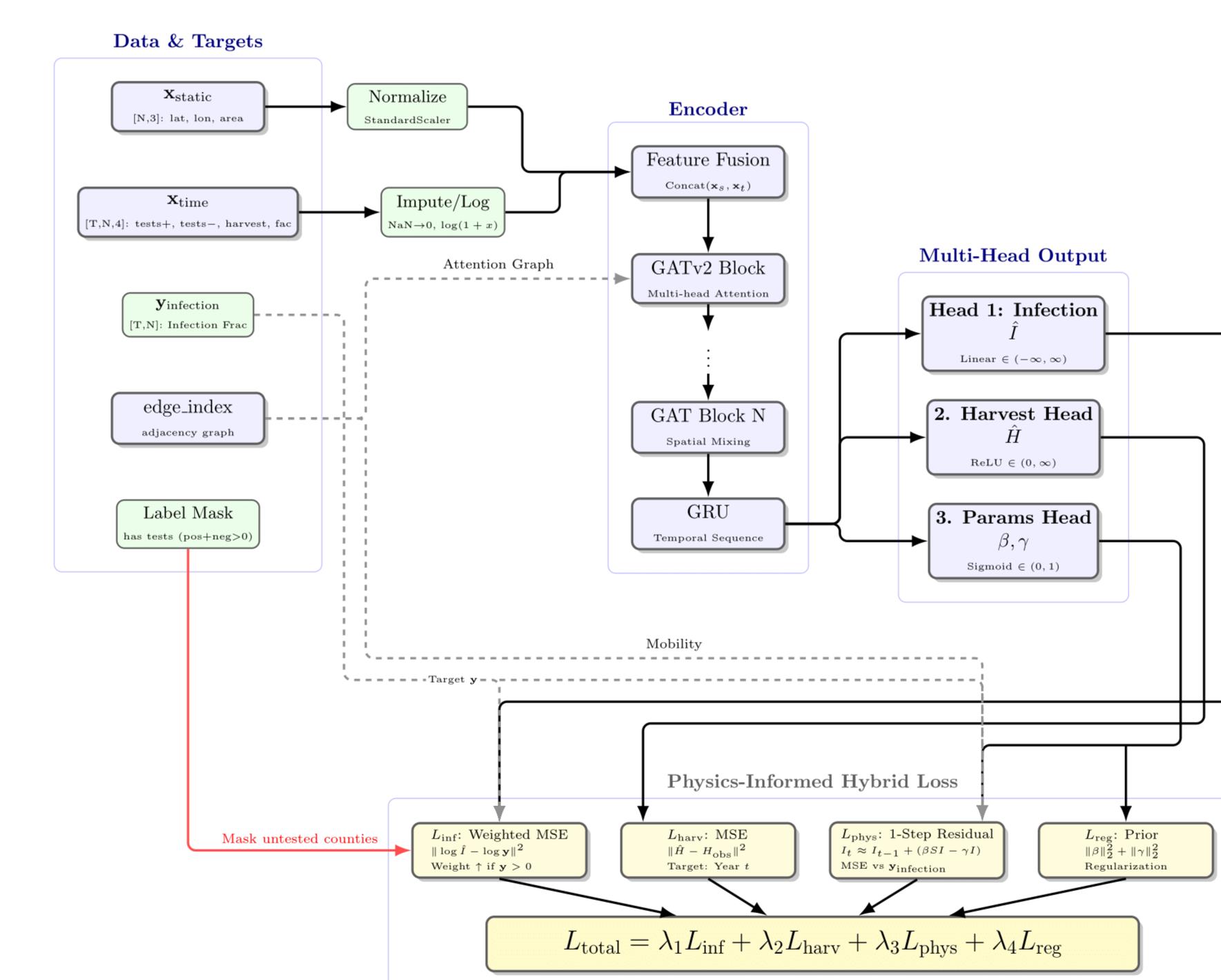


Figure 2. Overview of the Metapopulation-SIR informed Graph Neural Network (GNN) architecture.

The node-level infection dynamics are guided by a discrete **Metapopulation-SIR** system. The movement term ΔX_i^{move} for any compartment $X \in \{S, I, R\}$ is:

$$\Delta X_i^{\text{move}} = \sum_j A_{ij} X_j \sigma_j - X_i \sigma_i$$

where $A_{ij} = 1$ if nodes i, j are adjacent and $\sigma_i = \frac{1}{D_i} \cdot s$. D_i = out-degree of node i , and s is a small scaling factor. The effective populations after inter-county movement are:

$$S_i^{\text{eff}} = S_i + \Delta S_i^{\text{move}}, \quad I_i^{\text{eff}} = I_i + \Delta I_i^{\text{move}}, \quad R_i^{\text{eff}} = R_i + \Delta R_i^{\text{move}}$$

The discrete update equations for the next time step (X_i^{new}) are:

$$S_i^{\text{new}} = S_i^{\text{eff}} - \beta S_i^{\text{eff}} I_i^{\text{eff}}, \quad I_i^{\text{new}} = I_i^{\text{eff}} + \beta S_i^{\text{eff}} I_i^{\text{eff}} - \gamma I_i^{\text{eff}}, \quad R_i^{\text{new}} = R_i^{\text{eff}} + \gamma I_i^{\text{eff}}$$

Note that since CWD is always fatal, $R_i(t)$ represents the deceased population of a given county over time.

Experiments and Results

We tested the proposed model against the models found in Table 1. The results found that a graph neural network trained on infection data (Base) with a Metapopulation-SIR loss term perform the best via Mean Absolute Error (MAE). We found that all models in Figure 3 were able to distinguish the high infection count areas. However, the neural network based model demonstrated an aggressive spread in comparison to a classical Metapopulation-SIR ODE model.

| Model | MAE |
|--------------------------------------|------|
| Base (infection data) | 2.93 |
| Base w/ harvest data | 2.15 |
| Base w/ harvest data & Meta-SIR loss | 2.11 |
| Base w/ Meta-SIR loss | 0.73 |
| AR(1) | 1.08 |
| Metapopulation SIR | 2.62 |
| Random Forest | 2.61 |

Table 1. MAE scores for different models.

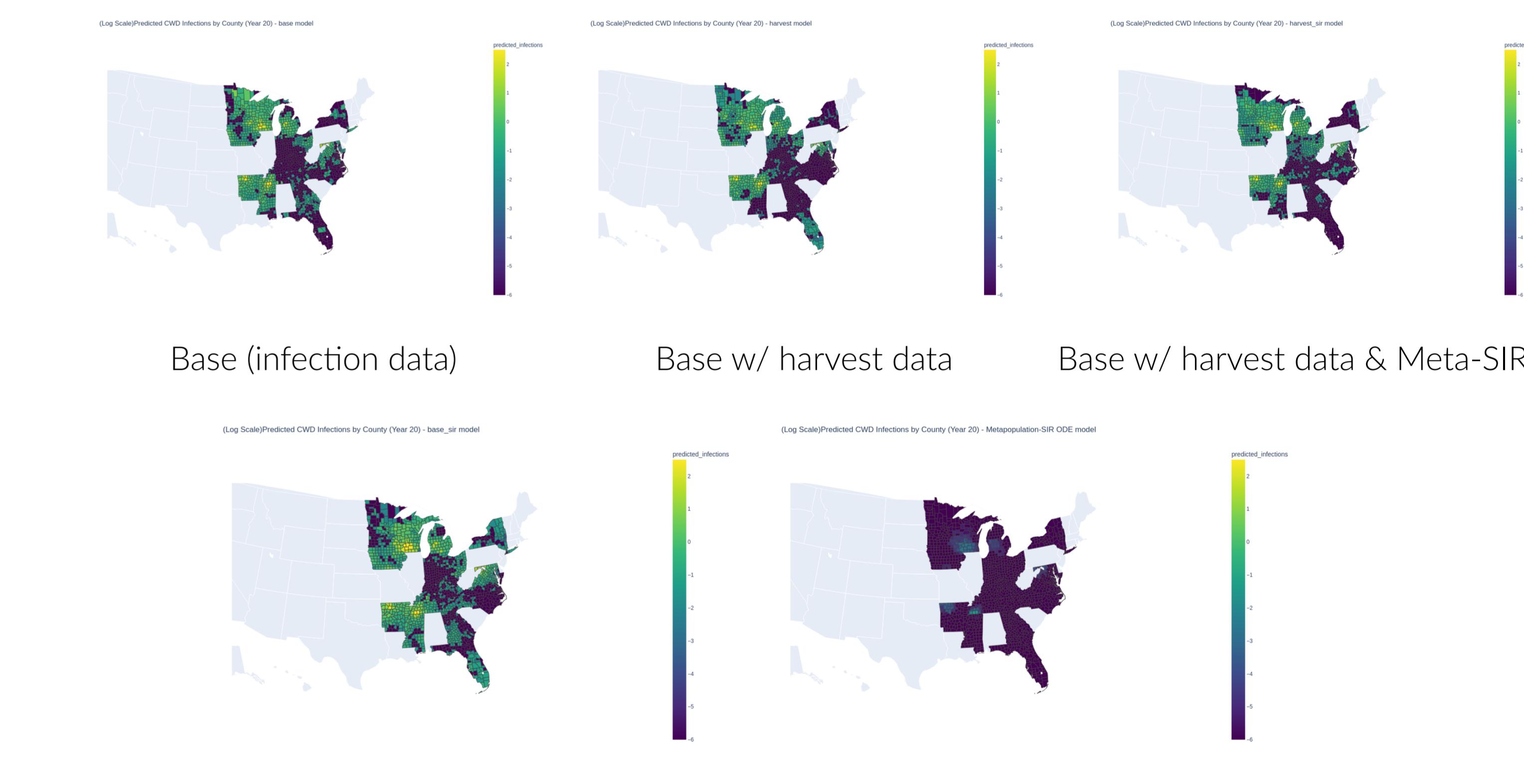


Figure 3. Predicted infection count per county for 2020-2021 season (log scale).

References

- [1] Centers for Disease Control and Prevention. chronic wasting disease in animals. 2024. Accessed: 2025-10-07.
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- [5] U.S. Census Bureau. County adjacency file. 2024. <https://www.census.gov/geographies/reference-files/time-series/geo/county-adjacency.html>. Accessed: 2025-11-03.