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# Recent and Forecasted Increases in Coccidioidomycosis Incidence Linked to Hydroclimatic Swings, California

## Appendix

**Appendix Table 1.** Variables included in the five models included in the ensemble. Green cells were used as main effects and blue cells were used as interactions. Models 1–4 were generalized linear models (GLMs) and model 5 was a random forest (RF).

| Variable | GLM 1 | GLM 2 | GLM 3 | GLM 4 | RF |
|---|---|---|---|---|---|
| Population (as an offset) | | | | | |
| Year | | | | | |
| Season (as a factor) | | | | | |
| Percent sand | | | | | |
| Impervious surface | | | | | |
| Elevation | | | | | |
| Total rainfall | | | | | |
| Lag 1 mo | | | | | |
| Lag 3 mo | | | | | |
| Lag 6 mo | | | | | |
| Lag 9 mo | | | | | |
| Lag 12 mo | | | | | |
| Lag 15 mo | | | | | |
| Lag 18 mo | | | | | |
| Lag 21 mo | | | | | |
| Lag 24 mo | | | | | |
| Lag 27 mo | | | | | |
| Lag 30 mo | | | | | |
| Lag 33 mo | | | | | |
| Lag 36 mo | | | | | |
| Average Temperature | | | | | |
| Lag 1 mo | | | | | |
| Lag 3 mo | | | | | |
| Lag 6 mo | | | | | |
| Lag 9 mo | | | | | |
| Lag 12 mo | | | | | |
| Lag 15 mo | | | | | |
| Lag 18 mo | | | | | |
| Lag 21 mo | | | | | |
| Lag 24 mo | | | | | |
| Lag 27 mo | | | | | |
| Lag 30 mo | | | | | |
| Lag 33 mo | | | | | |
| Lag 36 mo | | | | | |
| One year post drought (indicator) | | | | | |
| Two years post drought (indicator) | | | | | |

**Appendix Table 2.** Region-specific model weights used to generate the ensemble model. Weights were obtained using the out of sample prediction error (SSE) for each cross-validation fold and for each candidate algorithm. Using the weighted mean of each candidate algorithms' SSE across all folds, with weights proportional to the number of training years in the fold (e.g., folds with more training years had higher weights), model weights were calculated as the normalized inverse of the weighted mean.

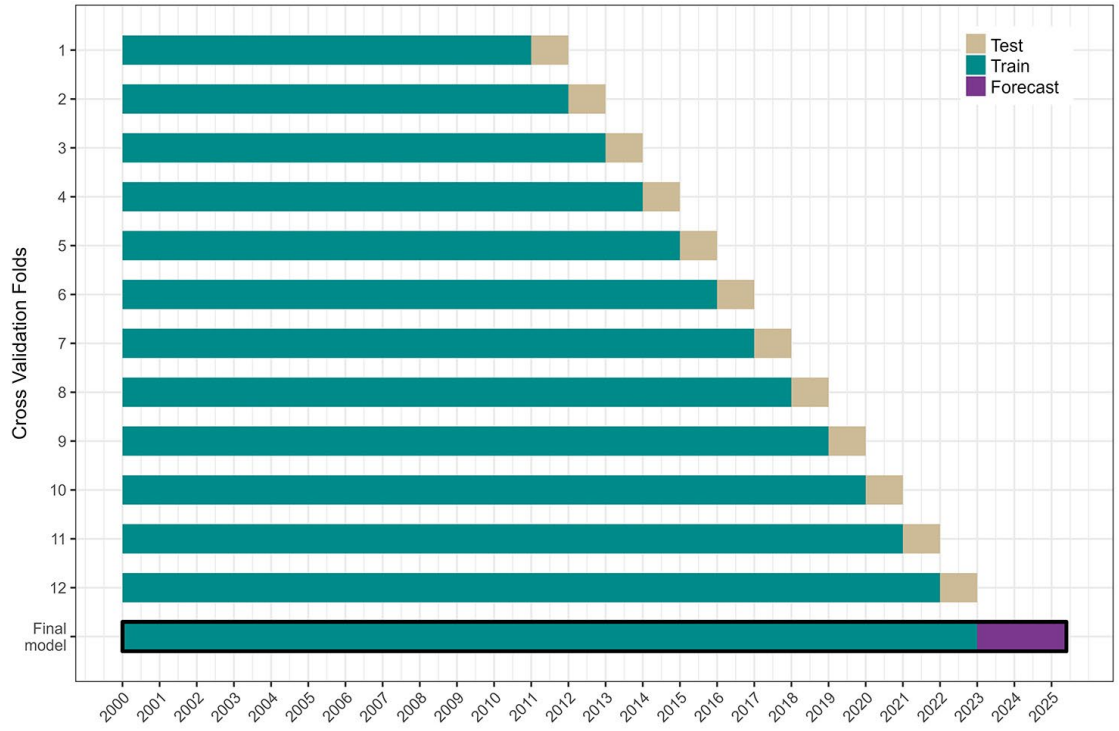
| Region | Model 1 | Model 2 | Model 3 | Model 4 | Model 5 |
|---|---|---|---|---|---|
| Bay Area | 0.207 | 0.206 | 0.207 | 0.207 | 0.173 |
| Eastern CA | 0.202 | 0.204 | 0.202 | 0.203 | 0.189 |
| Fresno | 0.231 | 0.353 | 0.121 | 0.039 | 0.255 |
| Kern | 0.192 | 0.199 | 0.195 | 0.198 | 0.215 |
| Kings | 0.209 | 0.191 | 0.176 | 0.217 | 0.207 |
| Madera | 0.198 | 0.203 | 0.199 | 0.201 | 0.199 |
| Merced | 0.199 | 0.212 | 0.204 | 0.175 | 0.211 |
| Monterey | 0.243 | 0.229 | 0.229 | 0.053 | 0.247 |
| Northern CA | 0.201 | 0.203 | 0.202 | 0.201 | 0.193 |
| Sacramento Valley | 0.19 | 0.214 | 0.213 | 0.212 | 0.171 |
| San Joaquin | 0.210 | 0.210 | 0.189 | 0.185 | 0.205 |
| San Luis Obispo | 0.199 | 0.185 | 0.187 | 0.217 | 0.211 |
| Santa Barbara | 0.198 | 0.222 | 0.192 | 0.173 | 0.214 |
| Southern Coast | 0.210 | 0.205 | 0.210 | 0.211 | 0.163 |
| Southern Inland | 0.203 | 0.204 | 0.204 | 0.203 | 0.186 |
| Stanislaus | 0.205 | 0.203 | 0.205 | 0.208 | 0.178 |
| Tulare | 0.200 | 0.206 | 0.202 | 0.200 | 0.192 |
| Ventura | 0.200 | 0.203 | 0.201 | 0.193 | 0.202 |

**Appendix Table 3.** Region-level forecasted incident cases and provisionally reported cases (as of December 2024) for 2023 and 2024. PI = prediction interval.

| Region | Provisional Cases (as of Dec. 2024) | 2023 Predicted (90% PI) | Provisional Cases (as of Dec. 2024) | 2024 Forecasted (90% PI) |
|---|---|---|---|---|
| Bay Area | 462 | 512 (469 – 568) | 603 | 536 (494 – 594) |
| Central Coast | 704 | 1,161 (999 – 1,385) | 1,284 | 1,053 (944 – 1,195) |
| Eastern California | 36 | 43 (31 – 73) | 39 | 47 (32 – 80) |
| Northern California | 25 | 34 (25 – 45) | 58 | 24 (17 – 33) |
| Northern San Joaquin Valley | 556 | 555 (472 – 644) | 978 | 769 (649 – 883) |
| Southern Coast | 2,174 | 2,968 (2,801 – 3,158) | 2,458 | 3,076 (2,928 – 3,261) |
| Southern Inland | 566 | 674 (611 – 745) | 648 | 692 (628 – 761) |
| Southern San Joaquin Valley | 4,273 | 5,331 (4,920 – 5,880) | 6,383 | 5,162 (4,768 – 5,705) |
| Southern Sacramento Valley | 81 | 148 (122 – 538) | 139 | 151 (127 – 256) |
| **Statewide** | **9,212** | **11,426 (10,804– 12,036)** | **12,590** | **11,509 (10,902– 12,182)** |

**Appendix Table 4.** Sensitivity analyses of our model specification.

| Sensitivity analysis | $R^2$ compared to original model predictions | Mean absolute error compared to original model predictions |
|---|---|---|
| Removal of highly co-linear temperature variables (>12-mo lags) | 0.98 | 0.034 |
| Including a natural spline on year (df = 3) rather than as a linear term | 0.90 | 0.012 |



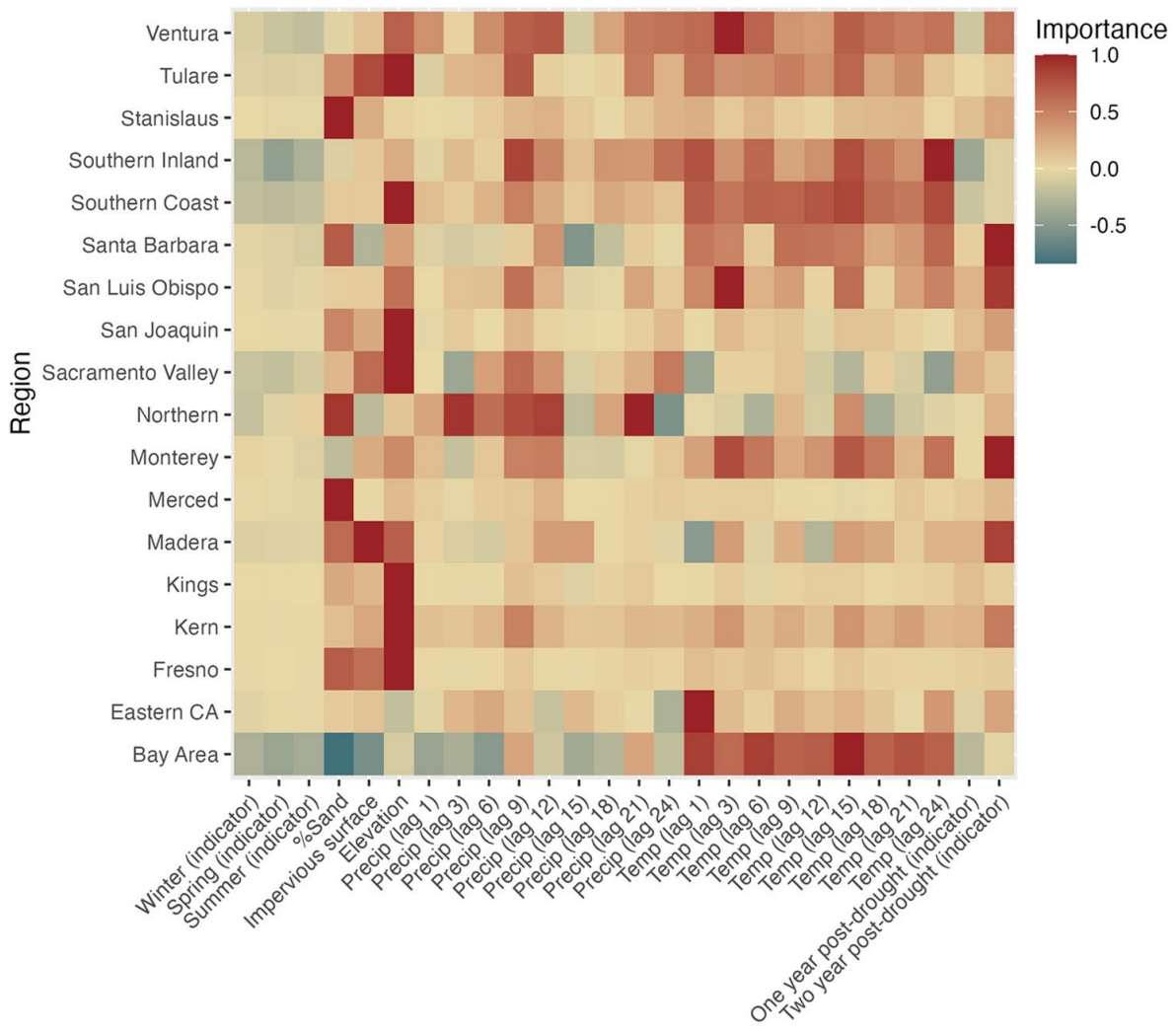

**Appendix Figure 1.** Schematic of the progressive time-series cross-validation approach used to generate weights for the ensemble model. Each progressive fold added an additional year to the training data (green) and predicted the following test year (beige). For example, we fit the models to data from 2000–2011 and predicted cases in 2012. We then fit the model to data from 2000–2012 and predicted cases in 2013, and so on. Individual models were then weighted by the inverse of their out-of-sample error across test years and used to forecast cases from Jan. 1st, 2023 – Mar. 31st, 2025 (purple).

**A**

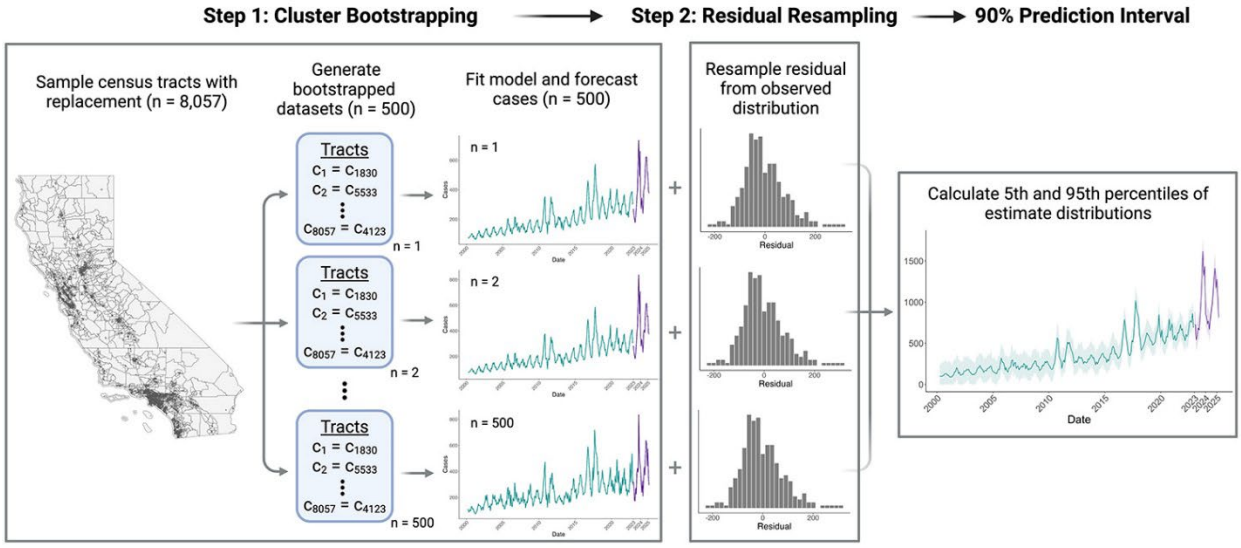

**B**

| | Region | Counties |
|---|---|---|
| 1 | Bay Area | Alameda, Contra Costa, Napa, San Francisco, San Mateo, Santa Clara, Santa Cruz, Solano, Sonoma, Marin, San Benito |
| 2 | Central Coast | Monterey, San Luis Obispo, Santa Barbara, Ventura |
| 3 | Eastern California | Inyo, Mono, Mariposa, Tuolumne, Alpine, Calaveras, Amador, El Dorado, Placer |
| 4 | Northern California | Butte, Colusa, Del Norte, Glenn, Humboldt, Lake, Lassen, Mendocino, Modoc, Nevada, Plumas, Shasta, Sierra, Siskiyou, Tehama, Trinity |
| 5 | Northern San Joaquin Valley | Merced, San Joaquin, Stanislaus |
| 6 | Southern Coast | Los Angeles, Orange, San Diego |
| 7 | Southern Inland | Riverside, Imperial, San Bernardino |
| 8 | Southern Sacramento Valley | Sacramento, Yolo, Yuba, Sutter |
| 9 | Southern San Joaquin Valley | Fresno, Kern ,Kings, Madera, Tulare |

**Appendix Figure 2.** Map of California counties by region. Starred regions are considered “high incidence”; counties within these regions were modeled independently.




**Appendix Figure 3.** Corrected Gini Importance Indices from each region's random forest model. Index values have been scaled by dividing each region's index values by the regional maximum for comparability across regions.




**Appendix Figure 4.** To generate 90% prediction intervals, we used a two-step bootstrapping process. In step 1, we sampled census tracts (n = 8057) with replacement to generate 500 datasets, fit the models to each dataset (n = 1–500), and forecasted cases using each model. In step 2, we then combined the estimates with resampled residuals from the observed residual distribution and calculated the 5$^{th}$ and 95$^{th}$ percentile of the resulting distribution to obtain 90% prediction intervals. Figure created with BioRender (https://www.biorender.com).