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Decoding Viral Diffusion: High-Resolution Modeling of COVID-19's First Waves of Expansion

Biology * Public Health * DNA

From Temporal Curves to Spatiotemporal Wavefronts

The rapid dissemination of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), a single-stranded RNA virus, challenged researchers to track a mutating pathogen across heterogeneous landscapes. While traditional epidemiological surveillance rooted in Kermack-McKendrick theory relies on temporal epidemic curves -- plotting aggregate case counts against time -- this unidimensional approach fails to capture the physical propagation of disease across space. Epidemics behave as physical waves originating from localized epicenters and diffusing outward through susceptible populations. Quantifying these spatiotemporal dynamics is essential for evaluating public health interventions, forecasting regional surges, and deploying medical resources.

Recent advances in computational biostatistics have enabled high-resolution spatiotemporal modeling of the first two major U.S. epidemic waves of SARS-CoV-2.[1] By synthesizing clinical surveillance streams through Bayesian nowcasting models and projecting daily incidence onto a uniform hexagonal grid, investigators quantified daily territorial expansion (km /day) and forward wavefront velocity (km/day), revealing how viral variant biology, decentralized non-pharmaceutical interventions (NPIs), and human mobility networks governed the physical speed of the pandemic.[1]

Biological Context: Variant Evolution, Viral Loads, and Baseline Immunity

Wave 1 (mid-September 2020 through February 2021) propagated through an immunologically naive population; vaccines were unavailable to healthcare workers until late December 2020 and to the general public until spring 2021.[1] Driven initially by ancestral wild-type lineages, Wave 1 later incorporated the Alpha variant (B.1.1.7) and competing lineages such as B.1.1.420, which exhibited natural selection at spike protein residues L452 and P681 that enhanced transmissibility.[1][2] Throughout autumn and winter 2020, physical spread was contested by widespread, though decentralized, NPIs including indoor capacity restrictions, masking mandates, and travel quarantines.[1]

Conversely, Wave 2 (early July to early September 2021) unfolded after millions of Americans had received mRNA or viral vector vaccines.[1] However, baseline population immunity was offset by the Delta variant (B.1.617.2), which possessed an estimated basic reproduction number (R0) of 5.08.[1][4] Genomic assays showed Delta infections generated 6.2 times more viral RNA copies per milliliter than Alpha -- and tenfold higher ORF1ab concentrations than wild-type strains -- shortening generation intervals and elevating effective reproduction numbers (Rt) by 1.45-fold in Massachusetts to 1.99-fold in Maine.[5][6][7][8] Simultaneously, broad rollbacks

of masking mandates, capacity limits, and domestic travel restrictions in summer 2021 accelerated multi-focal viral expansion.[1]

Methodological Architecture: Bayesian Nowcasting, Hexagonal Grids, and BYM2 Smoothing

Raw county case reports suffer from weekend reporting troughs, testing access disparities, and administrative lags.[3][9] To avoid measuring bureaucratic latency, investigators utilized daily county infection estimates from the COVIDestim Bayesian evidence-synthesis nowcasting framework, which jointly models reported cases, hospitalizations, and deaths while accounting for clinical progression and reporting delays.[1][9] COVIDestim reconstructions indicate that prior to January 1, 2021, only 22.4 percent of true U.S. SARS-CoV-2 infections were officially reported.[9]

Because the more than 3,000 U.S. counties vary drastically in area and population size, county-level rates were reapportioned onto a uniform continental hexagonal grid using 2019 U.S. Census Block Group data and Meta 30-square-meter population density maps.[1][10] Daily hexagonal incidence was then smoothed across space and time using a reparameterized Besag, York, and Molli hierarchical spatial model (BYM2) fitted via Integrated Nested Laplace Approximation (R-INLA) for each day from March 2020 through December 2021.[1][11][12] BYM2 resolves classical confounding between the Intrinsic Conditional Auto-Regressive (ICAR) spatial neighborhood component and unstructured Gaussian noise by parameterizing total combined variance alongside a spatial mixing proportion regularized by Penalized Complexity (PC) priors.[10][11][12]

Hexagons exceeding 190 daily infections per 100,000 residents (validated via sensitivity thresholds at 85 and 300 per 100,000) were classified as within an active epidemic wave.[1] From these daily contours, researchers computed the areal expansion rate (daily net km recruited into the high-incidence boundary) and wavefront speed (mean shortest orthogonal distance in km/day from each boundary vertex on day d to the advancing contour on day d+1).[1]

Comparative Wavefront Dynamics: Areal Expansion, Velocity, and Acceleration

Wave 1 (September 17, 2020 - February 19, 2021) originated from a contiguous epicenter spanning central South Dakota, eastern North Dakota, and northeastern Montana following the August 2020 Sturgis Motorcycle Rally, which drew 462,000 attendees from 61 percent of U.S. counties.[1][13] Meade County testing volume rose 199 percent (positivity climbing from 5 to 8 percent), while returning attendees generated a continental contagion externality across 56 percent of bordering states that merged into a single outward-moving wavefront.[13][14]

Wave 2 (July 3 - September 4, 2021) emerged in early July 2021 in southern Missouri's Ozarks -- where tourist hubs like Branson had reopened indoor venues without mask mandates -- followed rapidly by secondary epicenters in the Pacific Northwest seeded via domestic air travel.[1][5] Because multiple perimeters expanded simultaneously, Wave 2 outpaced Wave 1 in mean daily areal expansion by over 18,500 km /day (Table 1).[1]

| Spatial Metric | | Wave 1 (Fall/Winter 2020) | | Wave 2 (Summer 2021) |

| Predominant Viral Variant | | Wild-type, transitioning to Alpha | | Delta (B.1.617.2) |

| Initial Area Affected | | 134,200 square kilometers | | 23,100 square kilometers |

| Maximum Area Encompassed | | 6,515,300 square kilometers | | 7,573,500 square kilometers |

| Mean Daily Areal Expansion | | 101,287 km /day | | 119,848 km /day |

| Median Daily Areal Expansion | | 64,900 km /day | | 69,300 km /day |

| Interquartile Range (IQR) | | 20,350 to 199,650 km /day | | 29,700 to 192,500 km /day |

Orthogonal velocity measurements confirmed that Wave 2 advanced at an overall mean speed of 25.9 km/day versus 20.3 km/day for Wave 1, while sustaining a peak high-speed wavefront perimeter of 9,157 kilometers compared to 7,017 kilometers in Wave 1 (Table 2).[1]

| Velocity Metric | | Wave 1 | | Wave 2 |

| Overall Mean Wavefront Speed | | 20.3 km/day | | 25.9 km/day |

| Overall Median Wavefront Speed | | 20.6 km/day | | 20.6 km/day |

| Overall Interquartile Range (IQR) | | 0 to 35.6 km/day | | 0 to 35.6 km/day |

| IQR of Daily Mean Speeds | | 4.4 to 33.4 km/day | | 7.0 to 32.9 km/day |

| Max Length of High-Speed Wavefront | | 7,017 kilometers | | 9,157 kilometers |

Partitioning the 63 days prior to each national peak into 21-day intervals demonstrated exponential acceleration as infectious host density accumulated, with Wave 2 exceeding Wave 1 in every interval and reaching 40.8 km/day in the final three weeks before peak incidence (Table 3).[1]

| Chronological Interval | | Wave 1 Mean Speed (km/day) | | Wave 2 Mean Speed (km/day) |

| 63 to 43 Days Prior to Peak | | 3.8 | | 6.8 |

| 42 to 22 Days Prior to Peak | | 17.0 | | 19.8 |

| 21 to 0 Days Prior to Peak | | 33.9 | | 40.8 |

Methodological Critiques and Wastewater Surveillance Integration

Peer review of the BYM2 wavefront framework highlights two structural caveats: global mean velocity metrics average rapid urban corridor transmission with slower rural spread, and nearest-neighbor orthogonal boundary distances can underestimate long-distance saltatory jumps driven by aviation networks.[1] Furthermore, as unreported at-home antigen testing degraded clinical notification streams, wastewater-based epidemiology emerged as an objective spatial anchor.[15] Longitudinal sewage surveillance in Saxony, Germany, confirmed that regression models incorporating flow discharge rates and lead/lag dynamics accurately reconstruct community prevalence, offering a bias-free input for future BYM2 spatial models.[15]

Conclusion: Predictive Spatial Epidemiology and Pandemic Preparedness

High-resolution spatiotemporal modeling proves that baseline population immunity alone cannot contain a respiratory pathogen whose biological evolution yields a sixfold surge in upper-respiratory viral shedding while non-pharmaceutical behavioral mitigations are simultaneously relaxed.[1] By pairing Bayesian evidence-synthesis nowcasting and municipal wastewater surveillance with standardized hexagonal spatial smoothing, public health agencies can track advancing epidemic wavefronts in real time -- shifting from reactive universal lockdowns to targeted, preemptive medical and clinical resource deployment directly ahead of an approaching viral surge.[1][15]

Updates (Nov 20, 2026): Consolidated preprint and broken duplicate links to the peer-reviewed March 4, 2026 PLOS Computational Biology DOI (10.1371/journal.pcbi.1013983), replaced blocked mirrors and secondary links with canonical DOIs and verified publication dates, split grouped citation markers, and removed numbered section prefixes.

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