



GISDD: a comprehensive global integrated sequence and genotyping databases platform for dengue virus, facilitating a stratified coordinated surveillance strategy

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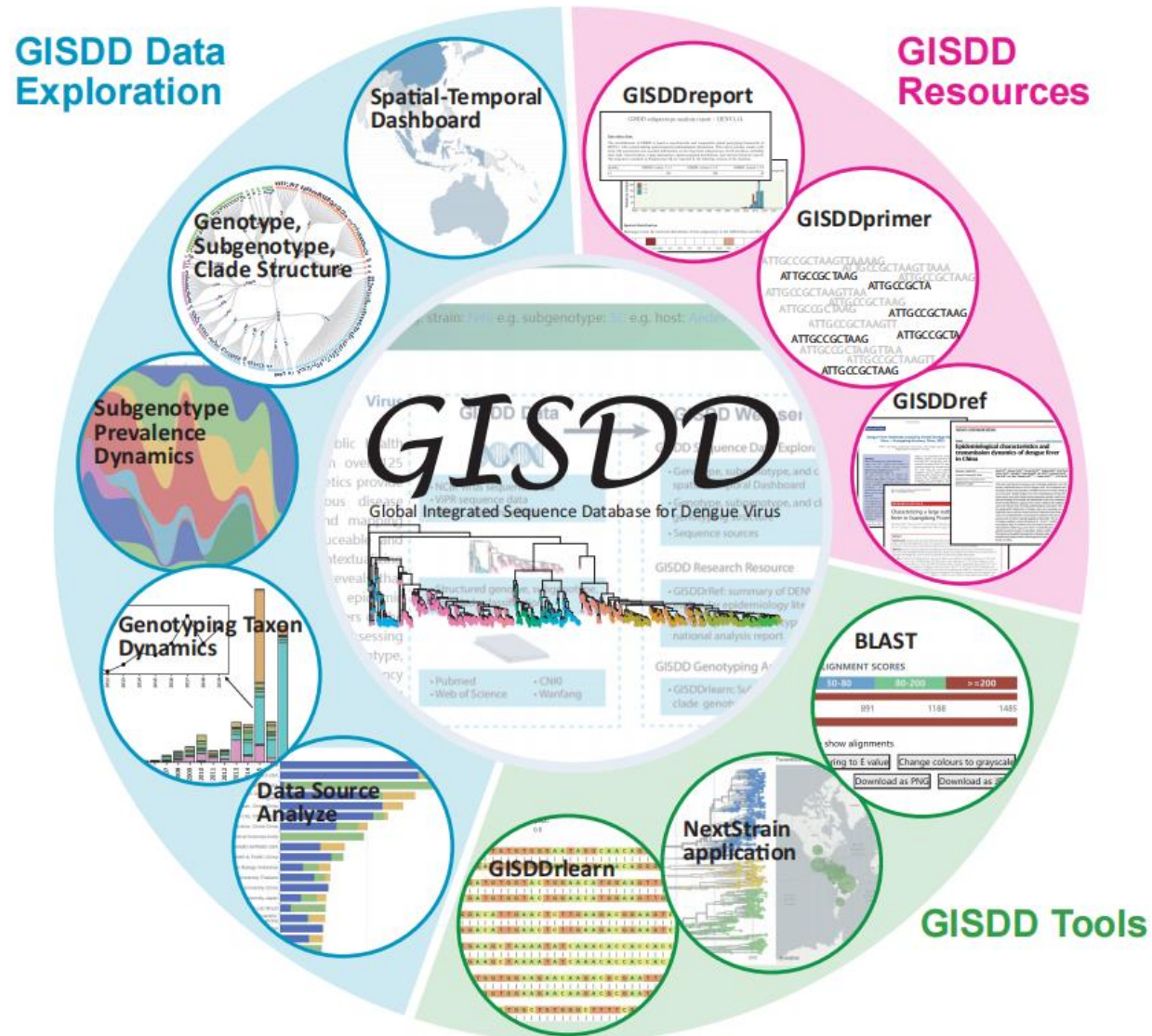
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Highlights



A platform facilitating a stratified coordinated surveillance strategy

Features of GISDD data

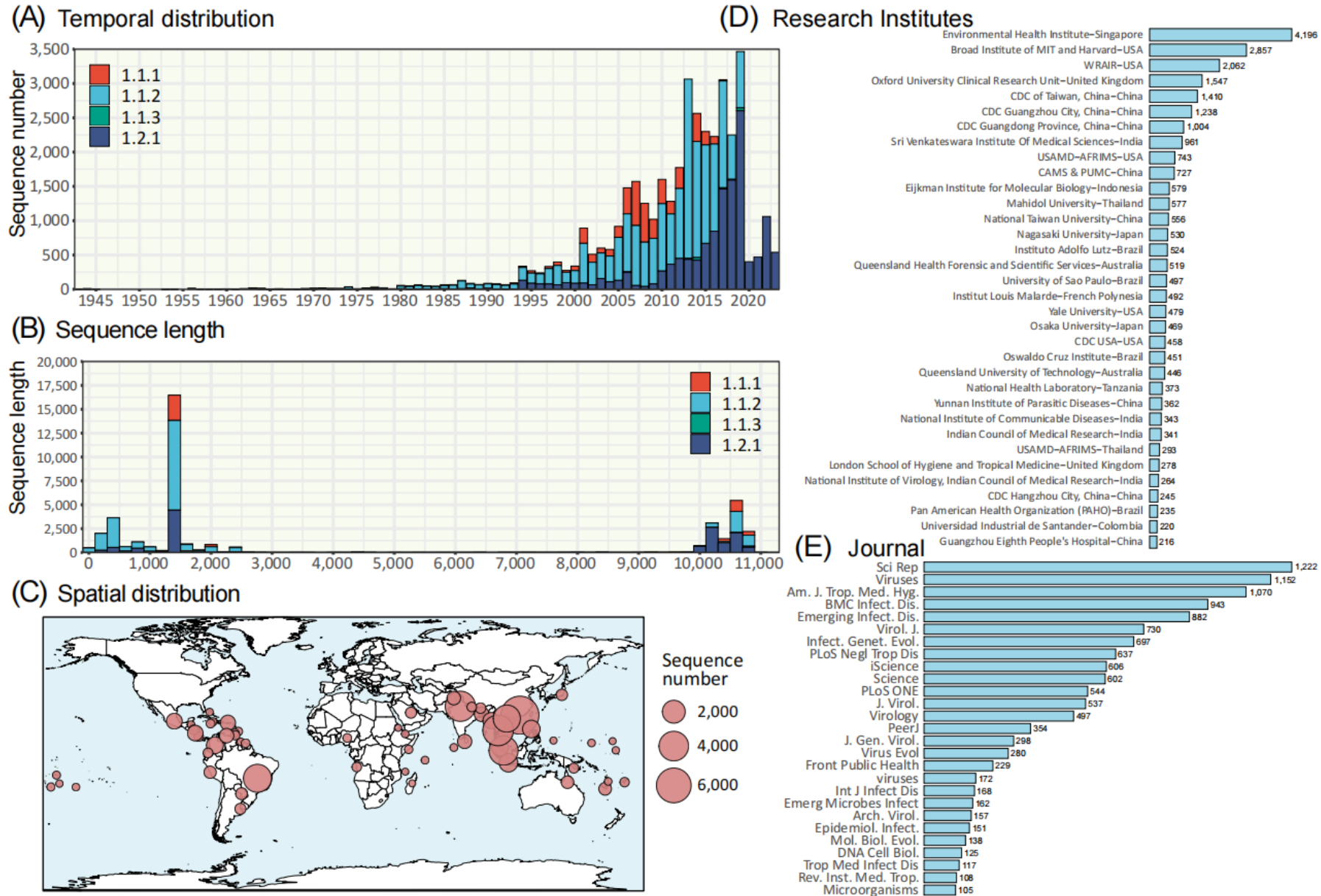


Figure 1. Key features of GISDD.

Resources & Tools in GISDD

The figure illustrates the user interface of the Global Integrated Sequence Database for Dengue Virus (GISDD) for data exploration. The interface is divided into several key sections:

- Header:** Features the GISDD logo and a search bar with example queries: "e.g. strain: N46", "e.g. subgenotype: 5C", and "e.g. host: Aedes albopictus".
- Navigation Menu:** Includes links for Home, WorkFlow, Browse, Explore, Resources, Tools, and About.
- Explore Section:** A sub-menu with options for "Spatial-temporal distribution", "Genotype, subgenotype, and clade structure", and "Data sources analyze".
- Parameters Options:** A form with various filters including Serotype, Subgenotype, Clade, Genome, Country, City, Genotype, Quality, E, Year, and Province. A "Submit" button is located at the bottom left.
- Results:** Displays two main visualizations:
 - Temporal distribution:** A stacked bar chart showing the number of sequences (Y-axis, 0-250) over time (X-axis, 2008-2018). The chart is color-coded by serotype: 1.1.1 (blue), 1.1.2 (green), and 1.1.3 (yellow).
 - Spatial distribution -- Global:** A world map showing the geographic distribution of sequences, with a legend for the number of strains per region (0, 1-10, 11-100, 101-1000, 1001-10000, >10000).

Red arrows and numbered circles (1-4) indicate the user's navigation path: 1. From the main menu to the Explore section; 2. From the Explore section to the Parameters Options form; 3. From the Parameters Options form to the Results section; 4. From the Results section back to the main menu area.

Figure 2: The user interface of data exploration in GISDD.



SIR Workflow in GISDD

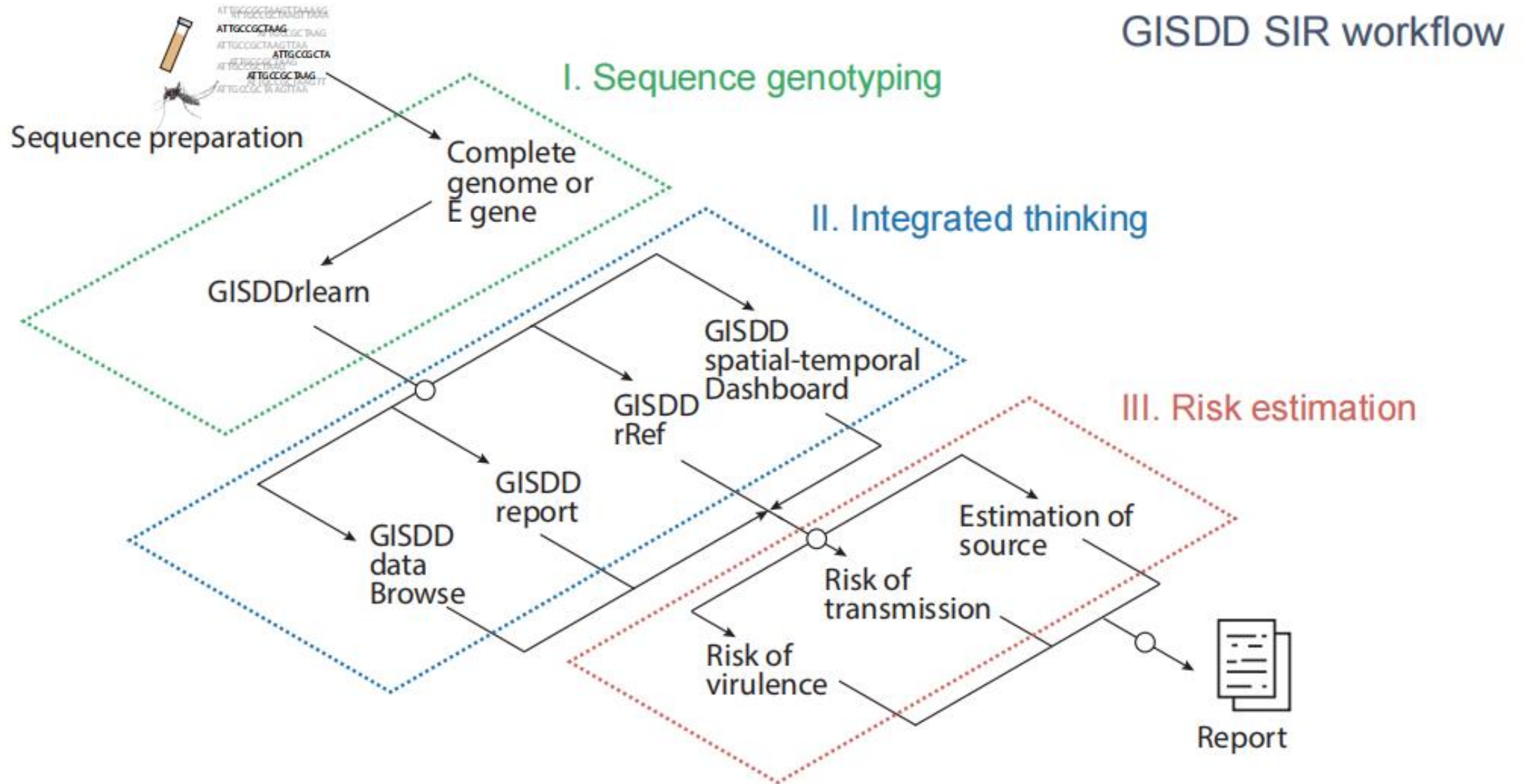
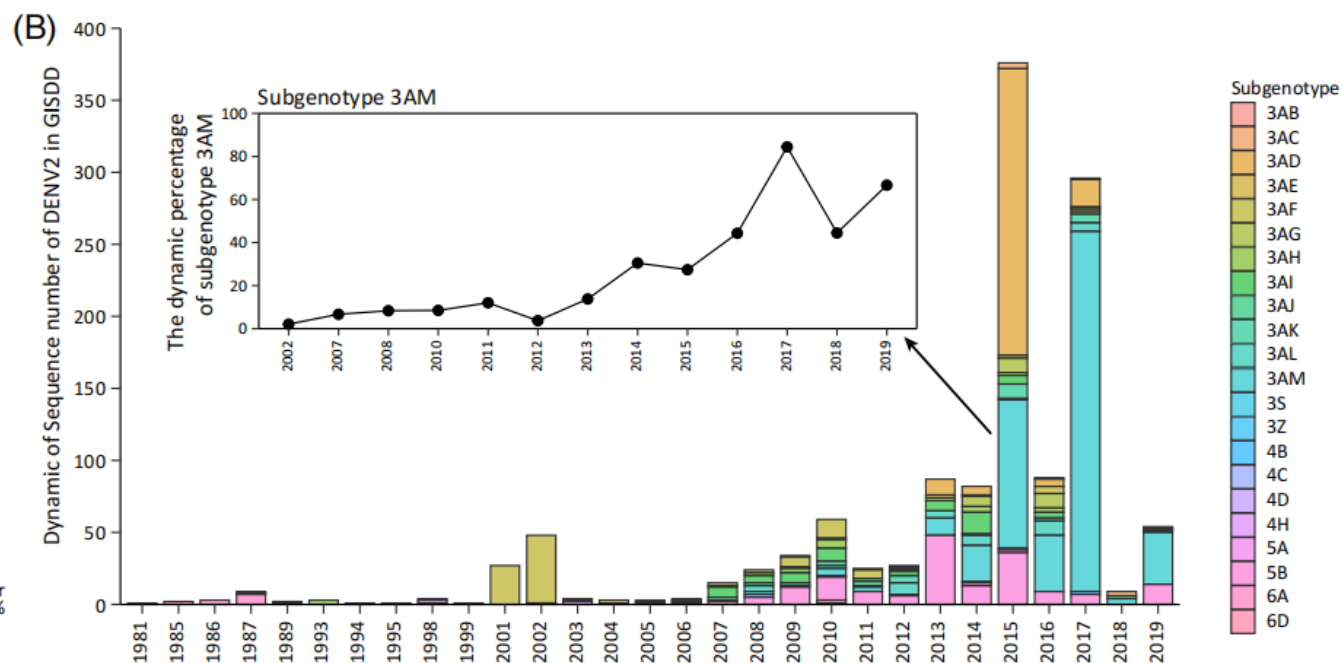
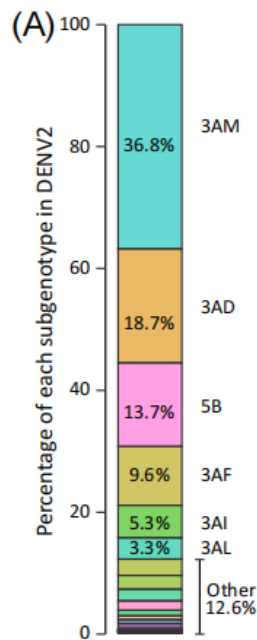


Figure 3. Overview of GISDD Sequence genotyping-Comprehensive thinking-Risk estimation (SIR) workflow.

SIR workflow implementation two cases

In Case 1



In Case 2

(C) Feature Score Subgenotype 3AM in China

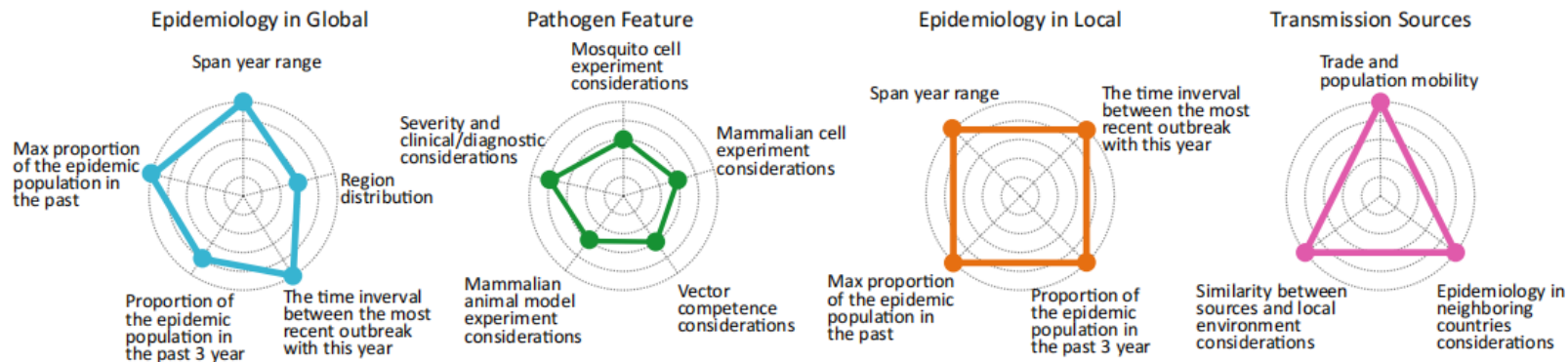


Figure 4. SIR workflow implementation two cases.

Summary

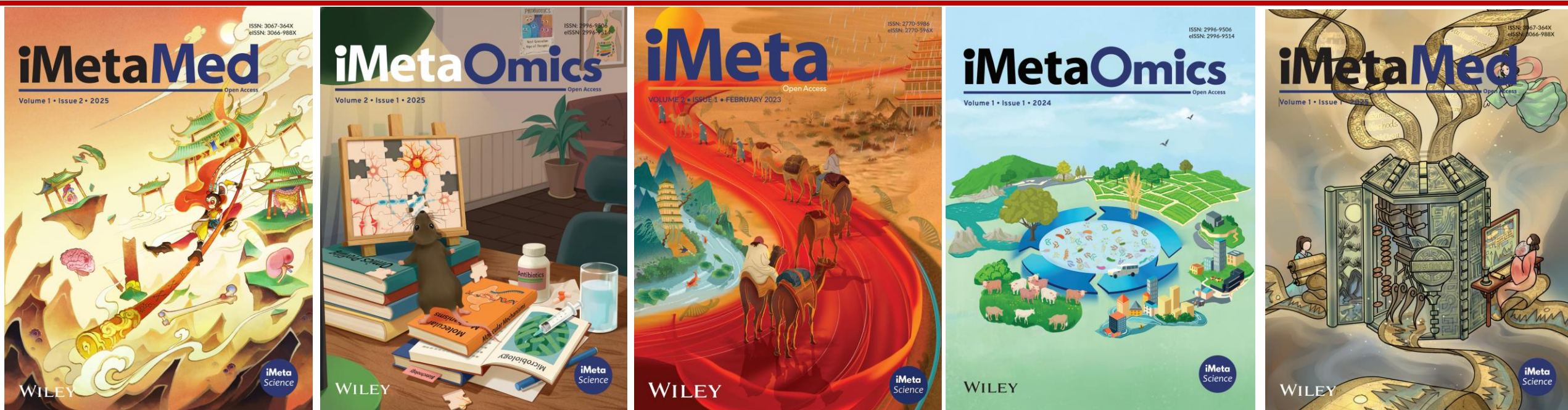


- ❑ GISDD integrates advanced online tools to enable rapid genotyping and tracing of DENV subgenotype and clade, enhancing molecular epidemiology insights.
- ❑ The database bridges critical surveillance gaps by mapping temporal-geographical spread patterns of dengue outbreaks.
- ❑ SIR workflow in GISDD enabling users to directly submit their sequences through a webpage for analysis and receive the corresponding reports.

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