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Data Descriptor

Synthetic and Encoded Database of Dengue, Zika, Chikungunya, and Influenza Derived from the Literature

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Abstract

This work presents a synthetic binary database of Dengue, Zika, Chikungunya, and Influenza constructed entirely from clinical information extracted from the scientific literature. Due to the limited availability and heterogeneity of clinical records in medical units—particularly for arboviral diseases—existing datasets are often insufficient for developing robust Machine Learning models. To address this limitation, an extensive search of PubMed and Google Scholar was conducted between February 2024 and May 2025, following strict selection criteria focused on diagnostic confirmation. The resulting dataset comprises 48,214 records and 67 standardized signs and symptoms, homogenized across all pathologies. Each record is fully binary, contains no missing values, and represents symptom presence or absence. The composition includes 22,379 Dengue records, 7135 Zika records, 7959 Chikungunya records, and 10,741 Influenza records. Symptom prevalence was analyzed, revealing consistency with patterns reported in epidemiological and clinical studies, supporting the dataset's plausibility. This database enables statistical exploration and direct integration into Machine Learning pipelines without the need for imputation. It has been used in an in silico predictive study of arboviral diseases, employing Influenza as a negative control, and serves as a reproducible, literature-derived resource for computational modeling.

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Keywords: Dengue; Zika; Chikungunya; database

1. Summary

Clinical data collected for diseases such as Dengue, Zika, and Chikungunya in medical units are often not sufficiently extensive to achieve generalization using Machine Learning (ML) techniques. Therefore, we undertook the task of gathering data from the existing literature with the purpose of employing it in ML models. This paper describes a synthetic binary database (https://doi.org/10.5281/zenodo.17902345) comprising four pathologies—Dengue, Zika, Chikungunya, and Influenza—with a total of 48,214 records. A set of 67 different signs and symptoms is presented across these diseases, and sensitive information such as age, sex, nationality, and socioeconomic status is excluded. This database was used for an in silico predictive study on arboviral diseases, employing Influenza as a negative control, currently under review, as well as in other works where F1-scores and AUC values above 90% were obtained throughout the performance of the ML models [1,2].

2. Data Description

The data included in this database represent patients exhibiting symptomatology indicative of one of the aforementioned diseases. The Excel file is divided into four sheets, each corresponding to one pathology. All sheets contain the same number and type of columns, corresponding to the label (pathology) and the features (symptoms).

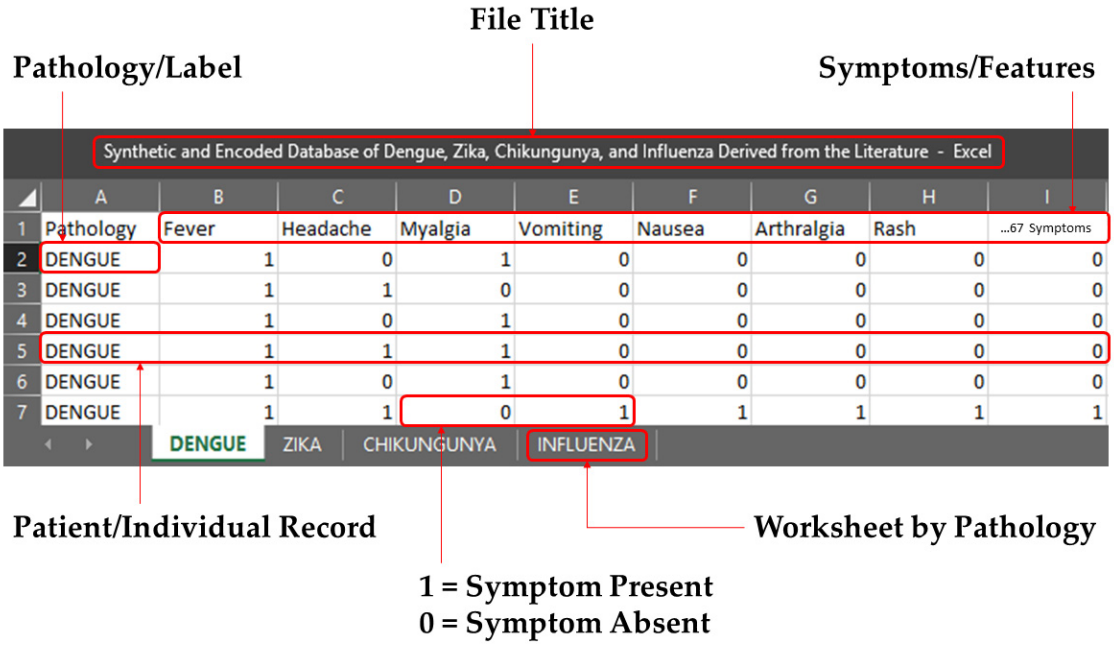
The pathologies included—Dengue, Zika, Chikungunya, and Influenza—share signs and symptoms during their early symptomatic phase, the febrile stage. The first three are arboviral diseases, that is, viral infections transmitted through the bite of infected arthropods, primarily Aedes aegypti and Aedes albopictus. In addition to sharing vectors and certain symptoms, these diseases also share geographic distribution and even seasonality, as vector activity increases under specific climatic conditions. Ultimately, laboratory tests are ultimately required to confirm infection; however, diagnosis for all three diseases is initially clinical [3–5].

Influenza was included because a previous study hypothesized that adding a negative control to predictive models would allow for a more accurate evaluation of arboviral diseases. Thus, if a patient's data did not match any arboviral infection, Influenza could serve as the alternative diagnosis. Influenza also shares several symptoms with the three arboviral diseases and is prone to epidemic outbreaks [6], making it a meaningful comparative dataset.

The database consists of 22,379 Dengue records, 7135 Zika records, 7959 Chikungunya records, and 10,741 Influenza records: 48,214 records in total. For Dengue, data were collected from patients diagnosed with Dengue without warning signs and Dengue with warning signs, but do not include severe Dengue cases. For Influenza, records include Influenza A, B, and seasonal Influenza.

2.1. Dataset

All values are binary. Each row represents an individual record, beginning with the label followed by values of 1 if the clinical sign was present and 0 if absent. No missing values or NaNs (not a number) are present. This structure allows for direct statistical analysis and integration into ML models without the need for imputation. Figure 1 shows a screenshot of the Excel file.



	A	B	C	D	E	F	G	H	I
1	Pathology	Fever	Headache	Myalgia	Vomiting	Nausea	Arthralgia	Rash	...67 Symptoms
2	DENGUE	1	0	1	0	0	0	0	0
3	DENGUE	1	1	0	0	0	0	0	0
4	DENGUE	1	0	1	0	0	0	0	0
5	DENGUE	1	1	1	0	0	0	0	0
6	DENGUE	1	0	1	0	0	0	0	0
7	DENGUE	1	1	0	1	1	1	1	1

Figure 1. Screenshot of the database file.

Individually, Dengue presented 37 symptoms, Zika 33, Chikungunya 31, and Influenza 35; collectively, they totaled 67 symptoms, 12 of which were shared among all four diseases. While laboratory data is not included, clinically relevant outcomes such as thrombocytopenia, leukopenia, and elevated hematocrit were incorporated as binary indicators. Table 1 summarizes the number of records and symptoms per disease.

Table 1. Records and symptoms.

Pathology	Records	Number of Symptoms
Dengue	22,379	37
Zika	7135	33
Chikungunya	7959	31
Influenza	10,741	35

2.2. Symptom Co-Occurrence and Disease Similarity Analysis

The symptoms are grouped into those shared among the pathologies and those observed only in each pathology. Table 2 presents all observed signs and symptoms, grouped into those shared between pathologies and those specific to each pathology.

Table 2. Symptoms observed in the synthetic database.

Symptom	DEN	ZIK	CHI	FLU	Category
1. Abdominal pain, 2. Anorexia, 3. Arthralgia, 4. Chills, 5. Cough, 6. Diarrhea, 7. Fatigue, 8. Fever, 9. Headache, 10. Myalgia, 11. Nausea, 12. Vomiting	*	*	*	*	Shared all
13. Bleeding, 14. Edema, 15. Pruritus, 16. Rash, 17. Retro-orbital pain	*	*	*		Triple (DEN-ZIK-CHI)
18. Conjunctivitis, 19. Lethargy, 20. Lymphadenopathy, 21. Malaise, 22. Sore throat		*	*	*	Triple (ZIK-CHI-FLU)
23. Constipation, 24. Leucopenia, 25. Petechiae	*	*			Dual (DEN-ZIK)

Table 2. *Cont.*

Symptom	DEN	ZIK	CHI	FLU	Category
26. Melena, 27. Tachycardia, 28. Tachypnea	*			*	Dual (DEN-FLU)
29. Dizziness		*	*		Dual (ZIK-CHI)
30. Erythema, 31. Low Back pain, 32. Rhinorrhea		*		*	Dual (ZIK-FLU)
33. Difficulty breathing, 34. Oliguria, 35. Seizures			*	*	Dual (CHI-FLU)
36. Adenoids, 37. Cutaneous hypersensitivity, 38. Dysuria, 39. Hematocrit, 40. Hepatomegaly, 41. Impaired consciousness, 42. Low SBP, 43. Maculopapular rash, 44. Mouth sore, 45. Mucosal bleeding, 46. Pharyngeal hyperemia, 47. Plasma leakage, 48. Shock, 49. Thrombocytopenia	*				DEN
50. General pain, 51. Odynophagia, 52. Paresthesia, 53. Photophobia		*			ZIK
54. AKI, 55. Concentration disorder, 56. Dysgeusia, 57. Sleeping disorder, 58. Vertigo			*		CHI
59. Ageusia, 60. Anosmia, 61. Chest pain, 62. Nasal congestion, 63. Otitis, 64. Rhinitis, 65. Sneezing, 66. Sputum, 67. Wheezing				*	FLU

* Mark the disease where the symptom was observed. DEN, Dengue; ZIK, Zika; CHI, Chikungunya; FLU, Influenza; SBP, systolic blood pressure; AKI, acute kidney injury.

Since the analyzed database is composed of binary variables that indicate the presence or absence of clinical characteristics, the Jaccard similarity index (Equation (1)) was used to quantify the degree of overlap between the diseases studied. This index is particularly suitable for asymmetric binary data, as it only considers positive matches, i.e., the shared presence of a feature in the subsets, and ignores simultaneous absences, which lack clinical relevance and can introduce biases in the estimation of similarity.

$$J = \frac{M_{11}}{M_{01} + M_{10} + M_{11}} \quad (1)$$

When working with binary variables, the Jaccard Index can be expressed in terms of a contingency table (Figure 2), where M_{11} denotes the number of features present in both pathologies, M_{10} the number of features present only in the first disease, and M_{01} the number of features present only in the second. Simultaneous absence matches (M_{00}) are not considered in the calculation, as they do not provide relevant clinical information.

The Jaccard Index shows values between 0 and 1, where values close to 1 indicate a high degree of similarity, reflecting that most of the features present in at least one of them are shared. On the other hand, values close to 0 indicate low similarity, implying that the pathologies share few clinical characteristics and present clearly distinguishable profiles. In clinical terms, high values suggest significant symptomatic overlap and, therefore, a greater likelihood of diagnostic confusion, especially in the early stages of the disease.

Consequently, the use of the Jaccard Index allows not only robust quantification of the similarity between infectious diseases with partially overlapping manifestations, such as Dengue, Zika, Chikungunya, and Influenza, but also direct interpretation of the results in a clinical and epidemiological context. The combination of the similarity matrix and its graphical representation provides an intuitive tool for identifying overlapping patterns, supporting comparative analysis between diseases, and methodologically justifying subsequent analyses, such as unsupervised clustering or multiclass classification models.

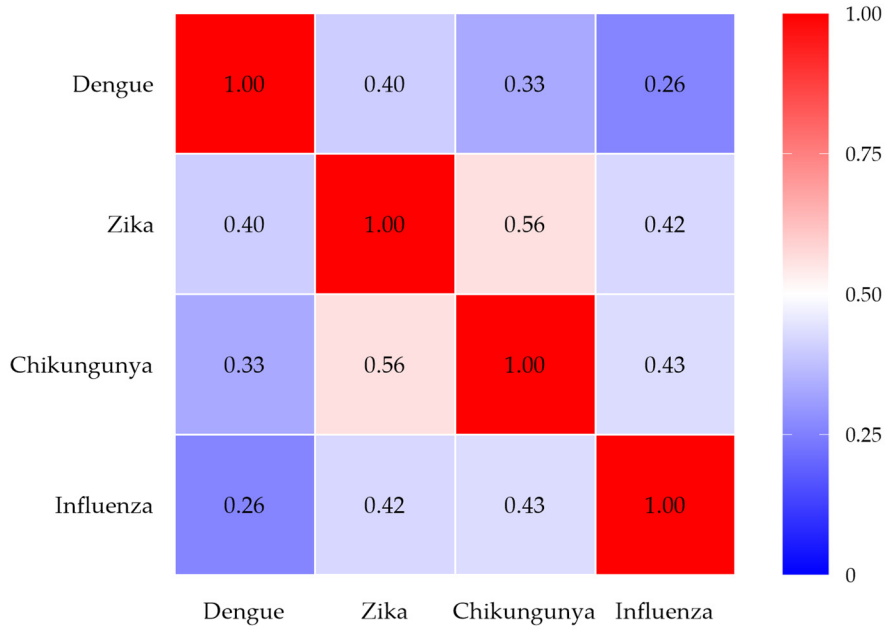


Figure 2. Jaccard Index among this group of pathologies. This value shows how similar the data are between each subset; 1 means they are the same and 0 means they are completely different.

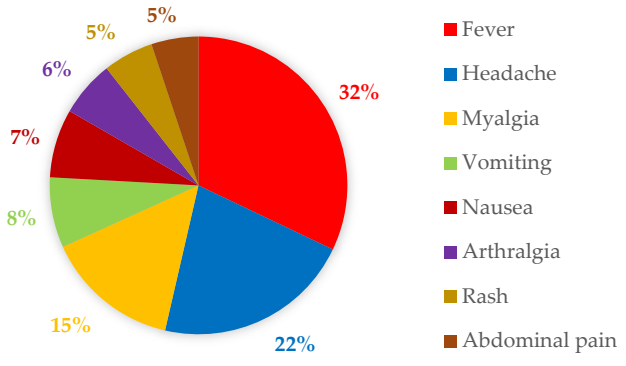
2.3. Prevalence Analysis

The prevalence of symptoms described in Appendix A is calculated using Equation (2)

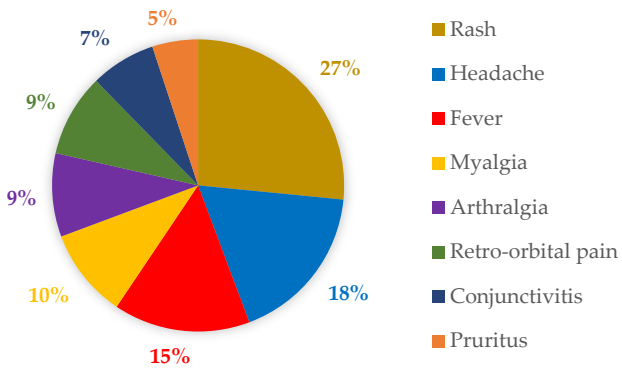
$$P_{s,d} = \frac{\sum_{i=1}^{N_d} X_{i,s}}{N_d} \quad (2)$$

where $P_{s,d}$ is the prevalence of the symptom s for disease d, $X_{i,s}$ represents the state of the symptom for an individual patient i of the specific symptom s, and N_d is the total number of patients analyzed for that specific disease.

Highlighting the eight most frequent symptoms per disease, these symptoms had a prevalence greater than 0.15, meaning that 15 out of every 100 patients presented with each symptom (see Figure 3).

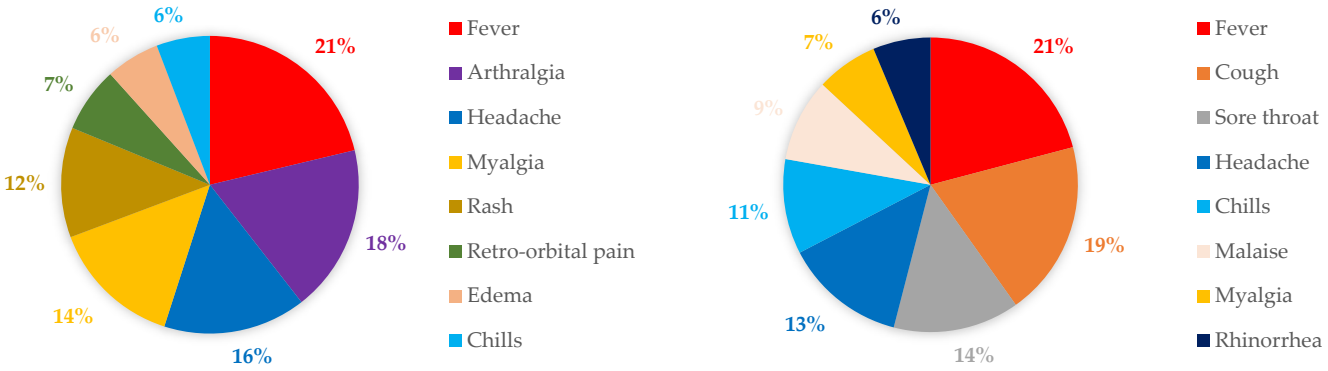


(**a**) Dengue



(**b**) Zika

Figure 3. *Cont.*



(**c**) Chikungunya (**d**) Influenza

Figure 3. Most prevalent symptoms for each pathology. The eight most prevalent symptoms per disease are highlighted.

3. Methods

In general, the database was compiled from existing literature; that is, the PubMed and Google Scholar search engines were used to identify papers containing clinical data on the pathologies of interest. Selection criteria were applied to the studies from this search to extract their clinical data, which were then transformed into a binary database. Figure 4 illustrates the methodological process.

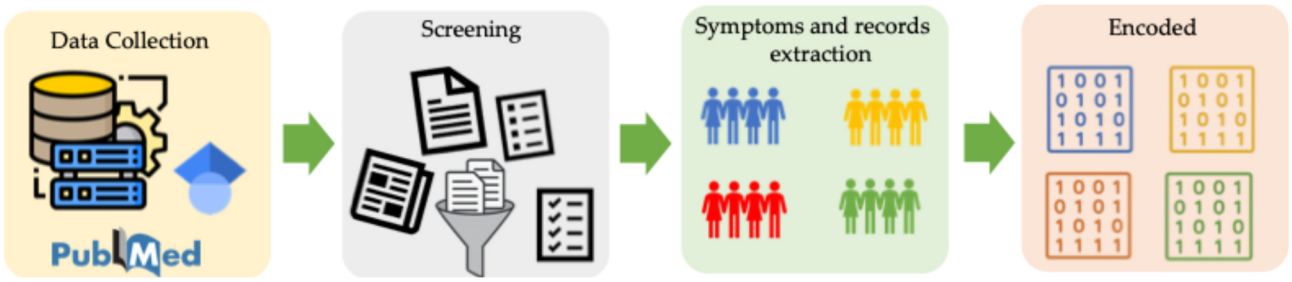


Figure 4. Methodological process of the database.

3.1. Data Collection

An exhaustive search was conducted in the PubMed and Google Scholar databases between February 2024 and May 2025. The extended duration was due to the manual nature of the search and selection process; furthermore, the database was built in blocks, one disease at a time. For this search, the following keywords were used: for Dengue: "DENGUE", "PREVALENCE", and "CLINICAL SYMPTOMS"; for Zika: "ZIKA", "PREVALENCE", and "CLINICAL SYMPTOMS"; for Chikungunya: "CHIKUNGUNA", "PREVALENCE", and "CLINICAL SYMPTOMS"; and for Influenza: "INFLUENZA", "PREVALENCE", and "CLINICAL SYMPTOMS".

3.2. Screening

The studies retrieved from the search had to meet the following selection criteria:

- Report at least twenty patients confirmed and diagnosed with the target pathology.
- Report all symptoms and signs observed in the patients.
- Symptoms had to be observed within the first five days of illness onset.
- At least four different symptoms had to be described.
- The patients must not have presented coinfection or reinfection.

The selected studies were carefully reviewed to minimize redundancy and ensure that each offered unique and relevant information. Additionally, including studies from

different countries, hospitals, and years allows for retrospective analysis of trends without interfering with the original clinical contexts.

A total of 125 studies were collected: 52 studies for Dengue [7–58], 32 for Zika [59–90], 30 for Chikungunya [91–120], and 11 for Influenza [121–131]. Studies originated from a wide range of scientific journals, including The American Journal of Tropical Medicine and Hygiene [17,22,55,65,105,116], Journal of Infection and Public Health [23,25,74,96], BMC Infectious Diseases [24,88,114,126], PLOS Neglected Tropical Diseases [27,43,49,50,53,56, 62,66,89,91,103,107,115], Science Advances [54], and The Lancet Infectious Diseases [86], among many others. Data in the studies came from several sources, including hospital records, surveillance datasets, and open access, among others.

3.3. Symptoms and Record Extraction

Based on the selection criteria, clinical data were extracted from the selected studies, excluding sensitive information such as age, sex, nationality, socioeconomic status, and the medical center where the patient received care. Regarding the laboratory data reported in the studies, abnormal results were considered clinically indicative of the disease; for example, studies showing a circulating leukocyte count < 4000 cells/mm^3 in patients were marked as "Leukopenia present" ("1"). In cases where symptoms were expressed using continuous data, such as the measured temperature, these values were converted to binary if they exceeded known limits. For example, values < 38 °C/100.4 °F were marked as fever present ("1"), and values below that limit were marked as absent ("0"). Transforming Boolean data (yes/no) to binary is simpler: affirmative values were marked as present (yes = 1), and negative values as absent (no = 0). Nominal data, such as those expressing the severity of a sign, were marked as present regardless of the severity level.

The exclusion of sensitive data is intended to generalize the dataset, making it suitable for statistical or AI modeling. The transformation to binary data allows for the standardization of the different types of data collected. This same transformation also allows for the analysis of outliers, labeling errors, and/or duplicate records—errors that can occur during manual data collection. The main objective is to ensure the quality of the synthetic database.

3.4. Encoding

Therefore, the extracted data is represented in a binary matrix, meaning that the encoding includes signs and symptoms represented by ones and zeros, indicating presence or absence. To homogenize the number of clinical features across all records, signs and symptoms belonging to other pathologies were added with a value of "0", meaning absent. Consequently, each record for each pathology contains 67 features. The matrix is expressed by Equation (2):

$$Z = \begin{pmatrix} z_{1,1} & z_{1,2} & \cdots & z_{1,n} \\ z_{2,1} & z_{2,2} & \cdots & z_{2,n} \\ \vdots & \vdots & \ddots & \vdots \\ z_{m,1} & z_{m,2} & \cdots & z_{m,n} \end{pmatrix} \tag{3}$$

where m is the total number of patients, n is the total number of symptoms evaluated, each row represents a patient, and each column represents a specific symptom. The binary coding is defined by Equation (3):

$$z_{ij} = \begin{cases} 1 \text{ if symptom } j \text{ is present in patient } i \\ 0 \text{ if symptom } j \text{ is absent in patient } i \end{cases} \tag{4}$$

where the element Z_{ij} corresponds to row i and column j, a value of 1 indicates the confirmed presence of the symptom, and a value of 0 indicates the absence of the symptom.

In summary, the Excel sheets present a bidimensional data structure where each column contains data of the same type, each row represents a single observation, and each sheet corresponds to a specific pathology.

4. Similarity of the Synthetic Database to Public Databases

To assess similarity with existing datasets, several published datasets are described. For example, Endy et al. [132] published a dataset including Dengue, Zika, and Chikungunya cases collected in Machala, Ecuador, divided into laboratory-confirmed patients (98 records) and non-laboratory-confirmed patients (534 records). This dataset includes a mix of binary and continuous variables such as symptoms, age, sex, waist and arm circumference, and height, among others. Mahalingam et al. [133] presented a dataset of 303 infants with Dengue, containing continuous data and scaled values (1–7) for variables including sex, age, symptoms, laboratory values, and diagnostic labels (dengue fever or complicated dengue).

Wheeler et al. [134] compiled clinical data for 47 infants in Brazil diagnosed with congenital Zika syndrome, including continuous and binary variables describing measurements, symptoms, and maternal history. For Influenza, Anderson et al. [135] presented 4572 records, of which 1493 were laboratory-confirmed Influenza cases, containing variables such as age, sex, symptoms (in Boolean values), and laboratory confirmation. Finally, Kandemir (2025) [136] published a dataset of 182 Turkish patients with Influenza reporting only binary symptom data (eight symptoms). Table 3 summarizes these datasets.

Table 3. Comparison with public databases.

Study	No. of Records	Data	Type of Data	Pathology	Country
Endy et al. [132]	632	Symptoms, demographic data, laboratory data.	Binaries, continuous	Dengue, Zika and Chikungunya	Ecuador
Mahalingam et al. [133]	303	Symptoms, demographic data, laboratory data.	Continuous	Dengue	Brazil
Wheeler et al. [134]	47	Symptoms, demographic data, laboratory data, anthropometric.	Binaries, continuous	Congenital Zika Syndrome	Brazil
Anderson et al. [136]	4572	Symptoms, demographic data, laboratory data.	Binaries, continuous, Boolean	Influenza	Thailand
Kandemir (2025) [136]	182	Symptoms	Binaries	Influenza	Turkey
Present database	48,214	Symptoms	Binaries	Dengue, Zika, Chikungunya, and Influenza	Global

Author Contributions: Conceptualization, E.C.-P. and G.V.-E.; methodology, E.C.-P. and C.M.L.-D.; software, E.C.-P., C.M.L.-D., G.V.-E., H.A.C.-F., and I.M.; validation, C.M.L.-D., L.P.-C.M., A.E.P.-R., M.T.H.-H., C.R.-D., A.D.P.-S., E.P.-C.M., I.A.G.-M., L.M.-M., H.M.-R., M.E.A.-V., H.A.C.-F., and M.M.C.; formal analysis, C.M.L.-D.; investigation, C.M.L.-D., E.C.-P., and E.L.P.-C.; writing—original draft preparation, E.C.-P., C.M.L.-D., and E.L.P.-C.; writing—review and editing, C.M.L.-D. and E.L.P.-C.; visualization, H.A.C.-F.; supervision, C.M.L.-D.; project administration, E.L.P.-C. and C.M.L.-D. All authors have read and agreed to the published version of the manuscript.

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Conflicts of Interest: The authors declare no conflicts of interest.

Abbreviations

The following abbreviations are used in this manuscript:

ML	Machine Learning
AUC	Area Under the Curve
NaN	Not a number
DEN	Dengue
ZIK	Zika
CHI	Chikungunya
FLU	Influenza
SBP	Systolic blood pressure
AKI	Acute kidney injury

Appendix A

Table A1 shows the prevalence of the 67 symptoms in the four pathologies. Prevalence values greater than 0.15 are indicated in bold, and the order of the symptoms is alphabetical.

Table A1. Prevalence of the sixty-seven symptoms.

	DEN	ZIK	CHI	FLU
Abdominal pain	**0.154**	0.047	0.066	0.115
Adenoids	0.011	0	0	0
Ageusia	0	0	0	0
AKI	0	0	0.003	0
Anorexia	0.032	0.043	0.007	0.007
Anosmia	0	0	0	0
Arthralgia	**0.182**	**0.286**	**0.815**	0.104
Bleeding	0.043	0.001	0.032	0
Chest pain	0	0	0	0.004
Chills	0.021	0.046	**0.26**	**0.468**
Concentration disorder	0	0	0.011	0
Conjunctivitis	0	**0.224**	0.065	0.001
Constipation	0.008	0	0	0
Cough	0.114	0.036	0.052	**0.867**
Cutaneous hypersensitivity	0.003	0	0	0
Diarrhea	0.067	0.042	0.057	0.045
Difficulty breathing	0	0	0.017	0.139
Dizziness	0	0.001	0.01	0
Dysgeusia	0	0	0.008	0
Dysuria	0.001	0	0	0
Edema	0.002	0.057	**0.262**	0
Erythema	0	0.034	0	0
Fatigue	0.064	0.096	0.053	0.009
Fever	**0.962**	**0.468**	**0.952**	**0.939**
General pain	0	0.007	0	0
Headache	**0.645**	**0.55**	**0.694**	**0.6**
Hematocrit	0.037	0	0	0

Table A1. *Cont.*

	DEN	ZIK	CHI	FLU
Hepatomegaly	0.035	0	0	0
Impaired consciousness	0.005	0	0	0
Lethargy	0	0.027	0.032	0.007
Leucopenia	0.136	0.012	0	0
Low back pain	0	0.094	0	0.003
Low SBP	0.005	0	0	0
Lymphadenopathy	0	0.02	0.007	0.001
Maculopapular rash	0.003	0	0	0
Malaise	0	0.026	0.033	**0.409**
Melena	0.004	0	0	0.001
Mouth sore	0.009	0	0	0
Mucosal bleeding	0.004	0	0	0
Myalgia	**0.438**	**0.307**	**0.641**	**0.304**
Nasal Congestion	0	0	0	0.064
Nausea	**0.223**	0.107	**0.223**	0.073
Odynophagia	0	0.014	0	0
Oliguria	0	0	0.001	0
Otitis	0	0	0	0.003
Paresthesia	0	0.005	0	0
Petechiae	0.018	0.039	0	0
Pharyngeal hyperemia	0.106	0	0	0
Photophobia	0	0.021	0	0
Plasma leakage	0.004	0	0	0
Pruritus	0.008	**0.157**	0.069	0
Rash	**0.164**	**0.823**	**0.535**	0
Retro-orbital pain	0.097	**0.283**	**0.318**	0
Rhinitis	0	0	0	0.015
Rhinorrhea	0	0.023	0	**0.284**
Seizures	0	0	0.001	0
Shock	0	0	0	0
Sleeping disorder	0	0	0.017	0
Sneezing	0	0	0	0.003
Sore throat	0	0.048	0.04	**0.622**
Sputum	0	0	0	0.009
Tachycardia	0.01	0	0	0.001
Tachypnea	0.003	0	0	0.007
Thrombocytopenia	0.116	0	0	0
Vertigo	0	0	0.033	0
Vomiting	0.229	0.11	0.106	0.096
Wheezing	0	0	0	0.008

Prevalence values greater than 0.15 are highlighted in bold. DEN, Dengue; ZIK, Zika; CHI, Chikungunya; FLU, Influenza; SBP, systolic blood pressure; AKI, acute kidney injury.

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