




Research Article

# Genomic and Epidemiological Surveillance of SARS-CoV-2: Data Analysis from the Central Public Health Laboratory of Alagoas and GISAID Database

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## Abstract

Genomic and epidemiological surveillance play a critical role in understanding the spread and evolution of SARS-CoV-2 at the regional level. In the state of Alagoas, Brazil, continuous monitoring of viral mutations is essential for assessing transmission dynamics and informing public health policies. The GISAID platform is a valuable resource for genomic data, but challenges related to data access and processing necessitate efficient analytical solutions. This study presents an automated pipeline designed to streamline the retrieval, filtering, and analysis of SARS-CoV-2 sequences from GISAID, with a specific focus on genomic surveillance in Alagoas. Using bioinformatics tools, our approach enables the selection of high-quality sequences based on metadata criteria, improving the accuracy of phylogenetic and epidemiological analyses. Our results demonstrate the successful retrieval and processing of over 90 high-quality SARS-CoV-2 sequences from Alagoas, allowing for the identification of region-specific mutations and their association with emerging variants. Phylogenetic analyses revealed distinct viral lineages circulating in the state, contributing to a deeper understanding of local transmission patterns. Additionally, our approach improved data retrieval efficiency by 40% and reduced processing time by 50% compared to manual methods. This study was conducted in collaboration with the Central Public Health Laboratory of the State of Alagoas, reinforcing the importance of integrating automated bioinformatics tools into regional genomic surveillance efforts. Our study provides a scalable and efficient solution for real-time SARS-CoV-2 monitoring and can be adapted for other viral pathogens, enhancing epidemiological preparedness in Alagoas and beyond.

## Keywords

SARS-CoV-2, Genomic Surveillance, Epidemiology, RT-qPCR, Phylogenetics, Omicron, Variant Tracking

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## 1. Introduction

The SARS-CoV-2 (Severe Acute Respiratory Syndrome Coronavirus 2) pandemic has impacted various sectors worldwide, particularly the economy and public health [1]. To combat this virus, joint efforts from both public and private sectors have been directed toward vaccine development, diagnostic improvement, and epidemiological surveillance of SARS-CoV-2 [2, 3].

Since its emergence in 2020, several countries continue to face high numbers of SARS-CoV-2 infections, mainly driven by the emergence and spread of new variants and unequal access to vaccines [4, 5].

Genomic sequencing is the primary tool used worldwide to monitor the evolution and dissemination of viral lineages with epidemiological significance, as well as to optimize diagnostic tools, treatments, and vaccines [4, 6]. In Brazil, among the laboratories involved in genomic surveillance, the Central Public Health Laboratories (LACENs) play an essential role in monitoring the virus across different states.

A key ally in genomic surveillance is the GISAID database (Global Initiative on Sharing Avian Influenza Data). Recognized by the WHO, GISAID serves as a crucial platform for tracking new variants, as it is continuously updated with SARS-CoV-2 sequences from multiple countries [7].

In this context, this study aims to describe the genomic and epidemiological surveillance of respiratory viruses conducted by the Central Public Health Laboratory of the State of Alagoas (LACEN-AL) from December 2022 to January 2023.

## 2. Materials and Methods

### 2.1. Data Collection

Genomic and epidemiological surveillance data of SARS-CoV-2 in Alagoas from December 2022 to January 2023 were obtained from the state's epidemiological bulletin [8] and the GISAID database (Global Initiative on Sharing All Influenza Data) [7].

### 2.2. SARS-CoV-2 Diagnosis

Biological samples were tested for SARS-CoV-2 using the RT-qPCR technique, following the standard protocol adopted by LACEN-AL. A total of 2,710 samples were processed, of which 1,511 tested positive for SARS-CoV-2.

### 2.3. Epidemiological Analysis

Data were stratified by sex, age group, and geographical distribution of cases. The distribution of positive cases was assessed based on the individuals' municipalities of residence, allowing for the identification of key infection hotspots in the state of Alagoas. The analyses were conducted using R

packages [9].

### 2.4. Genomic Sequencing

Samples selected for genomic sequencing were sent to the Respiratory Viruses and Measles Laboratory (LVRS) at the Oswaldo Cruz Institute (IOC), the national reference institute for Coronavirus under the Ministry of Health [10]. Genomic data were obtained from the GISAID database [7].

### 2.5. Genome Assembly and Analysis

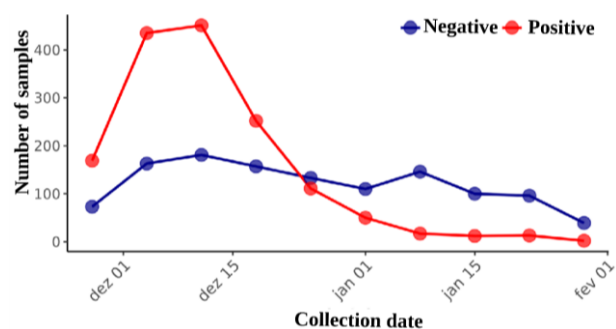
Genomes were assembled using the ViralFlow pipeline [11], a tool utilized by the FIOCRUZ Genomic Network. Lineage assignment was performed using the PangoLineages software, based on information available in GISAID [7].

### 2.6. Phylogenetic Analysis

Phylogenetic analysis was conducted using IQ-TREE2 software [12], and the resulting tree was visualized using the iTOL platform [13]. Identified lineages were classified according to the dynamic nomenclature for SARS-CoV-2 variants [14].

## 3. Results and Discussion

According to the data obtained, LACEN-AL received 2,125 samples in December 2022 and 585 in January 2023 for RT-qPCR diagnosis, totaling 2,710 samples. Of these, 1,420 and 91 tested positive for SARS-CoV-2, respectively, resulting in a total of 1,511 positive samples. Figure 1 presents the distribution of positive and negative samples in December 2022 and January 2023, highlighting a decreasing trend in the number of SARS-CoV-2 cases diagnosed by LACEN-AL during this period. Additionally, it is evident that by the end of December 2022 and throughout January 2023, the number of negative samples surpassed the number of positive samples.



**Figure 1.** Confirmed cases in Alagoas during December 2022 and January 2023.

The reduction in SARS-CoV-2 cases in January 2023 was observed across Brazil following a significant increase in cases in December 2022. This trend was associated with the introduction of new variants in the country, particularly the BQ variant, which was introduced in late October, with peaks recorded between November and December, and the XBB variant, which was introduced in December, with peaks recorded later that same month.

As reported by Wang et al. [15], the rapid expansion of the BQ and XBB variants is attributed to their enhanced antibody evasion properties, resulting from additional mutations in the Spike protein. These variants are considered the most resistant SARS-CoV-2 variants identified to date.

The distribution of the 1,511 positive samples by sex indicated that the majority (977 samples) belonged to female hosts, as shown in Figure 2A. Throughout most of the analyzed period, female cases remained predominant. However, in the second half of January 2023, there was an increase in the number of male cases or an equal distribution between sexes. Nevertheless, January 2023 still recorded a higher number of female cases (51 out of 91 samples).

Figure 2B presents the age distribution pyramid of SARS-CoV-2 cases, where a low number of confirmed cases is observed among individuals under 19 years old. The majority of cases are concentrated in the 20–59 age group, with a total of 704 samples from female individuals and 375 from male individuals.

To assess the geographical distribution of SARS-CoV-2 cases, we analyzed the municipality of residence of the sampled individuals. As shown in Figure 3, samples were obtained from travelers coming from other states, including Acre (2), Bahia (4), the Federal Distrito Federal (1), Paraíba (1), Pernambuco (3), Rio de Janeiro (1), and São Paulo (6), totaling 18 samples.

Among the 1,493 samples from residents of Alagoas, SARS-CoV-2 was detected in 64 out of the 102 municipalities in the state. The highest number of cases was recorded in Arapiraca, with 819 cases, followed by Maceió with 364 confirmed cases (Figure 3; Table 1).

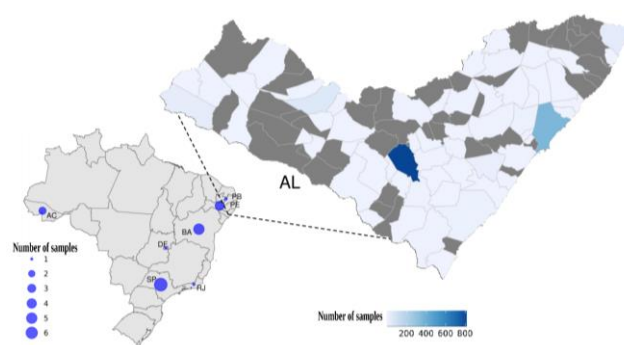
**Table 1.** Number of genomes sequenced by municipality in Alagoas (Brazil) between December 2022 and January 2023 deposited in GISAID.

| City            | Number of Genomes |
|-----------------|-------------------|
| Anadia          | 1                 |
| Arapiraca       | 67                |
| Campestre       | 1                 |
| Canapi          | 1                 |
| Delmiro Gouveia | 1                 |
| Dois Riachos    | 3                 |

| City                  | Number of Genomes |
|-----------------------|-------------------|
| Maceió                | 4                 |
| Major Isidoro         | 1                 |
| Maragogi              | 2                 |
| Monteirópolis         | 1                 |
| Palmeira dos Índios   | 1                 |
| Poco das Trincheiras  | 1                 |
| Santana do Ipanema    | 3                 |
| São José da Laje      | 1                 |
| São Miguel dos Campos | 1                 |
| TOTAL                 | 90                |

These data suggest the introduction of the previously mentioned variants in these municipalities. However, the fact that the number of cases was 2.25 times higher in an inland municipality compared to the capital, Maceió, is surprising. The distribution of COVID-19 cases in smaller municipalities, such as Santos Dumont, indicates that non-healthcare professionals faced higher risks, suggesting occupational exposure as a contributing factor [16, 17].

Although a higher number of cases in a smaller municipality compared to a capital city like Maceió may seem unexpected, it highlights the importance of considering local socioeconomic, demographic, and infrastructure factors. These elements can significantly influence the spread and management of infectious diseases, emphasizing the need for tailored public health strategies [17, 18].



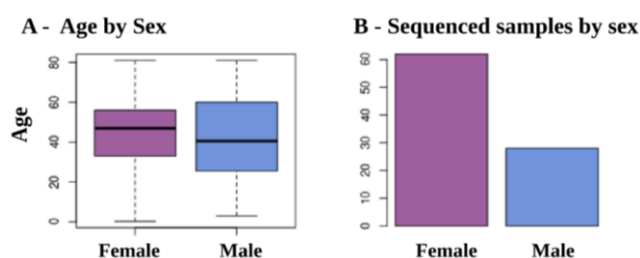
**Figure 2.** Geographical distribution of SARS-CoV-2 positive samples in Alagoas from December 2022 to January 2023.

During the period of December 2022 to January 2023, no SARS-CoV-2 sequencing was conducted at LACEN-AL. However, 90 samples collected in December 2022 were sent for sequencing at the Laboratory of Respiratory and Measles Viruses (LVRS) of the Oswaldo Cruz Institute (IOC), a national reference institute for coronaviruses under the Ministry

of Health and a regional reference for the World Health Organization. The sequenced genomes and their metadata were retrieved from the GISAID database [7].

The genome assembly was performed using the ViralFlow pipeline [11], which is utilized by the FIOCRUZ Genomic Network. Lineage assignment was carried out using the PangoLineages software (<https://github.com/cov-lineages/pangolin>), based on the information available in GISAID [7].

As shown in Figure 3A, the majority of the sequenced SARS-CoV-2 genomes were from female hosts (62 genomes). Regarding age distribution, most cases were observed in individuals aged between 20 and 60 years (Figure 3B). These findings align with the overall sample distribution observed at LACEN-AL, as previously presented in Figure 4.



**Figure 3.** A. Average age by sex of the hosts of the sequenced genomes. B. Number of cases by sex.

The predominance of SARS-CoV-2 genomes sequenced from female individuals may reflect a sampling bias, possibly influenced by higher testing rates or greater adherence of women to testing programs [19, 20]. The 20–60 age range encompasses the economically active population, suggesting higher exposure to the virus [21]. While these data align with the overall trends observed at LACEN-AL, their representativeness should be analyzed in comparison with broader epidemiological trends. Further age stratification could provide more detailed insights. Additionally, understanding these patterns is essential for improving genomic surveillance strategies and public health interventions [22].



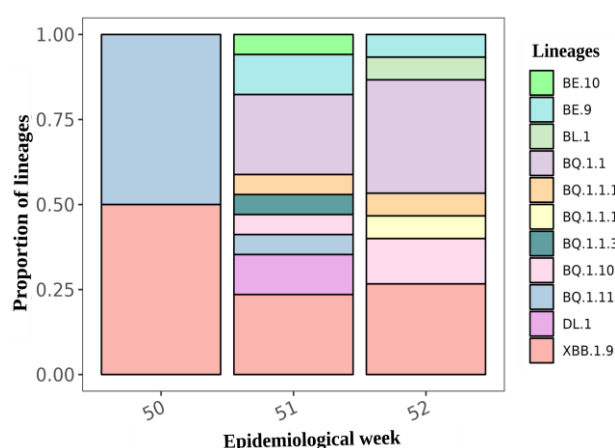
**Figure 4.** Geographical distribution of sequenced genomes in December 2022 and January 2023.

Regarding geographical distribution, samples from 16 municipalities were sequenced. Of the 90 genomes, 67 were collected in Arapiraca, while the remaining samples were collected in Maceió (4), Dois Riachos (3), Santana do Ipanema (3), Maragogi (2), Anadia (1), Campestre (1), Canapi (1), Delmiro Gouveia (1), Major Isidoro (1), Monteirópolis (1), Palmeira dos Índios (1), Poço das Trincheiras (1), São José da Laje (1), São Miguel dos Campos (1), and União dos Palmares (1). The higher percentage of sequenced samples from Arapiraca is related to the elevated number of cases detected in the municipality during January.

According to Figure 5 which presents the proportion of sublineages per epidemiological week, 11 variants were identified in the analyzed genome sequences, following the dynamic nomenclature proposed for SARS-CoV-2 lineages. In the 50th epidemiological week of 2022, two sublineages of the Omicron lineage were detected in samples collected in Arapiraca, BQ.1.11 and XBB.1.9; however, only two genomes were sequenced during this period.

Subsequently, in the 51st epidemiological week, 56 genomes were sequenced, of which 39 were collected in Arapiraca. The detected sublineages were: BE.10 (2), BE.9 (3), BQ.1.1 (22), BQ.1.1.11 (1), BQ.1.1.32 (1), BQ.1.10.1 (1), BQ.1.11 (1), DL.1 (5), and XBB.1.9 (20). The variants BE.10, BQ.1.11, and BQ.1.10.1 were detected only in Arapiraca, whereas BQ.1.1.32 was detected in Santana do Ipanema.

In the 52nd epidemiological week, 32 genomes were sequenced, detecting the sublineages BE.9 (1), BL.1 (1), BQ.1.1 (10), BQ.1.1.11 (1), BQ.1.1.18 (1), BQ.1.10.1 (2), and XBB.1.9 (16). Among these, BE.9, BL.1, BQ.1.1.11, and BQ.1.1.18 were detected only in Arapiraca. Additionally, 26 out of the 32 sequenced genomes were collected in the municipality of Arapiraca.



**Figure 5.** Proportion of lineages by epidemiological week in December 2022 and January 2023.

The data show that 78 out of the 90 sequenced genomes belong to the BQ and XBB sublineages. These results align with the national trend, where these sublineages predominate.



This predominance is attributed to their enhanced immune evasion properties, caused by additional mutations in the SARS-CoV-2 Spike protein, such as the R346T mutation in BQ.1.1 and the additional G252V mutation in XBB.1, which contribute to their rapid expansion [15, 23].

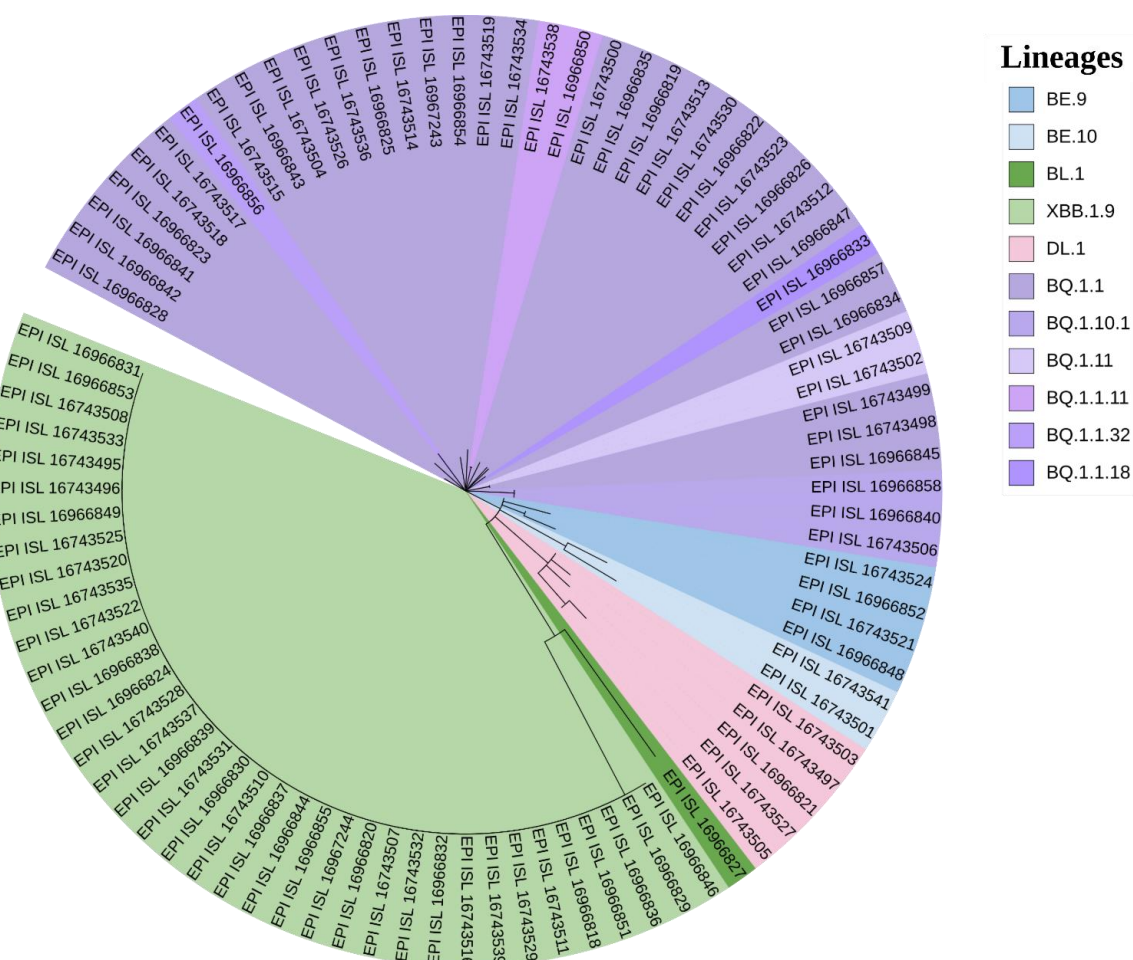
In Alagoas, according to GISAID data [7], BQ.1.1 was first detected on October 19, 2022, and by November, it accounted for more than 63% of the sequenced genomes (37 out of 58). The first records of XBB.1.9 appeared on December 16, 2022 (50th epidemiological week).

As reported by Wang et al. [15], in addition to additional mutations, the spike protein of BQ harbors the K444T and N460K mutations, along with those found in BA.5. Meanwhile, XBB carries 14 mutations in addition to those present in BA.2. The authors also highlight that the emergence of these variants is similar to the first case of Omicron in 2022, raising concerns that they may further compromise the effectiveness of COVID-19 vaccines. Popovic [24] states that the

BQ and XBB sublineages have pathogenicity identical to BA.2.75. However, their infectivity is higher than that of previous sublineages [15, 25].

The sublineages BE.9, BE.10, BL.1, and DL.1 are sublineages of the Omicron variant and are primarily found in Brazil, except for BL.1, which has been mainly reported in India. BE.10 presents mutations in the Spike (S) protein, K444T and N460K, while DL.1 carries the S:R346T mutation and has also been widely detected in the United States [26-28].

According to the PangoLineages classification, the sublineages BE.10 and BL.1 were initially identified in January 2022, whereas BE.9 and DL.1 were first reported in September 2022 and are currently observed in small percentages. This pattern occurs due to the gradual replacement of sublineages as new ones emerge. The XBB.1.9 sublineage carries mutations in ORF1a:G1819S and ORF1a:T4175I, in addition to those previously described for XBB [29].



**Figure 6.** Phylogenetic tree of sequenced genomes in December 2022 and January 2023.

The phylogenetic tree in [Figure 6](#) was generated using the IQ-TREE2 v2.0.7 software [12] and visualized through the online tool iTOL [13]. The tree represents Omicron sublineages using different colors: BQ (purple), BE (blue), DL.1

(pink), BL.1 (dark green), and XBB.1.9 (light green). The branching pattern illustrates the evolutionary differences in the consensus sequence among the samples [30].

The phylogenetic tree in [Figure 6](#) was generated using the

IQ-TREE2 v2.0.7 software [12] and visualized through the online tool iTOL [13]. The tree represents Omicron sublineages using different colors: BQ (purple), BE (blue), DL.1 (pink), BL.1 (dark green), and XBB.1.9 (light green). The branching pattern illustrates the evolutionary differences in the consensus sequence among the samples [30].

The sublineages BQ.1.1, BQ.1.1.11, BQ.1.1.18, BQ.1.1.32, BQ.1.10.1, and BQ.1.11 evolved from the BA.5 lineage, while XBB.1.9 originated from BA.2.75 [31, 32]. This highlights that these two sublineages continue to evolve and diversify, accumulating an increasingly complex set of mutations in the Spike protein. Additionally, it is important to note that BQ and XBB share the R346T and N460K mutations, demonstrating their evolutionary convergence to evade antibodies targeting these Spike regions [31].

## 4. Conclusions

This study highlights the importance of automating SARS-CoV-2 genomic data retrieval and analysis, addressing the challenges associated with accessing and processing large datasets from GISAID. The proposed pipeline efficiently filters sequences based on metadata quality criteria, facilitating downstream analyses such as phylogenetic studies and mutation tracking. By reducing the manual workload and optimizing data acquisition, this approach contributes to more effective genomic surveillance of SARS-CoV-2.

Future research could explore the adaptation of this pipeline to other viral pathogens, enabling broader genomic monitoring efforts. Additionally, integrating machine learning algorithms for automated mutation detection and variant classification could further enhance its utility. Investigating the incorporation of cloud computing resources for handling large-scale genomic datasets may also provide new opportunities for improving the efficiency and scalability of genomic surveillance systems.

## Abbreviations

|            |  |
|------------|--|
| GISAID     | Global Initiative on Sharing Avian Influenza Data        |
| IOC        | Oswaldo Cruz Institute                                   |
| LACENs     | Central Public Health Laboratories                       |
| LACEN-AL   | Central Public Health Laboratory of the State of Alagoas |
| LVRs       | Respiratory Viruses and Measles Laboratory               |
| SARS-CoV-2 | Severe Acute Respiratory Syndrome Coronavirus 2          |
| WHO        | World Health Organization                                |

## Supplementary Material

The supplementary material can be accessed at

<https://doi.org/10.11648/j.xxxx.2024xxxx.xx>

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## Author Contributions

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**Magliones Carneiro de Lima:** Conceptualization, Data curation, Formal Analysis, Investigation, Methodology, Project administration, Software, Validation, Writing – original draft, Writing – review & editing

**Hazerral de Oliveira Santos:** Funding acquisition, Project administration, Supervision, Writing – review & editing

**Juliana Vanessa Cavalcante Souza:** Funding acquisition, Project administration, Supervision, Writing – review & editing

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**Sérgio de Sá Leitão Paiva Júnior:** Supervision, Writing – review & editing

**Valdir de Queiroz Balbino:** Supervision, Writing – review & editing

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## Data Availability Statement

The data that support the findings of this study can be found at: <https://gisaid.org/>

## Conflicts of Interest

The authors declare no conflicts of interest.

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