



Negative Binomial tv-DINGARCH Models for Monthly DHF Cases in Surabaya, Indonesia (2015–2025)

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Abstract

Count time series data are commonly encountered in epidemiological studies, including monthly reports of Dengue Hemorrhagic Fever (DHF) cases. This study analyzes 132 monthly observations spanning January 2015 to December 2025, obtained from the Surabaya City Health Office. INGARCH models have been widely used to account for temporal dependence and overdispersion. However, standard INGARCH models assume constant dispersion, whereas the dispersion level may vary over time because of epidemiological factors. This study applies a time-varying dispersion INGARCH (tv-DINGARCH) model to monthly DHF case counts in Surabaya. A tv-DINGARCH(1,1,1,1) model with a negative binomial distribution is employed, allowing ϕ_t to evolve dynamically. Parameters are estimated in R using conditional maximum likelihood estimation. The tv-DINGARCH model yields AIC and BIC values of 967.24 and 984.54, respectively, both lower than those of the standard INGARCH model (AIC = 1038.55 and BIC = 1050.08). The likelihood ratio test yields an LR statistic of 75.31 with a p -value below 0.000001, providing evidence against constant dispersion. The sum of the stationarity coefficients is $\beta_1 + \beta_2 + \alpha_1 + \alpha_2 = 0.9976$, which is close to the nonstationarity boundary and indicates high persistence. However, the Ljung–Box test of the residuals remains significant ($p < 0.05$), indicating that some temporal dependence is not fully captured. These findings suggest that, although the tv-DINGARCH model provides an improved in-sample fit, further refinement is needed.

Keywords: count time series; overdispersion; tv-DINGARCH; conditional maximum likelihood; dengue forecasting

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1. Introduction

The present study focuses on count time series analysis using the integer-valued generalized autoregressive conditional heteroscedastic (INGARCH) framework. The term “INGARCH” originates from the property of the Poisson distribution that its conditional mean and variance are equal, as documented in earlier studies [1–3]. Consequently, specifying the mean structure simultaneously determines the variance dynamics, analogous to the conventional GARCH model proposed by Bollerslev [4]. However, this terminology should be used with care because standard

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GARCH models capture time-varying volatility, whereas INGARCH models are designed for count data.

For $p, q \in \mathbb{N}$, the Poisson INGARCH(p, q) process $\{Y_t\}_{t \in \mathbb{Z}}$ is defined by

$$Y_t | \mathcal{F}_{t-1} \sim \text{Poisson}(\lambda_t), \quad \lambda_t \equiv E(Y_t | \mathcal{F}_{t-1}) = \beta_0 + \sum_{i=1}^p \beta_i Y_{t-i} + \sum_{j=1}^q \alpha_j \lambda_{t-j}, \quad (1)$$

where $\mathcal{F}_t = \sigma\{Y_s : s \leq t\}$, $\beta_0 > 0$, $\beta_i \geq 0$, and $\alpha_j \geq 0$. Because $E(Y_t | \mathcal{F}_{t-1}) = \text{Var}(Y_t | \mathcal{F}_{t-1}) = \lambda_t$, the model establishes a dynamic link between the conditional mean and variance.

In many practical settings, the degree of dispersion is not constant but changes over time. This poses a challenge for standard Poisson and negative binomial INGARCH models, which assume a constant dispersion parameter. To address this limitation, Barreto-Souza et al. [5] introduced the tv-DINGARCH model, which allows both the conditional mean and the dispersion parameter to evolve over time. The model is defined by

$$Y_t | \mathcal{F}_{t-1} \sim \text{MP}(\lambda_t, \phi_t), \quad \lambda_t = \beta_0 + \beta_1 Y_{t-1} + \beta_2 \lambda_{t-1}, \quad \phi_t = \alpha_0 + \alpha_1 Y_{t-1} + \alpha_2 \phi_{t-1}, \quad (2)$$

where $\beta_0, \alpha_0 > 0$, $\beta_1, \beta_2, \alpha_1, \alpha_2 \geq 0$, and MP denotes a mixed Poisson distribution. When the mixing component follows a gamma distribution, the negative binomial (NB) distribution is obtained, with $\text{Var}(Y_t | \mathcal{F}_{t-1}) = \lambda_t + \lambda_t^2 / \phi_t$. Thus, overdispersion can change over time because ϕ_t evolves dynamically. Count time series often exhibit two key features: overdispersion and time-varying volatility. The proposed model is better equipped than standard approaches to accommodate these characteristics because of its greater structural flexibility. Extensions and generalizations of INGARCH models have been widely explored in the literature, including flexible and robust mixed Poisson models [6], varying-dispersion models [7], zero-inflated Poisson and negative binomial INGARCH models [8], bivariate INGARCH processes [9], and systematic reviews [10]. In addition, quasi-likelihood inference [11] and time-varying autoregressive models [12] have been developed for count time series, while applications to dengue fever [13] and epidemic volatility [14] have also been explored. A preprint version of the tv-DINGARCH framework is available [15].

Time-varying dispersion is epidemiologically meaningful for DHF in Surabaya because dengue transmission is characterized by complex dynamics influenced by seasonal rainfall patterns, temperature fluctuations, vector-control interventions, and population immunity. During periods of high transmission, such as the rainy season, variability in case counts tends to increase because of heterogeneous exposure, reporting delays, and localized outbreaks. Conversely, during low-transmission periods, case counts tend to be more stable and less variable. Standard INGARCH models assume constant dispersion and therefore ignore this phenomenon. Capturing time-varying dispersion may help public health officials anticipate periods of heightened uncertainty in disease incidence, which is important for resource allocation and outbreak preparedness. For example, if the dispersion coefficient α_1 is estimated to be positive and significant, a surge in cases in the previous month would indicate not only a higher expected number of cases but also greater uncertainty in the current month's case count.

Although the tv-DINGARCH model has been applied to measles data in Germany [5], its application to DHF data in an endemic Indonesian setting remains unexplored. Previous studies of DHF in Indonesia have employed seasonal ARIMA models [16] and GSTAR models [17] for Surabaya, as well as SARIMA models [18] for Malang, to capture temporal patterns. However, these approaches assume constant variance and do not accommodate time-varying overdispersion. Other studies have applied standard INGARCH models to dengue data in other regions, but none have considered the possibility that the dispersion parameter may itself evolve over time in response to changing epidemiological conditions. To the best of our knowledge, no previous study has applied the tv-DINGARCH model to DHF case data in Indonesia, particularly in Surabaya. Unlike previous approaches that assume constant variance, the tv-DINGARCH

model allows both the mean and dispersion to evolve dynamically, providing a more flexible framework for understanding DHF transmission dynamics. Therefore, this study applies a tv-DINGARCH(1,1,1,1) model with a negative binomial distribution to DHF cases in Surabaya over the period 2015–2025.

The main contributions of this study are threefold. First, unlike previous studies employing ARIMA, GSTAR, or SARIMA models that assume constant variance, this study provides empirical evidence of time-varying overdispersion in DHF transmission dynamics in Surabaya using the tv-DINGARCH framework. Second, it evaluates the tv-DINGARCH model against the standard INGARCH model using the Akaike information criterion (AIC), Bayesian information criterion (BIC), and a likelihood ratio test. Third, it compares the in-sample fit of the two models to determine which specification better captures the dynamics of DHF case counts.

The remainder of this paper is organized as follows. Section 2 describes the tv-DINGARCH methodology, including the stationarity conditions, parameter estimation via CMLE, Monte Carlo simulations, and the test for constant dispersion. Section 3 presents the empirical results for the DHF data from Surabaya, including model comparisons, PIT plots, and forecasting results. Section 4 concludes the study by summarizing the findings and providing recommendations for future research.

2. Methods

This section presents the methodological framework used in the study. First, the tv-DINGARCH model is formally introduced, followed by its stationarity and ergodicity properties. The conditional maximum likelihood estimation procedure and the design of the Monte Carlo simulation study are then described. The section concludes with a discussion of the bootstrap procedures used to test for constant dispersion.

2.1. The tv-DINGARCH Model

The time-varying dispersion INGARCH (tv-DINGARCH) model employed in this study follows the definition provided by Barreto-Souza et al. [5]. A tv-DINGARCH(1,1,1,1) process with a negative binomial distribution is defined as follows.

A linear tv-DINGARCH(1,1,1,1) process $\{Y_t\}_{t \in \mathbb{N}_0}$ satisfies

$$Y_t | \mathcal{F}_{t-1} \sim \text{MP}(\lambda_t, \phi_t; D),$$

$$\lambda_t = \beta_0 + \beta_1 Y_{t-1} + \beta_2 \lambda_{t-1}, \quad (3)$$

$$\phi_t = \alpha_0 + \alpha_1 Y_{t-1} + \alpha_2 \phi_{t-1}, \quad (4)$$

where $\mathcal{F}_t = \sigma\{Y_s : s \leq t\}$, $\beta_0, \alpha_0 > 0$, $\beta_1, \beta_2, \alpha_1, \alpha_2 \geq 0$, and MP denotes a mixed Poisson distribution. Mixed Poisson INGARCH models have been studied extensively, including flexible and robust versions [6], varying-dispersion models [7], and zero-inflated extensions [8].

The mixed Poisson distribution is defined hierarchically as follows. Let D be a mixing distribution with mean 1 and variance $1/\phi_t$. Then

$$\Lambda_t | \mathcal{F}_{t-1} \sim D \left(\text{mean} = \lambda_t, \text{variance} = \lambda_t^2 / \phi_t \right),$$

$$Y_t | \Lambda_t, \mathcal{F}_{t-1} \sim \text{Poisson}(\Lambda_t).$$

The resulting marginal distribution of Y_t , conditional on $\mathcal{F}_{t-1}$, is a mixed Poisson distribution. Of particular interest in this study is the negative binomial (NB) model, which is obtained when the mixing distribution D is gamma. Specifically, if $\Lambda_t \sim \text{Gamma}(\text{shape} = \phi_t, \text{rate} = \phi_t / \lambda_t)$, then, marginally,

$$Y_t | \mathcal{F}_{t-1} \sim \text{NB}(\text{mean} = \lambda_t, \text{dispersion} = \phi_t).$$

Accordingly, the conditional probability mass function of Y_t , given $\mathcal{F}_{t-1}$, is

$$P(Y_t = y \mid \mathcal{F}_{t-1}) = \frac{\Gamma(y + \phi_t)}{y! \Gamma(\phi_t)} \left(\frac{\lambda_t}{\lambda_t + \phi_t} \right)^y \left(\frac{\phi_t}{\lambda_t + \phi_t} \right)^{\phi_t}, \quad y \in \mathbb{N}_0. \quad (5)$$

The negative binomial distribution is selected because its dispersion parameter ϕ_t can be modeled dynamically. The conditional mean is $E(Y_t \mid \mathcal{F}_{t-1}) = \lambda_t$, and the conditional variance is $\text{Var}(Y_t \mid \mathcal{F}_{t-1}) = \lambda_t + \lambda_t^2 / \phi_t$. A small value of ϕ_t indicates substantial overdispersion, whereas the model approaches the Poisson INGARCH model as $\phi_t \rightarrow \infty$.

The tv-DINGARCH framework yields several simpler model specifications under particular parameter restrictions. For example, imposing $\alpha_1 = \alpha_2 = 0$ recovers the standard linear mixed Poisson INGARCH model. If $\beta_1 = \beta_2 = 0$, the pure INGARCH (P-INGARCH) model is obtained. This model has a constant mean and time-varying variance, analogous to the classical GARCH model [4].

2.2. Stationarity and Ergodicity

To investigate the stationarity properties of the tv-DINGARCH process, Barreto-Souza et al. [5] express the latent processes λ_t and ϕ_t in vector form. Defining $\xi_t = (\lambda_t, \phi_t)^\top$, $\tau = (\beta_0, \alpha_0)^\top$, $\mathbf{A} = \text{diag}(\beta_2, \alpha_2)$, and $\mathbf{B} = \text{diag}(\beta_1, \alpha_1)$, the process $\{\xi_t\}$ can be represented as $\xi_t = \tau + \mathbf{B}(Y_{t-1}, Y_{t-1})^\top + \mathbf{A}\xi_{t-1}$.

According to Barreto-Souza et al. [5, Theorem 1], if the spectral radius $\rho(\mathbf{A} + \mathbf{B}) < 1$, then the process $\{\xi_t\}$ has at least one stationary distribution. For the first-order case, this condition simplifies to $\beta_2 + \alpha_2 + \beta_1 + \alpha_1 < 1$, which is the stationarity condition used in this study. Furthermore, a stronger condition is required to guarantee ergodicity and the geometric moment contraction (GMC) property: $\|\mathbf{A}\|_p + 2^{1-1/p}\|\mathbf{B}\|_p < 1$ for some $p \in [1, \infty]$. For $p = 1$, this ergodicity condition becomes $\beta_2 + \alpha_2 + 2(\beta_1 + \alpha_1) < 1$. The stationarity condition $\beta_2 + \alpha_2 + \beta_1 + \alpha_1 < 1$ is sufficient to ensure the consistency and asymptotic normality of the CMLE, as established by Barreto-Souza et al. [5, Theorem 3].

In addition to stationarity, Barreto-Souza et al. [5] establish moment boundedness for the tv-DINGARCH process. Their Theorem 2 states that if $\|\mathbf{A}\|_1 + \|\mathbf{B}\|_1 < 1$, then, for every natural number k , $E|Y_t|^k < \infty$, $E|\lambda_t|^k < \infty$, and $E|\phi_t|^k < \infty$. In other words, all moments of the tv-DINGARCH process are finite under the stationarity condition. The proof employs Tweedie's criterion for Markov chains and the recursive moment properties of the negative binomial distribution.

2.3. Parameter Estimation Using CMLE

Let $\theta_1 = (\beta_0, \beta_1, \beta_2)^\top$, $\theta_2 = (\alpha_0, \alpha_1, \alpha_2)^\top$, and $\theta = (\theta_1^\top, \theta_2^\top)^\top = (\beta_0, \beta_1, \beta_2, \alpha_0, \alpha_1, \alpha_2)^\top$ denote the parameter vector. Let $Y_1, \dots, Y_n$ be a sample from an NB tv-DINGARCH process. The conditional log-likelihood function of $Y_2, \dots, Y_n$, given $Y_1 = y_1$, is, up to an additive constant,

$$\ell(\theta) = \sum_{t=2}^n \ell_t(\theta), \quad (6)$$

where

$$\ell_t(\theta) = y_t [\log \lambda_t - \log(\lambda_t + \phi_t)] + \phi_t [\log \phi_t - \log(\lambda_t + \phi_t)] + \log \Gamma(y_t + \phi_t) - \log \Gamma(\phi_t),$$

for $t = 2, \dots, n$. The dependence of λ_t and ϕ_t on θ is suppressed for notational simplicity.

The computation of the log-likelihood function depends on the initial values λ_0 and ϕ_0 . Denoting the initial values of the latent processes by $\tilde{\lambda}_0$ and $\tilde{\phi}_0$, the observed log-likelihood function is given by

$$\tilde{\ell}(\theta) = \sum_{t=2}^n \tilde{\ell}_t(\theta), \quad (7)$$

where

$$\tilde{\ell}_t(\theta) = y_t \left[\log \tilde{\lambda}_t - \log(\tilde{\lambda}_t + \tilde{\phi}_t) \right] + \tilde{\phi}_t \left[\log \tilde{\phi}_t - \log(\tilde{\lambda}_t + \tilde{\phi}_t) \right] + \log \Gamma(y_t + \tilde{\phi}_t) - \log \Gamma(\tilde{\phi}_t),$$

with $\tilde{\lambda}_t = \beta_0 + \beta_1 Y_{t-1} + \beta_2 \tilde{\lambda}_{t-1}$ and $\tilde{\phi}_t = \alpha_0 + \alpha_1 Y_{t-1} + \alpha_2 \tilde{\phi}_{t-1}$.

The conditional maximum likelihood estimator (CMLE) of θ , denoted by $\hat{\theta}$, is given by

$$\hat{\theta} = \arg \max_{\theta \in \Theta} \tilde{\ell}(\theta), \quad (8)$$

where $\Theta = (0, \infty) \times [0, \infty)^2 \times (0, \infty) \times [0, \infty)^2$ denotes the parameter space.

The initial values $\tilde{\lambda}_0^{(0)}$ and $\tilde{\phi}_0^{(0)}$ are set to their unconditional means under the stationarity assumption, namely, $\tilde{\lambda}_0^{(0)} = \beta_0/(1 - \beta_2)$ and $\tilde{\phi}_0^{(0)} = \alpha_0/(1 - \alpha_2)$. These values serve only as numerical starting points for the L-BFGS-B optimization algorithm. They are updated recursively during the estimation procedure and are not expected to materially affect the final parameter estimates, provided that the stationarity conditions are satisfied and the optimization algorithm converges successfully. This approach avoids the potential bias associated with using the sample mean and sample variance as initial values.

Estimation was performed in the R environment using the L-BFGS-B optimization algorithm, with the maximum number of iterations set to 1000 and the tolerance parameter **factr** set to 10^7 . Non-negativity constraints were imposed on all parameters, and the stationarity condition $\beta_2 + \alpha_2 + \beta_1 + \alpha_1 < 1$ was enforced throughout the optimization. The Hessian matrix was computed numerically to obtain standard errors, enabling the construction of confidence intervals. Convergence was successfully achieved for all estimated models, and no parameter estimates reached the boundary constraints, indicating stable and reliable estimation. Quasi-likelihood inference for negative binomial time series models is discussed in [11].

2.4. Monte Carlo Simulation

The finite-sample behavior of the CMLE for the NB tv-DINGARCH(1,1,1,1) model was investigated through a Monte Carlo study comprising 1000 replications for trajectory lengths of $n = 500$ and $n = 1000$. Two parameter configurations, derived from the actual DHF data, were used to represent high-case and low-case conditions:

Setting I (high-case): $(\beta_0, \alpha_0, \beta_1, \beta_2, \alpha_1, \alpha_2)^\top = (4.00, 0.34, 0.81, 0.00, 0.11, 0.07)^\top$.

Setting II (low-case): $(\beta_0, \alpha_0, \beta_1, \beta_2, \alpha_1, \alpha_2)^\top = (2.00, 0.17, 0.41, 0.01, 0.05, 0.03)^\top$.

Stationarity and uniqueness of the simulated tv-DINGARCH processes were ensured by verifying that $\beta_2 + \alpha_2 + \beta_1 + \alpha_1 < 1$. For Setting I, this condition gives $0.81 + 0.00 + 0.11 + 0.07 = 0.99 < 1$; for Setting II, it gives $0.41 + 0.01 + 0.05 + 0.03 = 0.49 < 1$. Thus, both configurations satisfy the stationarity requirement. All results were obtained using restricted optimization to enforce the stationarity condition during parameter estimation.

The results for Settings I and II are summarized in Table 1. The empirical Monte Carlo means are consistently close to the true parameter values, and the standard deviations decrease as the sample size increases, supporting the consistency of the CMLE.

Evidence of the asymptotic normality of the CMLEs for Setting I is provided in Figure 1. Nonparametric density estimates of the standardized parameters are plotted alongside the standard Gaussian density, represented by the solid line. The dashed and dotted curves represent the estimated densities for sample sizes of $n = 500$ and $n = 1000$, respectively. Although the estimated density curves overlap substantially, a modest improvement in estimation accuracy is evident as the sample size increases.

2.5. Testing Constant Dispersion

A Monte Carlo study was conducted to assess restricted and unrestricted bootstrap procedures for testing constant dispersion. Under H_0 , 200 observations were generated from the NB tv-DINGARCH process, with 500 Monte Carlo replications and $B = 500$ bootstrap replications. Four parameter configurations were considered, as shown in Table 2.

Table 1: Monte Carlo estimates (empirical means and standard deviations) for the NB tv-DINGARCH model parameters under Settings I and II.

Setting I		$\beta_0 = 4.00$	$\alpha_0 = 0.34$	$\beta_1 = 0.81$	$\beta_2 = 0.00$	$\alpha_1 = 0.11$	$\alpha_2 = 0.07$
$n = 500$	Mean	3.9262	0.3494	0.7881	0.0227	0.1081	0.0899
	SD	0.6286	0.1002	0.0397	0.0339	0.0152	0.0949
$n = 1000$	Mean	3.9046	0.3473	0.7952	0.0165	0.1094	0.0779
	SD	0.4299	0.0714	0.0286	0.0240	0.0117	0.0698
Setting II		$\beta_0 = 2.00$	$\alpha_0 = 0.17$	$\beta_1 = 0.41$	$\beta_2 = 0.01$	$\alpha_1 = 0.05$	$\alpha_2 = 0.03$
$n = 500$	Mean	1.9149	0.1619	0.3947	0.0483	0.0501	0.0689
	SD	0.3420	0.0297	0.0649	0.0796	0.0110	0.0928
$n = 1000$	Mean	1.9389	0.1655	0.4012	0.0374	0.0495	0.0541
	SD	0.2357	0.0212	0.0457	0.0569	0.0074	0.0635

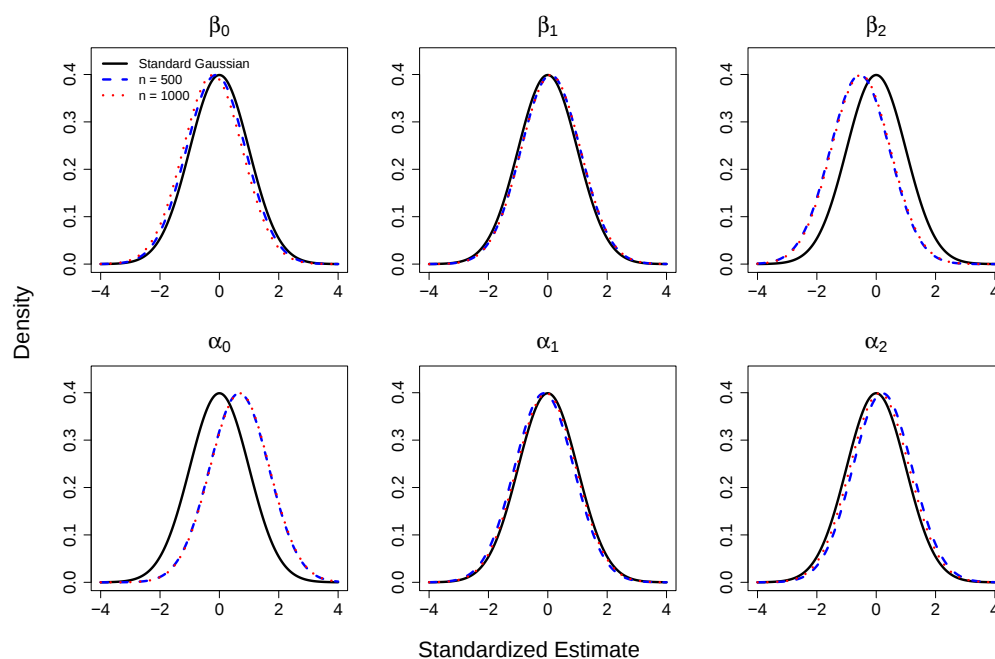


Fig. 1: Kernel density plots of standardized estimates from Setting I for $n = 500$ and $n = 1000$. The solid line shows the standard Gaussian density function.

As shown in Table 2, for configuration C1, characterized by large mean effects ($\beta_1 = 0.81$, $\beta_2 = 0.00$), the restricted bootstrap yielded a rejection rate of 0.40 at the 5% nominal level, compared with 0.50 for the unrestricted bootstrap. At the 1% nominal level, the corresponding rejection rates were 0.18 and 0.50, respectively. Both procedures overestimated the significance level, with the unrestricted bootstrap showing a more pronounced overestimation.

For configuration C2, characterized by smaller mean effects ($\beta_1 = 0.41$, $\beta_2 = 0.01$), the restricted and unrestricted bootstrap procedures produced rejection rates of 0.04 and 0.06, respectively, at the 5% level, both of which are close to the nominal level. For configuration C3, the restricted bootstrap yielded rejection rates of 0.60 at the 5% level and 0.45 at the 1% level, whereas the unrestricted bootstrap yielded a rejection rate of 0.75 at both levels. For configuration C4, with very small mean effects ($\beta_1 = 0.20$, $\beta_2 = 0.00$), the restricted bootstrap yielded rejection rates of 0.04 at the 5% level and 0.00 at the 1% level, closely approximating the nominal values.

Overall, the simulation results indicate that the unrestricted bootstrap consistently yields higher rejection rates than the restricted bootstrap, particularly in configurations with pronounced

Table 2: Achieved significance levels of the likelihood ratio test for constant dispersion using restricted and unrestricted bootstrap procedures.

Configuration	Nominal Level	Restricted Bootstrap	Unrestricted Bootstrap
C1: $\beta_0 = 4.00, \alpha_0 = 0.34$	0.05	0.40	0.50
$\beta_1 = 0.81, \beta_2 = 0.00$	0.01	0.18	0.50
C2: $\beta_0 = 2.00, \alpha_0 = 0.17$	0.05	0.04	0.06
$\beta_1 = 0.41, \beta_2 = 0.01$	0.01	0.00	0.06
C3: $\beta_0 = 3.50, \alpha_0 = 0.25$	0.05	0.60	0.75
$\beta_1 = 0.70, \beta_2 = 0.20$	0.01	0.45	0.75
C4: $\beta_0 = 1.00, \alpha_0 = 0.05$	0.05	0.04	0.06
$\beta_1 = 0.20, \beta_2 = 0.00$	0.01	0.00	0.06

mean effects (C1 and C3). As discussed by Cavaliere, Nielsen, and Rahbek [19], the classical unrestricted bootstrap is not valid when parameters lie on the boundary of the parameter space. Because the DHF data exhibit strong mean effects, the bootstrap p -value should be interpreted with caution. We therefore rely primarily on the AIC and BIC comparisons and on asymptotic theory [15].

3. Results and Discussion

This section presents the empirical findings of the study. It begins with a descriptive analysis of the DHF case data, followed by the parameter estimation results for the *tv*-DINGARCH and standard INGARCH models. The predictive calibration of the competing models is then evaluated using probability integral transform (PIT) plots, and their forecasting performance is assessed using RMSFE. The section concludes with a comparative discussion of the two models.

3.1. Analysis of Dengue Hemorrhagic Fever Case Data

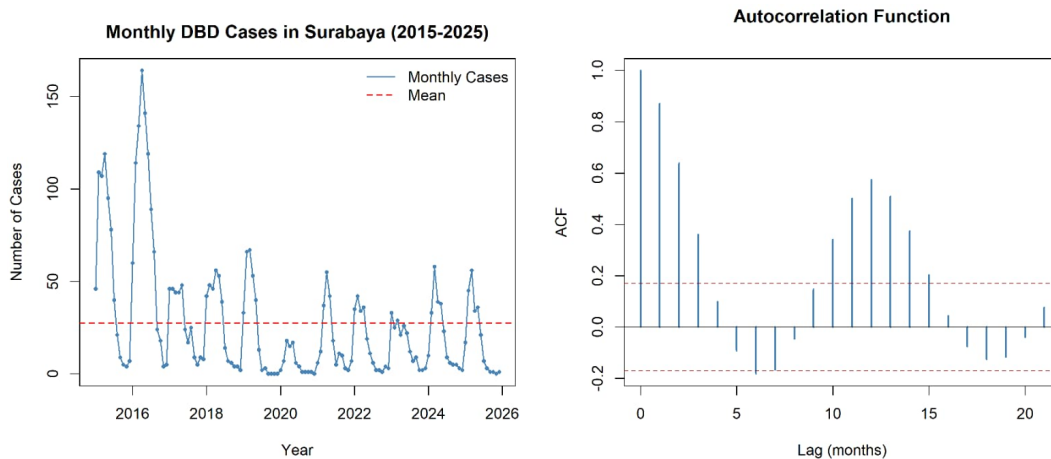


Fig. 2: Monthly DHF cases reported in Surabaya, Indonesia, from 2015 to 2025 (left) and the autocorrelation function of the series (right).

To illustrate the practical utility of the *tv*-DINGARCH framework, this study applies the model to monthly Dengue Hemorrhagic Fever (DHF) case counts recorded in Surabaya, Indonesia, from January 2015 to December 2025. The dataset consists of 132 monthly observations obtained from the Surabaya City Health Office. Two competing specifications are compared: the *tv*-DINGARCH model, which permits time-varying dispersion, and the standard INGARCH model, which assumes a constant dispersion parameter. Both models have the same mean structure; therefore, the comparison is based solely on their dispersion dynamics.

The left panel of Figure 2 displays the monthly DHF case counts in Surabaya from January 2015 to December 2025. The series exhibits substantial fluctuations, reaching a maximum of 164 cases in April 2016. The right panel presents the autocorrelation function (ACF) of the series, which shows significant autocorrelation at lags 1 and 2 and therefore indicates strong temporal dependence.

The sample variance of the series is 1083.47, and the sample mean is 27.43, yielding a variance-to-mean ratio of 39.50. This value substantially exceeds 1, confirming extreme overdispersion in the DHF case counts and motivating the use of a negative binomial distribution.

3.2. Parameter Estimation Results

The parameter estimates obtained by conditional maximum likelihood estimation for both models are summarized in Table 3.

Table 3: Parameter estimates, standard errors, and 95% confidence intervals for the $\mathcal{M}_{tv}$ and $\mathcal{M}_{ord}$ models fitted to monthly DHF case counts in Surabaya, Indonesia.

Parameter	tv-DINGARCH		INGARCH	
	Estimate (SE)	95% CI	Estimate (SE)	95% CI
β_0	3.4319 (0.4299)	(2.5893, 4.2745)	3.8288 (1.9078)	(0.0894, 7.5682)
β_1	0.6074 (0.0286)	(0.5513, 0.6634)	0.8754 (0.2463)	(0.3927, 1.3581)
β_2	0.2158 (0.0240)	(0.1687, 0.2628)	0.0000 (0.2282)	(0.0000, 0.4473)
α_0	0.3900 (0.0714)	(0.2501, 0.5300)	0.9619	
α_1	0.0705 (0.0117)	(0.0475, 0.0934)	—	
α_2	0.1039 (0.0698)	(0.0000, 0.2407)	—	

The log-likelihood of the tv -DINGARCH model was -477.6213 , whereas that of the standard INGARCH model was -515.2761 . The tv -DINGARCH model yielded AIC and BIC values of 967.2426 and 984.5394, respectively, whereas the standard INGARCH model yielded AIC = 1038.5523 and BIC = 1050.0835.

The estimated parameters provide important epidemiological insights. The coefficient $\beta_1 = 0.6074$ (95% CI: 0.5513, 0.6634) is statistically significant, indicating that the number of DHF cases in the previous month has a strong positive effect on the current conditional mean. The dispersion equation yields a significant coefficient of $\alpha_1 = 0.0705$ (95% CI: 0.0475, 0.0934), providing evidence that overdispersion increases after months with high case counts. The stationarity condition is satisfied because $\beta_1 + \beta_2 + \alpha_1 + \alpha_2 = 0.9976 < 1$.

A likelihood ratio test was conducted to assess $H_0 : \alpha_1 = \alpha_2 = 0$ (constant dispersion) against H_1 : at least one of α_1 and α_2 is nonzero. Under the null hypothesis, the test statistic asymptotically follows a χ^2 distribution with 2 degrees of freedom. The test yielded an LR statistic of 75.31 with an asymptotic p -value below 0.000001, leading to rejection of the null hypothesis. Although bootstrap procedures were considered in the simulation study in Section 2.5, the asymptotic p -value is reported here based on the sample size ($n = 132$) and the CMLE performance observed in the Monte Carlo simulations in Table 1, which support the use of the asymptotic approximation for this dataset.

The lower AIC and BIC values of the tv -DINGARCH model indicate a better in-sample fit than the standard INGARCH model. The likelihood ratio test also provides evidence that the dispersion parameter varies over time, suggesting that the tv -DINGARCH model is more appropriate for this dataset.

3.3. Predictive Calibration: PIT Plots

Probability integral transform (PIT) plots were generated to assess the predictive calibration of both models. For count data, the randomized PIT approach proposed by Czado, Gneiting, and Held [20] was employed to account for the discrete nature of the observations. The randomized PIT is defined as $u_t = F(y_t | \mathcal{F}_{t-1}) + v_t f(y_t | \mathcal{F}_{t-1})$, where $v_t \sim \text{Uniform}(0, 1)$, F is the conditional

cumulative distribution function, and f is the conditional probability mass function. Under a correctly specified model, the randomized PIT values should be uniformly distributed on $(0, 1)$.

The PIT plot for the standard INGARCH model exhibited a pronounced inverted U-shaped pattern, suggesting that the constant-dispersion assumption does not adequately account for the overdispersion in the data. In contrast, the PIT plot for the tv-DINGARCH model was closer to uniformity. A Kolmogorov–Smirnov test for uniformity yielded a p -value of 0.08 for the tv-DINGARCH model, compared with $p < 0.01$ for the standard INGARCH model, indicating improved, although still imperfect, calibration of the tv-DINGARCH specification.

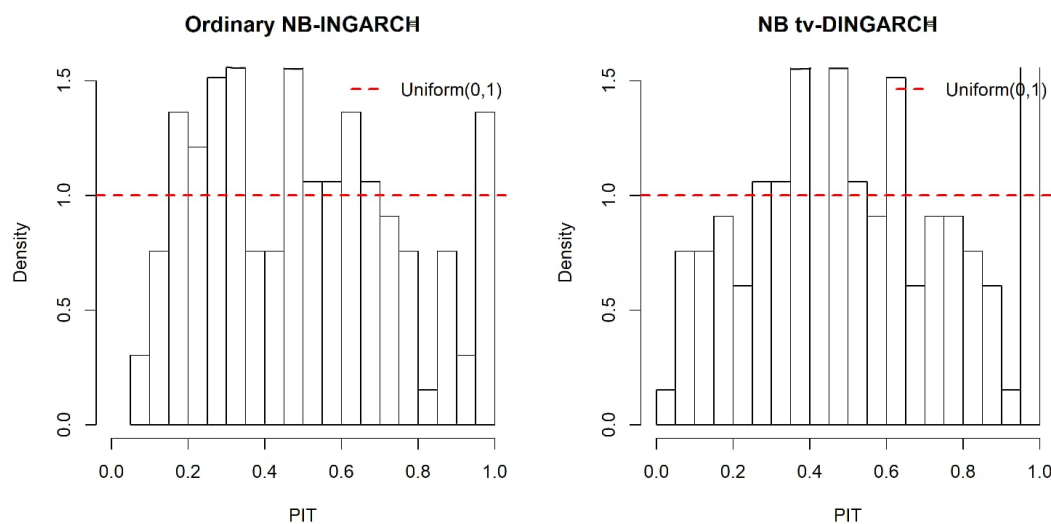


Fig. 3: PIT plots for $\mathcal{M}_{ord}$ (left) and $\mathcal{M}_{tv}$ (right).

3.4. Forecasting Performance and RMSFE

Table 4: Selected 12-month-ahead forecasts for Surabaya DHF cases using the tv-DINGARCH model, with prediction intervals accounting for parameter uncertainty and process variability.

Month	Mean Prediction	Median	95% Prediction Interval
1	4.28	3	(0, 14)
6	16.63	9	(0, 82)
12	28.24	10	(0, 150)

To evaluate the predictive capability of the competing models, a recursive one-step-ahead forecasting exercise was conducted using a rolling-window approach. The first 120 observations, from January 2015 to December 2024, were used for training, and the remaining 12 observations, from January to December 2025, were used for testing. Predictions were obtained using both the mean and median of the predictive distribution. Table 4 presents selected forecasts from the tv-DINGARCH model for forecast months 1, 6, and 12. The widening prediction intervals reflect increasing uncertainty at longer horizons; for month 12, the interval ranges from 0 to 150 cases, indicating very high forecast uncertainty.

Table 5: Out-of-sample forecasting performance (RMSFE) for one-step-ahead predictions based on a rolling window with 120 training observations and 12 test observations (January 2025–December 2025).

Model	Mean Prediction	Median Prediction
tv-DINGARCH	19.46	18.51
Standard INGARCH	12.59	12.48

The RMSFE values presented in Table 5 show that the standard INGARCH model outperforms

the tv-DINGARCH model over the 12-month test period. Thus, although the tv-DINGARCH model provides a better in-sample fit, as measured by the AIC, BIC, and likelihood ratio test, its out-of-sample forecasts are less accurate over this particular test period than those of the simpler INGARCH model. For both models, median predictions yield smaller RMSFE values than mean predictions, reflecting the robustness of the median to the skewed predictive distributions typical of overdispersed count data.

The progressive widening of the prediction intervals in Table 4 as the forecast horizon increases reflects the substantial overdispersion and inherent uncertainty in the DHF data. In particular, the interval for month 12 ranges from 0 to 150 cases, indicating extremely high forecast uncertainty. This uncertainty limits the practical strength of the forecasting results and suggests that further model refinement is needed before either model can be recommended for operational early warning systems.

In summary, the analysis of the Surabaya DHF case data indicates that the tv-DINGARCH model provides a better in-sample fit and better predictive-distribution calibration than the standard INGARCH model. However, the out-of-sample results show that the standard INGARCH model achieves a lower RMSFE over this particular test period, while the wide prediction intervals from the tv-DINGARCH model indicate substantial uncertainty. These findings suggest that further refinement, such as the incorporation of seasonal components or external covariates, is necessary.

4. Conclusion

Based on the analysis of DHF case data in Surabaya from 2015 to 2025, several conclusions can be drawn. The data exhibit extreme overdispersion, with a variance-to-mean ratio of 39.50, as well as significant temporal dependence. The NB tv-DINGARCH(1,1,1,1) model was successfully estimated and satisfied the stationarity condition, with $\beta_1 + \beta_2 + \alpha_1 + \alpha_2 = 0.9976 < 1$; however, this value is close to the nonstationarity boundary, indicating high persistence.

The likelihood ratio test ($LR = 75.31$, $p < 0.000001$) rejected the null hypothesis of constant dispersion, indicating that the dispersion parameter evolves dynamically. The information criteria consistently favored the tv-DINGARCH model, with $AIC = 967.24$ and $BIC = 984.54$, compared with $AIC = 1038.55$ and $BIC = 1050.08$ for the standard INGARCH model. The estimated parameters $\beta_1 = 0.6074$ and $\alpha_1 = 0.0705$ were statistically significant, indicating that past DHF cases influence both the conditional mean and the degree of overdispersion. The Monte Carlo simulations also supported the consistency of the CMLE.

However, the Ljung–Box test of the residuals remained significant ($p < 0.05$), indicating that the tv-DINGARCH(1,1,1,1) model does not fully capture the temporal dependence in the data. Future research may consider seasonal tv-DINGARCH models, higher-order lag structures, the inclusion of external covariates such as rainfall, temperature, humidity, and vector-control interventions, and out-of-sample validation using a clearly defined training–test split. Overall, although the tv-DINGARCH model provides a better in-sample fit than the standard INGARCH model for this dataset, the remaining residual dependence and near-boundary stationarity indicate that further refinement is necessary before the model can be recommended for operational early warning systems.

CRedit Authorship Contribution Statement

Aminatuz Zahro: Conceptualization, Methodology, Software, Data Curation, Writing–Original Draft, Visualization. **A’yunin Sofro:** Conceptualization, Methodology, Validation, Writing–Review.

Declaration of Generative AI and AI-Assisted Technologies

Generative AI was used solely for language editing and proofreading. The authors reviewed and verified the revised text and remain fully responsible for all content presented.

Declaration of Competing Interests

The authors declare that they have no competing interests.

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Data and Code Availability

The DHF case data examined in this study were obtained through a formal request submitted to the Surabaya City Health Office (Dinas Kesehatan Kota Surabaya). In accordance with institutional policies and confidentiality agreements, the dataset is not publicly available. The R code supporting the findings of this study is available from the corresponding author upon reasonable request.

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