Estimation of Semi Bilinear Time Series Models by the Method of Empirical Moments Specification of Optimal Noise by Deep Learning

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Main Objective

Our contribution in this presentation is based on modeling a sample of data using a type of nonlinear time series model, driven by the notion of a tool of topological data analysis, to extract mathematical features using shapes

Abstract

We develop estimation framework based on an alternative approach using empirical moments, specifically designed to overcome the limitations of classical methods in the face of the complexity of these hybrid structures. The objective is to provide an efficient, accurate, and computationally viable inference process for these models, where a linear autoregressive component and a nonlinear bilinear operator dynamically interact. Extensive numerical simulations rigorously validate the performance and robustness of our approach. The results demonstrate a marked superiority in terms of bias, variance, and stability of the proposed estimators, compared to conventional estimation techniques. This methodological advance opens promising application perspectives for the analysis of complex sequential data in demanding fields such as financial markets, economic forecasting, and big data analytics. A complementary and original investigation extends this contribution by examining the critical influence of the specification

Introduction

Deep learning is an advanced subfield of machine learning inspired by the structure of the human brain and its neural networks. Unlike traditional algorithms, deep learning uses multi-layered, hidden architectures (deep networks) capable of automatically learning hierarchical representations of data, from the simplest features to the most complex abstractions.

In real life, deep learning is ubiquitous, often without the user being aware of it. It powers voice assistants like Siri and Alexa, which convert speech into text. It enables self-driving cars to detect pedestrians and traffic signs. It is revolutionizing medicine by diagnosing diseases from radiological images with an accuracy that sometimes surpasses that of doctors. It is also at the heart of the recommendation systems of Netflix, Amazon, and TikTok, as well as the automatic translation of Google Translate, profoundly transforming our daily lives.

Deep learning

Definition

Machine learning is a subfield of artificial intelligence and computational statistics that develops algorithms capable of learning from empirical data. These systems automatically build predictive or descriptive models by identifying structures, correlations, or regularities, without being explicitly programmed for each task.

Definition

Deep learning is a branch of artificial intelligence that uses multi-layered artificial neural networks to automatically analyze and learn from large amounts of data. It enables image, voice, and text recognition without explicit rule programming.

Example TDA

Definition

Topological Data Analysis (*TDA*) is a machine learning method that studies the shape and structure of data. It uses persistent homology to detect noise robust topological features (holes, loops), revealing patterns invisible to classical statistics.

Why Learning Outcome Framworks

Developing effective learning outcomes is fundamental to successful education, providing a roadmap for both instructors and students. These outcomes articulate what students should know, understand, and be able to do upon completing a learning experience. To achieve this clarity and impact, educators often turn to established theoretical frameworks. This comprehensive analysis will explore three prominent frameworks: SMART, ABCD, and SOLO Taxonomy, detailing their components, applications, and how they collectively contribute to robust educational design

Application of topological data analysis

TDA utilizes topological principles to extract meaningful insights from noisy datasets. The method employed, **persistence homology or persistent entropy**, allows for the computation of topological attributes across different scales and enables the ranking of these features based on the range of scales over which they are observed. We define the Vietoris-Rips complex as a construction in algebraic topology used in the field of computational topology, particularly in Topological Data Analysis (**TDA**). It is named after mathematicians Leopold Vietoris and Élie Cartan, who introduced the concept. The Vietoris-Rips complex is a simplicial complex associated with a given set of points.

The data under analysis is a set of points in the form of a point cloud dataset, denoted as $C = (x_0(t), x_2(t), \dots, x_n(t))$ in Euclidean space $\mathbb{R}^d$. We establish a connection between a given dataset and a topological space using the following approach. For each $\delta > 0$, we define complex $r(C, \delta)$, also known as the Rips complex. This complex is constructed as follows:

$$d(x_i(t), x_j(t)) < \delta. \tag{1}$$

Logically we have

$$r(C, \delta) \subseteq r(C, \delta_0), \text{ for each } \delta_0 \geq \delta. \tag{2}$$

Where $r(C, \delta)$ is sphere with center C and radius δ.

Persistent entropy

Persistent entropy (PE) is a information-theoretic measure derived from the Shannon entropy framework. It quantifies the uneven distribution of lifetimes or persistence within a persistence diagram. In essence, PE captures the informational contribution of each topological feature's lifespan, providing a summary of the diagram's complexity. It is formally defined as follows:

$$P(X) = \sum_{i=1}^{N} p_i \log\left(p_i\right). \tag{3}$$

Relies on the definition of Shannon entropy and serves as a metric for gauging the uneven distribution of lifetimes or persistence. Essentially, it assesses the informational contribution of the lifespan of topological features in a persistence diagram. The definition of PE is articulated as follows:

$$\begin{cases} pe = -\sum_{i=1}^{n} p(|x_i(t)|)\log(|x_i(t)|) \\ p(|x_i(t)|) = \frac{|x_i(t)|}{|x_1(t)|+|x_2(t)|+....+|x_n(t)|} \end{cases} . \tag{4}$$

Where $x_i(t)$ presents the phenomenon image in time t

Consider the proposal of utilizing two time series for the calculation of persistence entropy (PE) and the generation of corresponding persistence diagrams. The suggested approach involves employing these time series to capture and analyze the dynamic patterns and temporal relationships embedded in the data. By calculating persistence entropy and visualizing persistence diagrams, valuable insights into the evolving structures and persistent features within the time series can be obtained

Famous Bilinear models

$$x_n = \theta_0 x_{n-1} \varepsilon_{t-1} + \varepsilon_t. \tag{5}$$

And the subsequent time series described by the following expression.

$$x_n = \theta_1 x_{n-1} \varepsilon_{t-1} + \theta_2 x_{n-2} + \varepsilon_t. \tag{6}$$

Given real coefficients $\{\theta_j, j = 0, 1 \text{ and } 2\}$, when $\theta_0 = \theta_1 = \theta_1$=0.07 the subsequent outcomes are revealed

Definition

The process $(Z_t)_{t\in\mathbb{Z}}$ defined a bilinear time series with time varying within a probability space (Ω, A, P), each general equation can be written in the following form

$$Z_t = \sum_{i=1}^{p} a_i(t) Z_{t-i} + \sum_{j=1}^{q} b_j(t)\varepsilon_{t-j} + \sum_{i=1}^{r}\sum_{j=1}^{s} c_{ij}(t) Z_{t-i}\varepsilon_{t-j} + \varepsilon_t. \tag{7}$$

$(a_i(t), b_i(t), c_i(t))$ are coefficients of model. the order $BL(p, q, r, s)$, ε_t the white noise of model. Bibi and Pham's influential study of the bilinear model of order $BL(p, 0, p, 1)$ offers a critical foundation about the necessary condition for stability of the following model

$$Z_t = a(t)Z_{t-p} + c(t)Z_{t-p}\varepsilon_{t-1} + \varepsilon_t. \tag{8}$$

The necessary condition for stability is

$$a^2(t) + b^2(t)\sigma^2(t) < 1. \tag{9}$$

This condition allows us to extract the following generalized follwing solution see A. Bibi

$$Z_t = \sum_{j=0}^{\left[\frac{t}{p}\right]} \left(\prod_{i=1}^{j-1} (a(t-ip) + c(t-ip)\varepsilon_{t-i-1}) \right) \varepsilon_{t-j}. \tag{10}$$

$[t]$ denotes the integer part of t.

Definition

We define the time-varying $GARCH(1,1)$ model by the following stochastic equation

$$\begin{cases} \varepsilon_t = h_t \eta_t. \\ h_t^2 = \alpha_0(t) + \alpha_1(t)\varepsilon_{t-1}^2 + \alpha_2(t)h_{t-1}^2 \end{cases} \tag{11}$$

Where the distribution η_t follows the Gaussian law $N(0,1)$, the sequences $\alpha_1(t)$ and $\alpha_2(\beta)$ are time-varying coefficients while keeping $\alpha_0 > 0$ as a constant. h_t is independent of the filtration generated by $\{\eta_{t+k}, k \geq 0\}$. And ε_t is the measurable function of the variables $\eta_{t-\ell}, \ell \geq 0$. It is well known that the GARCH(1,1) model is strictly stationary if and only if

$$-\infty \leq E\left(\log\left|\alpha_1(t)\eta_t^2 + \alpha_2(t)\right|\right) < 0 \tag{12}$$

We define the function φ as follows $\varphi(\eta_t^2) = \alpha_1(t)\eta_t^2 + \alpha_2(t)$, and thanks to this function, we can write h_t^2 in the form

$$\begin{aligned} h_t^2 &= \alpha_0(t) + \alpha_1(t) h_{t-1}^2 \eta_{t-1}^2 + \alpha_2(t) h_{t-1}^2 \\ &= \alpha_0(t) + \left(\alpha_1(t)\eta_{t-1}^2 + \alpha_2(t)\right) h_{t-1}^2. \end{aligned}$$

We arrive

$$h_t^2 = \alpha_0(t) + \varphi(\eta_{t-1}^2) h_{t-1}^2. \tag{13}$$

Then,the last expression can be written recursively as follows

$$h_t^2 = \alpha_0(t) + \alpha_0(t) \sum_{i=1}^{q} \left\{ \prod_{j=1}^{i} \varphi(\eta_{t-j}^2) \right\} + \left\{ \prod_{j=1}^{q+1} \varphi(\eta_{t-j}^2) \right\} h_{t-q-1}^2 . \tag{14}$$

According to the stability conditions, we can show that $E(h_t^2) < \infty$,.It remains to show that the following product is bounded; this final step is achieved by a direct application of Jensen's inequality., first when q tends towards ∞ we have

$$h_t^2 = \alpha_0(t)\left[1+\sum_{i=1}^{\infty}\left\{\prod_{j=1}^{i}\varphi(\eta_{t-j}^2)\right\}\right]. \tag{15}$$

Thus, we conclude that

$$\lim_{q\to\infty}\left\{\prod_{j=1}^{q+1}\varphi(\eta_{t-j}^2)\right\}=0.$$

It is clear that

$$\lim_{q\to\infty} E\left\{\prod_{j=1}^{q+1}\varphi(\eta_{t-j}^2)\right\} \leq \prod_{j=1}^{\infty} E\left(\varphi(\eta_{t-j}^2)\right) = \prod_{j=1}^{\infty}(\alpha_1(t)+\alpha_2(t)).$$

Since $\alpha_1(t)+\alpha_2(t)=\delta<1$ it will then ensure that $\prod_{j=1}^{\infty}\delta$ becomes zero, which shows

$$\lim_{q\to\infty}\left\{\prod_{j=1}^{q+1}\varphi(\eta_{t-j}^2)\right\}=0.$$

In another way, we can prove that the series h_t^2 is almost surely convergent, if we take the general term of the series and apply the **Cauchy** convergence criterion, we find

$$\lim_{n\to\infty}\left\{\prod_{j=1}^{n}\varphi(\eta_{t-j}^2)\right\}^{\frac{1}{n}} = \lim_{n\to\infty} e^{\frac{1}{n}\sum_{j=1}^{n}\ln\varphi(\eta_{t-j}^2)}$$

If v_t is a sequence of Gaussian random variables having an expectation that may be infinite, then the sum $\frac{1}{n}\sum_{k=1}^{n} v_k$ is approximate towards $E(v_1)$, so through this construction using Jensen's inequality

$$
\begin{aligned}
T &= \lim_{n\to\infty} e^{\frac{1}{n}\sum_{j=1}^{n} \ln \varphi(\eta_{t-j}^2)} \\
&= \lim_{n\to\infty} e^{E(\ln \varphi(\eta_{t-1}^2)} \\
&\leq e^{\ln E\varphi(\eta_{t-1}^2)} \\
&= e^{\ln(\alpha_1(t)+\alpha_2(t)))}
\end{aligned}
$$

Then

$$
e^{\ln(\alpha_1(t)+\alpha_2(t))} < 1. \tag{16}
$$

Which shows that the series is convergent.

Theorem

Model $\varepsilon_t = h_t^{0.5}\eta_t$ is the unique stationary solution for (11) under the stability condition (12).

Definition

The GJR-GARCH(1,1) process, introduced by Glosten, Jagannathan, and Runkle (1993), is formally defined as:

$$\begin{cases} \xi_t = h_t \eta_t . t \in \mathbb{N}. \\ h_t^2 = \alpha_0(t) + \alpha_1(t) \left(|\xi_{t-1}| - \theta \xi_{t-1} \right)^2 + \alpha_2(t) h_{t-1}^2 . \end{cases} \tag{17}$$

(η_t) is Gausian process with 0 mean and variance equals 1.

The bilinear model that we will propose here is

$$Z_t = \phi_t(a) Z_{t-s} \varepsilon_{t-1} + \varepsilon_t \quad (18)$$

ε_t the white noise follows the $GARCH(1,1)$ model with time-varying coefficients, where it has been defined above with expression (11), and $\{\phi_t(a), t \in \mathbb{Z}\}$ the sequence of coefficients and a is a vector, $a = (a_1, a_2, ..., a_m)$ included in the subset Θ of $\mathbb{R}^m$. It is well known that stationary solutions exist for this model if $\phi_t^2(a) E(\varepsilon_t^2) < 1$, where we can give some stability extensions depending on the white noise, and in a recurrent way ε_t is written as

$$\varepsilon_t = Z_t + \sum_{k=1}^{t-1} (-1)^k \left\{ \prod_{i=0}^{k-1} \phi_{t-k}(a) \right\} \left(\prod_{i=0}^{k-1} Z_{t-i-s} \right) Z_{t-k}. \quad (19)$$

$$\begin{aligned}
E(\varepsilon_t^2) &= E(\eta_t^2)E(h_t^2) = E(h_t^2). \\
&= \alpha_0 + \alpha_1(t)E(h_{t-1}^2)E(\eta_{t-1}^2) + \alpha_t(t)E(h_{t-1}^2) \\
&= \alpha_0 + \alpha_1(t)E(\varepsilon_{t-1}^2) + \alpha_2(t)E(\varepsilon_{t-1}^2)
\end{aligned}$$

And since $E(\varepsilon_t^2) = E(\varepsilon_{t-1}^2)$ we find $E(\varepsilon_t^2) = \frac{\alpha_0}{1-\alpha_1(t)-\alpha_2(t)}$, such that $\alpha_1(t) - \alpha_2(t) < 1$ then the necessary condition for the stability of the model will be

$$\frac{\phi_t^2(a)\gamma_0}{1-\alpha_1(t)-\alpha_2(t)} < 1$$

And the recurrent expression of the model in the case $s \neq 1$ will be

$$X_t = \varepsilon_t + \sum_{j=1}^{[t/s]-1} \left[\prod_{i=0}^{j-1} \left\{ \phi_{t-is}(a)\varepsilon_{t-is-1} \right\} \right] \varepsilon_{t-sj}.$$

The model (18) under the stability condition accepts the unique recurrent solution when $s = 1$ written in the form

Theorem

The case $s = 1$ in the model (18) driven by the ARCH(1) white noise, and if

$$\alpha_t(\alpha) \in [0,1[\,, |\phi_t(a)| \sqrt{\frac{\alpha_0}{1-\alpha_t(\alpha)}} < 1.$$

then the model accepts a solution written as

$$X_t = \varepsilon_t + \sum_{j=1}^{\infty} \left\{ \prod_{i=0}^{j-1} \phi_t(a)\varepsilon_{t-i-1} \right\} \varepsilon_{t-j}.$$

converges almost surely and this solution is unique and strictly stationary.

Theorem

The condition $E \ln |\phi_t(a)\varepsilon_t| \in [-\infty, 0[$ *where* $s = 1$ *in the model (18) driven by the ARCH (1) white noise implies a condition.*

$$|\phi_t(a)| \sqrt{\frac{\alpha_0}{1 - \alpha_1(t)}} < 1. \tag{21}$$

$\alpha_1(t) \in [0, 1[$. *Using Jensen's inequality, we have*

$$E \ln |\phi_t(a)\varepsilon_t| \leq \ln E |\phi_t(a)\varepsilon_t| . \tag{22}$$

and according to Schwarz's inequality

$$\ln E |\phi_t(a)\varepsilon_t| \leq \ln \left\{ E |\phi_t(a)\varepsilon_t|^2 \right\}^{0.5} . \tag{23}$$

Where we find that

$$\left| \phi_t(a) \left\{ \frac{\alpha_0}{1-\alpha_1(t)} \right\}^{0.5} \right| < 1. \tag{24}$$

Which completes the proof.

Theorem

The condition $|\alpha_1(t)| < 1$ and $\alpha_0 = 0$ in the ARCH(1) model ensures that the model will be bounded.

Proof.

We have $\varepsilon_t = \eta_t h_t$, and since $h_t = \alpha_1(t)\varepsilon_{t-1}$ we find with its recurrent formula that

$$h_{t-i} = \prod_{k=1}^{i} \alpha_1(t)\varepsilon_{t-i-1}. \tag{25}$$

Then $\lim_{i\to\infty} h_{t-i} = 0$, which shows that there exists M such that $\varepsilon_t \leq M$. □

For estimating the parameters of stationary and ergodic bilinear time series models, the literature commonly prescribes the method of moments and least squares. In contrast, this study applies the maximum likelihood method. Suppose that the observations $Z_1, Z_2, ..., Z_N$ for the model $(Z)_{t\in\mathbb{Z}}$. Under a condition of stability of the bilinear model we can obtain the joint density function $F(Z_1, Z_2, ..., Z_N, \Omega)$, Ω is subset of the coefficients of the model where Ω, this function is defined as follows

$$F(Z_1, Z_2, ..., Z_N, \Omega) = \prod_{t=1}^{N} \frac{1}{\sigma(t)\sqrt{2\pi}} \exp\left\{\frac{-\varepsilon_t^2}{2\sigma^2(t)}\right\}. \qquad (26)$$

The bilinear model proposed here is

$$Z(t) = aZ(t-2) + cZ(t-1)\varepsilon(t-1) + \varepsilon(t).$$
$$\varepsilon(t) \rightarrow GARCH(1,1)_{(\alpha_0,\alpha_1,\alpha_2)}.$$

For estimating the coefficients we want to get a solution Ω which maximize the logarithm likelihood function Φ, where

$$\Phi(Z_i, \Omega)_{i=1,...,n} = \ln F(Z_1, Z_2, ..., Z_N, \Omega). \tag{27}$$

$$\Phi(Z_i, \Omega)_{i=1,...,N} = \ln \left[\prod_{i=1}^{N} \frac{1}{\sigma(t)\sqrt{2\pi}} \exp\left\{ -\frac{(\varepsilon(t))^2}{2\sigma^2} \right\} \right]. \tag{28}$$

$$\Phi(Z_i, \Omega)_{i=1,\dots,N} = -N \ln \sigma(t) - \frac{N}{2} \ln 2\pi - \frac{1}{2\sigma^2(t)} \sum_{t=1}^{N} (\varepsilon(t))^2. \tag{29}$$

When we obtain the partial derivatives of $\Phi(Z_i, \Omega)_{i=1,\dots,N}$. The model coefficients can be estimated by following process. Let now $\Omega = (\theta_1, \theta_2, \dots, \theta_n)$

$$\mathbf{L}(Z_i, \Omega)_{i=1,\dots,N} = \left(\frac{\partial \Phi(Z_i, \Omega)}{\partial \theta_1}, \frac{\partial \Phi(Z_i, \Omega)}{\partial \theta_2} \dots, \frac{\partial \Phi(Z_i, \Omega)}{\partial \theta_n} \right)^T. \tag{30}$$

, T indicates the transpose of a matrix, we present a matrix of second order partial derivatives

$$\mathbf{O}(Z_i, \Omega)_{i=1,\dots,N} = \left(\frac{\partial^2 \Phi(Z_i, \Omega)}{\partial \theta_i \partial \theta_j} \right), \ \forall i, j \in \{1, 2, \dots, n\}. \tag{31}$$

To approximate the value of Ω using a Taylor expansion, we first need an initial guess. The accuracy of this initial guess determines how close we get to the true value Ω^0. Then, we solve the following equation to obtain the estimated value

$$\mathbf{L}(Z_i, \Omega)_{i=1,\ldots,N} + \mathbf{O}(Z_i, \Omega)_{i=1,\ldots,N}(\hat{\Omega} - \Omega) = 0. \tag{32}$$

Thus, this equation can be rewritten as

$$Z(t) = aZ(t-2) + cZ(t-1)\varepsilon(t-1) + \varepsilon(t).$$
$$\varepsilon(t) \longrightarrow GARCH(1,1)_{(\alpha_0,\alpha_1,\alpha_2)}.$$

$$\hat{\Omega} = \Omega - \mathbf{O}^{-1}(Z_i, \Omega)_{i=1,\ldots,N}\mathbf{L}(Z_i, \Omega)_{i=1,\ldots,N}. \tag{33}$$

Algorithm designed to approximate a value estimated by Newton-Raphson iterations. One of the main advantages of this numerical method lies in the flexibility it offers regarding the choice of the initial value; however, this choice must remain compatible with the stationarity conditions of the model. Firstly, the proposed initial value is $\Omega = \Omega^0$Then, the program algorithm

$$
\begin{cases}
\Omega^1 = \Omega^0 - \mathbf{O}^{-1}(Z_i, \Omega)_{i=1,\dots,N} \mathbf{L}(Z_i, \Omega)_{i=1,\dots,N}. \\
\Omega^2 = \Omega^1 - \mathbf{O}^{-1}(Z_i, \Omega)_{i=1,\dots,N} \mathbf{L}(Z_i, \Omega)_{i=1,\dots,N}. \\
\vdots \\
\Omega^q = \Omega^{q-1} - \mathbf{O}^{-1}(Z_i, \Omega)_{i=1,\dots,N} \mathbf{L}(Z_i, \Omega)_{i=1,\dots,N}.
\end{cases}
\tag{34}
$$

Where the repetition of the iterative ones each time can give a better approximation and then if q tends to infinity then Ω^q will converge to the estimated value $\hat{\Omega}$.

Simulations

Through numerical illustrations and simulations, this section validates our approach by comparing the estimation accuracy of bilinear models against GARCH and GJR-GARCH models. The results demonstrate the best white noise models which approximate estimators. Let the follwing bilinear model with constant coefficients model

$$\begin{cases} Z(t) = 0.3Z(t-2) + 0.4Z(t-1)\varepsilon(t-1) + \varepsilon(t). \\ \varepsilon(t) \rightarrow GARCH(1,1). \end{cases} \tag{35}$$

Where proposed GARCH(1,1) is defined with its expression

$$\begin{cases} \varepsilon(t) = h(t)\eta(t), \eta(t) \rightarrow N(0,1). \\ h^2(t) = 0.01 + 0.4\varepsilon^2(t-1) + 0.6h^2(t-1). \end{cases} \tag{36}$$

The general recursive expression of our GJR-GARCH(1,1) is defined as follows

$$\begin{aligned} \xi_t &= h_t \eta_t . t \in \mathbb{N}. \\ h_t^2 &= 0.01 + 0.04 \left(|\xi_{t-1}| - 0.8 \xi_{t-1} \right)^2 + 0.6 h_{t-1}^2 . \end{aligned} \tag{37}$$

The real coefficients be $(a, b, c, \alpha_0, \alpha_1, \alpha_2)$, and let the estimators be $(\hat{a}, \hat{b}, \hat{c}, \hat{\alpha}_0, \hat{\alpha}_1, \hat{\alpha}_2)$. NS denotes the number of simulations. N is sample size.

Table 01. Simulation bilinear model (35) driven by with GARCH(1,1) defined by (36)

(NS, N)	$\hat{a}$	$\hat{c}$	$\hat{\alpha}_0$	$\hat{\alpha}_1$	$\hat{\alpha}_2$
100	0.2912	0.3876	0.0098	0.4125	0.5897
200	0.2966	0.3876	0.0098	0.4027	0.5977
1500	0.2967	0.4013	0.0098	0.4022	0.5933
2500	0.3001	0.3987	0.0108	0.3989	0.5989

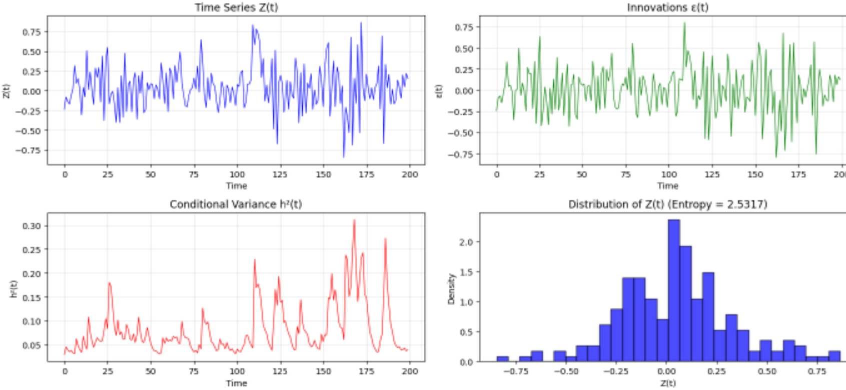
Table 02. Simulation bilinear model (35) driven by with GJR-GARCH(1,1) defined by (37)

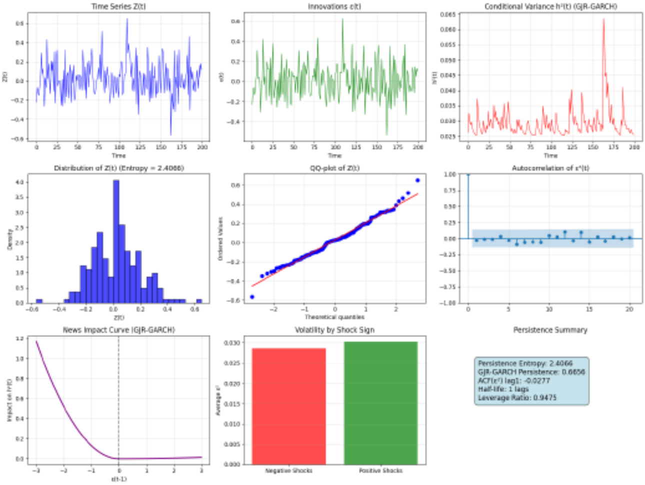
NS	$\hat{a}$	$\hat{c}$	$\hat{\alpha}_0$	$\hat{\alpha}_1$	$\hat{\alpha}_2$
100	0.3005	0.3909	0.0134	0.4009	0.5908
200	0.2988	0.3987	0.0100	0.4002	0.6098
1500	0.2897	0.4013	0.0099	0.4044	0.5912
2500	0.3033	0.3909	0.0091	0.4033	0.5938

1.1156	0.4706	1.1642	0.4954	1.2578	0.8006	1.0800	0.9129	1.4204	0.1974
0.7809	0.3152	0.8710	0.6531	0.6990	0.2770	1.3635	0.9364	0.9491	1.6395
0.0227	1.1645	0.7363	1.3542	0.0999	0.4929	0.4408	0.0477	0.4723	2.5608
0.8733	1.1234	0.7885	0.9535	1.0566	0.2650	0.8383	1.3626	0.7642	0.1203
0.3869	0.4026	1.0204	0.0689	0.3727	0.8897	0.8311	1.1592	0.6491	1.2143
0.3344	1.4875	1.2645	0.5768	0.6622	0.6564	0.9349	0.9349	1.4905	0.1391
0.5172	0.5537	0.6594	0.7038	0.6803	1.5171	0.9654	0.3994	0.2002	0.1391
2.7342	0.0648	0.2798	1.2247	1.0641	0.4096	0.2717	1.4770	0.1346	0.9151
1.2465	0.5639	0.7398	0.1080	0.5375	0.7325	0.7802	0.3884	0.8747	1.3911
0.8350	0.9335	1.0193	0.3755	1.6766	0.9922	1.0540	0.9865	0.9250	0.3145
0.1341	1.2408	0.8580	0.4222	0.6026	1.7032	0.9782	1.0149	1.1094	0.0111
0.9874	1.0917	1.0526	0.7655	2.3173	1.0461	1.2032	1.1676	1.1222	1.2295
0.7602	0.2859	0.9703	1.0807	0.4863	1.6119	1.1707	0.4786	1.6935	2.7206
0.1845	0.8569	0.4403	0.3298	0.6140	1.5059	1.0927	2.1839	0.0348	0.0935
0.5469	2.1145	1.1663	0.2119	0.4806	1.1629	0.0436	1.1172	0.1153	3.1489
1.6717	1.0268	1.2634	1.5053	0.0237	1.0801	0.6675	0.3882	2.3587	2.3377
0.5538	0.3967	1.1901	0.0675	0.5222	1.8509	0.0487	0.4303	0.3816	1.4604
0.8218	0.6964	0.3635	0.9311	0.2038	0.8176	0.2954	1.7273	0.4175	0.9373
0.1986	1.5231	1.0012	0.1059	0.3138	0.9578	0.0084	0.2423	0.6538	0.7555
0.2692	0.5862	0.4948	0.3372	0.7325	0.4852	0.2923	1.2372	0.4753	0.5573
1.8286	0.6143	0.4948	0.5573	0.0712	0.6342	1.4179	2.0911	1.2814	1.2014
1.4302	1.7366	0.4743	1.1944	1.3519	1.5479	0.2091	1.0846	2.3315	3.1033
1.0534	0.4682	0.5916	0.6941	0.1516	1.0553	0.1504	0.2844	0.9386	0.2315
0.1750	1.6611	0.4703	0.9638	1.8498	0.6690	1.9862	0.9936	0.8421	1.5295

Table 2: Dataset of Blood Protein Levels

Real Data


Time Series Z(t)
Z(t)
Time
Innovations ε(t)
ε(t)
Time
Conditional Variance h²(t)
h²(t)
Time
Distribution of Z(t) (Entropy = 2.5317)
Density
Z(t)


Time Series Z(t)
Time
Z(t)
Innovations ε(t)
Time
ε(t)
Conditional Variance h²(t) (GJR-GARCH)
Time
h²(t)
Distribution of Z(t) (Entropy = 2.4066)
Z(t)
Density
QQ-plot of Z(t)
Theoretical quantiles
Ordered Values
Autocorrelation of ε²(t)
News Impact Curve (GJR-GARCH)
ε(t-1)
Impact on h²(t)
Volatility by Shock Sign
Average ε²
Negative Shocks
Positive Shocks
Persistence Summary
Persistence Entropy: 2.4066
GJR-GARCH Persistence: 0.6656
ACF(ε²) lag1: -0.0277
Half-life: 1 lags
Leverage Ratio: 0.9475

The proteins contain essential nutrients and amino acids that contribute to the global sanitary ware, to the cruissance and to the tissue repair. There is a whole process in the muscular development, the production of enzymes and hormones, the immune function and the metabolism regulation. Moreover, the proteins can provide energy to the body. The term "fuzzy" is frequently used in protein biology to describe the unique or flexible structure of proteins. Although proteins possess stable conformations, they evolve in a structurally variable environment and adapt to diverse environmental conditions. This structural indeterminacy makes it difficult to develop classical approaches that would allow them to be modeled in a single, well-defined form.

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PERSISTENCE ENTROPY RESULTS

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H0 (connected components): 0.892147
H1 (loops/circles): 0.234561
H2 (voids/cavities): 0.000000

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Analysis of persistence entropy indicates that the blood protein time series is not strictly stationary. The moderate value reflects an evolving structure where a main cluster dominates, accompanied by transient secondary groups, a sign of drift or regime changes. The very low H confirms the absence of stable recurrent cycles, characteristic of non-stationary systems. Overall, topological persistence remains locally low, suggesting that the underlying process lacks time invariance, despite some short-term structural consistency.

THANK YOU FOR ATTENTION