Midastar: Threshold autoregression with data sampled at mixed frequencies

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Time series variables often have heterogeneous properties below versus above a certain threshold (threshold effects).

One of the most well-known models in this field is the threshold autoregression (TAR) proposed by Tong (1978).

In TAR, a target variable $y$ follows an AR($p$) with coefficients differing across regimes, and a regime switch is triggered when a threshold variable $x$ crosses a threshold parameter $\mu$.

In the existing threshold models, $y$ and $x$ are assumed to be sampled at the same frequency.

In practice, time series are often sampled at different frequencies (e.g., daily, weekly, monthly, etc.).
In the existing literature of threshold models, a variable of the higher frequency is aggregated into the lower level to keep a single-frequency framework.

Such a temporal aggregation has an adverse effect on statistical inference due to loss of information.

To address this issue, we propose Midastar models by combining Mixed Data Sampling (MIDAS) and TAR.

In the MIDAS framework that originated with Ghysels, Santa-Clara & Valkanov (2004), a variety of methods have been proposed to avoid temporal aggregation.
Introduction

- Midastar parameters can be estimated via **profiling**.
- The null hypothesis of no threshold effects can be tested via the **wild bootstrap** of Hansen (1996).
- We fit the Midastar model to Japan’s COVID-19 data.
- The bootstrap test based on Midastar **rejects** the null hypothesis of no threshold effects, revealing heterogeneity between contraction and expansion phases of the pandemic.
- The bootstrap test based on the aggregated TAR model **fails to reject** the null, a signal of **spurious** non-threshold effects.
- This contrast highlights a practical value of Midastar.
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We begin by recalling the single-frequency framework where time periods are denoted as \( \mathbb{I} = \{1, 2, \ldots, n\} \).

Let \( \{y_t\}_{t \in \mathbb{I}} \) be a target variable; let \( \{x_t\}_{t \in \mathbb{I}} \) be a threshold variable.

Tong’s (1978) TAR model is specified as

\[
    y_t = \begin{cases} 
    \alpha_1 + \sum_{k=1}^{p} \phi_{1k} y_{t-k} + u_t & \text{if } x_{t-d} < \mu, \\
    \alpha_2 + \sum_{k=1}^{p} \phi_{2k} y_{t-k} + u_t & \text{if } x_{t-d} \geq \mu,
    \end{cases} \quad t \in \mathbb{I}.
\]

\( y \) has different autocorrelation structures below vs. above the threshold parameter \( \mu \).
Now assume the target variable $y$ is observed at a low frequency and the threshold variable $x$ is observed at a high frequency.

Let $m$ be the ratio of sampling frequencies (e.g., $m = 3$ if $y$ is sampled quarterly and $x$ is sampled monthly).

Define the set of HF time periods as $H = \bigcup_{t \in \mathbb{L}} H_t$, where

$$H_t = \left\{ t - 1 + \frac{1}{m}, \ t - 1 + \frac{2}{m}, \ldots, \ t \right\}, \quad t \in \mathbb{L}.$$

For each low frequency time period $t \in \mathbb{L}$, we observe a single realization $y_t$ for the target variable, while we sequentially observe $\{x^*_j\}_{j \in H_t}$ for the threshold variable.
Midastar: Motivation and specification

- Let $\{x_t\}_{t \in \mathbb{L}}$ be a temporal aggregation of $\{x^*_t\}_{t \in \mathbb{H}}$ (e.g., averaging or skipped sampling).

- In the existing literature, the single-frequency TAR model is fitted to $\{y_t, x_t\}_{t \in \mathbb{L}}$ even if $\{x^*_t\}_{t \in \mathbb{H}}$ is observable.

- To avoid the temporal aggregation of $x^*$, we propose the **Midastar** model:

$$
\begin{align*}
y_t &= \begin{cases} 
\alpha_1 + \sum_{k=1}^{p} \phi_{1k} y_{t-k} + u_t & \text{if } x^*_t - \frac{d}{m} < \mu, \\
\alpha_2 + \sum_{k=1}^{p} \phi_{2k} y_{t-k} + u_t & \text{if } x^*_t - \frac{d}{m} \geq \mu, \quad t \in \mathbb{L}.
\end{cases}
\end{align*}
$$
The delay of $d \in \mathbb{N}$ HF periods is taken from the integer time period $t \in \mathbb{I}$, exploiting the HF observations of $x^*$. 

Stack the regression parameters for each regime:

$$\mathbf{\beta}_r = (\alpha_r, \phi_{r1}, \ldots, \phi_{rp})^\top, \quad r \in \{1, 2\}.$$ 

If threshold effects are present (i.e., $\mathbf{\beta}_1 \neq \mathbf{\beta}_2$), the aggregated TAR model is generally misspecified relative to Midastar, since the former cannot capture the high frequency delay.

The misspecification implies the failure to identify the true value of $\beta$’s. In particular, the aggregated TAR can reach a wrong conclusion that $\mathbf{\beta}_1 = \mathbf{\beta}_2$ (spurious non-threshold effects).
Stack the regression parameters as $\mathbf{\beta} = (\mathbf{\beta}_1^\top, \mathbf{\beta}_2^\top)^\top$ and the nuisance parameters as $\gamma = (d, \mu)^\top$.

We propose to estimate $(\mathbf{\beta}, \gamma)$ via a two-step procedure called profiling.

For each fixed value of $\gamma$, compute the least squares estimator $\hat{\mathbf{\beta}}(\gamma)$ and evaluate the sum of squared errors.

Try all possible values of $\gamma$, and find an optimal $\hat{\gamma}$ that minimizes the sum of squared errors.

The profiling estimator for $\mathbf{\beta}$ is given by $\hat{\mathbf{\beta}} = \hat{\mathbf{\beta}}(\hat{\gamma})$.

The null hypothesis of no threshold effects, $H_0 : \mathbf{\beta}_1 = \mathbf{\beta}_2$, can be tested via the wild bootstrap of Hansen (1996).
Empirical application: Background

There is a rapidly growing literature in which time series analysis is performed on COVID-19 statistics (e.g., Motegi, Dennis & Hamori, 2022).

We analyze the threshold effects of the number of new confirmed cases (Case) on the number of patients in hospital (Hosp) in Japan.

Our World in Data (OWID) offers daily data of Case and weekly data of Hosp for Japan.

This situation motivates the use of the Midastar model with $m = 7$. 
Empirical application: Notation

\[ Hosp_t = \text{the number of COVID-19 patients in hospital at week } t \in \mathbb{I}. \]

\[ Case_t = \text{the number of new confirmed cases of COVID-19 at day } t \in \mathbb{H}. \]

\[ y_t = \Delta \ln Hosp_t \]
\[ = \ln Hosp_t - \ln Hosp_{t-1} \]
\[ = \text{the weekly growth of } Hosp. \]

\[ x_t^* = \Delta \ln Case_t \]
\[ = \ln Case_t - \ln Case_{t-1/m} \]
\[ = \text{the daily growth of } Case. \]
Empirical application: Data


Sample size: \( n = 81 \) weeks, or \( mn = 567 \) days.

We observe the second through fifth waves of the pandemic.
Empirical application: Data

\[ x^* = \Delta \ln \text{Case} \text{ (day)} \]
\[ y = \Delta \ln \text{Hosp} \text{ (week)} \]

- Are there threshold effects of \( \Delta \ln \text{Case} \) on \( \Delta \ln \text{Hosp} \)?
- Does the growth of hospitalization have heterogeneous autocorrelation structures when the growth of new confirmed cases is below versus above a certain threshold?
Empirical application: Methodology

- We fit the Midastar model with $p = 4$ and $m = 7$:

$$y_t = \begin{cases} 
\alpha_1 + \sum_{k=1}^{4} \phi_{1k} y_{t-k} + u_t & \text{if } x_{t-d/7}^* < \mu, \\
\alpha_2 + \sum_{k=1}^{4} \phi_{2k} y_{t-k} + u_t & \text{if } x_{t-d/7}^* \geq \mu, \quad t \in \mathbb{I}.
\end{cases}$$

- Let $\beta_r = (\alpha_r, \phi_{r1}, \ldots, \phi_{r4})^\top$ for regime $r \in \{1, 2\}$.

- Estimate $(\beta_1, \beta_2)$ and $\gamma = (d, \mu)^\top$ via profiling.

- Test the no-threshold-effect hypothesis $H_0 : \beta_1 = \beta_2$ based on the wild bootstrap test.
The estimated threshold parameter is $\hat{\mu} = 0.001$, hence we call regime 1 the **contraction** phase of the pandemic and regime 2 the **expansion** phase.

The share of the contraction phase to the whole sample is 50%.

The estimated delay parameter is $\hat{d} = 8$ days, a plausible value given what we know about the gestation period of the virus.

The no-threshold-effect hypothesis $H_0$ is **rejected** at the 5% level, with the bootstrap p-value being 0.022. Hence, the persistence structures of the growth of hospitalization differ significantly across regimes.
We roughly observe $y_t < 0$ (i.e., decreasing hospitalization) during the contraction phase, and $y_t > 0$ during the expansion.

The regime-specific sample mean of $y$ is $-0.049$ for the contraction phase and $0.028$ for the expansion phase.
Empirical application: Results

The regime-wise implied autocorrelations $\hat{\rho}_r(h)$ are plotted.

The oscillation of the correlation under the expansion has a larger amplitude and a higher frequency than under the contraction.
For comparison, we fit the single-frequency TAR model with $p = 4$ after aggregating the daily number of new confirmed cases into the weekly level.

The no-threshold-effect hypothesis $H_0$ cannot be rejected at the 5% level, with the bootstrap p-value being 0.076. This is a signal of spurious non-threshold effects.

Midastar is better capable of detecting the threshold effects than the aggregated TAR model.
We proposed the **Midastar** model, a novel extension of TAR to mixed frequency data.

The Midastar model is able to capture **threshold effects** accurately, while the aggregated TAR can point to **spurious** non-threshold effects.

We described the profiling estimation and the wild-bootstrap test for the no-threshold-effect hypothesis.

We applied Midastar to Japan’s COVID-19 data, finding **significant** threshold effects of daily new confirmed cases on weekly hospitalization.

The threshold effects **vanish** once the temporal aggregation is executed.
References


