New covariates selection method in dynamic regression models with a public implementation in R language

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Introduction

The **linear dynamic regression model (DRM)** defines the linear dependence between a stochastic process Y_t and a set of processes $\mathcal{X} = \{X_t^{(1)}, ..., X_t^{(m)}\}$:

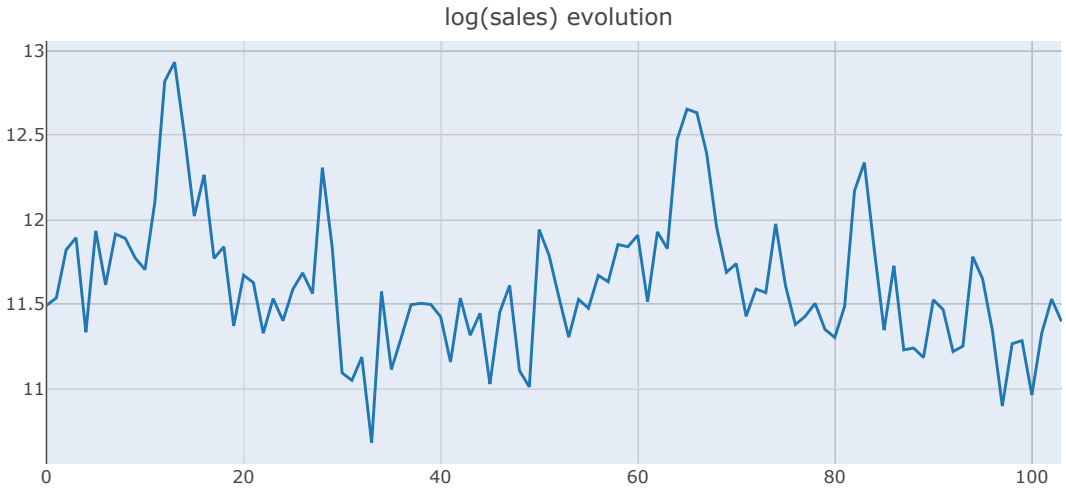
$$Y_t = \beta_0 + \beta_1 X_{t-r_1}^{(1)} + \cdots \beta_m X_{t-r_m}^{(m)} + \eta_t$$

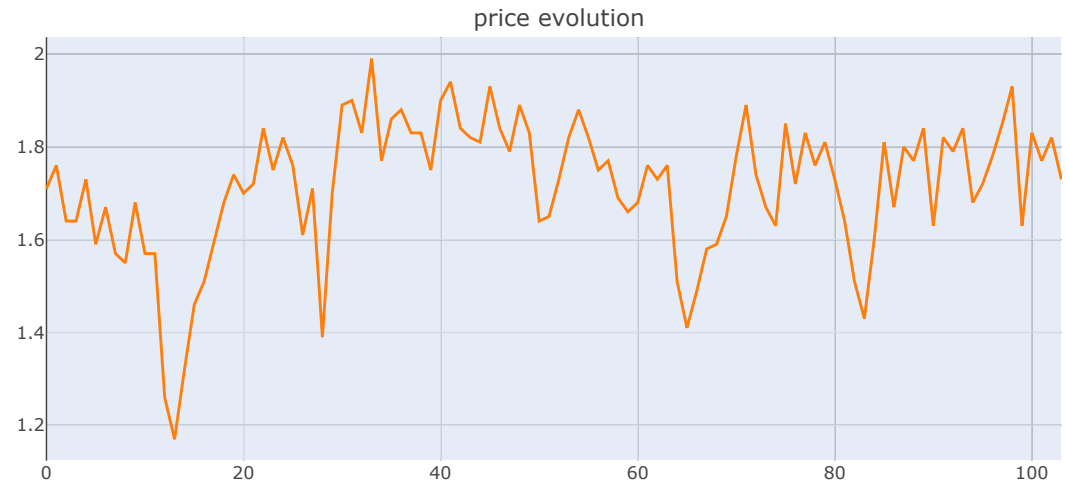
constrained to $r_i \geq 0$ for $i = 1, ..., m$ and $\eta_t \sim \text{ARMA}(p, q)$[1].

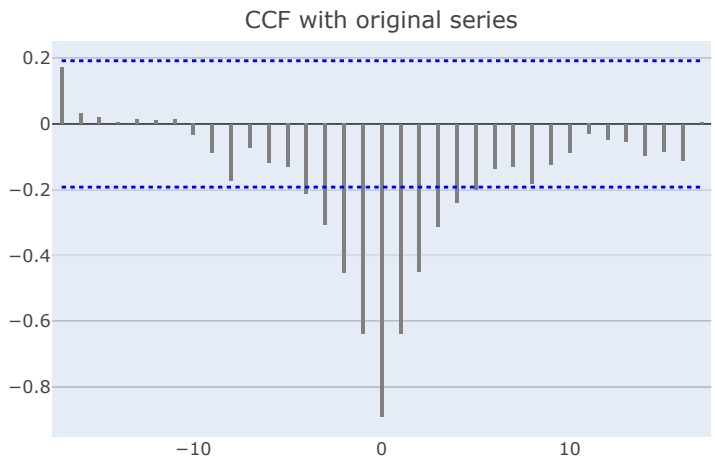
- [Cryer and Chan, 2008] proposed the *prewhitening* as a technique for removing spurious correlation between processes in order to detect linear correlation.
- We propose a forward-selection method that iteratively adds regressor variables (from a set of candidates) Y_t is *significantly* dependent with using the *prewhitening* technique.

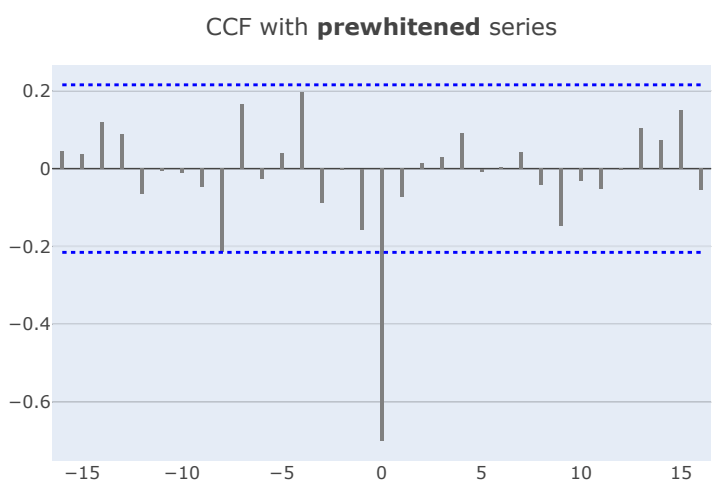
[1] here we denote the AutoRegressive Moving Average model as ARMA.

Prewhitening









Methodology

Let Y_t be the dependent variable and $\mathcal{X}$ the set of covariates candidates. Thus, selection proceeds as follows:

1. Initialization. Consider X_t^{best} as the covariate (lagged r moments) obtained via *prewhitening* that minimizes the IC of the constructed model with Y_t:

$$X_t^{\text{best}} = \underset{X_t \in \mathcal{X}}{\arg\min} \left\{ \text{IC} \left(Y_t = \beta_0 + \beta_1 X_{t-r}^{\text{best}} + \eta_t \right) \right\}$$

2. Iteration. Use the regression errors (η_t) of the last model created to check if some correlation exists between the rest of the covariates not yet added to the model. Find again the "best" variable and add it to the model to obtain a new IC value. If this value improves the last one achieved, repeat this step. If it does not, stop the iteration.
3. Finalization. The errors of the last fitted model must satisfy the stationary property. In other case, consider the regular differentiation of all data and start again the procedure.

Simulation procedure

1. Artificially construct Y_t:

$$Y_t = \beta_0 + \beta_1 X_{t-r_1}^{(1)} + \beta_2 X_{t-r_2}^{(2)} + \beta X_{t-r_3}^{(3)} + \eta_t$$

where $\eta_t \sim \text{ARMA}(p, q)$, $\beta_0, ..., \beta_3$, $r_i \in [0, 6]$ and $X_t^{(1)}$, $X_t^{(2)}$ and $X_t^{(3)}$ are randomly generated.

2. Consider the set of candidates:

$$\mathcal{X} = \{X_t^{(1)}, X_t^{(2)}, X_t^{(3)}, \underbrace{X_t^{(4)}, X_t^{(5)}, X_t^{(6)}}_{\text{not in the model}}\}$$

3. Selection method was tested with different configurations:
   - Changing the IC with three different options: AIC, BIC or AICc.
   - Changing the method to check stationary: via the Dickey-Fuller test or via adjusting an ARIMA and checking the differentiation order.

Results of multiple simulations where $\eta_t \sim$ ARMA(p,q)

Table 1: Percentage data results when residuals are stationary

	AIC	**BIC**	**AICc**	**AIC**	**BIC**	**AICc**
adf.test	97.66%	97.66%	97.66%	3.66%	1.33%	3.66%
auto.arima	98.33%	98.33%	98.33%	3.66%	1.33%	3.66%
	correctly added (TP)			incorrectly added (FP)		

	AIC	**BIC**	**AICc**	**AIC**	**BIC**	**AICc**
adf.test	96.33%	98.66%	96.33%	2.33%	2.33%	2.33%
auto.arima	96.33%	98.66%	96.33%	1.66%	1.66%	1.66%
	correctly **not** added (TN)			incorrectly **not** added (FN)		

Results of multiple simulations where $\eta_t \sim$ ARIMA(p,d,q)

Table 2: Percentage data results when residuals are non-stationary

	AIC	**BIC**	**AICc**	**AIC**	**BIC**	**AICc**
adf.test	93.33%	93.33%	93.33%	4.33%	0.30%	4.33%
auto.arima	94.33%	94.66%	95.33%	5.00%	1.33%	5.00%
	correctly added (TP)			incorrectly added (FP)		

	AIC	**BIC**	**AICc**	**AIC**	**BIC**	**AICc**
adf.test	95.00%	98.66%	95.00%	6.66%	6.66%	6.66%
auto.arima	94.66%	99.66%	95.66%	4.66%	5.33%	4.66%
	correctly **not** added (TN)			incorrectly **not** added (FN)		

Example of one simulation result

Figure 1: Code output when launching the function `drm.select()` that implements our approach

```
beta0 <- -0.6; beta1 <- 1.7; beta2 <- -2.2; beta3 <- 1.3; r1 <- 2; r3 <- 3
Y <- beta0 + beta1*lag(X1,-r1) + beta2*X2 + beta3*lag(X3,-r3) + residuals
xregs <- cbind(X1, X2, X3, X4, X5, X6)
ajuste <- drm.select(Y, xregs, ic='aicc', st_method='adf.test', show_info=F)
```

```
print(ajuste$history, row.names=F)
```

```
 var lag                ic
  X2   0 -1156.68486061937
  X1  -2 -2171.66958134745
  X3  -3 -3108.15443209894
```

```
print(ajuste, row.names=F)
```

```
Series: serie
Regression with ARIMA(0,0,4) errors

Coefficients:
         ma1     ma2  ma3     ma4  intercept       X2      X1      X3
      0.2498  0.3360    0  0.1589    -0.5947  -2.1868  1.6949  1.3083
s.e.  0.0304  0.0302    0  0.0300     0.0033   0.0105  0.0089  0.0320

sigma^2 = 0.002377:  log likelihood = 1562.15
AIC=-3108.3   AICc=-3108.15   BIC=-3069.26
```

Example of the iterative selection step by step

Table 3: From worldmeters source, model the evolution of *exitus* cases in Spain due to the COVID-19 considering other country data

Covariate	**Lag**	**Coefficient est. (s.e)**	**AICc**
confirmed_spain	0	0.0064 (0.0009)	5596.641
recovered_portugal	-1	-0.0337 (0.0063)	5550.963
recovered_france	0	0.0646 (0.0142)	5540.655
confirmed_france	0	-0.0033 (0.0007)	5522.699
confirmed_portugal	-13	0.0395 (0.0085)	5504.169
recovered_spain	-7	-0.0669 (0.0176)	5500.573

- **Note**: This model was fitted with differentiated data.
- deaths_england, deaths_france, confirmed_england, recovered_england and deaths_portugal were not included in the model.
- The residuals of the model follow an ARMA$(1,1) \times (1,1)_7$ with parameters:

$$\phi_1 = 0.9724(0.0131),\ \theta_1 = -0.7508(0.0370),$$
$$\Phi_1 = 0.6958(0.1892),\ \Theta_1 = -0.5512(0.2215)$$

Application to COVID19 evolution

Table 4: Information about the dynamic regression model constructed via selection of multiple vaccination variables to model COVID19 evolution

Covariate	**Lag**	**Coefficient est. (s.e)**
vac4565	-3	-0.0410 (0.0057)
vac6580	-2	-0.0468 (0.0120)
vac1845	-6	-0.0901 (0.0047)
vac1218	Not included in the model	
vac80	Not included in the model	
residuals	ARIMA(4, 0, 0)	$\phi_1 = 2.0816(0.0810)$ $\phi_2 = -1.2837(0.1152)$ $\phi_4 = 0.1919(0.0432)$

- There is a lagged negative correlation between the vaccination data and COVID-19 evolution.
- The vaccination of the young population (from 18 up to 45 years old) has a greater impact in the COVID19 evolution.
- The vaccination of the population older than 80 years has no significative impact in the COVID19 confirmed cases.

Publicly implementation of the method

- This method was implemented in R and optimized in order to parallelize some independent tasks of the method.
- All code is openly available in:

  `https://github.com/anaezquerro/dynamic-arimax`

- The main user-friendly functions of our implementation are:
  - `auto.fit.arima()`: Fits the optimal valid ARIMA/ARIMAX model (via some information criterion) where all coefficients are significative and the resultant residuals of the model satisfy the properties of independence and zero-mean.
  - `drm.select()`: Implements our selection method and optionally provides some information about the partial fits that are generated in process.
  - `forecast_model()`: Given the fit ARIMAX model of `drm.select()` function, returns and displays point predictions in original units.

  Detailed examples of these functions can be consulted in `EXAMPLES.md` file of the repository.

Conclusions and future work

- Our method successfully covers a widespread application in financial, economic and biomedical fields.
- As future work, other covariates might be considered, such as discrete or functional variables.
- Our implementation is intended to be published as an R package once more functionalities are added (such as the aforementioned covariates extension or make it available as an interactive web application with Shiny).

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