





CoRoNNa: A Deep Sequential Framework to Predict Epidemic Spread from Mobility and Viral Diffusion Trajectories

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Introduction on Epidemic Spread Prediction

- Characteristics:
 - Long-term sequence of measurements
 - Regular intervals between events
 - Hidden long-term dependencies within the sequence
- Task: Epidemic prediction on viral spread of COVID-19

• This paper: Analysis of the mobility containment policies effect on the viral spread and prediction of *daily positive cases* in the infection trajectories

Related work

• Diffusion models [1-6]:

- Based on specific infection parameters of the virus
- Usually augmented with environmental and weather data
- <u>Example</u> SIR, SEIR, LT

Trajectory-based models:

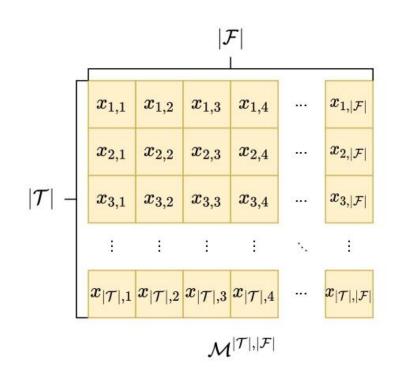
- Stationary linear stochastic models [7-10] predict the value at instant t by regressing its past values
- Deep sequential models learn long-term patterns in sequential data [11,12]

Related work

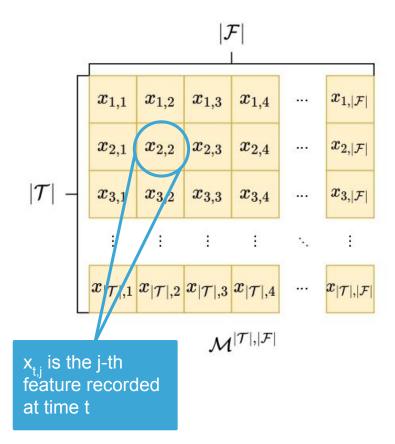
- Diffusion models are sensitive to the epidemiological parameters (i.e. infectivity period)
 - Unstable and less effective when the parameters are highly variable

- Stochastic models are not effective with long historical data
 - The COVID-19 spread depends on mobility containment policies to combat the disease
 - The effect of the containment policies is visible after several days/weeks
- Deep sequential methods are more promising:
 - No need to encode epidemiological parameters explicitly
 - Detection of underlying patterns and long-term dependencies

- The COVID-19 spread in a population is time-dependent
 - Number of infected, recovered and deceased patients change in time
- Time-series is a discrete sequence of random variables $\{x_t\}$ ordered in time $t \in T \subset R$
- Let M^{|T|,|F|} be a time-matrix of |T| rows and |F| columns:
 - T is the set of timestamps
 - F is the collection of time-variables (features)

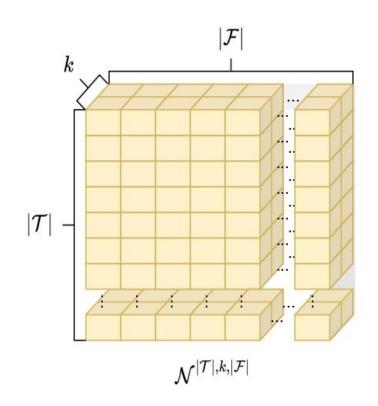


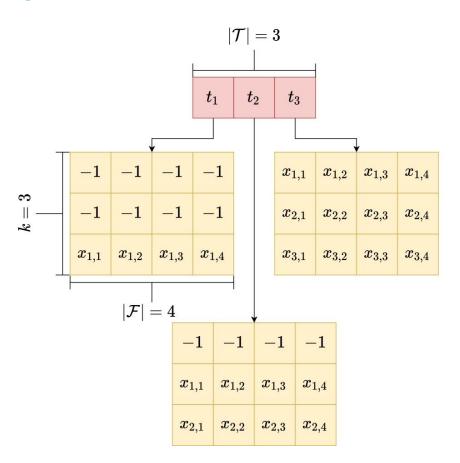
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- Temporal lag and lead
 - Lag (k) = the number of days to look back
 - Lead (ℓ) = the number of days to predict in the future
- Extend M^{|T|,|F|} into a time-tensor N^{|T|,k,|F|} to represent the lag
- For each $t \in T$, $i \in [1,k]$, $j \in [1,|F|]$ we have:

$$N_{t,i,j} = egin{cases} \mathcal{M}_{t-k+i,j} & ext{if } t-k+i > 0 \ -1 & ext{otherwise} \end{cases}$$





Predictive strategy

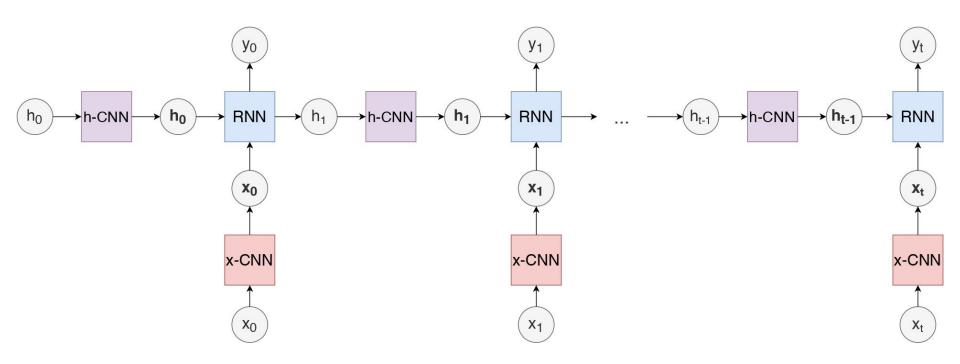
CNN + RNN = CoRoNNa

3 modules:

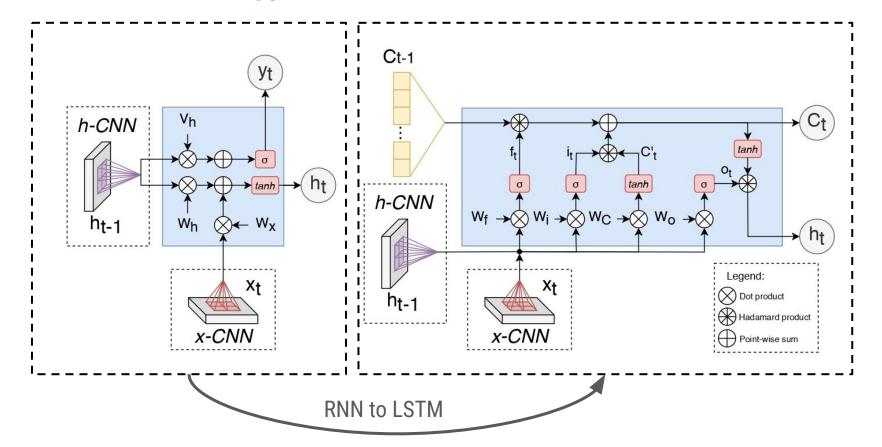
- x-CNN = convolution on the input trajectory at time t
- h-CNN = convolution on the hidden vector at time t-1
- Main RNN = finds features on the curves of daily infected patients

- Polymorphic and agile structure
 - Plug-in-plug-out architecture
 - Fully-configurable components

Predictive strategy



Predictive strategy



Datasets

	Covid spread infection data	Mobility patterns	COVID-19 features
Italy (A)	<u>Protezione Civile - Emergenza</u> <u>Coronavirus</u>	Google and Apple mobility patterns	 N° of daily positive cases N° of deceased persons N° of daily swab tests N° of daily ICU admissions
Switzerland (A)	Our World in Data	//	//
South Korea (B)	//	//	//
Japan (B)	//	//	//
Brazil (C)	//	//	*missing N° of daily swab tests
Texas, US (C)	//	//	//

A = countries with severe lockdown policies; B = light containment; C = no constraints

Mobility patterns

- Google mobility data: mobility trends related to specific places
 - Retail & Recreation (restaurants, cafes, shopping centers...)
 - Grocery & Pharmacy
 - Parks, Transit Stations, Workplaces
 - Residential

- Apple mobility data: trends related to directions request
 - Walking
 - Driving (private car)
 - Transit (public transport)

Experimental setup

Objectives:

 Assess the predictive power of infection (F1) and mobility (F2) trajectories in countries with containment strategies, compare with countries with no or little containment

Compare the quality of predictions of the models

Experimental setup

- Metrics:
 - RMSE

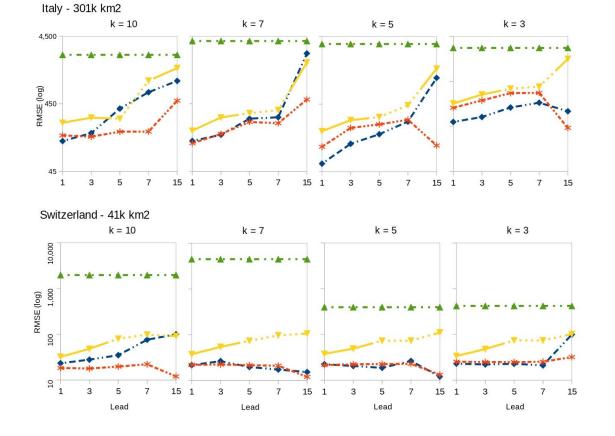
- Time-window:
 - Combination of all $k \in \{3,5,7,10\}$ and $l \in \{1,3,5,7,15\}$
- Training:
 - 60:10:30 split into training, validation, and test sets
 - Splitting is done sequentially in the time axis

Experimental setup

Competitors:

LSTM-Yang [12] with 25 cells and a sigmoid activation function

- VAR
 - Dependency evaluation between DPC and other series
 - Quadratic detrending for stationarity to be met

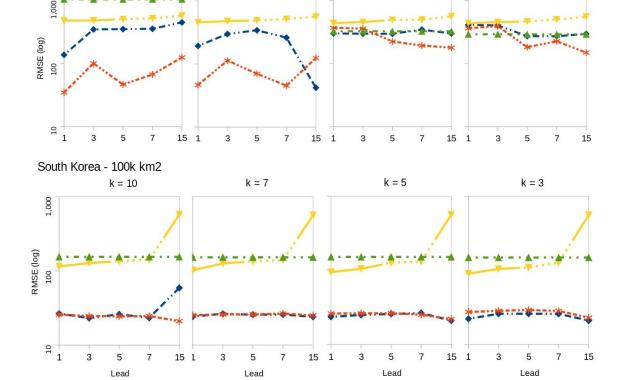


Legend:

- * LSTM-Yang
- * CoRoNNa
- * Random Forest
- * VAR

Japan - 377k km2

k = 10



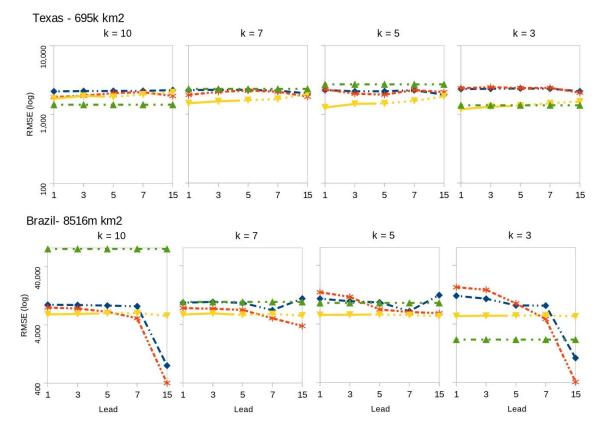
k = 5

k = 3

k = 7

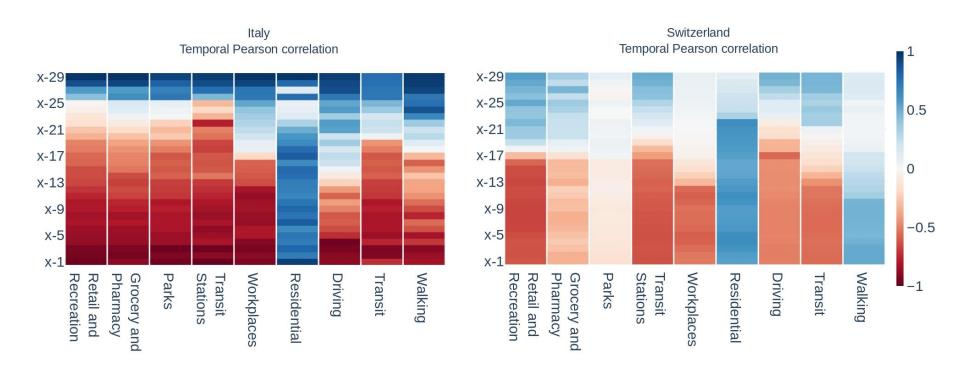
Legend:

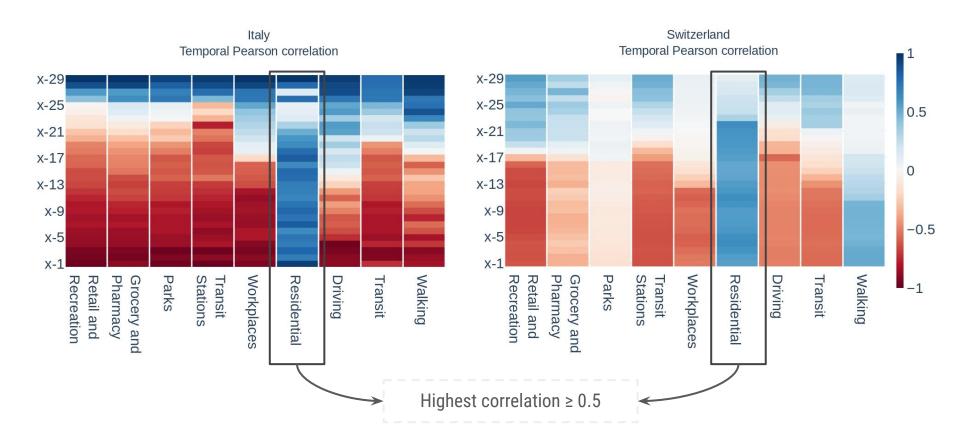
- * LSTM-Yang
- * CoRoNNa
- * Random Forest
- * VAR

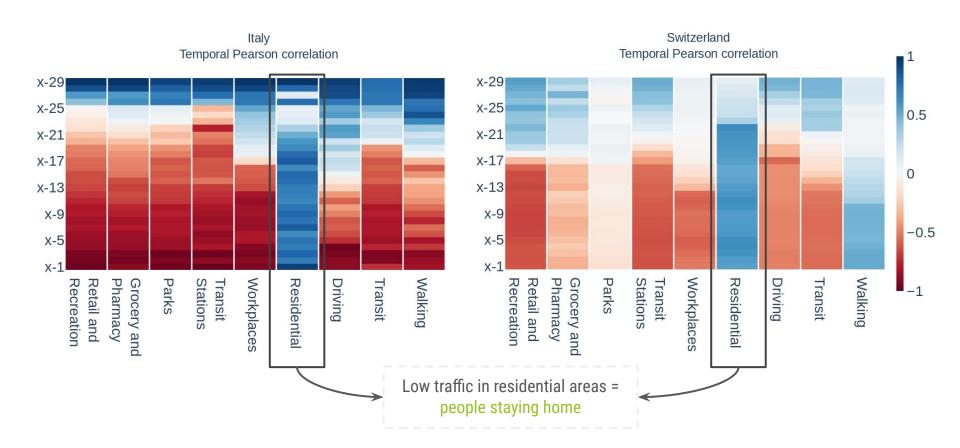


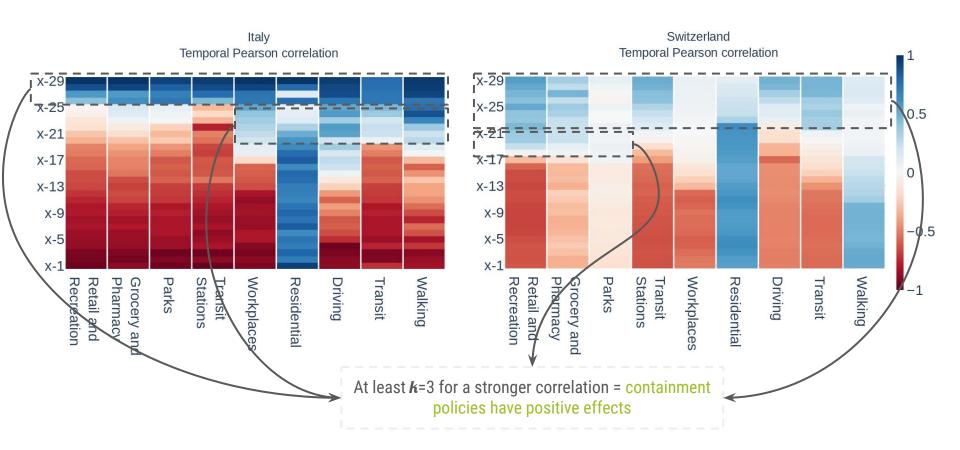
Legend:

- * LSTM-Yang
- * CoRoNNa
- * Random Forest
- * VAR

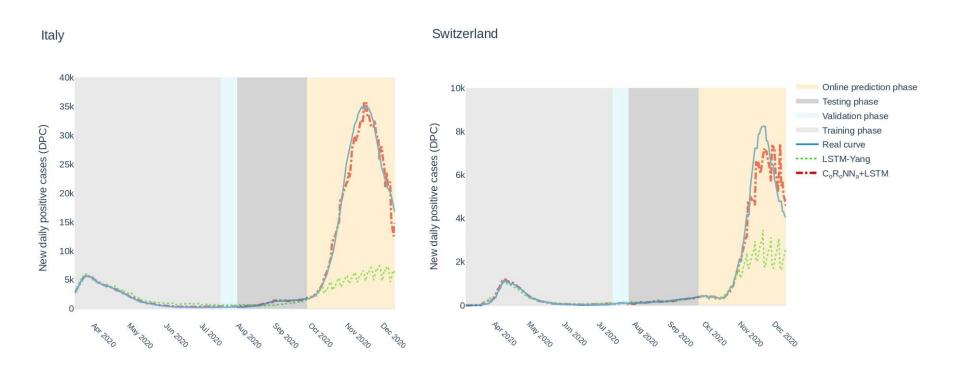








Results (Comparison of methods)



Conclusions

- Diffusion models are less effective at predicting the viral spread of infections
 - Epidemiological parameters have different manifestations from individual to individual

CoRoNNa is flexible and makes far fewer assumptions on input variables

- Changes in mobility data are good predictors of future infections
 - Stronger correlation with daily positive cases at longer lags
 - CoRoNNa shows superior ability at capturing long-term dependencies







THANK YOU

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