Identical trends of SARS-Cov-2 transmission and retail and transit mobility during non-lockdown periods

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Appendix

Estimation of $R_{eff}(t)$

Classically $R_{eff}(t)$ is estimated by the ratio of the number of new infections generated at time t, to the total infectiousness of infected individuals at time t. For the COVID-19 epidemic, considering of the data needed for the estimation of the reproductive numbers, these methods have many shortcomings due to the characteristics of the transmission of this virus namely its silent transmission and major time variation in the reporting of cases due to lack of timely or appropriate testing (O'Driscoll et al., 2020; Pitzer et al., 2020; Gostic et al., 2021).

A complementary approach is to infer changes in transmission using mathematical models, and computing R_{eff} based on its proportionality with the transmission rate. Accounting for all uncertainties associated with SARS-Cov-2 transmission, we propose using a framework that has been introduced to tackle non-stationarity in epidemiology (Cazelles et al., 2018). This framework uses diffusion models driven by Brownian diffusion to model time-varying parameters of major epidemiological significance embedded in a stochastic framework coupled with Bayesian inference methods (Cazelles et al., 2018).

For estimating $R_{eff}(t)$ we have proposed a simple model that incorporates the available information to examine the dynamics of Covid-19 epidemics. The model is described in Fig. A1 (Cazelles et al., 2021). Our model is an extended stochastic SEIR model also accounting for asymptomatic transmission and the hospital system. It includes the following variables: the susceptibles S, the infected non-infectious E, the symptomatic infectious I, the asymptomatic infectious A, the removed people R, and the hospital variables: hospitalized people H, people in intensive care unit ICI, cured people G, and deaths at hospital D. We have also introduced Erlang-distributed stage durations (with a shape parameter equal tow 2) for the E, I, A and H compartments. The differential equations below describe the deterministic version of our model, however it is important to note that we have used its stochastic version:

$$\frac{dS}{dt} = -\beta(t).\left(I_1 + q_1.I_2 + q_2.(A_1 + A_2)\right)$$

$$\frac{dE_1}{dt} = \beta(t).\left(I_1 + q_1.I_2 + q_2.(A_1 + A_2)\right) - \frac{\sigma}{2}.E_1$$

$$\frac{dE_2}{dt} = \frac{\sigma}{2}.(E_1 - E_2)$$

$$\frac{dI_1}{dt} = (1-\tau_A).\frac{\sigma}{2}.E_2 - \left(1-\tau_H - q_I.\tau_I\right)\frac{\gamma}{2}.I_1$$

$$\frac{dI_2}{dt} = \left(1-\tau_H - q_I.\tau_I\right)\frac{\gamma}{2}.I_1 - \frac{\gamma}{2}.I_2$$

$$\frac{dA_1}{dt} = \tau_A.\frac{\sigma}{2}.E_2 - \frac{\gamma}{2}.A_1$$

$$\frac{dA_2}{dt} = \frac{\gamma}{2}.(A_1 - A_2)$$

$$\frac{dR}{dt} = \frac{\gamma}{2}.\left(\left(1-\tau_H - q_I.\tau_I\right).I_2 + A_2\right) + (1-q_D.\tau_D).\frac{\kappa}{2}.H_2 \qquad \text{(A1)}$$

$$\frac{dH_1}{dt} = \tau_H.\frac{\gamma}{2}.\left(I_1 + I_2\right) - \frac{\kappa}{2}.H_1$$

$$\frac{dH_2}{dt} = \left(1-\tau_I - q_D.\tau_D\right).\frac{\kappa}{2}.H_1 + (1-\tau_D).\delta - \frac{\kappa}{2}.H_2$$

$$\frac{dICU_1}{dt} = q_I.\tau_I.\frac{\gamma}{2}.\left(I_1 + I_2\right) + \tau_I.\frac{\kappa}{2}.H_1 - \delta.ICU$$

$$\frac{dG}{dt} = \left(1-q_D.\tau_D\right).\frac{\kappa}{2}.H_2$$

$$\frac{dD}{dt} = q_D.\tau_D.\frac{\kappa}{2}.\left(H_1 + H_2\right) + \tau_D.\delta.ICU$$

The main characteristic of this model is the time-varying transmission rate $\beta(t)$ that follows a Brownian diffusion process:

$$d\log(\beta(t)) = \nu.dB(t) \qquad \text{(A2)}$$

In the model ν is the volatility of the Brownian process (dB), σ is the incubation rate, γ the recovery rate, $1/\kappa$ the average hospitalized period, $1/\delta$ the average time spent in ICU, τ_A the fraction of asymptomatics, τ_H the fraction of infectious hospitalized, τ_I the fraction of ICU admission, τ_D death rate, q_1 and q_2 reduction of transmissibility. As the peaks of those hospitalized and those admitted to ICU are concomitant we consider that a weak fraction, $q_I.\tau_I$ of infectious with severe symptoms go directly to ICU. Even if the majority of deaths occur in the ICU, a small fraction, $q_D.\tau_D$, can occur in hospital but not in intensive care. Then q_I and q_D are the reduction of admission in ICU and of death rate respectively.

With this model R_{eff} can be computed as:

$$R_{eff}(t) = \left(\frac{(1+q_1)}{2}.(1-\tau_A) + q_2.\tau_A\right).\frac{\beta(t)}{\gamma}.\frac{S(t)}{N} \qquad \text{(A3)}$$

Inference

Accounting for all the numerous shortcomings associated with positive cases, we used, for the model inference, hospitalized multiple datasets for France and Ireland. For these two countries the hospitalized data are published on open platform.

Due to the use of a diffusion equation (A2) for the dynamic of the time-varying parameters, the model is stochastic. Thus equations (A1-A2) are considered in a stochastic framework solved with the Euler-Maruyama algorithm (Kloeden and Platen, 1999) implemented in the SSM platform (Dureau et al., 2013). Since the epidemiological propagation mode is stochastic, its likelihood is intractable and it is estimated with particle filtering methods (Sequential Monte Carlo). In order to estimate the parameters of the system, the particle filter is embedded in a Markov Chain Monte Carlo framework, leading to the PMCMC algorithm (Andrieu et al., 2010). More precisely, the likelihood estimated by the particle filter is used in a Metropolis Hasting scheme (particle marginal Metropolis Hastings) (Andrieu et al., 2010).

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Supplementary figures

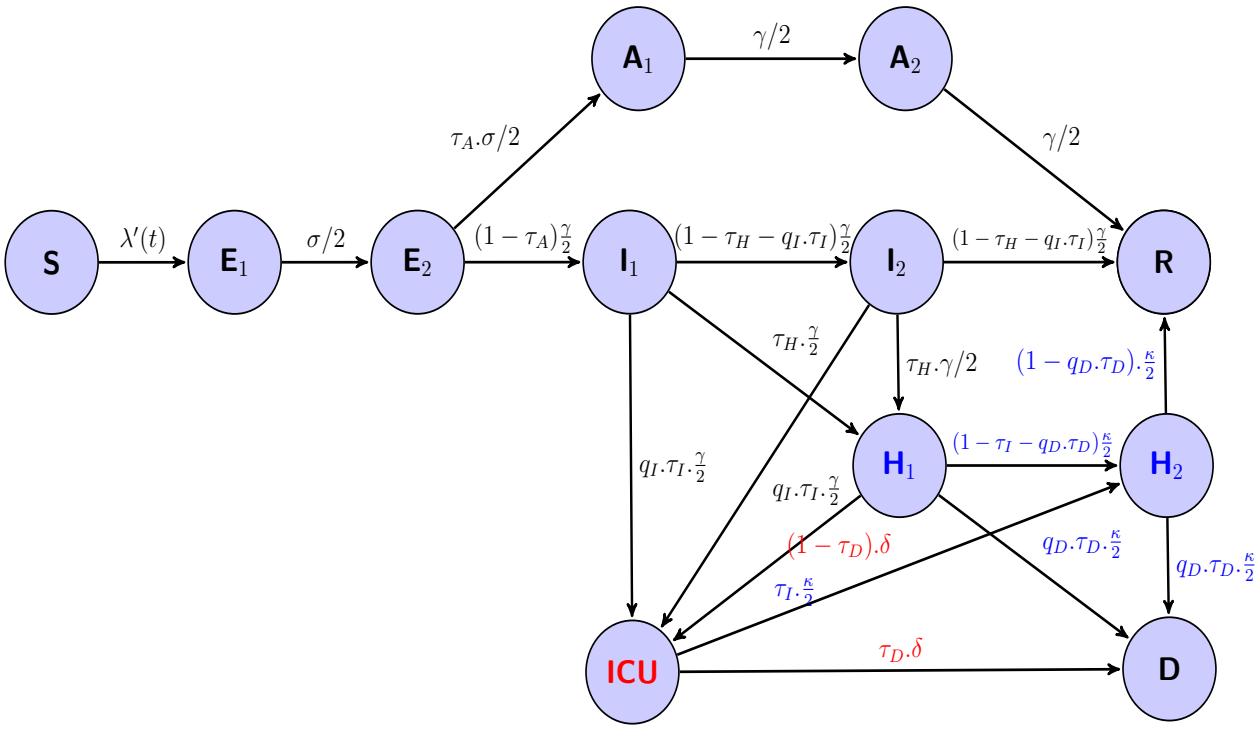

FIGURE A1 – Flow diagram of the model used. It ncludes the following variables : the susceptibles S, the infected non-infectious E, the infectious symptomatic I, the infectious asymptomatic A, the removed people R, and the hospital variables : hospitalized people H, people in intensive care unit ICU, hospital discharge G, and deaths at hospital D. Erlang-distributed stage durations is also introduced for the E, I, A and H compartments to mimic a gamma distribution for stage duration in these compartments.$\lambda'(t) = \beta(t).(I1 + q_1.I_2 + q_2.(A_1 + A_2))/N$ then the force of infection is $\lambda(t) = \lambda'(t).S(t)$. $\beta(t)$ is the time-varying transmission rate, σ the incubation rate, γ the recovery rate, $1/\kappa$ the average hospitalized period, $1/\delta$ the average time spent in ICU, τ_A the fraction of asymptomatics, τ_H the fraction of infectious hospitalized, τ_I the fraction of ICU admission, τ_D the death rate, q_1 and q_2 the reduction of transmissibility of I_2 and A_i, q_I the reduction of the fraction of people admitted in ICU and q_D the reduction of the death rate. The subscripts 1 and 2 are for the 2 stages of the Erlang distribution of the considered variable. Flows in blue are from hospital (H_i) and flow in red from ICU.

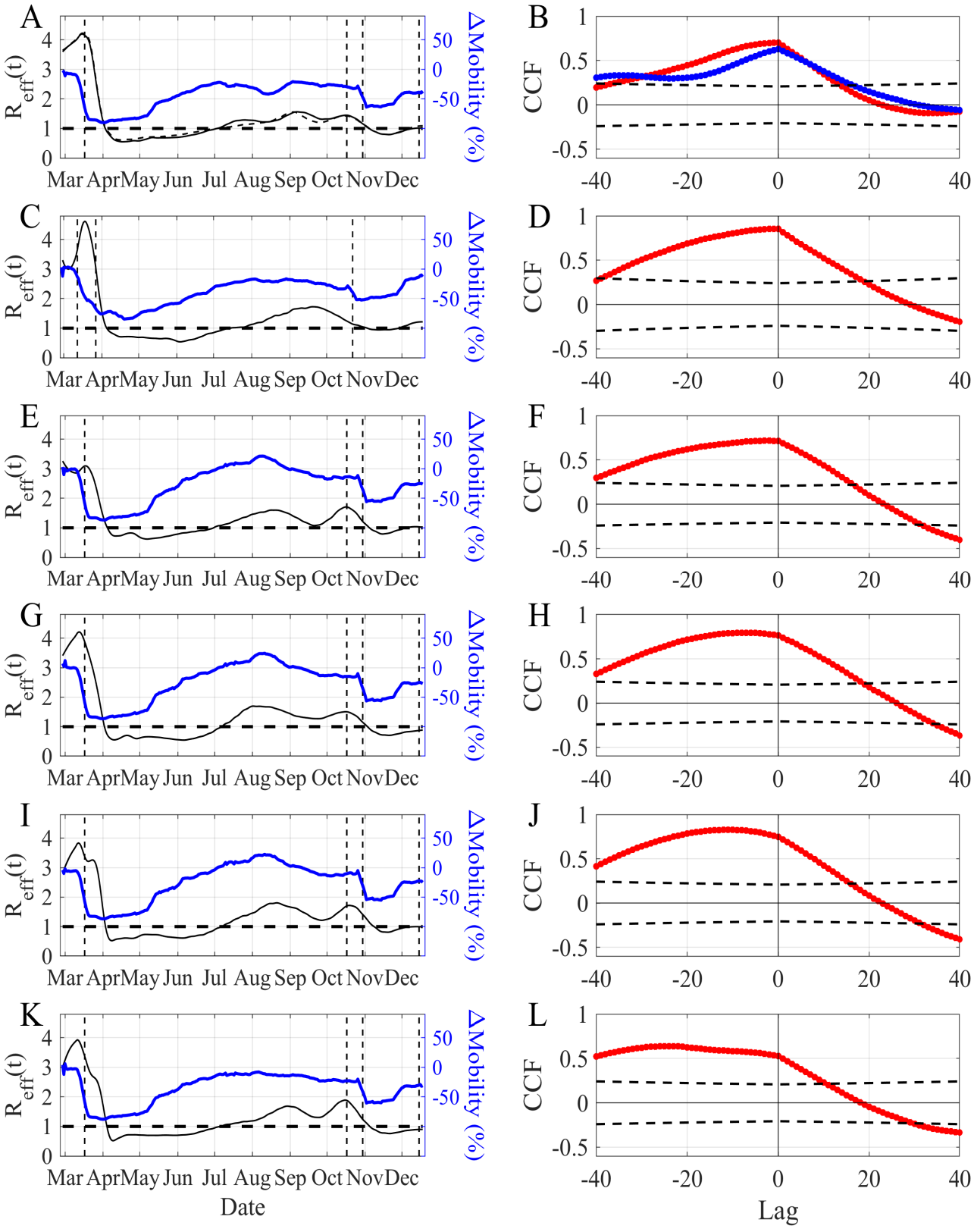

FIGURE A2 – Correlations between the effective reproduction number and retail and recreation mobility. Left column : Time evolution of the estimated $R_{eff}(t)$ (black line) and retail and recreation mobility (blue line). Right column : Cross-correlation functions between the estimated $R_{eff}(t)$ and retail and recreation mobility computed between 15-05-2020 and 15-10-2020. The dashed black lines delimit the significant region at 0.1%. (A-B) Ile de France region, (C-D) Ireland ; (E-F) Provence Alpes Côte d'Azur region, (F-G) Occitanie region, (H-I) Nouvelle-Aquitaine region, (J-K) Auvergne Rhône Alpes region.

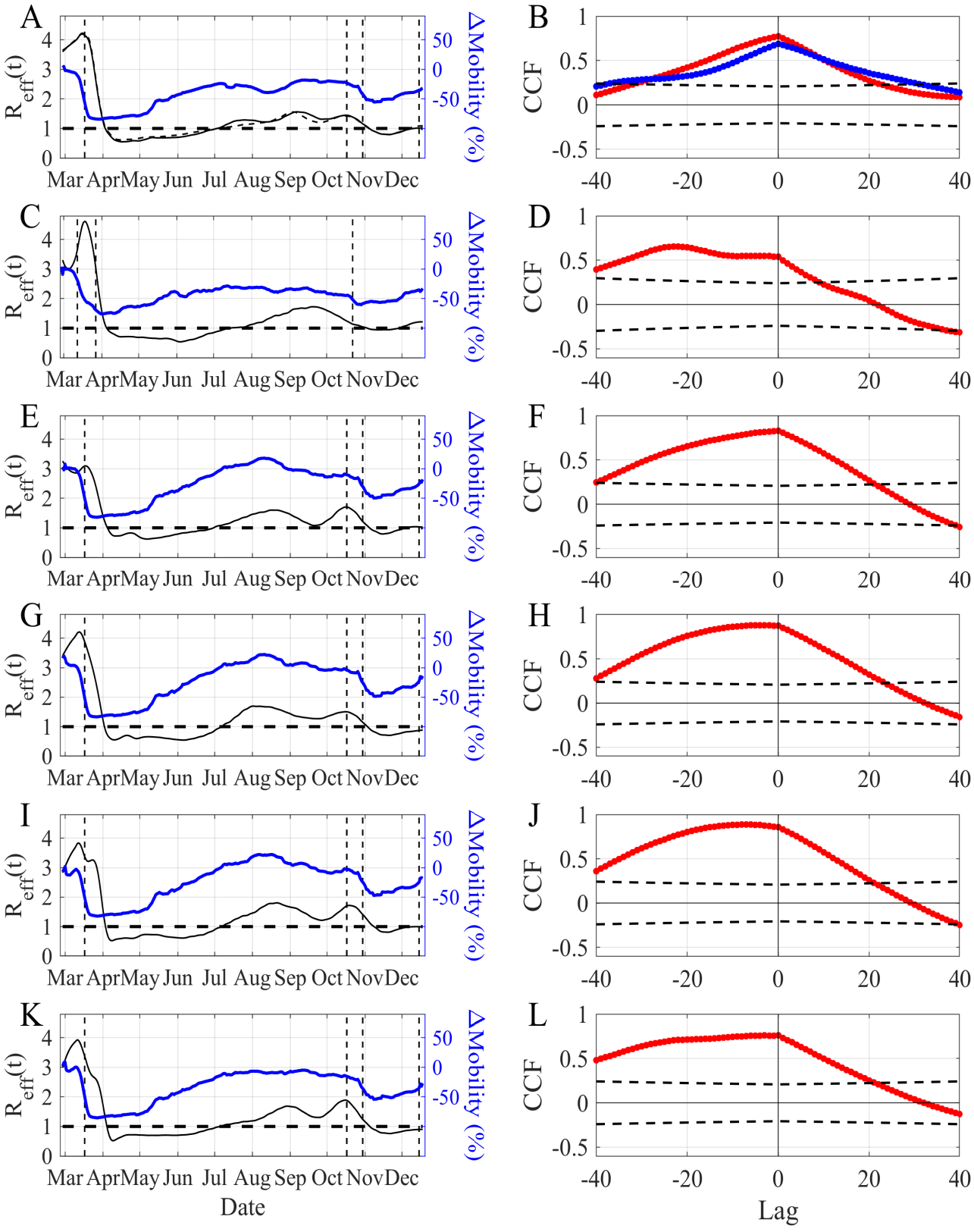

FIGURE A3 – Correlations between the effective reproduction number and public transport mobility. Left column : Time evolution of the estimated $R_{eff}(t)$ (black line) and public transport mobility (blue line). Right column : Cross-correlation functions between the estimated $R_{eff}(t)$ and public transport mobility computed between 15-05-2020 and 15-10-2020. The dashed black lines delimit the significant region at 0.1%. (A-B) Ile de France region, (C-D) Ireland ; (E-F) Provence Alpes Côte d'Azur region, (F-G) Occitanie region, (H-I) Nouvelle-Aquitaine region, (J-K) Auvergne Rhône Alpes region.