A model for COVID-19 spreading

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- We have ℓ regions, where each region can correspond do a "regione" or a "provincia."

- For each region r we will consider a compartment model, for example SIR. (We can consider also more accurate models, but let's start simple.) Let us consider a particular region r.

- At compartment r, at time t, the total population $N_r(t)$ is divided into three groups: $S_r(t)$, $I_r(t)$, $R_r(t)$.

- $S_r(t)$: People who are *susceptible* at time t, those who can contact the disease. Initially the whole population.

- $I_r(t)$: People who are *infected* at time t, those who currently have the disease and can infect others.

- $R_r(t)$: People who are *removed* at time t, those who have passed the disease and cannot get again infected.

- The standard equations are:

$$\frac{dS_r(t)}{dt} = -\beta_r \cdot \frac{I_r(t)S_r(t)}{N_r(t)}$$
$$\frac{dI_r(t)}{dt} = \beta_r \cdot \frac{I_r(t)S_r(t)}{N_r(t)} - \gamma_r \cdot \frac{I_r(t)}{N_r(t)}$$
$$\frac{dR_r(t)}{dt} = \gamma_r \cdot \frac{I_r(t)}{N_r(t)}$$

- Typically there is only one region r and there exist closed form solutions by making t continuous. Here we want to extend and we will use the model for simulations.

- We consider some fixed time unit, x days (e.g., $x = 1, 3, 5, 7, 10$)

- As a start we can assume that the population movement between the regions is fixed, that is, for each r: $N_r(t) = N_r(0)$.

- The parameter γ_r is probably fixed and independent of the region $\gamma_r = \gamma$.

- Instead we should change the infection rate. Let $L_{r',r}(t)$ be the number of people from r' who traveled to r during t. Then we could replace the term

$$\beta_r \cdot \frac{I_r(t)S_r(t)}{N_r(t)}$$

with

$$\beta_r \cdot \frac{\left(I_r(t) + \sum_{r' \neq r} p_{r'} \cdot L_{r',r}(t) \cdot \frac{I_{r'}(t)}{N_{r'}(t)} + o_r(t) \right) S_r(t)}{N_r(t)},$$

where $p_{r'}$ captures the change in the probability that someone who is infected will travel (we can have it equal to 1 initially), where as $o_r(t)$ captures the probability that someone is infected from externas sources (e.g., international travel).

Also the parameter β_r can be region-independent ($\beta_r = \beta$), and we should also probably make it depend on the measures taken.

0.1 Modeling the parameters

Each of the set of parameters $\beta_r(t)$, $o_r(t)$, and $p_r(t)$ depends on various factors, including the cultural behavior of the people in the particular country, or region and on the measures adopted by the govenment to reduce the epidemic.

We consider the following potential restrctions [**?**]:

label	Name
R^1	school_closing
R^2	workplace_closing
R^3	cancel_public_events
R^4	restrictions_on_gatherings
R^5	close_public_transport
R^6	stay_at_home_requirements
R^7	restrictions_on_internal_movement
R^8	international_travel_controls

Define

$$x_r^i(t) = \begin{cases} 1, & \text{if } R^i \text{ is in place in region } r \text{ during period } t, \\ 0, & \text{otherwise.} \end{cases}$$

Now we can use them to define the parameters of the model.

$o_r(t)$ depends only on R^i, so we could models it with a simple linear regression:

$$o_r(t) = \alpha_r^o \cdot x_r^8(t) + c_r^o.$$

$p_r'(t)$ is a probability and depends only on R^7, so we can use a logistic model:

$$\ln \frac{p_r(t)}{1 - p_r(t)} = \alpha_r^p \cdot x_r^7(t) + c_r^p.$$

The other restrictions affect the intra-regional infection rate, so we use them to model $\beta_r(t)$:

$$\beta_r(t) = \sum_{i=1}^{6} \alpha_{r,i}^\beta \cdot x_r^i(t) + c_r^\beta.$$

Important variants to try.

- We can consider a model where p_r is constant depending on the region r, given that the restrictions have an effect on the flow.

- Here all the parameters are different for different regions. We can can also try a model where they are the same; for instance $o_r(t) = o_r'(t)$, $p_r(t) = p_r'(t)$, and so on. For different countries it should be different though.