

ECON 605 - APPLIED MICROECONOMETRICS  
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**Applications of Transfer Learning  
With The SIR Model**

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I hope to present a novel approach to assessing the movements of a disease or virus in one region, recognize it, then recognize similar movements elsewhere to create a map that minimizes the response time by policymakers. For instance, if we know the behavior of COVID-19 across one city or state, with certain parameters, we can predict the movement of COVID-19 elsewhere. Transfer learning allows for world-class work with fewer resources and less data. Not many people have published any research on this. Thus, I want to apply this to the SIR model and see if we can find a new, faster approach to predicting disease and virus spread.

To motivate this idea, transfer learning is defined in terms of domains and tasks. A domain  $\mathcal{D}$  consists of a feature space  $\mathcal{X}$  (which is just a vector space with vectors of explanatory variables and we need this to do statistical inference), and a marginal probability distribution  $P(X)$ , where  $X = \{x_1, \dots, x_n\} \in \mathcal{X}$ . Given some domain,  $\mathcal{D} = \{\mathcal{X}, P(X)\}$ , a task has two parts, that is, a label space  $\mathcal{Y}$  and an objective prediction function  $f : \mathcal{X} \rightarrow \mathcal{Y}$ . The function  $f$  is used to predict the corresponding label  $f(x)$  of a new instance  $x$ . The task is denoted as  $\mathcal{T} = \{\mathcal{Y}, f(x)\}$ , is learned from the training data, which consists of pairs  $\{x_i, y_i\}$ , where  $x_i \in X$  and  $y_i \in \mathcal{Y}$ .

Given a source domain  $\mathcal{D}_S$  and learning task  $\mathcal{T}_S$ , a target domain  $\mathcal{D}_T$  and learning task  $\mathcal{T}_T$ , where  $\mathcal{D}_S \neq \mathcal{D}_T$  or  $\mathcal{T}_S \neq \mathcal{T}_T$ , transfer learning aims to help improve the learning of the target predictive function  $f_T(\cdot)$  in  $\mathcal{T}_T$  using the knowledge of the domains,  $T$  and  $S$ .

The SIR model is a simple compartmental model with three parts. First,  $\mathcal{S}$  is the number of susceptible individuals. When someone in the set of  $\mathcal{S}$  gets infected, he moves to  $\mathbf{I}$ .  $\mathbf{I}$  is the number of infected or infectious individuals. They are capable of infecting susceptible individuals,  $\mathcal{S}$ .  $\mathbf{R}$  is the number of removed (and immune, or recovered) or deceased individuals. We construct these variables as a function of time,  $t$ , that is,  $\mathcal{S}(t), \mathbf{I}(t), \mathbf{R}(t)$ . This model is set in continuous time,  $t \in [0, \infty)$  and individuals are partitioned into groups,  $j = 1, \dots, J$  with  $N_j$  initial members. We normalize this such that  $\sum_{j=1}^{\infty} N_j = 1$ .

Moreover, the dynamics of  $\mathbf{I}$  depends on the following ratio,  $R_0 = \frac{\beta}{\gamma}$ , known as the basic reproduction number. We arrive to this fraction from examining the time between contacts,  $T_c = \beta^{-1}$  and the typical time until removal,  $T_r = \gamma^{-1}$ . Thus, the number of contacts by an infectious individual with others before the infectious are removed is  $T_r/T_c$ . Simple operations give us our ratio,  $R_0 = \frac{\beta}{\gamma}$ .

So I am still thinking how to infuse this with transfer learning to build a tractable model. One avenue I will try to take is through Recurrent Neural Networks to see if embedding the outputs of the SIR will make a difference, but I am not sure yet. I believe that for some state  $i$  we can embed the outputs into our transfer learning model and minimize the outputs that are outside some confidence interval, given some prior distribution. Essentially, we can

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parameterize our new model such that layers become vectors, and we can make inference out of the predictions.