Chiara Poletto
EPIcx-Lab, INSERM & UPMC UMR S 1136
chiara.poletto@inserm.fr
chiara-poletto.weebly.com
Hôpital St Antoine, 27 rue Chaligny, 75012, Paris

The research work within the EPIcx-lab is devoted to the spread of infectious diseases seen as a complex system phenomenon. Pathogen epidemics result from the concurrence of mechanisms taking place at different scales from the pathogen/immune system interactions to the contagion mediated by human contacts, up to the spatial propagation on the top of the human mobility network. A wide array of quantitative approaches needs to be combined to tackle open questions in infectious disease epidemiology, such as network theory, reaction-diffusion models, information theory and advance statistical approaches.

We are seeking a candidate to work on one of the following internship projects. In each case the internship can be followed by a PhD on the same subject.

Analysis visualization and modeling of influenza global circulation
The four circulating subtypes of seasonal influenza virus show a complex dynamics with patterns of subtype dominance/co-dominance highly variable across countries and seasons. The unpredictability of the virus composition of an approaching season is a major obstacle to the public health attempt to contain and mitigate the disease. Despite worldwide data of subtype distribution by country are freely available from the FluNet platform, little has been done so far to characterize the phenomenology of the co-circulation dynamics, as emerging from these data, and identify its drivers. The student will analyze FluNet (co-)dominace time-series obtained for each country with the goal of identifying spatiotemporal correlations, quantifying their level of predictability and establish causal links. A wide array of data analysis approaches can be deployed, such as motif extraction, clustering, information theory, Bayesian networks. In particular, permutation entropy[1, 2] will be used to quantify the level of complexity of a time-series assumed to be linked to its degree of predictability. On the other hand, Dynamical Baysian Networks technique[3, 4] will be used to establish causal associations. This technique, introduced for the study of gene regulatory networks, can successfully capture relationships among variables of different nature (e.g. linear, non-linear, combinatorial, stochastic and other type of relationships). In this context DBN will allow identifying causal links between (co-)dominace time-series and possible socio-environmental drivers, such as local weather, demography and local mobility. The student will take care of the design and implementation of the data analysis algorithms, along with their use to characterize the behavior of the spatiotemporal co-circulation dynamic.

[1] Bandt C, Pompe B, Phys Rev Lett, 88, 2002
[2] Garland J, James R, Bradley E, Phys Rev E, 90, 2014

[3] Trairatphisan P, Mizera A, Pang J, Tantar AA, Schneider J, Sauter T, Cell Commun Signal, 11, 2013
[4] Berestovsky N, Nakhleh L, PLOS ONE, 8 2013

Multi-scale modeling of pathogen emergence dynamics

The ecological dynamics of infectious diseases is often driven by the competitive interaction between different variants of the same pathogen. Novel variants emerge through mutation and their fate (rapid extinction or wide spread in the population) is driven by the co-occurrence of biological mechanisms taking place at different scales, from the pathogen/immune system interaction, occurring within the individual, to the human-to-human transmission and spread ruled by human behavior. A multiscale approach is thus needed to characterize the phase space of possible dynamics regimes. The student will be introduced to the metapopulation modeling framework where the infection dynamics is described as a reaction-diffusion process [1,2]. Pathogens are represented as discrete particle units; reaction rules are introduced to describe biological interactions taking place within the individuals (here described as subpopulations of the metapopulation system), and a mechanism of diffusion is introduced to account for transmission from one individual to another. The approach will be used to model the dynamics of an emerging variant of influenza virus (minority variant) and its interaction with the circulating one [3]. The theoretical model developed will thus provide a quantitative ground to explain the structure of viral population observed by ultra-deep sequencing genetic data collected during the course of two influenza seasons in France. The student will take care of model design, its numerical implementation and its use to reconstruct the system phase diagram. The simplicity of the modeling framework will make possible analytical understandings. The project will be in the context of a collaboration with the CNR (Centres de Référence Nationaux for Influenza) at Institute Pasteur.

[1] Colizza C, Pastor-Satorras R, Vespigani A, Nature Physics 3, 2007
[2] Poletto C, Meloni S, Colizza V, Moreno Y, Vespignani A, PLoS Comp Biol 9(8), 2013
[3] Pepin KM, Volkov I, Banavar JR, Wilke CO, Grenfell BT, J Theor Biol 265, 2010