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Systems Biology of next epidemics: 3 dimensions of emergence and ORCHESTRA experience

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Motivation and Aim: Systems Biology aims to understand biological emergence from the interactions of biomolecules, e. g. by integrating the knowledge about these interactions into a computer model and thereby reconstructing biological behavior in silico. In relation to the human, such an in silico replica of the whole body is the so-called Silicon Human. We can add medical aspects to this model and, using the patient's genome, transcriptome, and proteome data, parameterize a Silicon Human for any patient individually (Silicon Patient), for modeling any systems biological disease [1, 2], including so-called Long Covid caused by SARS-CoV-2 virus. On this level, personalized physiological behavior emerges from interactions between biomolecules, like in many other systems' biological models [3–5].

However, when talking about epidemics, there is also a second dimension of emergence. Interactions between susceptible, recovered, immune, or infected individuals lead to the emergence of epidemics. The chance of an individual being infected is now state-dependent on the spread of the virus in the population [6].

Moreover, there is also a third, level of emergence, where interactions between various players (researcher, clinical data manager, medical doctors, nurses, etc) collecting and processing different pieces of data lead to the emergence of the project. We should notice that the scientific concept is evolving during the study and thus the project itself is a Complex Adaptive System. The data collection process becomes state-dependent and data becomes live in a sense that they change with the evolution of the whole system. So, data should become not only Findable, Accessible, Interoperable, and Reusable (FAIR) [7] but also Emergable (FAIRE) and the goal as a systems-forming factor should be incorporated into the design of the network for epidemics-related projects.

Methods and Algorithms: Our of COVID-19 epidemics [6] is a modification of the classical SIER model. Model diagrams were generated using CellDesigner, a graphical front-end for creating process diagrams of biochemical networks in Systems Biology Markup Language. CellDesigner-generated models were transferred to COPASI (www.copasi.org), which is another Systems Biology Markup Language-compliant program, but with a wider variety of analysis options. The comprehensive dynamic model described in vitro data sets from two independent laboratories. The model and its description is available at FAIRDOMHub [8, 9].

Results: In the presentation, I will analyze the lessons from our COVID-19 modeling, where the model of epidemics [6] was performed along with COVID–19–related clinical data management in the ORCHESTRA EU Horizon 2020 project [https://orchestra-cohort.eu/] focused on:

1. Standardizing and harmonizing COVID-19-related data collection methodologies across participating institutions to ensure consistency and interoperability.
2. Facilitating the sharing of COVID-19 data among researchers and public health authorities across Europe to support collaborative research efforts.
3. Promoting collaboration among researchers from various disciplines to conduct comprehensive studies on COVID-19, including epidemiological modeling, vaccine development, therapeutic interventions, and public health strategies.
4. Providing a platform for rapid data analysis and dissemination of findings to inform decision-making and public health responses to the COVID-19 pandemic [10].

Conclusion: Based on the previous System's Biological experience in COVID-19 modeling and ORCHESTRA clinical data management, I will present the next steps, which could facilitate our preparations for the next potential epidemics.

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