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Description

In the previous project, EPIC, we developed a consistent methodological framework for the exploration of disease comorbidity at the molecular level. EPIC provides a first overview of disease interactions from the general level to the one of individual patients. Particularly interesting is the network of patient-subgroups that matches, in a statistically significant manner, previous disease comorbidities extracted from medical records.

We propose to develop a computational framework (EPICstemic) to systematically investigate the underlying basis of comorbidities combining network based approaches (i.e. multilayer networks and AI/ML components) and molecular modeling (i.e. logical models of signaling networks, as well as metabolic models) adapted to the BSCs HPC environment. EPICstemic will be designed to expand the current disease network with additional molecular information (RNAseq and other OMIC datasets), as well as with epidemiological information directly extracted from medical records from two different populations. The deployment of EPICstemic will enable the systematic extraction of temporal comorbidity trajectories associated to patients drug treatments, differentiating cases by gender and age, and linking them to specific molecular entities (potential markers).

Finally, we will collaborate with epidemiologists and medical doctors in the application of EPICstemic to a practical use case. We will study a recently reported complex comorbidity relationship linking COPD, diabetes, asthma and pancreatic cancer, with the aim of providing comorbidity markers associated to each potential comorbidity risk, as well as possible drug treatments to be further explored. In the long run, our aim is to use the experience gained in this pilot project to adapt EPICstemic to its use in medical environments for the study of comorbidities at the level of individual patients.

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