Elucidating drug-drug interactions underlying drug polypharmacy profiles

Supervisors	Cristina Leal Rodríguez, Gianluca Mazzoni
Type	Data analysis
Requirements	Programming in Python and R, Bioinformatics, Cytoscape
Skills	Programming, advanced bioinformatics

Description

Many adverse drug reactions and drug interactions that impact large part of the patient population lead to hospitalizations and substantial healthcare expenses. Often these noxious and unintended responses go unnoticed during the preclinical and clinical trial phases of a drug. Longitudinal data and electronic health records (EHR) have proven to provide potential insights to uncover useful fine-grained phenotyping of individual patients in a real world context. The reuse of this existing clinical data is seen world-wide as a major driver for precision medicine. Over the last years, the Translational Disease Systems Biology group has developed several workflows and pipelines for working with structured (diagnosis, medical procedures, medication) and unstructured (clinical notes, discharge summaries, biomedical abstracts) biomedical and clinical data and has published a number of well cited papers in the field.

This project aims to characterize drug interaction profiles. The student will make use of available clinical and phenotypic data and results from ongoing projects in the group. This includes text mined adverse drug reactions from clinical notes and drug co-exposure profiles. Analysis of the data will help finding out potential biological functions in which drug interactions are involved by using different clustering algorithms and topological network analyses. The results will be compared and overlaid with available knowledge on drug interaction databases (i.e., Drugbank, Micromedex, Interaktionsdatabasen, pharmGKB). The student will be involved in quite substantial efforts in data mining and machine learning, in the use of sensitive big data stored in secure clouds (www.computerome.dk), and in network and integrative data approaches. Lastly, the project also encourages the student to describe the feasibility, advantages and limitations of the approaches used in pharmacovigilance.

References

Jensen,P.B. *et al.* (2012) Mining electronic health records: Towards better research applications and clinical care. *Nat. Rev. Genet.*

Jensen,A.B. *et al.* (2014) Temporal disease trajectories condensed from population-wide registry data covering 6.2 million patients. *Nat. Commun.*, **5**, 1–10.

Eriksson,R. *et al.* (2014) Dose-specific adverse drug reaction identification in electronic patient records: Temporal data mining in an inpatient psychiatric population. *Drug Saf.*, **37**, 237–247.

Gustafsson,M. *et al.* (2014) Modules, networks and systems medicine for understanding disease and aiding diagnosis. *Genome Med.*, **6**, 82.

Mizutani,S. *et al.* (2012) Relating drug-protein interaction network with drug side effects. *Bioinformatics*.