An integrative Systems Biology approach to advance in the understanding and treatment of prostate cancer

Luis Tobalina
tobalina@combine.rwth-aachen.de

David Henriques
henriques@combine.rwth-aachen.de

Julio Saez-Rodriguez
saezrodriguez@combine.rwth-aachen.de

RWTH-Aachen University Hospital, Joint Research Centre for Computational Biomedicine (JRC-COMBINE), Aachen, Germany

PrECISE

Motivation

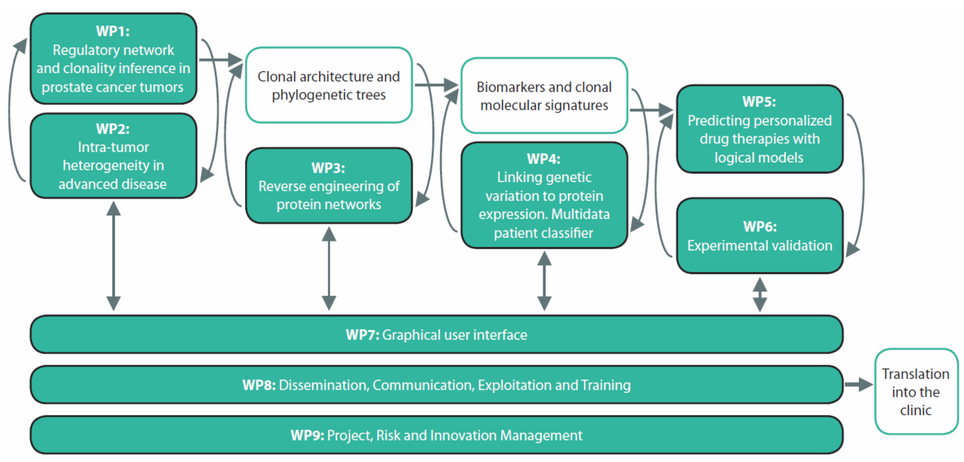
Prostate cancer is one of the top three most common types of cancer affecting men around the world. Screening techniques have allowed the detection of this type of cancer at early stages, yet not all of them will develop into aggressive life threatening tumours. In addition, prostate cancer turns out to be a highly heterogeneous disease, but currently therapeutic regimens are not designed based on tumour profiling.

Objectives

- Development of a comprehensive computational methodology to integrate different sources of data
- Characterization of intra-tumour heterogeneity
- Suggestion of therapeutical strategies
- Development into deployable, easy to use software tools

Description

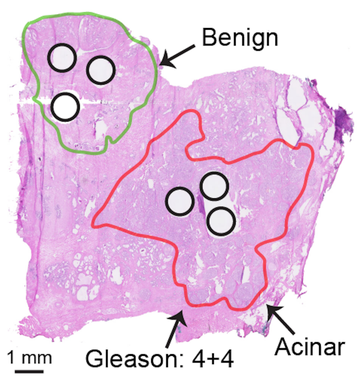
Here, we present the European H2020 PrECISE Project (Personalized Engine for Cancer Integrative Study and Evaluation), an international collaboration that aims to translate into clinical advances many of the technical and methodological developments achieved during the last years.

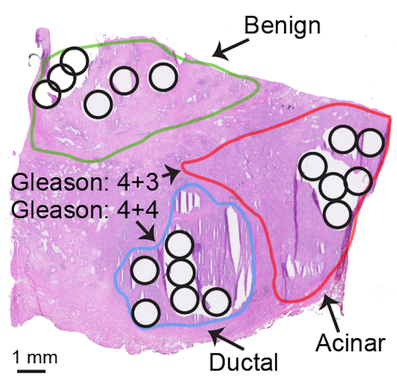


Data

The project will make use of different kinds of data:

- gene expression data
- sequencing and mutation data
- proteomics data
- phosphoproteomics data





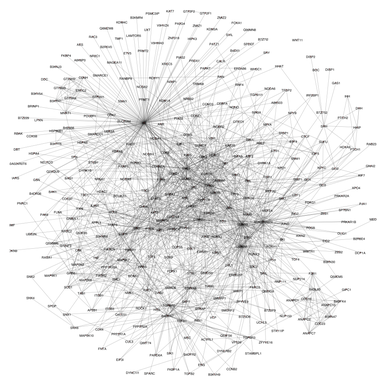
Multiple samples from the same tumour will be taken at different places to study the clonality landscape of prostate cancer.

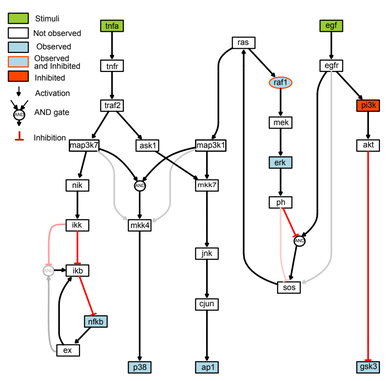
Drug perturbation experiments will be conducted on prostate cancer cell lines and their measurements incorporated into network models.

Methods

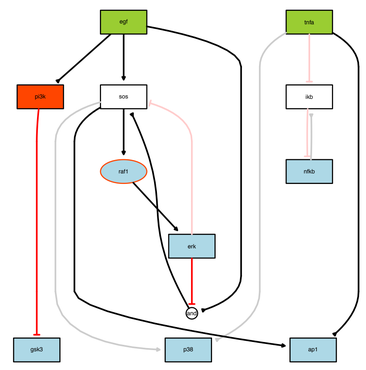
We are currently working on the pipeline to build interaction networks for increasing our understanding of prostate cancer tumours. The wealth of data generated will be encoded into mathematical models, both qualitative and quantitative.

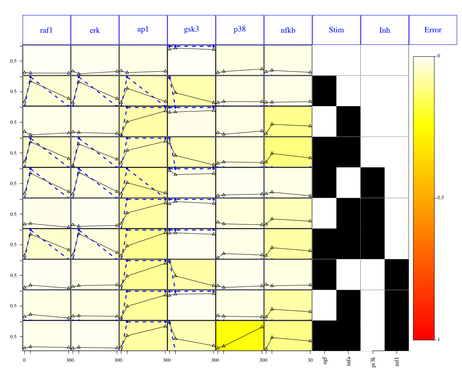
The incorporation of prior biological knowledge into these models will be eased by Omnipath, a new resource that gathers information from several signalling databases.

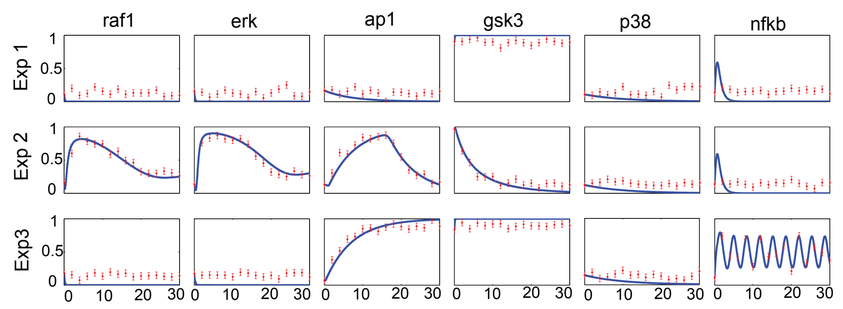




We will use our approaches for logic modeling to model, simulate and make predictions about cell signalling pathways relevant to the biology of prostate cancer.







The models will describe tumor, cell type, patient and clone specific features along with current knowledge on prostate cancer biology. Eventually, they will be used to propose patient focused therapeutic strategies.

Project Partners

IBM · University of Zurich[UZH] · ETH zürich · Technische Universität Darmstadt · Joint Research Center for Computational Biomedicine · RWTH Aachen University · institut Curie · TECHNIKON · Baylor College of Medicine · astridbio

Resources

Project website: www.precise-project.eu

Omnipath: www.omnipathdb.org

CellNOpt: www.cellnopt.org

Funding

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 668858.

This work is supported (in part) by the Swiss State Secretariat for Education, Research and Innovation (SERI) under contract number 15.0324-2. The opinions expressed and arguments employed therein do not necessarily reflect the official views of the Swiss Government.