PrECISE - PERSONALIZED ENGINE FOR CANCER INTEGRATIVE STUDY AND EVALUATION

Newsletter

December 2016 - Issue 2

PrECISE

Main Project Information

The aim of PrECISE is to **improve the treatment of patients suffering from prostate cancer** via identification of disease mechanisms and provision of treatment recommendations based on therapeutic biomarker for individual patients. The main objectives are:

- Development of a **comprehensive computational methodology**
- Characterization of **intra-tumour heterogeneity**
- Suggestion of **chemotherapy drugs** and **targeted therapies**
- Development into **deployable, easy to use** software tools

The expected outcome of the PrECISE project is the development of **a software framework** serving as a proof of concept, that provides intuitive tools to **deposit, share, analyze** and **visualize molecular and clinical data** to **infer prognosis, elucidate implicated mechanisms** and **recommend therapy** accordingly.

In this Issue

Message from the Coordinator

The year 2016 draws to an end and with that we are looking back on a successful first year of the PrECISE project. The first months were characterized by initial activities like literature surveys, feasibility analysis and state-of-the-art research to build a stable basis for the upcoming work. After the first 6 months the consortium met again in Villach, Austria at the premises of Technikon.
The main goal of this meeting was to keep the consortium updated about the ongoing activities of each partner and to foster the collaboration between different research teams.

PrECISE technical meeting in Villach, Austria

Reflecting on year 1, there was an emphasis on dissemination activities of the research interests and the results of the project. Workshops and tutorials were given, talks were held and posters have been presented on well-known conferences. In addition, there have been appearances in video clips and in European TV news sessions. Needless to say, the last month was dedicated to the world famous Movember, where the moustache and November join up together each year to raise awareness of cancer. Partners of the consortium actively joined the movement and helped changing the face of men's health.

Currently the PrECISE team is collaborating on model solutions that allow the formalization of what is already known and what needs to be interrogated. Therefore, the consortium teamed up for special conference calls where respective partners presented their ongoing work in the two work packages mainly dedicated to modelling (WP3 "Reconstruction of protein interaction networks from high-dimensional proteomic maps and IBM-Watson technology", WP5 "Logic models of prostate cancer patients: predicting personalized drug therapies"). The results of this calls are summarized in the following.

Key Data:

Start Date:	1 January 2016
End Date:	31 December 2018
Duration:	36 months
Project Reference:	668858
Project Costs:	€ 5.695.712,50
Project Funding:	€ 3.090.312,50

Consortium:	9 partners (6 countries)
Project Coordinator:	Dr. Klaus-Michael Koch coordination@precise-project.eu
Technical Leader:	Dr. María Rodríguez Martínez mrm@zurich.ibm.com
Scientific Leader:	Prof. Julio Saez-Rodriguez jsaez@ukaachen.de

Project Website: www.precise-project.eu

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Summary of the Presentations on **Modelling**

The **Technische Universität Darmstadt** (TUDA) was the first beneficiary presenting in the modelling calls, talking about network reconstruction via graphical lasso techniques. Network reconstruction aims to understand how products of genes interact and how they are regulated. TUDA worked specifically on protein — protein interaction networks describing how the function and activity of a protein is influenced when interacting with other proteins. They are using computational methods based on graphical lasso techniques to reverse-engineer and interpret these interactions in prostate cancer.

IBM Research Laboratory Zurich (IBM) presented the progress of ongoing work on the building of interactomes of prostate cancer. They are currently taking datasets, databases and publications into account to develop a high performance systems biology network reconstruction. Regarding the datasets, IBM is working on inference methods applied to synthetic data generated using yeast network. For publications, they are working on word embeddings to map words or phrases from the vocabulary to vectors of real numbers as a tool of natural language processing.

Institut Curie (CI) presented their ongoing work on logical modelling of prostate cancer based on resources like like Omnipath and the Human Prostate Cancer Hallmarks Map. They are working on the description of mechanisms that are altered in prostate resistant cancer patients and the stratification of patients based on model solutions (i.e. Phenotypes). The presentation was concluded showing encouraging simulation results coming from the manually curated generic model.

RWTH Aachen University Hospital (UKAACHEN) presented their work on the integration, analysis and extraction of signalling networks from literature curated resources (using the Omnipath database and Pypath). Working on drug response prediction clearly showed that the more data they have for training predictive models, the better performance these will show. Moreover, they showed that gene expression and proteomics provide similar models in terms of predictive performance. Using gene set and pathway methods may provide an additional way to characterize samples and lead to better predictive models.

Baylor College of Medicine Corporation (BCM) showed the collaborating work with IBM regarding cellular composition from exome sequencing. All expressed genes in a genome are called exome — it is the protein-coding region of the human genome. Exome sequencing means reduced efforts compared against sequencing of the whole genome and is therefore very cost-effective. Coding variants including genetic disease and cancer studies can be efficiently identified.

PrECISE Upcoming Public Deliverables

- **D2.1** *Targeted ultra-deep sequencing of cancer-gene loci* **IBM, M12—December 2016**
- **D3.2** *Network reconstruction algorithms for MS data* **TUDA, M12—December 2016**
- **D4.1** *Interactome of molecular interactions in prostate cancer* **IBM, M12—December 2016**
- **D5.1** *Generic model* **CI, M12—December 2016**

PrECISE Public Deliverables submitted

- **D8.2** *Data Management Plan (DMP)* **UZH, M06—June 2016**
- **D3.1** *Computational pipeline to extract prior network information at the proteomic level* **UKAACHEN, M08—August 2016**

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