PrECISE - PERSONALIZED ENGINE FOR CANCER INTEGRATIVE STUDY AND EVALUATION

Newsletter

May 2016 - Issue 1

PrECISE

Main Project Information

The PrECISE project is a **pilot project** that combines **hypothesis-driven strategies** with **data-driven analysis** in a novel mathematical and computational methodology for the integration of genomic, epigenetic, transcriptomic, proteomic, and clinical data with the goal of risk-stratifying patients and **suggesting personalized therapeutic interventions.** The project targets the following specific **objectives**:

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

In this Issue

Message from the Coordinator

The intention of this Newsletter is to open a new communication channel in order to provide news on the project progress and to discuss ongoing topics relevant to PrECISE for internal and external project partners, stakeholders and all other interested bodies. For more detailed information about and around the project we warmly invite you to have a look on our project website, which is constantly kept up-to-date with the latest project related news: www.precise-project.eu. The project has successfully started with the Kick-off meeting in January 2016 at IBM in Zurich and since then the project has been in its initial stages of formation. Regulatory networks have been constructed, sequencing data for 39 samples of the Prostate Cancer Outcomes Cohort (ProCOC) was distributed among the partners, and the foundations for infer clonality were laid. A comprehensive summary about the state of the art methods for the reconstruction of protein-protein interaction networks was provided. Furthermore, the team has started to look at The Cancer Genome Atlas (TCGA) data in order to understand the main mechanisms of disease development, which is necessary to investigate the interactions between different levels of omics data. Moreover, the generic model of prostate cancer is currently in the process of being constructed and the SmartBiobank clinical data storage technology is under development.

The PrECISE project has a well-balanced and focused consortium - comprising nine partners from six countries - and forms a complete chain stretching from basic research and service design, via applied research, up to end-user oriented service providers. It is well-balanced intellectually and geographically and also in terms of the mix of partners involved.

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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Technical Approach

The PrECISE project is planned to run for 36 months. It is organized into 9 work packages (WPs) with significant dependencies and expected synergies between them. **WP1 Regulatory network and clonality inference in prostate cancer tumours** provides the basis for clone identification and associated biomarkers. Therefore, regulatory networks and clonality analyses of proCOC tumour biopsies as well as public prostate genomic profiles are used. **WP2 Identification of sub-clonal genomic alterations** determines sub-clonal genomic alterations and describes intratumour heterogeneity in prostate cancer through protein profiling and ultra-deep sequencing in the proCOC samples an additional selected Castration-Resistant Prostate Cancer (CRPC). **WP3 Reconstruction of protein interaction networks from high-dimensional proteomic maps and IBM—Watson technology** provides data-driven context-specific interaction networks out of the SWATH mass spectrometry for the proCOC samples, prostatic cell lines and public proteomic data. Another focus will be on network reconstruction algorithms that incorporate automatic text-mining capabilities through the Watson cognitive computer. **WP4 Linking genetic variation to protein expression** aims at incorporating genomic, transcriptomic and proteomic maps into a comprehensive molecular map, which is then utilized to detect clusters of proteins enriched in genomic alterations. It shall also identify key pathways and molecular mechanisms that underlie cancer progression specific clones and it shall help to develop a multi-data patient classifier to group patients in clinically meaningful groups. **WP5 Logic models of prostate cancer patients: predicting personalized drug therapies** aims at developing a mathematical model that includes the key molecular players identified in upstream WPs and that can provide a qualitative understanding of cancer underlying molecular mechanisms. **WP6 Experimental validation of prognostic biomarkers and targeted drug predictions** is a validation WP that creates quantitative proteomic and genomic datasets from selected samples. These new data will be used to validate inferred biomarkers and dysregulated pathways. **WP7 Graphical user interface** provides an interface for analyses and prognostic inference from molecular profiles. A dashboard is established that contains all project data in order to select, control, execute or display the analyses. **WP8 Dissemination, Communication, Exploitation and Training** focuses on communication and dissemination of scientific research results achieved within the individual WPs to outside parties as well as to participating entities. Furthermore, this WP will support the partners to exploit the achieved results and impact the European as well as the international market. **WP9 Project, Risk and Innovation Management** ensures a successful project lifetime with respect to all risk and innovation management. There are dependencies to all other work packages as this WP coordinates the tasks so that they are in line with the project work plan in order to reach the objectives of PrECISE.

PrECISE Upcoming Public Deliverables

- D8.2 "Data Management Plan" (M06)
- D3.1 "Computational pipeline to extract prior network information at the proteomic level" (M08)
- D2.1 "Targeted ultra-deep sequencing of cancer-gene loci" (M12)
- D3.2 "Network reconstruction algorithms for MS data" (M12)
- D4.1 "Interactome of molecular interactions in prostate cancer" (M12)
- D5.1 "Generic model" (M12)
- D9.2 "1st Interim Progress Report" (M12)

PrECISE Public Deliverables submitted

- D8.1 "Internal and external IT communication infrastructure and project website" (M03)
- D9.1 "Project quality plan (M03)

Milestone successfully accomplished:

- MS1 "Successful project start" (M01)

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