



The partners of iPC have already developed a variety of open source software within the project. A total of 25 different softwares have been developed within the project framework so far. The factsheet briefly describes three of these - INtERAcT, CONSIFER and DECODE.

**INTERACT** is an unsupervised method for extracting interactions from a corpus of biomedical articles and was developed by IBM Zurich. The software uses a vector representation of words computed on a corpus of domain-specific knowledge and implements a new metric that estimates an interaction value between two molecules in the space where the corresponding words are embedded. INtERAcT is used to reconstruct the molecular pathways of 10 different cancers using corpora of disease-specific articles, using the STRING database as a benchmark. The metric outperforms currently used approaches and is very robust to parameter choices, leading to the identification of known molecular interactions in all cancer types studied. Furthermore, this approach does not require text annotation, manual curation or the definition of semantic rules based on expert knowledge and can therefore be efficiently applied to different scientific domains.

**COSIFER** was also developed by IBM and it's a Python package with a companion web based platform, that provides a service for inferring gene interaction networks from molecular data. COSIFER integrates ten different inference methods, chosen due to their performance, complementary theoretical approaches and scientific acceptance. A user can select different pre-processing approaches, inference methods and consensus strategy to process expression data, and COSIFER returns pairwise interaction networks between the measured molecular entities. Although many methods for network inference have been proposed, no method systematically outperforms all others in terms of robustness and reconstruction accuracy on heterogeneous datasets, and CONSIFER therefore exploits the collective knowledge gathered by a community of complementary inference approaches to produce more robust and stable predictions.

**DECODE** is an easy-to-use and customisable computational pipeline also developed by IBM for extracting binding rules from any black-box model designed to predict the TCR-epitope binding. DECODE provides a set of analysis and visualisation tools to assist the user in extracting such rules. IBM demonstrates the pipeline on a recently released TCR binding prediction model called TITAN, and shows how the quality of the computed rules is demonstrated by the computed rules provided. TITAN achieves high performance in the prediction of specificity of unseen TCRs surpasses the results of the current state-of-the-art by a large margin.

In the list below, you will find the other open source software that were developed within iPC:

### IBM: CURIE: PaccMann BIODICA PaccMann RL CalinTrajAn DeepMS scycle TITAN ElPiGraph MonoNet clustMMRA NaviCell 3.0 BSC: cd2sbgnml iPC text mining workflow CmmD multiAffinity Explainable Synthetic Data BCM: Generator

## UGent:

deconv benchmark deconv benchmark 2.0 XLAB: Patherea

**UNINA: DPFREP** 

LongHorn BigHorn

CHOP: FHIR Data Model

### SHORT PROJECT INFO

Cancer is a very heterogeneous disease that arises in patients with a great variety of genomes, epigenomes and clinical history, and especially the treatment of paediatric cancers presents particular challenges that differ from the treatment of adult cancers. Therefore, the iPC aims to integrate high quality data sources and their analyses using knowledge-based and artificial intelligence models

to increase the performance of individual datasets and improve therapeutic decision-making in paediatric cancers. The project's approach is based on the development of virtual patient models, i.e. in-silico avatars that resemble the molecular and clinical landscape of the paediatric patient and can be used for computer-assisted personalised diagnosis and treatment recommendations. iPC will

therefore develop a computer-based platform that will also allow caregivers to interrogate the models to deduce the pros and cons of specific treatment combinations for each child. More information about iPC and its vision, motivation and objectives can be found on the project website.











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More information about the consortium can be found on the project website

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