JOINT TRANSNATIONAL CALL 2017:

"Translational Research on Rare Cancers"

PARTNER REQUEST/COLLABORATION OFFER

If you would like to have your profile published on the TRANSCAN-2 website, "Looking for a research partner" webpage, please fill out this form and send it to ✉
If you have any questions about this form, please do not hesitate to contact us at ✉

Note: Fields marked with a * are mandatory

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***I agree with the publication of my contact data and of this form on the TRANSCAN-2 Website:**

☑ YES

SEARCH FOR A COLLABORATOR

IF YOU ARE LOOKING FOR A PARTNER IN YOUR SUGGESTED PROPOSAL, PLEASE SPECIFY ALSO THE NEEDED EXPERTISE

Project proposal
Project title (draft):
Short description of the project in preparation and of the consortium; description of the areas of expertise needed (Max. 2000 words):

OFFER FOR COLLABORATION

IF YOU PROPOSE YOURSELF AS A PARTNER IN A CONSORTIUM, PLEASE DETAIL YOUR EXPERTISE

Short description of the areas of interest and expertise (Max. 2000 words):

Mathematical modelling is a mean to analyse and explain biological processes putting together pieces of knowledge and results of experiments in a mathematical form. In the age of massive data generation modelling is a tool to exploit experimental results in an automatic way. Modelling enables to find contradictions in knowledge we have and skip a number of experiments if they become unnecessary after analysis of model behaviour.

We are modellers but our background is different: computer science, control theory, mathematics and biology. We are flexible in terms of object of research as mathematical methods remain the same independent on the organism and process of interest. To enter a new area of research we need specialists of that field to communicate with and to get information suitable for our models. To develop a model we choose the best way to describe the rules known about the process after consulting with specialists of the process of interest. The initial model then is a starting point for iterative improvement of the model performance until the model is acceptable representation of reality. Then usually we start optimisation to learn the optimal dose of a drug, necessary changes in organism or environment aso.

In case of demanding tasks we develop (and sometimes publish) own software (http://biosystems.lv/index.php/software).

Some fields where we have experience:

1. **Kinetic modelling using ordinary differential equations.**

Analysis of process changes in time can be analysed by kinetic models that consist from a set of ordinary differential equations. Time course is a typical product of kinetic modelling.

Our particular strength is the experience in use of global stochastic optimisation methods in parameter estimation and optimisation tasks. In both cases we are implementing different types of constraints to improve the credibility of results. This type of kinetic modeling can be applied for **metabolic pathways, signaling pathways, protein-protein interaction networks, pharmacokinetic/pharamacodynamic, therapeutic effects on networks and others.**

Our main modeling tool is the software COPASI. We have used COPASI alone and in combination with COPASI wrapper SpaceScanner to manage parallel optimisation runs of global stochastic optimisation methods.

2. Boolean modelling.

Boolean modelling is applied when detailed information about interactions of elements in networks is not available and model elements have just “0” or “1” values. This kind of modelling was initially applied for gene regulation networks and Boolean modeling turned out to be highly effective. Now there are several modifications of this approach available and the spectrum of applications has grown to **wide spectrum of regulatory and signalling networks.**

For Bollean modeling we use GinSim, CellNetAnalyzer and Cellcollective software tools.

3. Stoichiometric modelling of metabolism.

Stoichiometric modeling approach can be used for analysis of feasible steady states (metabolite concentrations are not changing in time) of metabolic network and minimally need information just about reaction stoichiometry. Additional constraints like lower and upper bounds of fluxes, reaction directionality and others can make the model predictions more accurate. Small amount necessary of information per reaction enable development of large models.

That has enabled the development of human metabolic reconstruction Recon2 (Thiele et al., 2013, Nature Biotechnology) with 7440 reactions and 5063 metabolites in it. The work is continued at Recon3 with much more elements in it. That is also a basis for creation of cell specific models. There is a convenient platform – Virtual Metabolic Human (https://vmh.uni.lu/) - for application of mentioned tools.

The genome scale models can be used for **personalised analysis of metabolism as well as for drug predictions for metabolic diseases**. Recent publications underline the potential of genome scale metabolic models to predict **anticancer drug targets** for various cancer types (Robinson and Nielsen, 2017, Current opinion in systems biology).

We have used several software platforms COBRA, ScrumPy and COBRApy.

We have developed some software for stoichiometric modeling like Paint4Net for COBRA, AltFluxes for COBRA.