Services offered by ISBE

Service/Tool Name	Description	Contact	Mode of access
doRiNA	doRiNA is a database for RNA binding protein binding sites and microRNAs	Altuna.akalin [at] mdc-berlin.de http://dorina.mdc-berlin.de/	Open access
methylKit	methylKit is an R package for DNA methylation analysis and annotation from high-throughput bisulfite sequencing. The package is designed to deal with sequencing data from RRBS and its variants, but also target-capture methods such as Agilent SureSelect methyl-seq. In addition, methylKit can deal with base-pair resolution data for 5hmC obtained from Tab-seq or oxBS-seq. It can also handle whole-genome bisulfite sequencing data if proper input format is provided.	https://code.google.com/p/methylkit	Open access
genomation	This is an R package that contains a collection of tools for visualizing and analyzing genome-wide data sets. The package works with a variety of genomic interval file types and enables easy summary and annotation of high throughput data sets with given genomic annotations.	http://bioinformatics.mdc-berlin.de/genomation/	Open access
Web app under development for cell type determination from omics data	Computational analysis: Determination of cancer sample type identity from molecular signatures such as gene expression, SNPs and copy number variation Approach applicable for subtype detection and survival estimation Currently applicable to cancer setting		Open access with selection procedure based on scientific soundness and technical feasibility of the project (CORBEL Open Call)

	Support for proper data processing		
ISBE.NL **Dynamic network modelling and model analysis**	Modelling service 1. Building the network diagram for modelled process in SBML format (Systems Biology Markup Language) with CellDesigner - open source software (http://www.celldesigner.org/). 2. Converting network diagram into a toy dynamic model in COPASI (another open source software www.copasi.org). 3. Fitting the dynamic model to experimental data. 4. Model analysis; e.g. sensitivity analysis, looking for network targets, metabolic control analysis etc. 5. Available datasets will be used to refine and tune the model. **Online self-learning course** ISBE.NL provides an online self-learning course in systems biological modelling, where a customer will be able to download standard models, follow online tutorial steps, address questions about the model and the biology of the model, obtain the answers, check them with the online test system, and thereby learn modelling as well as the utilization of pre-existing models. If any question arises, there will be an option for contacting the instructor.	alexeykolodkin [at] @gmail.com H.V.Westerhoff [at] uva.nl	Open access with selection procedure based on scientific soundness and technical feasibility of the project (CORBEL Open Call)
FAIRDOM	Data and model management service facility for systems biology. It enables Systems Biology projects to make their Data, Operating procedures and Models, Findable, Accessible, Interoperable and Reusable (FAIR).	http://fair-dom.org/ http://fairdomhub.org	Open access to FAIRDOMHub, open source data and model management platform.
e-cyanobacterium	model and experimental data repository dedicated to cyanobacteria	ecyano [at] fi.muni.cz http://www.e-cyanobacterium.org	

PRODAN	Access to the new and easy to use proteomic data analysis software PRODAN ,which can analyse mass-spectrometry based high-throughput proteomic dataset - differential expression analysis between control and non-control groups - basic analysis and visualization of differentially expressed proteins - direct vs indirect interactome analysis - condition centric gene ontology and pathway enrichment analysis - clustering - cluster centric gene ontology and pathway enrichment analysis - protein interaction network reconstruction and visualization - complex identification in PPI networks functional analysis of identified protein complexes	Tapesh Santra prodanhelpdesk [at] gmail.com http://www.prodanonline.com/index.html	
Systems metabolomics facility	Access to a state-of-the-art metabolomics facility to obtain data specific for systems biology-oriented modeling. • Untargeted Profiling of Primary Metabolism by GC- or LC-QTOF Mass Spectrometry • Metabolic profiling Metabolic Flux Analysis	info [at] sysbio.it http://www.sysbio.it	
COSYS - COmputational SYStems Biology platform	SYSBIO Italy web modelling services, currently available in beta version (first stable version: end of march 2017): - a data analysis layer, with various omics tools, such as new bioinformatics methods for transcriptome analysis and PPI map design - simulation of biological systems, using deterministic	helpdesk-cosys [at] sysbio.it http://www.sysbio.it/isbe	Open access with free registration (registrations are used only for stats)

	and/or stochastic methods, accelerated on GPU to reduce calculation times, for: -multi-level models of yeast metabolism, growth and cell cycle, molecular dynamic models of various cell cycle modules (G1/S transition, onset DNA replication, etc.) -constraint-based models of cancer metabolism - constraint-based models of yeast metabolism - an inference layer to estimate unknown parameters required for simulation, or for reverse engineering of parts of the model		
Toolbox for easy network analysis in plant sciences	*Arabidopsis thaliana* and *Solanum tuberosum* knowledge network, consisting from manually constructed model on hormonal signalling and data available from different public resources on PPI, transcriptional regulation and co-expression.	kristina.gruden [at] nib.si	
SteatoNet model	SteatoNet model plus SysBio library: Systems Biology library, which can be used straightforwardly in the design of complex systems medicine and systems biology models in Modelica environment.	adviti.naik [at] fri.uni-lj.si	