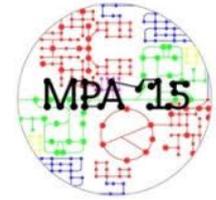


## Participants list in the MPA 2015 conference poster sessions



### Poster session 1: Tuesday 9th June (5 pm - 8:00pm)

Title	Presenting author
Integrated Contextualisation and Analysis of Metabolic Networks	Thomas Pfau
Shifts in the bacterial metatranscriptome accompanying draught in Namibian agricultural soils	Sixing Huang
FECorr: An algorithm to improve FBA predictions using transcriptomic data	Abdelmoneim Desouki
Impact of intermediate toxicity on the regulation of metabolic pathways	Jan Ewald
Dynamic constraint-based modeling of phototrophic metabolism	Alexandra-Mirela Reimers
Genome-scale and Flux modeling in the Lemnaceae ( <i>Spirodela polyrhiza</i> ) isoprenoid pathway for predictive metabolic engineering	Nadine Toepfer
Biofuel production with cyanobacteria: new strain design strategies revealed by computational modeling.	Philipp Erdrich
The steady-state assumption for oscillating and growing systems	Arne Reimers
Evaluation of methods for the reconstruction of specific models from omics data	Sara Correia
Investigation of physiological impacts of knockout mutants using a genome scale model of Arabidopsis.	Kailash Adhikari
Hub Reactions in Storage of Selected Compounds in Heterotrophic Plant Cell Network.	Marie Beurton-Aimar
Drug target identification in a <i>Salmonella Typhimurium</i> metabolic model	Hassan Hartman
A comparison between Flux Balance Analysis and cellular constrained models of simplified metabolic networks	Hugo Dourado
Flux variability analysis to understand <i>Arabidopsis</i> response to sulfur limitation.	Alex Calderwood
Interpreting systematic properties of the tomato photorespiratory metabolism by using a genome-scale metabolic model	Huili Yuan
Ancestral metabolic networks and phenotypic evolution in <i>E. coli</i>	Tin Yau Pang
Reconstruction and validation of <i>iTR383</i> , a genome-scale metabolic model for <i>Helicobacter pylori</i> 26695	Tiago Resende
The severity of enzyme mutations strongly influences the number of affected metabolic pathways	Deya Alzoubi
Dynamic modelling of cell metabolic behaviour: A work in progress	Mario Jolicoeur
A Model for the Expression Dynamics of the Nicotinic Acid Degradation Pathway in <i>Pseudomonas Putida</i> KT2440	Noah Mesfin
Imputing enzyme kinetic constants	Martin Lercher
Dynamic metabolic flux analysis of hybridoma cells cultivated in perfusion mode	Sofia Fernandes de Sousa

Reconstruction of a genome-scale metabolic model for <i>Actinobacillus succinogenes</i>	Sonia Carneiro
Metabolic modeling of microalgae growth and lipids production during day/night cycles and nitrogen starvation	Caroline Baroukh
Visualizing omics data in the OptFlux workbench	Paulo Maia
Mathematical models of glucosinolate metabolism in plants	Suraj Sharma
Evaluation of carbon sources for recombinant enzymes production in <i>E. coli</i> – an <i>in silico</i> analysis of the host metabolism	Sindélia Freitas
In silico analysis of retinoid metabolism	Jennifer Chase
The evolutionary footprint in metabolic genes of <i>Arabidopsis thaliana</i>	Ahmad Mannan
Flux balance analysis of integrated host-virus metabolic models	Sean Aller

#### Poster session 2: Thursday 11th June (5 pm - 8:00pm)

Title	Presenting author
An adaptive scenario for the origins of complex innovations	Claus Jonathan Fritzeimer
TDPS - Turnover dependent phenotypic simulation: a quantitative constraint-based simulation method that accommodates all main strain design strategies	Rui Pereira
The effect of light on the evolution of C <sub>4</sub> plants	Esther Sundermann
Context-specific metabolic model extraction based on regularized least squares optimization	Semidan Robaina
Analysis of pathways involved in glycerol fermentation by two novel anaerobic bacteria	Alfons Stams
<i>Escherichia coli</i> redox metabolism for the production of polyhydroxybutyrate using different substrates	Mariana Velasco Alvarez
Markov-Chain Monte-Carlo sampling of metabolite concentrations to identify thermodynamically feasible reaction directionalities for flux balance analysis	Ulrich Wittelsburger
Enhancing the production of mannosylglycerate in <i>S. cerevisiae</i> through <i>in silico</i> driven metabolic engineering	Cristiana Faria
Metabolic analysis of EBPR phosphate/glycogen accumulating organisms	Leonor Guedes da Silva
SAT-based Metabolics Pathways Analysis without Compilation	Sabine Peres
Exploring the Consequences of Species Heterogeneity in <sup>13</sup> C-Flux Analysis: A Case Study	Salah Azzouzi
Analysis of 140 published GSMs and identification of the most common representation problems	Paulo Vilaça
Serine and glutamine metabolism in cancer cells.	Anna Zhukova
Including cofactor concentrations into dynamic Flux Balance Analysis	Antonella Succurro

Stochastic modelling of fatty acid synthesis	Elahe Radmaneshfar
Integrated analysis of metabolomics and transcriptomics data in tobacco cultivars grown in various regions of China	Lifeng Jin
<i>GlobalFit</i> : Automatically refining metabolic network models by simultaneously matching sets of experimental growth and non-growth data	Daniel Hartleb
Modeling nutrient assimilation in a species of <i>Chloroidium</i> isolated from the United Arab Emirates	David Nelson
Computer simulation of mitochondrial metabolism in cardiomyocytes during hypoxia	Filmon Eyassu
Phylogenomic signature fluidity in metabolic network of a key species with plant and animal affinities	Bushra Dohai
Integration of biomass functions of genome-scale metabolic models with experimental data reveals universally essential cofactors in prokaryotes	Joana Xavier
VIRTUAL MITOCHONDRION :A Modular and Multi Level Whole-Mitochondrion Model	Jean-Pierre MAZAT
Systems level metabolic pathway analysis for understanding antibiotic resistance in <i>Chromobacterium violaceum</i>	Deepanwita Banerjee
<i>merlin</i> latest developments for pathways analysis	Oscar Dias
Metabolic flux prediction in cancer cells with altered substrate uptake	Jean-Marc Schwartz
Elementary flux mode analysis of irradiance-induced stress acclimation strategies in the thermophilic cyanobacterium <i>Thermosynechococcus elongatus</i> BP-1	Ashley Beck
Uncovering the metabolic capacities of <i>H. pylori</i> 26695 using <sup>13</sup> C labeling experiments	Daniela Marques Correia
Compensatory mechanisms in mitochondrial diseases revealed by computer modelling	Alan Robinson
Analysis of <i>Salmonella typhimurium</i> pathways and metabolic model improvement	Teresa Zangirolami
Elucidate robust redox metabolism of <i>Clostridium thermocellum</i>	Cong Trinh