Nick Jagiella
INRIA ROCQUENCOURT, PARIS, FRANCE
e-mail: `nick.jagiella@inria.fr`
Benedikt Müller[1], Irene Vignon-Clementel[2], Margareta Müller[1], Dirk Drasdo[2]
[1] DKFZ, HEIDELBERG, GERMANY, [2] INRIA ROCQUENCOURT, PARIS, FRANCE

From Data Analysis to Model Parameterization & Prediction of Tumor Growth and Therapy

In order to establish a predictive model for in-vivo tumor growth and therapy a multi-scale model has to be set-up and calibrated individually in a stepwise process to a targeted cell type. As a proof of principle we will present the process chain of model construction and parameterization from different data sources for the EMT6/Ro and the SK-MES-1 cell line.

In a first step the model has been built up and validated with EMT6/Ro mouse mammary carcinoma multi-cellular cell spheroid data from literature. For this cell line it predicted the growth kinetics to be controlled by spatial restrains over a wide range of oxygen and glucose medium concentrations. Only if both, oxygen and glucose are very limiting saturation was observed which the model could explain by cells switching from aerobic to anaerobic glycolysis.

In a seconde step the model was adapted to the SK-MES-1 cell line. The growth kinetics was calibrated quantitatively in comparison with growth curves and qualitatively by image analysis of spheroid cryosections stained for apoptosis and proliferation.