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Predictive biological networks - an EGEE GRID application

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Predicting the effect of perturbations of complex biological systems is key to being able to solve important problems, in particular in the case of human diseases. It is highly likely, that such predictions will have to be based on computer models that represent all relevant components of the networks involved as well as their interactions in sufficient detail and accuracy. Establishment of such models is however complicated by the fact, that relevant parameters are either completely unknown, or can at best be measured under highly artificial conditions. We provide a logical framework for constructing predictive models of such complex biological processes in the absence of accurate knowledge on parameter values. This approach is based on massive parallel simulations and subsequent statistical testing. We have implemented the approach on the EGEE GRID in order to gain sufficient computing power and applied this strategy to predict the effects of drugs on a large cancer-relevant network involving 20 signaling pathways and 767 model components.

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