1048-93-312 **Carsten Conradi*** (conradi@mpi-magdeburg.mpg.de), Max-Planck-Institute Magdeburg, Sandtorstr. 1, 39106 Magdeburg, Germany. *Multistationarity in subnetworks of biochemical reaction networks.* Preliminary report.

The standard model of biochemical reaction networks with mass action kinetics is a set of first order ODEs. The right hand side of this vector ODE is given by the product of the stoichiometric matrix N and a vector of reaction rates. If the matrix N does not have full row rank, the state is confined by a system of affine equations. Multistationarity is then equivalent to a positive answer to the following question: is there a vector of rate constants such that two different positive steady state solutions exist that satisfy the same algebraic constraints?

To answer this question we previously proposed a decomposition of the overall network in subnetworks based on generators of the pointed polyhedral cone defined by the intersection of the kernel of N with the nonnegative orthant. Under some mild constraints each subnetwork can be analysed by the deficiency one algorithm (thus multistationarity can be established by linear inequality systems).

Here we show that multistationarity for the subnetworks can always be established by analysis of linear inequality systems (regardless, whether or not the deficiency one algorithm can be applied). An algorithm to obtain parameterizations of all pairs of steady states is also presented. (Received February 10, 2009)