Lumping of Reaction Networks: Generic and Critical Parameters

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Abstract

Lumping methods reduce biochemical reaction networks by aggregating species concentrations via algebraic conditions that hold globally. We study linear lumping for parameter-dependent mass action systems, asking how lumpability depends on rate constants. Our first result shows that for generic parameters—those ranging over a non-empty open subset of parameter space—exact linear lumping yields only "obvious" reductions: elimination of non-reactant species or projections along stoichiometric first integrals [2]. This characterization extends to product-form kinetics, including Michaelis–Menten and Hill-type rate laws, and structurally explains why parameter-independent approaches such as CLUE [3] often fail to find nontrivial reductions.

Beyond generic parameters, we develop an algorithmic approach to identify critical parameter sets—algebraic subvarieties where non-trivial lumpings become available. Determining critical parameters reduces to solving finitely many polynomial systems, and extends naturally to constrained lumping. For proper lumpings of quadratic systems, covering all networks with at most bimolecular reactions, we provide a complete characterization via block-structured Jacobian conditions. Applications to a self-replicator model [4] and a two-pathway enzyme mechanism show that critical parameters reveal hidden conservation laws, with approximate lumpings available near these values [5].

References

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