



# Hamilton Institute

## Analysis of Metabolic Responses

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Wednesday, March 21<sup>st</sup>, 2007

### **Abstract:**

Predicting the responses of intact cellular systems to environmental and genetic changes has not been an easy task. Two of the major challenges to understand metabolic responses are the structural complexity of the molecular networks sustaining cellular functioning and the non-linearity inherent in the interaction and kinetic laws involved. In the development of metabolic control analysis (MCA), some strategies have been devised to deal with these difficulties.

Regarding network complexity, top-down or modular strategies have been proposed. To deal with non-linearity two assumptions have been made. The first is that metabolic perturbations and responses are small, so that they can be described using a first order infinitesimal treatment. The second assumption is that *in vivo* enzyme catalysed reaction rates are proportional to the corresponding enzyme concentrations. However, many, if not most, of the responses exhibited by metabolic systems subject to environmental changes or genetic manipulations involve large changes in metabolic variables.

To deal with this problem, we proposed an extension of MCA that can be applied to arbitrarily large responses. Control and elasticity coefficients for large changes are defined. These fulfil summation and connectivity theorems, from which expressions for the control coefficients as a function of elasticity coefficients (and the inverse design expressions) are obtained. In addition, the new formalism can be applied in a top-down way to study the control of large metabolic responses in intact cells. This will be exemplified with data reported in the literature.

**Venue:** Seminar Room, Hamilton Institute, Rye Hall, NUI Maynooth

**Time:** 1.30 - 2.30pm (followed by tea/coffee)

Travel directions are available at [www.hamilton.ie](http://www.hamilton.ie)

