A Chemical Perturbation Spectroscopy to Elucidate Dynamic Responses of Cellular Networks

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We have developed a "chemical perturbation spectroscopy (CPS)" approach to apply temporal perturbations to cellular signaling and regulatory networks and measuring the response (eliciting the response function) to such perturbations. The approach is complementary to the "omics" methods that are pervasive in that CPS gives the response of an entire (selected) network to perturbations rather than the action of single components. We have shown that a previously reported model of the cell cycle network in Caulobacter crecentus needs to be revisited to account for the new response function (i.e. the phase resetting curve) obtained by CPS. [1] To augment the CPS studies, we have recently developed an automated microscopy (imaging) and data analysis method that allows measuring >10,000 growth curves of single cells for each experimental condition. The resulting high (statistical) precision measurements allow determination of the exponential growth law, an Arrhenius temperature dependence of the rate constant, size ratio scaling at division, and the functional scaling relation of the temperature-dependent division time distributions.[2] Pulsatile expression of a master cell cycle regular protein allows obtaining synchronization and also provides mechanistic insights into the aforementioned scaling; synch occurs by relaxation of the constant size ratio at division rather than the growth rate constant. Finally, pulsatile changes of the environment allow controllable induction of senescence.

***Keywords* — chemical perturbation spectroscopy, Arrhenius, scaling, single cell, synchronization, Caulobacter crecentus**

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REFERENCES

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