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Systems Biology

S&T Campaign: Materials Research
Biological and Bio-Inspired

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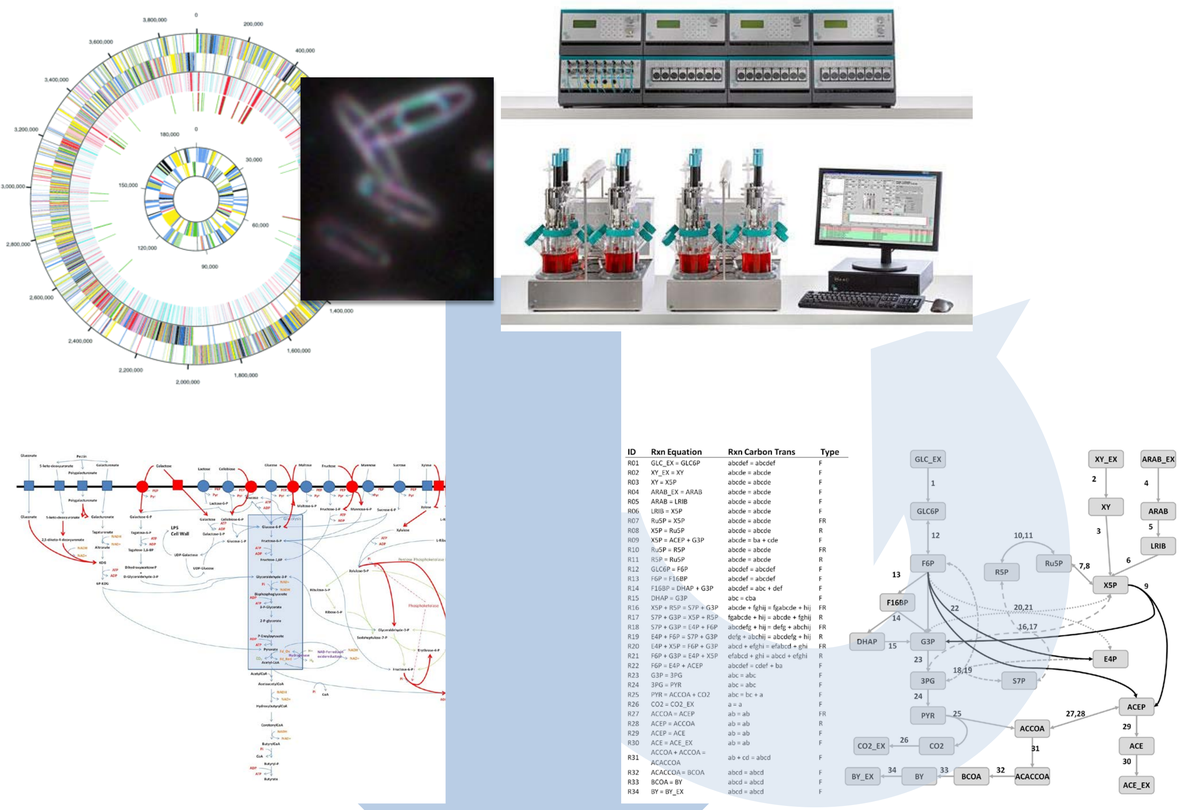
Research Objective

- Model and control microbial metabolism to produce technologies for increased sustainment
- Use state of the art experimentation and modeling to understand, predict, and control metabolism for generation of optimized bioprocesses.



Optimized Bioprocess

Iterative modeling-experimentation process used to understand, predict, and control microbial metabolism.

Challenges

- Current methods track metabolic flux, transcription, etc. in populations and do not capture heterogeneity
- Models of non-model organisms are time consuming to develop and are often inaccurate due to lack of organism specific knowledge
- Need advanced state-of-the-art in modeling heterogeneous systems to include multiple cell types based upon a single genetic code
- Characterize genetic circuitry to determine how individual species modulate responses to ecological conditions such
- Develop the tools for obtaining system-level information on individual cells in populations to better understand how natural phenotypic heterogeneity contributes to population phenotype

ARL Facilities and Capabilities Available to Support Collaborative Research

- Facilities and experience in systems biology of anaerobes
- Advanced capabilities in metabolic network reconstruction
- 12-vessel bioreactor with off gas analysis and in situ metabolite analysis
- Next generation sequencing – ordered
- Multi-Scale Biological Modeling

+

In Situ Raman Spectroscopy

+

Off Gas Analysis

Sund, C. J., Liu, S., Germane, K. L., Servinsky, M. D., Gerlach, E. S., and Hurley, M. M. Phosphoketolase flux in Clostridium acetobutylicum during growth on L-arabinose. Submitted.

Servinsky, M. D., Liu, S., Gerlach, E. S., Germane, K. L., and Sund, C. J. Fermentation of oxidized hexose derivatives by *Clostridium acetobutylicum.* Microb Cell Fact. 2014 Sep 18;13(1):139.

Servinsky, M. D., Germane, K. L., Liu, S., Clark, A. M., Shankar, J. and Sund, C. J. Arabinose is Metabolized via a Pentose Phosphoketolase Pathway in *Clostridium acetobutylicum* ATCC 824. Journal of Industrial Microbiology and Biotechnology. 2012 Dec;Volume 39, Issue 12, pp 1859-1867.

Servinsky, M. D., Kiel, J. T., Dupuy, N. F. and Sund, C. J. Transcriptional Analysis of Differential Carbohydrate Utilization in *Clostridium acetobutylicum*. SGM Microbiology. 2010 Nov;156(11):3478-3491.

Complementary Expertise/ Facilities/ Capabilities Sought in Collaboration

- Increased capabilities in proteomics
- Advanced chromatographic and mass spectrometric instrumentation / expertise for metabolomics

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