

Robot Scientists and model-driven strain design

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The current status of the model-design-build-test cycle will be considered with particular reference to *Saccharomyces cerevisiae* and other industrial yeasts. The strengths and limitations of existing metabolic models will be considered and the use of the *S. cerevisiae* model for strain design for biofuel production presented. The limitations of the current genome-scale metabolic model will be discussed and its improvement using machine-learning techniques, including the use of a Robot Scientist, illustrated. Finally, I will provide a prospectus for the development of a toolbox for the fabrication of multienzyme pathways, their assembly using high-capacity scaffolds, and the wholesale re-engineering of the yeast genome to optimize product formation. This prospectus will focus on the potential of the yeast 2.0 genome for pathway engineering.