Gene targets prediction for products biosynthesis by system biotechnology

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System biotechnology has given us promising methodology and perspective. Unfortunately it keeps the theoretical step yet, so we could not apply their feedback from *in silico*work of system biotechnology to correlatedwet experiment. Nevertheless many research groups try a lot of approaches again to fulfill their object that derives incalculable benefits as a result.

Among the approaches, strain optimization is very important object carrying out system biology. To increase onesproductivity, generally we should select modified gene target on the host genome based on qualitative biological knowledge. But there are immeasurable experimental conditions to verify difference in the diverse characteristics and our experimental perspective should be not sufficient to make best optimized cell. Although someone use common *in silico* tools with no particular strategy for the increasing productivity, it should be exhaustive computational work and their result is too hard to solve and understand. Also, considering complicated cellular property, our experimental perspective should be not sufficient to make best optimized cell. Because of this, strain optimization using methods of system biotechnology, is very attractive and novel approach in biotech and industrial field.

One of the accomplished *in silico* work is metabolic flux analysis which quantifies intracellular metabolic fluxes for characterizing and modifying the cellular processing in metabolic engineering. Based on metabolic flux analysis, we made various *in silico* strategies which were able to predict cell physiology and productivity inspecific disruption condition of interested gene for increasing product yield.

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