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## Description:

The application of microbial community traces back to the beginning of the human culture. Microbial community involves in principle in all the natural bioprocesses. However, due to the complexity of this system, it is difficult to quantify and understand the system dynamics and difficult to control it. This situation impeded the extension of its industrial application.

With the microbial conversion of glycerol with a defined microbial community we work on three new aspects.

**Technologically**, we explore the use of a co-culture of two defined species to develop new bioprocesses for a **more effective bioconversion of glycerol to value-added products** such as diols which have a wide range of applications in the chemical industry and as biofuels.

**Biologically**, the selected co-culture is used as a model system for a minimal microbial community to quantitatively study microbial interactions under controlled physiological conditions. A **two-chamber membrane bioreactor** is used to study the individual behaviour of species and their interactions.

**Methodologically**, mathematical models will be established to describe the kinetics of cell growth and metabolism of the microbial community. For a more fundamental understanding of the individual organisms and the microbial community intracellular metabolic fluxes should be estimated. **Metabolic fluxes of microbial communities** have been seldom studied; therefore the existing methods for flux estimation need to be further developed. The results from kinetic and flux analysis should help to identify possible limiting step(s) and key parameters for the development and optimization of the novel bioprocess.

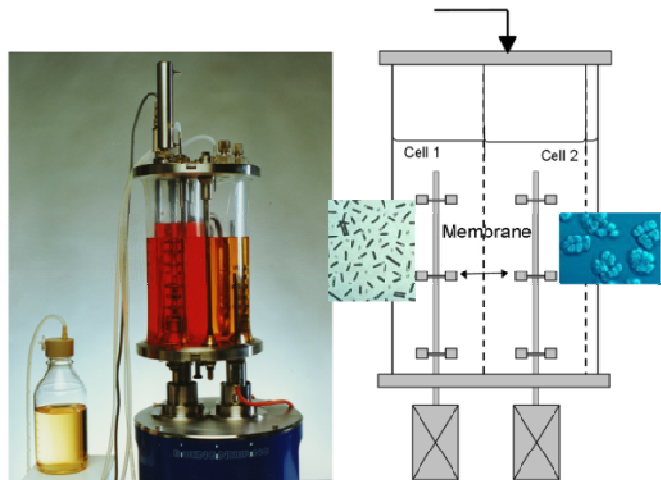


Fig 1: A two-chamber membrane bioreactor for realization of a defined microbial co-culture for glycerol degradation. Chamber 1: Glycerol degrader e.g. *Klebsiella pneumoniae* that produces self-inhibitive by-product such as acetate; Chamber 2: Acetate degrader *Methanosarcina spec.*

$$dX/dt = S \cdot V - b$$

X = Metabolite concentration

S = Stoichiometric matrix

V = Reaction fluxes

b = Net transport out

Steady state

$$S \cdot V = b$$

↓

$$(S \cdot S_{BOF}) \cdot \begin{pmatrix} V \\ V_{BOF} \end{pmatrix} = b$$

BOF = Biomass Objective Function

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Multiple objective optimization

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Fluxes estimated

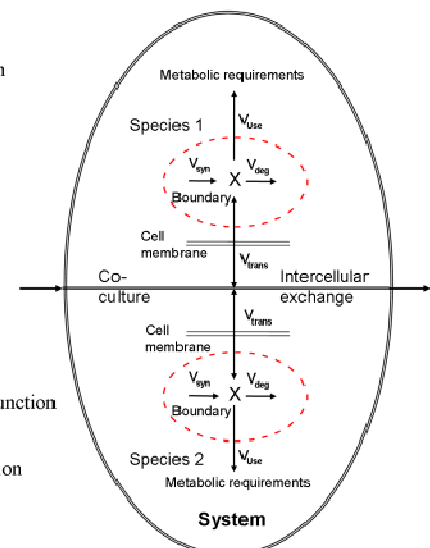


Fig. 2: Scheme for metabolic flux estimation in a microbial community

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