

MATHEMATICAL MODELING OF THE MODIFIED TRICKLING FILTER

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Abstract

A Mathematical Model for the Modified Trickling Filter (MTF) has been developed. The MTF employs polyurethane sponge (PU sponge) as the support media for biomass growth and immobilization. PU sponge offers several advantages over conventional media such as Raschig Rings. The Mathematical model can be an excellent tool to study various aspects associated with the different parameters whose sensitivity can be used for reactor design and calculate the performance.

The model includes many steps describing the biochemical and physicochemical processes. The biochemical processes include the degradation of organic carbonaceous material and ammonia oxidation by the heterotrophs and nitrifiers, respectively. The conversion of nitrates into nitrogen is done by the facultative heterotrophs under anoxic conditions. The physicochemical processes describe mass transport processes and how substrate transport is affected by the microbial reaction within the biofilm matrix.

In brief, the model consists of the following three components:

1. A biofilm model describes the substrate conversion kinetics within the differential section of the biofilm attached to the support media. The stoichiometric equations considered were taken from the literature. The substrate utilization rates were defined using the Monod kinetics and diffusion across the biofilm matrix following Fick's Law. Microscopic mass balance was written for different components within a microscopic differential section of the biofilm. The

component fluxes entering the biofilm surface can be obtained by solving the mass balance equations. These component fluxes can be viewed as the biofilm reaction rate.

2. A Reactor Model describes how biofilm is distributed within the reactor. The compartment model is used to describe the reactor model. One compartment can be considered a Completely Mixed Biofilm Reactor (CMBR). In a CMBR, biofilm is wholly mixed within the compartment.
3. A Reactor Flow Model links the Biofilm Model and the Reactor Model. The Reactor Flow Model describes how each compartment (CMBRs) is connected. The flow model is obtained by summing up all compartments to form the complete reactor. The CMBRs are thought to be connected in series in an MTF.

The rate law expressions for the biofilm kinetics were developed. The process involves converting the Biofilm Model into the dimensionless domain. Then formulating, the rate law expression in terms of dimensionless flux, which depends on a dimensionless number named 'Biofilm Number' (B) and a dimensionless algebraic function named Biofilm Kinetic Function $\Psi(S^*)$. The concept of maximum flux has been developed, equal to the Biofilm Number's square. The effectiveness factor of the biofilm has been formulated using the Biofilm Kinetic Function.

The Mathematical Model of the MTF has been proven using the experimental data from the findings (Shukla, 2021). The spatial distribution of heterotrophs and Nitrifiers plays a vital role in the conversion. The coexistence of Heterotrophs and Nitrifiers within the same biofilm is modeled according to two hypotheses: Bilayer Biofilm and Homogenous Biofilm. The predictions of Model simulations found that Bilayer Biofilm

Model is promising for the experimental data. The growth kinetics of each species strongly influences the structure and spatial distribution of species in the multispecies Biofilm.