A discrete model to study bacterial activity in activated sludge systems in wastewater

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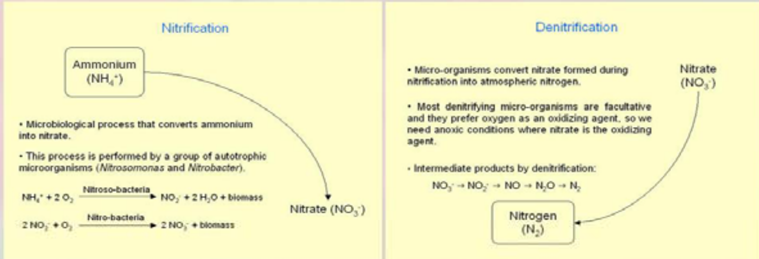
INTRODUCTION

Activated sludge systems have been applied and studied for a long time in wastewater treatments. In fact, several models have been developed in order to understand and interpret the phenomenas and biological mechanisms involved. Nevertheless all the models used are macroscopic models, they are based on average values of some properties of the microbial population involved in these treatments. Since real behavior of individual cells responsible for these transformations and reactions may diverge from average properties. Taking into account the property of biological systems to be discrete, the objective is to develop a discrete simulation methodology that stands on an individual-based model to deal with activated sludge systems in a Sequencing Batch Reactor. The simulator INDISIM-AS controls a set of rules of behavior for each kind of microorganism related to: uptake, metabolism, growth, reproduction, loss of cellular viability, death and lysis, and it also considers processes as organic matter decomposition, nitrification and denitrification.

Biological treatment of wastewater with an activated sludge system

This system takes advantage of the capacity of the micro-organisms, mainly bacteria, to transform organic matter to achieve energy for their cellular growth and maintenance. But biological treatments are used not only to decomposed organic matter, but also to transform N. Through a combination of processes were autotrophic and heterotrophic bacteria are involved, nitrogenous organic and mineral compounds are transformed. These processes are known as mineralization, nitrification and denitrification.



MODELLING ACTIVATED SLUDGE SYSTEMS

Classic models

Several models have been developed, the IAWPRC formed in 1983 a task group to review and promote the development of Activated Sludge (AS) models. The AS Model No. 1 (ASM1) [1] becomes the main reference for many scientific projects and the subsequent models have been implemented (Activated Sludge Model N° 2 - ASM2 [2], an extension of ASM2, the ASM2d [3], and the Activated Sludge Model N° 3 - ASM3 [4]), playing all of them an important role in practice. These models are based on average values of biomass composition (macroscopic models). This is probably a good approach as long as the biomass interacts primarily with cell external compounds. Bacterial communities in AS can store substrates as reserve polymers. The inclusion of storage polymers in the description of microbial growth processes makes relevant the choice of kinetic relations. In ASM2 and ASM3 cell internal storage compounds was also included .

Microscopic versus macroscopic biomass models [5] [6]

Today's models of activated sludge systems are based on average composition of biomass. Since the kinetics of most processes are not linear, adding up the behaviour of individual cells (microscopic models) does not result in the same model prediction as obtained when predictions are made with average cell composition [6].

INDIVIDUAL BASED MODELS [7]

(i) They usually make more realistic assumptions than state variable models.
(ii) They are a bottom-up approach which starts with the 'parts' of a system and then try to understand how the system's properties emerge from the interaction among these parts.
(iii) The simulations provide information on the collective behaviour by looking at the behaviour of each element of which it is composed.

INDISIM-AS, an adaptation from INDISIM to study an Activated Sludge system

INDISIM, a discrete simulation model that stands on individual based methodology to study microbial systems [8] [9]

1. Model the behaviour of each element that is considered outstanding for the evolution of the system in a domain, BIOTIC ELEMENTS (microbial cells) and ABIOTIC ELEMENTS (particles in the medium that represent the different kinds of compounds)
2. ACTIONS IN THE SYSTEM: Flows of these compounds going into/out of the system and periodic redistribution or diffusion of the compounds.
3. Implement the overall model in a computer code, following the behaviour of all those elements acting together.

MODEL OF THE SPATIAL DOMAIN

A cubic space divided into small spatial cells:

$$Domain = Q \times Q \times Q$$

In each spatial cell a set of variables is controlled:

$$D_Q(t) = \{S_{xyz}(w_1(t), w_2(t), \ldots, w_m(t)\}_{xyz=1,2,\ldots,Q},$$

S_{xyz} → a spatial cell of the grid,

w_i → a property depending on time, giving the amount of different types of particles

w_1 : readily biodegradable organic matter (OM)
w_2 : slowly biodegradable OM,
w_3 : inert soluble OM,
w_4 : inert particulate OM,
w_5 : ammonium plus ammonia nitrogen (NH_4^+-N + NH_3-N),
w_6 : nitrate plus nitrite nitrogen (NO_3^--N + NO_2^--N),
w_7 : dinitrogen (N_2),
w_8 : dissolved oxygen (O_2),
w_9 : alkalinity of the wastewater

Flows from complex compounds to simpler compounds due to the enzymatic action (hydrolysis of these macromolecules) and exit and/or input of diverse compounds

MODEL OF THE BACTERIAL POPULATION

A group of N bacterial cells is defined at time *t* with a set of variables:

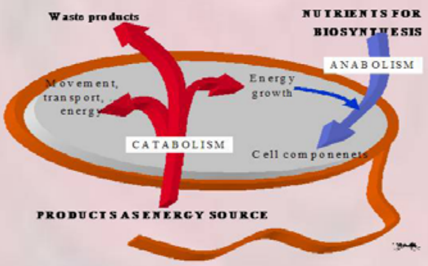
$$P_N(t) = \{n_i(v_1(t), v_2(t), \ldots, v_m(t)\}_{i=1,2,\ldots,N}$$

N = the total number of bacteria

n_i → a bacterium

v_i → gives the value of its individual characteristics

n_1 : biomass,
n_2 : prototype (heterotrophic or autotrophic bacteria)
n_3, n_4, n_5: spatial cell in cartesian coordinates (3D),
n_6 : reproduction biomass,
n_7 : state of its cellular cycle,
n_8: internal amounts of organic matter compounds



FOR EACH BACTERIUM AND TIME STEP IS CONTROLLED

- **Motion**
- **Uptake** of some surrounding particles, depending on diverse factors
- **Metabolism** of these particles in order to *achieve its maintenance energy and to produce new biomass, with the excretion of some end products to the medium. Theys follow different metabolic rules:*
  - *To synthesise new biomass (anabolism)*
  - *To produce energy (catabolism)*
- **Reproduction**
- **Cellular lysis,** with *the return of its biomass into the medium and the release of the non-metabolised internal compounds.*

The **SEQUENCING BATCH REACTOR** process is an activated sludge process in which the sewage is introduced into a Reaction Tank (or SBR Tank), one batch at a time. Wastewater treatment is achieved by a timed sequence of operations which occur in the same SBR Tank, consisting of filling, reaction (aeration), settling, decanting, idling, and sludge wasting.

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