Anaerobic Digestion Model (AM2) for the Description of Biogas Processes at Dynamic Feedstock Loading Rates

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The anaerobic digestion of biomass is a complex, dynamic, and highly nonlinear process. Hence, a mathematical model that is capable of describing the complete operability region with sufficient accuracy cannot be identifiable even with the most advanced process monitoring technology. The complexity of the anaerobic digestion model no. 1 (ADM1) leads to the application of either parameter-reduced versions of the ADM1 or simpler models as, e.g., the anaerobic digestion model AM2. A comparative study for the simulation of biogas formation at dynamic feedstock loading using maize silage was performed with both models.

Keywords: Anaerobic digestion, Anaerobic digestion model, Biogas, Identifiability

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1 Introduction

Anaerobic digestion (AD) for biogas production is an attractive technology, which can contribute to the overall goal for the reduction of fossil fuel energy consumption. However, due to the complexity of the process, a better understanding and prediction of the system is required to take advantage of the full potential of biogas production. Moreover, AD can be operated with various feedstocks in a flexible manner in order to better integrate such systems in dynamic networks, like electricity grids and local carbon cycles, which are oriented to the seasonal availability of substrate [1].

Temporary process instabilities occur from alternating process conditions, however, a poor process performance can typically be solved by adjusting the feedstock load and composition [2], if the problem is diagnosed correctly and promptly. Several suitable models for the complex digestion process to produce biogas were described. The description of the physicochemical interactions among the various biological stages [3] with modifications of the Monod-type kinetic equations for the consideration of the inhibition of volatile fatty acids (VFA) on methanogenesis [4] was the original basis for many models. Approaches, which considered two bacterial groups, namely acid and methane producing microorganisms [5], and even those, which considered four populations, were applied [6]. The latter model type was inspiring for further developments based on four populations, predicting the change of VFA, pH-value, and biogas production [7, 8]. Other models considered that the limiting step can change under altered operation conditions [9] or occurs in hydrolysis of degradable suspended solids [10]. These models were easy to use, but they were unable to describe the process properly under transient conditions. Lyberatos et al. [11] showed that the limiting step of the AD process changes with variable operation conditions, which represents a real challenge in terms of modeling.

Substrate conversion is a central aspect in the modeling of the biogas process [12], especially under transient or generally dynamic conditions. The latter term is understood to describe a state, in which transient conditions are occurring frequently. There are four models, which include more detailed kinetics that consider this type of process mode [13–15], the International Water Association (IWA) AD
model no. 1 – ADM1 [16] and its subsequent implementations [17], respectively.

The ADM1 was used for several applications, such as studies of biodegradability of wastes or substrates like olive mill wastewater [18], municipal solid with activated sludge wastes [19], agro-wastes as apple, pear, orange, rape, sunflower, pig manure, and glycerol wastes [20], and others like maize silage, grass, and cattle manure, which show reliable results [21]. The ADM1 was applied for state prediction from online measurements with pattern recognition. The modelled biogas process was predicted with an accuracy of 90% [22]. Nevertheless, a high computational effort is involved when applying the ADM1.

2 Materials and Methods

2.1 Digestion Process

Data of lab scale digestion was obtained from two continuously mixed reactors of a liquid volume of 50 L. Maize silage was used as feedstock and the experiment lasted 36 days. Most of the time feedstock was added once daily, feeding was suspended during the weekend (two days per week). The temperature was held constant at 39°C (mesophilic conditions). Biogas production, methane and CO2 content in the gas phase, temperature, and the pH-value (7.0) were measured online every hour. The hydraulic retention time (HRT) and organic loading rate (OLR) were 33.09 days and 3.58 kgODMm⁻³d⁻¹, respectively.

2.2 Model Validation

In a second experiment, two 15-L reactors fed with maize silage were investigated. The methane and CO2 content were measured daily. The pH-value was measured online. The process was started with an OLR of 3.165 kgODMm⁻³d⁻¹ for 10 days. After this period, the OLR was increased as follows: 4.22 kgODMm⁻³d⁻¹ (three days), 5.27 kgODMm⁻³d⁻¹ (four days), and 6.33 kgODMm⁻³d⁻¹ (three days). The experiment lasted throughout 20 days.

The concentration of VFAs in the culture broth was analyzed using an Agilent 1200 series HPLC system equipped with a refractive index detector (Agilent GmbH) and a HyperRez XP column (Thermo Fisher Scientific Inc.).

The substrate characterization as required for the ADM1 was applied also for the anaerobic digestion model AM2, which relies on the chemical oxygen demand (COD). In this work, a detailed characterization of the substrate was made for maize silage, applying the described method in [23], see supporting information.

2.3 Software

All models and graphical interfaces were written in Matlab R2013b (Mathworks Inc.). The ODE and DAE simulation were integrated using the SunDialsTB v.2.4.0 suite, OdeSol and Idas, respectively. Parameter estimations were computed using a Gauss-Newton based optimization program included in the TOMLAB optimization environment.

3 Results

3.1 The ADM1 – Evidence of Unidentifiability

Sensitivity analysis was conducted for all parameters to identify those that influence the predicted methane and biogas production rate at most. The study was performed for the 80 parameters of the ADM1 (Tab. S1 in the supporting information) as depicted in Fig. 1. The dilution rate for the feeding was 0.01 d⁻¹ and the substrate was sludge, which was gained from waste water treatment plant (WTP) operated at mesophilic conditions. The process lasted 95 days and the values for the methane and CO2 flow rate were taken every 0.01 d (14.3 min), which was the step size of simulation. Sensitivities with piecewise constant influent conditions were computed. The differential sensitivity analysis was performed keeping all parameters constant except the targeted parameter. This procedure was repeated for all parameters. The order of parameters in the program is shown in Tab. S1. The results of the sensitivity range of the parameters are depicted in Tab. 1. Parameters, which are not listed, were considered as sensitive. It can be seen that 6 parameters were insensitive and 11 parameters exhibited a lower to moderate degree of sensitivity. Sensitive parameters were found, which might cause variations in the output variables. Results indicate the requirement of parameter reduction of the ADM1 for the applied case with an increased identifiability, or alternative models are needed. If the AM2 is a suitable alternative remains to be evidenced in the following.

![Figure 1. Sensitivity analyses of 80 parameters of the ADM1. Shown is the parameter variance of the sensitivity analysis. The normal distribution of variance is 0–0.5.](image-url)
3.2 The AM2

In the AM2, only two bacterial populations are considered, namely the acidogenic and methanogenic microorganisms. The model performs well using sludge when compared to the ADM1 as reference model [24]. Modifications of the original model were implemented, like a term for describing the relation between inorganic nitrogen and alkalinity [24], hydrolysis and growth decay [25]. The model was applied once for the lab-scale description of cheese-way digestion. Although satisfying results were achieved to simulate the experimental data set, the fitting changed throughout the experimental period during 8 days, probably due to a biological adaptation of the microflora as suggested by the authors [25]. In the same study, a simulated data set was used to describe acidification with the AM2 for the purpose of proper parameter identification. So far, the simulation of data of a lab-scale biogas process fed with maize silage was performed once [26]. Therefore, the applicability of the AM2 to a close-to practice operated lab-scale biogas process is evaluated.

3.3 Comparison with ADM1 Model

The AM2 applied to the experimental data using maize silage as a substrate doesn’t fit well when it is compared to the ADM1 simulation (see supporting information). A different profile for the amount of acidogenic bacteria \( X_1 \) is shown between simulations with the AM2 and the ADM1. The methanogenic bacteria \( X_2 \) profile results in a higher concentration when the AM2 is applied. Alkalinity \( Z \) for the AM2 is a horizontal straight line, due to lack of terms, which include the growth rates of bacteria in the differential equation. The organic substrate \( S_1 \) is simulated to be higher in the AM2, in which the hydrolysis process is not clearly defined. The simulation profile for volatile fatty acids \( S_2 \) and inorganic carbon \( C \) are similar when applying both models.

### 3.3.1 AM2 with Growth Decay

As described in [24], the AM2 was applied using maize silage as a substrate, the differential equations of biomasses and the alkalinity were modified from the original AM2 [27]. The differential equations for biomasses \( X_1 \) and \( X_2 \) include the term of the decay rate of biomasses \( X_1 \) and \( X_2 \), \( k_{d1}, k_{d2} \), respectively, see Eqs. (1) and (2).

\[
\frac{dX_1}{dt} = (\mu_1 - \alpha D_m - k_{d1})X_1
\]

\[
\frac{dX_2}{dt} = (\mu_2 - \alpha D_m - k_{d2})X_2
\]

\( D_m \) is the dilution rate; \( \alpha \) is the fraction of bacteria in the liquid phase; \( \mu_1 \) and \( \mu_2 \) are the growth rate of acidogenic and methanogenic bacteria respectively. Terms to consider the contribution of the nitrogen species were integrated in the differential equation describing the alkalinity in the AM2, Eq. (3).

\[
\frac{dz}{dt} = D_m (Z_m - Z) + \left[ (k_1 N_{S1} - N_{bac}) \mu_1 X_1 - N_{bad} \mu_2 X_2 + (k_{d1} N_{bac} \mu_{1max} X_1) + (k_{d2} N_{bac} \mu_{2max} X_2) \right]
\]

\( Z_m \) is the influent value for alkalinity, \( N_{S1} \) describes the nitrogen content of the substrate and \( N_{bac} \) is the nitrogen content in the biomass.

### 3.3.2 Extended AM2

#### 3.3.2.1 Extension for Growth Rates

Three new extensions to the AM2 model of Ficara, et al. [24] were added. The first extension describes the growth rate of acidogenic and methanogenic bacteria, Eqs. (4) and (5), including a term of the pH inhibition, under consideration of a lower bound of \( \text{pH}_{1L} = 5.0 \) [28] and an upper bound of \( \text{pH}_{1H} = 8.5 \) [16].

\[
\mu_1 = \left( \mu_{1max} \frac{S_1}{S_1 + K_S} \right) - \left( \mu_{1max} \frac{S_1}{S_1 + K_S} \exp \left[ -3 \left( \frac{\text{pH} - \text{pH}_{1L}}{\text{pH}_{1H} - \text{pH}_{1L}} \right)^2 \right] \right)
\]

\[
\mu_2 = \left[ \frac{S_2}{S_2 + K_S + \left( \frac{S_1}{K_S} \right)} \right] - \left( \mu_{2max} \frac{S_2}{S_2 + K_S + \left( \frac{S_1}{K_S} \right)} \exp \left[ -3 \left( \frac{\text{pH} - \text{pH}_{1L}}{\text{pH}_{1H} - \text{pH}_{1L}} \right)^2 \right] \right)
\]
3.3.2.2 Extension for Hydrolysis

Hydrolysis is a step in the degradation of a substrate, when composites (Xc), carbohydrates (Xch), proteins (Xpr) and lipids (Xli) are broken into a smaller components. In this work, a description of the hydrolysis process was added to the AM2 from Ficara et al. [24], as in Eqs. (6) – (9).

\[
\begin{align*}
\frac{dX_h}{dt} &= -k_{dis}X_h + D_{in}(X_{ch} - X_h) + k_{dec}X_hX_1 \\
\frac{dX_{ch}}{dt} &= -k_{hyd,ch}X_{ch} + D_{in}(X_{ch} - X_{ch}) + f_{ch,X}k_{dis}X_c \\
\frac{dX_{pr}}{dt} &= -k_{hyd,pr}X_{pr} + D_{in}(X_{pr} - X_{pr}) + f_{pr,X}k_{dis}X_c \\
\frac{dX_{li}}{dt} &= -k_{hyd,li}X_{li} + D_{in}(X_{li} - X_{li}) + f_{li,X}k_{dis}X_c
\end{align*}
\]

(6) – (9)

\(k_{dis}\) is the first order parameter of the disintegration process from homogeneous particulates to carbohydrates, proteins, and lipids. The differential equation for organic substrate concentration, \(S_i\), was modified including the hydrolysis process as described in Eq. (10).

\[
\begin{align*}
\frac{dS_i}{dt} &= D_{in}(S_{i,in} - S_i) - (k_i\mu_iX_i) \\
&+ k_7(k_{dis}X_i - k_{dec}X_1 - k_{dec}X_2) \\
&+ k_8 \left[ (k_{hyd,ch}X_{ch} - f_{ch,X}k_{dis}X_c) + (k_{hyd,pr}X_{pr} - f_{pr,X}k_{dis}X_c) \right] \\
&+ (k_{hyd,li}X_{li} - f_{li,X}k_{dis})
\end{align*}
\]

(10)

\(k_7\) and \(k_8\) are the yield-coefficient of substrate disintegration and the yield-coefficient of carbohydrates, proteins, and lipids, respectively.

3.3.2.3 Extension for High Organic Loading Rates

Eq. (11) was incorporated into the AM2 from Ficara et al. [24] only when high organic loading rates up to 5.0 are present during the process.

\[
R_{OLR} = \tanh \left[ 2.5 \left( \frac{OLR_H - OLR_L}{OLR_H - OLR_L} \right)^2 \right]
\]

(11)

OLR_H and OLR_L are the high and low organic loading rates. This last equation was applied to the CO_2 and methane flow rate equations, \(q_c\) and \(q_m\), respectively [mol m^{-3} d^{-1}]. Eq. (12) and (13).

\[
\begin{align*}
q_c &= K_{fa}[C + S_2 - Z - (K_{H}P_{C})]R_{OLR} \\
q_m &= (k_q\mu_2X_2)R_{OLR}
\end{align*}
\]

(12) – (13)

3.3.3 Comparison Between the Extended AM2 vs the ADM1

The simulations of biogas and methane production and the state variables of the AM2 were compared between the model using the extension from Ficara et al. [24] and the ADM1. The simulations of the AM2 show a delay in the dynamics in comparison to the ADM1 (see supporting information). The acidogenic and methanogenic bacteria \((X_1\) and \(X_2\)) fit well to the ADM1 profiles. The comparison shows that both models simulate a similar tendency for the alkalinity \((Z)\) due to the lack of a term describing hydrolysis in the original version of the AM2. VFA \((S_i)\) and inorganic carbon content \((C)\) simulations of both models have a similar profile.

3.3.4 Comparison of the Extended AM2 vs the ADM1

Measured values and simulation results of the extended AM2 for biogas and the methane production rate of the first experiment in a 50-L reactor, which was discontinuously fed with maize silage, are depicted in Figs. 2b and c. Model outputs for gas production and online data correspond well. During the process, a decrease of the gas formation...
rate appeared due to reduced feeding, as it was the case after the 5th, 13th, 20th, 27th, and 34th day of operation. The period of time of each feeding into the reactor lasted 15 min. The organic loading rate is depicted in Fig. 2a. A comparison between biogas and methane production simulated with the ADM1 and AM2 is depicted in Figs. 3a - b. AM2 outputs for gas production and ADM1 values corresponded well.

The output of variables of the modified AM2 simulation $X_1$, $X_2$, $Z$, $S_1$, $S_2$, and $C$ are compared with the corresponding results of the ADM1 (see Figs. 4 and 5). The predictions of both models of the portion of acidogenic and methanogenic bacteria ($X_1$ and $X_2$) are very close to each other. The simulated profile of the organic substrate ($S_1$) depicts quite well the fluctuations caused by the discontinuous feeding into the reactor. The time course of the VFA concentration, alkalinity, and inorganic carbon content reflects this feeding profile as well. In these cases, the simulations of the two models are close to each other. The ADM1 simulates lower VFA concentrations due to a more diverse consumption of carbon and due to an increased number of conversion reactions. If this reflects a decreased overall prediction capability for the VFA content is further investigated during an acidification driven by an increased loading rate of the substrate in a follow-up experiment. The differences between experimental data and model simulation values for both, the biogas and the methane flow rate, were less than 7 %, which are acceptable for the process.

The simulation of the components of each variable from the ADM1 is shown in Fig. S5.

Key model parameters, which result in a satisfactory simulation of methane and biogas, are obtained through calibration, the initial values are taken from [27]. Output values are depicted in Tab. 2.


The 24 parameters of the extended version of the AM2 that can exert an influence on model results, were subjected to a sensitivity analysis. The order of analyzed parameters was the same as indicated in Fig. 6. Simulation outcomes of the sensitivity analysis when applied to the AM2 show that parameters $k_2$, $k_3$, and $k_{dis}$ are most insensitive, as can be seen in Fig. 6. The parameters $k_5$, $k_6$, and $k_{dec,cat}$ exhibit a low degree of sensitivity; all other parameters are considered as sensitive parameters. In general terms, the sensitivity analysis depicted six parameters with a low degree of sensitivity, but the ADM1 yielded twelve parameters of eighty, as shown in Fig. 1. Among the AM2 parameters, which are sensitive, are $k_1$, $k_4$, $k_7$, $k_9$, $\mu_{1\text{max}}$, $\mu_{2\text{max}}$, $K_{s1}$, $K_{s2}$, $K_{d1}$, $K_{d2}$, $K_{\text{hyd,ch}}$, $K_{\text{hyd,pr}}$, $K_{\text{hyd,li}}$, $f_{\text{ch,xc}}$, $f_{\text{pr,xc}}$, $f_{\text{li,xc}}$, and $K_{\text{dec,cat}}$. The parameters $k_1$, $k_4$, $K_{s1}$, $K_{s2}$, and $K_{d2}$ are from the original AM2 related to the substrate degradation, yield of CO$_2$, and half-saturation constants, respectively. They are markedly correlated to the equations for organic substrate, volatile fatty acids, and organic carbon in the model; $k_{41}$ and $k_{42}$ are both the decay rates of biomass, which are needed to obtain the real growth profiles of bacteria. $K_{s6}$, $K_{\text{hyd,ch}}$, $K_{\text{hyd,pr}}$, $K_{\text{hyd,li}}$, $f_{\text{ch,xc}}$, $f_{\text{pr,xc}}$, $f_{\text{li,xc}}$, and $K_{\text{dec,cat}}$ are parameters for the hydrolysis process, however, they have strong significance for the prediction output.

Still, since sensitivity analysis and model comparison are valid only in a restricted vicinity of the parameter values, the results obtained have a local nature. In the study conducted by [24] the ADM1 and AM2 were compared against each other. Parameter estimation was performed to adapt the AM2 further using the original values of the AM2 and a benchmark substrate. A new state variable accounting for the inorganic nitrogen was added. For the sake of keeping the simple structure of the AM2, the reaction terms of the new state were directly incorporated into the total alkalinity state variable. Along with the new state variable, two new parameters were introduced. The first one describes the nitrogen content of the organic substrate and biomasses, the second one the nitrogen content in the biomass, taken up from or released into the environment [24]. At a steady state, both the original and the extended version of the AM2 predict the outcome of all parameters well, except the ones pertaining to the inorganic states. In the original AM2 inorganic nitrogen ($S_{an}$) is neglected [24], while ADM1 defines alkalinity by Eq. (14), which involves the difference between cation ($S_{cat}$) and anion ($S_{an}$) concentrations in the solution and inorganic nitrogen. The alkalinity constituents in Eq. (14) are bicarbonates, VFA, hydroxide ions, and free ammonia. Neglecting nitrogen affects the bicarbonate equilibrium, especially the amount of ammonium bicarbonate ($\text{NH}_4\text{HCO}_3$) [24]. Deviances arise in the predicted amount of methane. Results of the original AM2 [24] indicates that due to the absence of the description of free ammonia inhibition, the growth of methanogenic populations is increased. Therefore, the simulation of methane production is actually higher in the AM2.

$$Z = S_{cat} - S_{an} + S_{in}$$  \hspace{1cm} (14)
3.4 Comparison with Original AM2

The AM2 is able to describe the experimental data of the biogas process using maize silage as a substrate, however, deviations from the real process appear in the biogas and methane rate production. The simulation made by the AM2 provides lower values than the experimental data after days 6, 13, and 28 when there is a two days period without feeding (see supporting information).

3.5 Experimental Study 2

In order to assess the quality of the optimized parameter set and their applicability in a biogas process, a validation study was performed. The model outputs were compared to measured data from an anaerobic digestion process conducted in two 15-L scale digesters operated at mesophilic conditions. The process was simulated applying the same implementation as described above without changing the previously optimized parameter set. The comparison of model outputs included experimental data for methane, CO₂, and volatile fatty acids. The OLR was increased in the following sequence during 20 days of the process: 3.16, 4.22, 5.27, and 6.33 kg ODM m⁻³ d⁻¹. The methane production increased to a higher value after an initial adaptation phase, and then sharply decreased after the increase in OLR (Fig. 7a). It can be noticed that the model predicted reasonably the dynamic behavior of the process with a slight delay to high values of the organic loading rate.

The simulation of the amount of VFAs in comparison with experimental results of the two reactors is depicted in Fig. 7b. The amount of volatile fatty acids increased due to an excess of organic material at an OLR of 5.27 and 6.33 kg ODM m⁻³ d⁻¹. Biogas production decreased under these conditions, which are known to be unfavorable for some methanogenic microorganisms. Particularly, the increase of the VFA concentration was predicted close to experimental data, although overestimated at the onset.

The standard procedure to increase model identifiability is to detect the parameters with a small sensitivity and high correlation and remove them from the parameter estimation problem. Nevertheless, the selection of these parameters, which are assumed to be highly correlated and of low sensitivity, is performed based on the Fisher Information Matrix (FIM), which is an approximation based on first order derivative information. This very rough approximation is only correct near the vicinity of the exact parameter values used to calculate the FIM. Therefore, ideally, all parameters should be considered in the parameter estimation. In order to take advantage of the information embedded in complex models, but allow its application in industrial plants without the need of improvement of the sensor system, methods to model reduction can be applied to tailor complex models to the needs of industrial processes. Representative examples are lumping [29, 30], sensitivity analysis [31], and time-scale analysis [32 – 34]. Beside many efforts, model reduction techniques still rely on process knowledge and experience in order to achieve the correct reduction of the model. In most cases, a combination of methods and...
case studies is required to achieve the most suitable result. Some examples of the applicability of model reduction in biological processes are available in the literature [35] including its applications for advanced monitoring and optimization [36–38]. However, the complexity of the biogas process and the concomitant limitation in sufficient data limits practical application. Therefore, the AM2 with the extensions made as described in this study seems to be a good compromise for achieving reduced models for the description of AD for biogas production.

4 Conclusions

Advanced methods for optimization and control are required to allow for a dynamic operation of biogas plants while risks of a failed process is kept low. Nevertheless, in order to apply existing computer based methods, a robust and tractable model that is able to predict the dynamics of the process with sufficient accuracy is needed. Biogas processes are known for their complexity and limited installed monitoring capacities. Although many monitoring methods exist [39], their real application is restricted. Hence, existing models need to be adapted to fit the demands of large scale biogas production plants. In other words, models that are tractable and identifiable with the quality of information that is usually available from a biogas plant has to be used.

Nowadays, feed control of full-scale biogas plants is often performed by rules of thumb or simple calculation, although some attempts were made for optimal control of the feed rate at stable operation conditions, e.g., based on the ADM1 [40]. A first step towards a closed loop control is the availability of suitable models. In this study, the AM2 was evaluated for the application at dynamic process operation, caused by a fluctuating feedstock load. The calibration of the AM2 at a pilot-scale biogas plant was only feasible with a verification of the uncertainty in the model parameters, due to the nonlinearity of the biogas process. Very slow reactions occur when anaerobic microorganisms are fed in a dynamic real-time process, so the optimization using a complex and nonlinear process model seems to be a suitable approach. This is of special interest, when the loading rate is changed, e.g., for a better integration of biogas production and energy generation from it into smart systems. Then, a certain variation of the biogas synthesis rate is achieved by changing the feeding intervals, thus, creating a dynamic provision of biogas and energy. First attempts in this way have shown that this concept is suitable to gain a 9-fold variation in the biogas production if the process was fed every two days with dried distillers' grains in lab-scale bioreactors [41]. If more demanding conditions are used, e.g., a combination of rapidly and slowly digestible feedstock, any model-based approach might be useful to predict the feedstock load for various biogas production scenarios and for control purposes.

In this work, the AM2 was further compared to the ADM1 and it was shown that a tradeoff has to be made between model complexity and tractability in order to obtain reliable results:

(1) the ADM1, which is the most complex representation of the process including 36 states and more than 80 parameters.

(2) the AM2, which is a model developed for control purposes and is also tractable with only 6 states.

The ADM1 showed to be non-identifiable, if the data that is obtained in an usual biogas plant is considered. Taking this into consideration, the implementation of the AM2 in an adaptive framework should be preferred.

Symptoms used

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ADF</td>
<td>acid detergent fiber</td>
</tr>
<tr>
<td>ADL</td>
<td>acid detergent lignin</td>
</tr>
<tr>
<td>CA</td>
<td>crude ash</td>
</tr>
<tr>
<td>C</td>
<td>carbon content</td>
</tr>
<tr>
<td>CF</td>
<td>crude fiber content of a substrate in dried form</td>
</tr>
<tr>
<td>cf</td>
<td>conversion parameter in COD</td>
</tr>
<tr>
<td>CL</td>
<td>crude lipid content of a substrate in dried form</td>
</tr>
<tr>
<td>COD</td>
<td>chemical oxygen demand</td>
</tr>
<tr>
<td>CP</td>
<td>crude protein content of a substrate in dried form</td>
</tr>
<tr>
<td>D_m</td>
<td>dilution rate</td>
</tr>
<tr>
<td>DM</td>
<td>dry matter</td>
</tr>
<tr>
<td>f</td>
<td>yield</td>
</tr>
<tr>
<td>FM</td>
<td>fresh matter</td>
</tr>
<tr>
<td>HRT</td>
<td>hydraulic retention time</td>
</tr>
<tr>
<td>k_{A,B}</td>
<td>acid-base kinetic parameter</td>
</tr>
<tr>
<td>k_d1</td>
<td>decay rate of biomass X1</td>
</tr>
<tr>
<td>k_d2</td>
<td>decay rate of biomass X2</td>
</tr>
<tr>
<td>k_{dis}</td>
<td>parameter for disintegration process</td>
</tr>
<tr>
<td>k_{hyd}</td>
<td>parameter for hydrolysis</td>
</tr>
<tr>
<td>k_{La}</td>
<td>volumetric gas-liquid mass transfer coefficient</td>
</tr>
<tr>
<td>k_m</td>
<td>maximum specific uptake rate</td>
</tr>
<tr>
<td>k_p</td>
<td>factor related to the friction of the gas outlet</td>
</tr>
</tbody>
</table>
\[ k_1 \text{[–]} \text{yield for substrate degradation} \]
\[ k_2 \text{[mol kg}^{-1}\text{]} \text{yield for VFA generation} \]
\[ k_3 \text{[mol kg}^{-1}\text{]} \text{yield for VFA consumption} \]
\[ k_4 \text{[mol kg}^{-1}\text{]} \text{yield for CO}_2\text{ production} \]
\[ k_5 \text{[mol kg}^{-1}\text{]} \text{yield for CO}_2\text{ consumption} \]
\[ k_6 \text{[mol kg}^{-1}\text{]} \text{yield for CH}_4\text{ production} \]
\[ k_7 \text{[–]} \text{yield for substrate disintegration} \]
\[ k_8 \text{[–]} \text{yield for carbohydrates, proteins and lipids} \]
\[ K \text{[kg m}^{-3}\text{]} \text{half-saturation constant} \]
\[ K_a \text{[kmol m}^{-3}\text{]} \text{acid-base equilibrium coefficient} \]
\[ K_H \text{[mol atm}^{-1}\text{m}^{-3}\text{]} \text{Henry-coefficient} \]
\[ K_{12} \text{[mol m}^{-3}\text{]} \text{inhibition constant} \]
\[ N \text{[mol kg}^{-1}\text{]} \text{nitrogen content} \]
\[ N_D \text{[mol m}^{-3}\text{]} \text{nitrogen-free extracts} \]
\[ O_M \text{[mol m}^{-3}\text{]} \text{organic loading rate} \]
\[ P_c \text{[atm]} \text{CO}_2\text{ partial pressure inside the fermenter} \]
\[ q \text{[mol m}^{-3}\text{d}^{-1}\text{]} \text{flow rate} \]
\[ S \text{[mol m}^{-3}\text{]} \text{organic substrate concentration} \]
\[ S_1 \text{[kgCOD m}^{-3}\text{]} \text{organic substrate concentration} \]
\[ S_2 \text{[mol m}^{-3}\text{]} \text{VFA concentration} \]
\[ X_1 \text{[kgCOD m}^{-3}\text{]} \text{Concentration of acidogenic bacteria} \]
\[ X_2 \text{[kgCOD m}^{-3}\text{]} \text{Concentration of methanogenic bacteria} \]
\[ X \text{[kgCOD m}^{-3}\text{]} \text{particulate fraction} \]
\[ Y \text{[kgCODX kgCODS]} \text{yield of biomass} \]
\[ Z \text{[mol m}^{-3}\text{]} \text{total alkalinity} \]

Greek symbols
\[ \alpha \text{[–]} \text{fraction of bacteria in the liquid phase} \]
\[ \mu \text{[d}^{-1}\text{]} \text{growth rate} \]

Sub- and superscripts
\[ \text{aa} \text{ amino acid} \]
\[ \text{ac} \text{ acetate} \]
\[ \text{an} \text{ anion} \]
\[ \text{bac} \text{ acetic acid} \]
\[ \text{bu} \text{ butyrate} \]
\[ \text{c} \text{ CO}_2\text{ cation} \]
\[ \text{ch} \text{ carbohydrates} \]
\[ \text{ch}_4 \text{ methane} \]
\[ \text{fa} \text{ fatty acid} \]
\[ \text{hCO}_3 \text{ hydrogen carbonate} \]
\[ \text{h}_2 \text{ hydrogen} \]

Abbreviations
\[ \text{AD} \text{ anaerobic digestion} \]
\[ \text{ADM1} \text{ anaerobic digestion model no. 1} \]
\[ \text{AM2} \text{ anaerobic digestion model} \]
\[ \text{FIM} \text{ Fisher information matrix} \]
\[ \text{IWA} \text{ International Water Association} \]
\[ \text{VFA} \text{ volatile fatty acids} \]
\[ \text{WTP} \text{ water treatment plant} \]

References


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