Modeling microbial response to temperature changes in anaerobic digestion: a novel approach

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Modeling microbial response to temperature changes in anaerobic digestion: a novel approach

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Abstract:

Present work details the inclusion and evaluation of a new, multi-faceted temperature-dependent microbial growth-limiting function in an existing anaerobic digestion model. The function was developed to address flexibility issues related to simulating anaerobic digestion processes with changing temperatures. Finally, the goodness of the extended model was evaluated using monitoring and 16s rRNA gene sequencing data from a laboratory-scale continuous experiment. The newly extended model showed increased flexibility in the simulation of different microbial temperature-dependence profiles. This finding was also supported by the simulation of the experimental data, where the best results were achieved during the shift from the established temperature-effect profile to the novel one. In conclusion, the novel temperature-dependence function was found to produce superior simulations compared to conventional ones and might benefit other, currently used models as well.

Keywords: modeling; microbial growth; temperature

Session: Modelling, instrumentation and control

Introduction

Anaerobic digestion (AD) is a dynamic process, during which relevant bacterial and archaeal species consume, produce and exchange chemical compounds, thus gradually converting insoluble substrates to organic acids and terminal gases. In such a dynamic system, ambient conditions change continuously, putting microbial productivity at potential risk. Fortunately, modeling can support the monitoring and control of these stochastic systems.

Using AD models, nevertheless, comes with assumptions, one of which involves the temperature-dependence of microbial growth. Such growth rates are generally modeled to be uniformly distributed in restricted ranges of mesophilic (20-40 °C) or thermophilic (45-60 °C) temperatures, although practice has shown that they can change significantly during swings in AD temperature or deliberate transitions from one temperature range to another (Lin et al., 2016).

In response to this deficiency, the objectives of present work were (1) to extend a multistep dynamic AD model with a novel, microbial growth-limiting temperature function and (2) to evaluate the model extension, by simulating an experimental study with temperature changes.

Materials and Methods
The AD model (BioModel) selected for the study was developed by Angelidaki and coworkers (Angelidaki et al., 1993), which was extended with a newly developed mathematical expression representing the temperature-dependence of microbial growth (Eq. 1). Considering previous work in the topic (Huang et al., 2011), the function was designed to be applicable for any temperature ranges potentially applied in AD.

\[
G = \frac{T_e \left( \frac{T_{\text{min}}}{T} \right)^{\alpha}}{1 + e^{(T_{\text{opt}} - T_{\text{max}})}}
\]

\[
\frac{T_{\text{opt}} e^{-\left( \frac{T_{\text{min}}}{T_{\text{opt}}} \right)^{\alpha}}}{1 + e^{(T_{\text{opt}} - T_{\text{max}})}}
\]

\[
\mu(T) = \mu_{\text{max}} * G
\]

In the above equations, \( G \) represents the growth-limiting temperature function and \( \alpha \) is a temperature coefficient, while \( \mu_{\text{max}} \) and \( \mu \) are the maximum and temperature-specific growth rates of a microbial group, respectively. \( T_{\text{min}}, T_{\text{opt}} \) and \( T_{\text{max}} \) are the minimum, optimal and maximum temperatures under which a microbial group is assumed to be active. For \( G \) to be conveniently normalized on the range 0 to 1, \( T_{\text{opt}} \) must have the value of \( T \) at which \( G \) is 1.

For model evaluation, a laboratory-scale AD experiment was carried out, using digestate from a thermophilic AD plant (Snertinge) for inoculation and manure as the sole substrate. The experiment was carried out in a CSTR at 53 °C and with an organic loading rate (OLR) of 2 g manure L\(^{-1}\) d\(^{-1}\). In order to simulate short-term temperature disturbances in the system, the reactor temperature was decreased to 40 °C on day 77 and was increased to 60 °C on day 105 for one day. After one day, the reactor was set back to the initial reaction temperature of 53 °C in both cases, resulting in two two-day operation periods under suboptimal temperature conditions. Long-term temperature changes were considered to alter the microbial community structure and were not considered.

**Results and Conclusions**

Through the novel extension and compared to the reference model, microbial growth rate equations became temperature-wise continuously differentiable. This made the model suitable for the potential simulation of large-scale AD processes with stochastic temperature changes. While using the same number of parameters as the reference function of the BioModel, a further advantage of the new implementation is that it can be calibrated to various microbial temperature-dependence profiles. An example for this can be seen in Figure 1, with the respective parameter values listed in Table 1.

<table>
<thead>
<tr>
<th>Reference</th>
<th>ADapT_1</th>
<th>ADapT_2</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \mu_{\text{max}} [\text{d}^{-1}] )</td>
<td>5.1</td>
<td>5.1</td>
</tr>
<tr>
<td>( T_{\text{min}} [\text{C}] )</td>
<td>50.0</td>
<td>50.0</td>
</tr>
<tr>
<td>( T_{\text{opt}} [\text{C}] )</td>
<td>55.0</td>
<td>55.0</td>
</tr>
<tr>
<td>( T_{\text{max}} [\text{C}] )</td>
<td>65.0</td>
<td>60.0</td>
</tr>
<tr>
<td>( \alpha )</td>
<td>0.0</td>
<td>-1.0</td>
</tr>
</tbody>
</table>
Results of the simulations using data from the laboratory experiment can be seen in Figure 2. During the reference simulation of methane production and total volatile fatty acid (VFA) concentration, the temperature parameters used by the growth function were taken from Angelidaki et al. (1993). Meanwhile, for the simulations with the extended model, the parameters were chosen similar to the cases marked $ADapT_1$ or $ADapT_2$ in Table 1 and close to the reference values.

It appears that the extended model with settings according to the $ADapT_2$ case provided the best simulation results, especially regarding the temperature decrease on day 77, which was previously not captured well by the reference model. This indicates that a shift is necessary and possible in modeling the temperature effects on microbial growth in AD, for which an initial solution is provided in this study.
References