COMPREHENSIVE LOCAL SENSITIVITY ANALYSIS OF THE ADM1-BASED ANAEROBIC DIGESTION PROCESS

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ABSTRACT

Anaerobic digestion is a popular method for treating waste and producing biogas. It remains challenging to automate and optimize the operation of the digester because of its complex process and it suffers from great uncertainty. Therefore, it is extremely crucial to understand the influence of different model parameters on the output variables. Although anaerobic digestion processes have been studied extensively, few of these have performed sensitivity analyses. The present study explores the potential effects of varying 48 stoichiometric and kinetic parameters and input variables in the well-known Anaerobic Digestion Model No. 1 (ADM1) on the 35 output variables. The sensitivity analysis enables the identification of key parameters and variables relevant to the model uncertainty. The python implementation of ADM1 was used to identify the system behavior and sensitivity to the input parameters and variables from the mathematical point of view. The analysis provides all the correlations and sensitivity indexes between input variables/parameters and output variables. pH, as one of the critical output variables, shows the highest sensitivity to T_{base}, $k_{dec,ac}$, and $S_{an.in}$, among all parameters and input variables. As another example, methane concentration in the gas phase is sensitive to temperature bases variables, namely T_{base} and T_{op}.

Keywords: sensitivity analysis, ADM1, anaerobic digestion, biogas, local sensitivity analysis.

1 INTRODUCTION

Anaerobic digestion is the process of treating organic matter biochemically in the absence of oxygen [1]. Digestion occurs in digesters and local chambers, where fermentation reactions are regulated and optimized. Anaerobic digestion of organic wastes and industrial byproducts is a multi-stage complex process leading to biogas production, primarily composed of methane (CH_4) [2]. This method of energy generation, which has been used for centuries, is a viable alternative for sustainable energy production. Nevertheless, it does present some challenges inherent in the operation of such a complex and unpredictable system [2]–[4]. The biogas consists of CH_4, CO_2, H_2, and H_2S [5].

The integrated anaerobic model, Anaerobic Digestion Model No. 1 (ADM1), was developed in 2002 by the International Water Association (IWA) Task Group for Mathematical Modeling of Anaerobic Digestion Processes [6]. ADM1 is one of the most common platforms for modeling and simulating anaerobic digestion [7]. ADM1 consists of processes simulating all possible reactions in anaerobic sludge, such as biological and physicochemical reactions. Biological reactions include disintegration, hydrolysis of suspended solids, microorganism uptake (growth), and decay. Ion association/dissociation and liquid–gas transfer are covered in physicochemical reactions [2]. The original ADM1 comprises 35 differential algebraic equations (DAE) organized into five groups used to simulate the concentrations and rates of numerous species in the liquid and gas phases. This categorization and the number of DAEs assigned to each group are shown in Table 1 [8], [9].

Apart from these differential equations, the ADM1 model has many parameters and input state variables, summarized in Table 2, affecting the process's performance [8], [9]. Due to anaerobic digestion's dynamic and nonlinear nature, it is very vulnerable to instabilities and uncertainty. Although most of the over one hundred parameters have precise and predictable

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Table 1: Classification and number of original ADM1 DAEs [8].

Liquid phase equations	
Soluble matter	12
ion states	6
Particulate matter	12
Cations and anions modeling	2
Gas-phase equations	
Gaseous products	3

Table 2: Classification and number of parameters and variables in ADM1 [8].

Parameters	
Stoichiometry	41
Biochemical	36
Physiochemical	25
Physical	2
State variables	
Input state variables	26

values, several are uncertain, such as the uncertain feedstock quality. On the other hand, input state variables in real-world applications are likewise subject to great uncertainty. As a result, the efficient operation of a biogas production unit requires an in-depth grasp of the system's uncertainties.

There are two different approaches to conducting a sensitivity analysis, local and global sensitivity analysis [10]. A local sensitivity analysis considers the sensitivity of a single parameter value change, whereas a global sensitivity analysis considers the sensitivity of the complete parameter distribution [11]. Anaerobic digestion processes have been extensively studied, but sensitivity analyses have been few and far between [12]. Barahmand and Samarakoon [13] conducted an extensive literature review of different approaches to dealing with the uncertainty inherent to anaerobic digestion processes. Baldé et al. [2] performed a sensitivity analysis on ADM1 to determine some ADM1 input state variables and related hydrolysis kinetics. Ramin et al. [14] conducted a global sensitivity analysis using BSM2 on a secondary settling tank in the wastewater treatment plant. They used two different tools to perform this global sensitivity analysis. First, standardized regression coefficients method using linear regression of Monte Carlo simulations and second Morris screening. Using local sensitivity analysis combined with a series of Monte Carlo simulations and a multivariate regression technique, Xu [15] proposed a partial least square method to validate the calibrated parameter set. Solon et al. [16] performed a global sensitivity study on ADM1 to determine the effect of uncertainty on the substrate composition, kinetics, stoichiometry, and mass transfer parameters. Two methods (Morris screening method and standardized regression coefficients) were used to perform the global sensitivity analysis. Trucchia and Frunzo [12] conducted a global sensitivity analysis on ADM1 to calibrate the model parameters.

The present study aims to conduct a comprehensive local sensitivity analysis (one-at-a-time methodology) on ADM1's input parameters and variables to investigate the effect of each on the output variables. This study employs the python implementation of Anaerobic Digestion Model No. 1 [17]. The remainder of the article is organized as follows: Section 2

provides the mathematical structure behind this model, Section 3 provides the results and discusses them, and Section 5 concludes the study.

2 MATHEMATICAL STRUCTURE

2.1 ADM1 mathematical framework

The ADM1 model is a complex nonlinear model commonly used to simulate anaerobic digestion. Anaerobic digestion is organized into five main stages in the ADM1 model: disintegration, hydrolysis, acid genesis, acetogenesis, and methanogenesis (Fig. 1). The first-order biochemical process is assumed for all extracellular processes, while a Monod type is assumed for all intercellular reactions [2]. The influent's chemical oxygen demand (COD) is divided into 13 input state variables, 11 biodegradable, including a composite substrate, carbohydrates, proteins, lipids, sugars, amino acids, long-chain fatty acids, butyrate, valerate, propionate, and acetate. Inert COD is also split into soluble and particulate components [18].

Each substrate was considered as a group of fractions degrading at varying rates. By definition, hydrolysis is the limiting rate for particulate fractions, so their disintegration rate was represented by first-order hydrolysis kinetics [19].

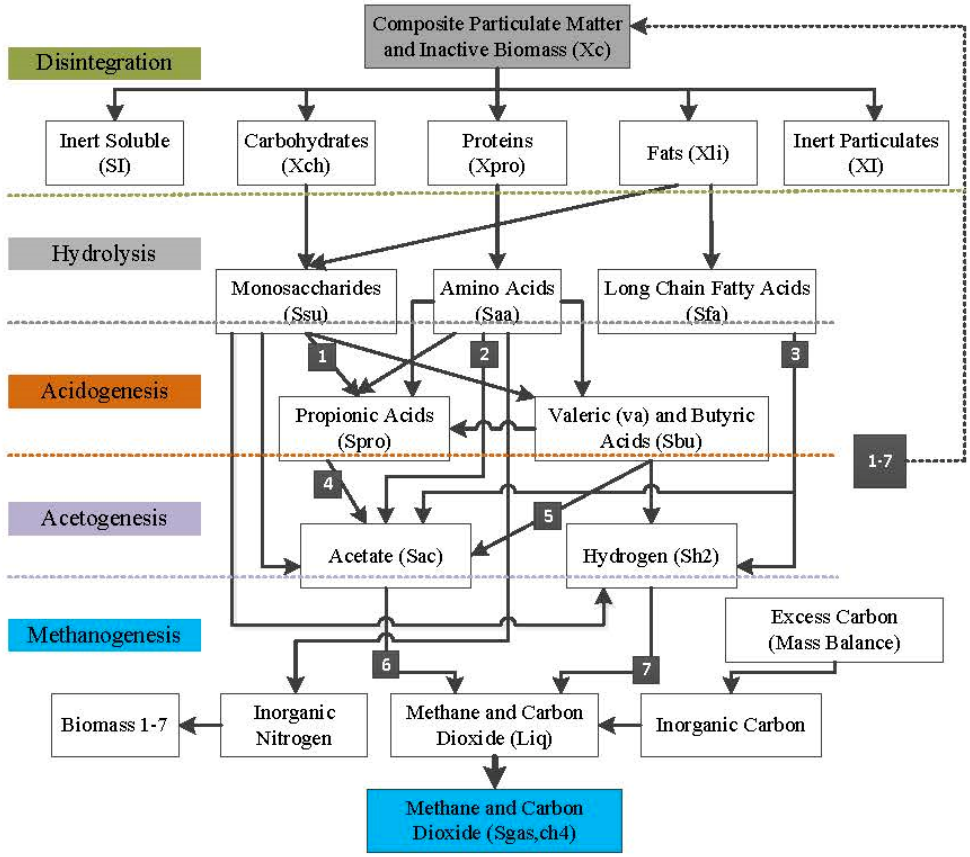

Figure 1: The reaction paths borrowed. *(Source: Adapted from [6].)*

Jeppsson and Rosen [9] implemented ADM1's ordinary differential equation (ODE) model. For the soluble matters, the general form of the differential equations 1–12 can be written as:

$$\frac{dS_z}{dt} = \frac{q_{in}}{V_{liq}}\left(S_{z,in} - S_z\right) + \mathcal{F}\left(\rho_a, f_{product,substrate}, N_c, Y_d, C_e\right), \quad (1)$$

where S_z is soluble substrate concentrations in $kg.COD.m^{-3}$, q_{in} in the influent volumetric flow rate in m^3d^{-1}, V_{liq} is the volume of the liquid in m^3, $S_{z,in}$ is the concentration of the influent soluble substrate in $kg.COD.m^{-3}$, $\mathcal{F}$ represents different functions and variables defined in Jeppsson and Rosen [9]. ρ_a represents 19 biochemical process rates, six acid-based rates, and three gas transfer rates in d^{-1}. $f_{product,substrate}$ is the yield (catabolism only) of the product on a substrate in $kg.COD.(kg.COD)^{-1}$, N_c is the nitrogen content of component c in $k,mole.N.(kg.COD)^{-1}$, Y_d is the yield of biomass on a substrate in $kg.COD.(kg.COD)^{-1}$, and C_e is the carbon content of component e in $k.mole.C.(kg.COD)^{-1}$.

The general form of differential equations 13–24 associated with particulate matters is:

$$\frac{dX_z}{dt} = \frac{q_{in}}{V_{liq}}\left(X_{z,in} - X_z\right) + \mathcal{F}(\rho_a, f_{product,substrate}, Y_d), \quad (2)$$

where X_z is the concentration of particulate component (biomass) z in $kg.COD.m^{-3}$, and $X_{z,in}$ is the concentration of influent biomass z in $kg.COD.m^{-3}$.

The general form of differential equations 25 and 26, cations and anions, does not include $\mathcal{F}$ term.

$$\frac{dS_{cat^+/an^-}}{dt} = \frac{q_{in}}{V_{liq}}\left(S_{cat^+/an^-,in} - S_{cat^+/an^-}\right), \quad (3)$$

where S_{cat^+} is the concentration of cation, S_{an^-} is anion concentration, and $S_{cat^+,in}$ and $S_{an^-,in}$ are input cation and anion all in $k.mole.m^{-3}$. Moreover, there are six differential equations 26–32 for ion states. The general form is:

$$\frac{dS_w}{dt} = -\rho_{A.i}, \quad (4)$$

where S is concentration, ρ is the acid-base rates. w and i are defined in Table 3.

Table 3: Defining w and i in eqn (4).

w	i
va^-	4
bu^-	5
pro^-	6
pro^-	7
ac^-	10
nh_3	11

The last three differential equations 33–35 are related to the gas phase with the general form of:

$$\frac{dS_{gas.u}}{dt} = -\frac{S_{gas.u}q_{gas}}{V_{gas}} + \rho_{T,l}\frac{V_{liq}}{V_{gas}}, \quad (5)$$

where $S_{gas.u}$ is the concentration of gases ($h_2.ch_4.co_2$) in $kg.COD.m^{-3}$, $\rho_{T,l}$ is the gas transfer rates in d^{-1}, and q_{gas} is the gas flow in Nm^3d^{-1}, and V_{gas} is the gs volume in m^3. Except for these differential equations, there are numerous intermediate equations such as biochemical process, acid-based and gas transfer rates, inhibition-related equations, and algebraic equations. Table 4 summarizes the number of equations in the ADM1 model.

Table 4: Classification of the ADM1 equations [9].

Model equations	No. of equations	Model equations	No. of equations
Process rates	**28**	*Process inhibition equations*	**15**
Biochemical process rates	19	*Differential equations*	**35**
Acid-base rates	6	Water phase equations	32
Gas transfer rates	3	*Soluble matter*	*12*
Algebraic equations	**30**	*Particulate matter*	*12*
Soluble matter	14	*Cations and anions*	*2*
Inhibition	5	*Ion states*	*6*
Ion states	4	Gas-phase equations	3
Gas-phase equations	7		

2.2 Sensitivity analysis

This study aims to verify the consequences of parameter variations on the output using the one-at-a-time methodology. Sensitivity analysis [20] is one of the most important steps in uncertainty analyses. Like many other cases, sensitivity analysis is tied with fuzzy set theory. To have a more realistic and robust model, it is crucial to define the fuzzy values accurately for the parameters with higher sensitivity [21]. Moreover, in complex systems such as ADM1, many inputs and outputs interact with each other.

Some input parameters have a positive coloration with the output parameters, and others negative. It is important to be aware of these correlations for uncertainty analysis tools such as fuzzy calculations and arithmetics. In Section 1, two different approaches (global and local) to sensitivity analysis were introduced. Zhou and Lin defined the local sensitivity analysis as "the assessment of the local impact of input factors' variation on a model response by concentrating on the sensitivity in the vicinity of a set of factor values" [22]. Sensitivity analysis can be defined by the sensitivity index (SI) defined below [23]:

$$SI = \frac{\%\ change\ in\ output\ variable}{\%\ change\ in\ input\ parameter}. \tag{6}$$

By changing the value of a single input parameter, the change of an output variable can be calculated, but it cannot be a measure of comparison with other variations. SI is a unitless number that allows one to compare the variations with different scales [24].

The present study selected 48 input variables and parameters to investigate the sensitivity analysis. These variables and parameters were classified into different groups according to their specific biological significance. The groups are biochemical, physiochemical, and physical parameter values and steady-state input variable values. Biochemical parameters include first-order parameters for hydrolysis ($k_{hyd,ch}$, $k_{hyd,pr}$, $k_{hyd,li}$), first-order decay rates for substrates ($k_{dec,su}$, $k_{dec,aa}$, $k_{dec,fa}$, $k_{dec,c4}$, $k_{dec,pro}$, $k_{dec,ac}$, $k_{dec,h2}$), half-saturation values ($k_{m,su}$, $k_{m,aa}$, $k_{m,fa}$, $k_{m,c4}$, $k_{m,pro}$, $k_{m,ac}$, $k_{m,h2}$), equivalent oxygen transfer

coefficient (k_{La}), the concentrations of the six microbial species in influent ($X_{su,in}$, $X_{aa,in}$, $X_{fa,in}$, $X_{c4,in}$, $X_{pro,in}$, $X_{ac,in}$, $X_{h2,in}$), influent substrate's volumetric flow rate (q_{in}), and system temperatures (T_{op}, and T_{base}), etc. On the other hand, as mentioned earlier, there are 35 differential equations needed to be solved. As a result, there are 35 output variables (Table 5). Moreover, *pH* also can be calculated indirectly using an algebraic equation in the ion state using S_{h+}. The full list of 48 input parameters/variables used in the sensitivity analysis is provided in Table 6. These parameters/variables were defined by Batston et al. [6].

3 RESULT AND DISCUSSION

3.1 Simulation setup

To perform this sensitivity analysis study, a python implementation of ADM1 was employed [17]. Initial values are required for the numerical solution of DAEs. As with many differential equation systems, the ADM1 is sensitive to initial values. This study employs these initial values reported in Barahmand [8]. These initial values are listed in Table 5.

Table 5: Initial values at steady-state [8].

Parameters/ variables	Initial values	Parameters/ variables	Initial values	Parameters/ variables	Initial values
S_{su}	0.012	X_{xc}	0.315	S_{h+}	3.45E-8
S_{aa}	0.006	X_{ch}	0.029	S_{va-}	0.012
S_{fa}	0.103	X_{pr}	0.108	S_{bu-}	0.014
S_{va}	0.012	X_{li}	0.026	S_{pro-}	0.016
S_{bu}	0.014	X_{su}	0.421	S_{ac-}	0.212
S_{pro}	0.016	X_{aa}	1.194	S_{HCO3-}	0.143
S_{ac}	0.213	X_{fa}	0.210	S_{CO2}	0.010
S_{h2}	2.44E-7	X_{c4}	0.437	S_{NH3}	0.004
S_{ch4}	0.055	X_{pro}	0.139	S_{NH4+}	0.126
S_{IC}	0.153	X_{ac}	0.749	$S_{gas.H2}$	1.06E-5
S_{IN}	0.130	X_{H2}	0.310	$S_{gas.CH4}$	1.622
S_I	0.320	X_I	25.601	$S_{gas.CO2}$	0.014
S_{cat}	0.040	S_{an}	0.020		

3.2 Sensitivity analysis results

As discussed earlier, local sensitivity analysis is a one-at-a-time methodology that studies the effect of variation in a single input parameter on the output variables when other input parameters are fixed with no variation. Table 6 provides the information about the applied step change for each input parameter/variable. By calculating percent changes in the output variable and applying them to eqn (6), the sensitivity index (SI) associated with each input parameter/variable and output variable can be obtained. Table 7 provides all the significant sensitivity indices (greater than 9e-4). The positive and negative SI indicates the positive and negative correlation between variables. A negative SI occurs when the output variable decreases by increasing an input variable. In the uncertainty analysis (specifically in mathematical approaches), both SI and its sign play a crucial role. For example, in fuzzy set theory, the higher SI means that the fuzzy input variables should be defined as realistic as

possible because the system's sensitivity is high. The sign of the SI, on the other hand, is important when the upper and lower limits (highest and lowest possible outcomes) should be calculated.

Table 6: The variations in the value of input parameters/variables.

No.	Inputs	From	To	No.	Inputs	From	To
1	T_{base}	298	300	25	$S_{va.in}$	0.001	0.0012
2	T_{op}	308	303	26	$S_{bu.in}$	0.001	0.0012
3	k_{dis}	0.5	5	27	$S_{pro.in}$	0.001	0.0012
4	$k_{hyd,ch}$	10	50	28	$S_{ac.in}$	0.001	0.0012
5	$k_{hyd,pr}$	10	50	29	$S_{h2.in}$	1.00E-8	1.20E-8
6	$k_{hyd,li}$	10	50	30	$S_{ch4.in}$	1.00E-5	1.20E-5
7	$k_{m,su}$	30	60	31	$S_{IC.in}$	0.04	0.048
8	$k_{m,aa}$	50	100	32	$S_{IN.in}$	0.01	0.012
9	$k_{m,fa}$	6	12	33	$S_{I.in}$	0.02	0.024
10	$k_{m,c4}$	20	40	34	$X_{xc.in}$	2	4
11	$k_{m,pro}$	13	26	35	$X_{ch.in}$	5	10
12	$k_{m,ac}$	8	16	36	$X_{pr.in}$	20	40
13	$k_{m,h2}$	35	70	37	$X_{li.in}$	5	10
14	$k_{dec,su}$	0.02	0.5	38	$X_{su,in}$	0.01	0.1
15	$k_{dec,aa}$	0.02	0.5	39	$X_{aa.in}$	0.01	0.1
16	$k_{dec,fa}$	0.02	0.5	40	$X_{fa.in}$	0.01	0.1
17	$k_{dec,c4}$	0.02	0.5	41	$X_{c4.in}$	0.01	0.1
18	$k_{dec,pro}$	0.02	0.5	42	$X_{pro.in}$	0.01	0.1
19	$k_{dec,ac}$	0.02	0.5	43	$X_{ac.in}$	0.01	0.1
20	$k_{dec,h2}$	0.02	0.5	44	$X_{h2.in}$	0.01	0.1
21	k_{La}	200	300	45	$X_{I.in}$	0.01	0.1
22	$S_{su.in}$	0.01	0.012	46	$S_{cat.in}$	0.04	0.08
23	$S_{aa.in}$	0.001	0.0012	47	$S_{an.in}$	0.02	0.04
24	$S_{fa.in}$	0.001	0.0012	48	q_{in}	170	180

Note: The units are based on [6] and [9].

In Table 7, the first column represents the 48 input parameters/variables listed in Table 6. For example, pH, as one of the critical output variables, shows the highest sensitivity to the base T_{base}, $k_{dec,ac}$, and $S_{an.in}$ (−0.204, −0.014, and −0.011 respectively) among all parameters and input variables. The negative sign in all sensitive parameters mentioned above means that increasing them leads to a pH drop. As another example, methane concentration in the gas phase is sensitive to temperature bases variables, namely T_{base} and T_{op}.The system's highest sensitivity belongs to the effect of T_{base} on S_{ac} by −32.01. Table 7 can be used as a reference in uncertainty studies on ADM1.

Table 7: Sensitivity index (SI) associated with each input parameter/variable and output variable.

	S_{su}	S_{aa}	S_{fa}	S_{va}	S_{bu}	S_{pro}	S_{ac}	S_{ac}	S_{h2}	S_{IC}	S_{IN}	S_I
1							-32.010		6.236	1.799	-0.012	0.027
2							-0.077		0.048	0.006		
3							0.001					0.010
4												
5							0.003			0.001	0.001	
6												
7	-0.506											
8		-0.505										
9			-0.557						0.001			
10				-0.515	-0.516		0.001					
11						-0.538	0.001					
12							-0.702		0.002	0.014		0.001
13			-0.030	-0.013	-0.013	-0.038		-0.509				
14	0.338						0.001					0.004
15		0.320					0.004			0.001	0.001	0.012
16			1.793						-0.002	0.001	0.001	-0.001
17				0.504	0.524						0.001	0.004
18						7.783	-0.011		-0.002	-0.006		
19	0.013	0.013	1.812	7.235	8.090	8.065	2.412	19.229	-0.024	-0.037	0.003	-0.006
20			0.024	0.010	0.010	0.031	0.001	0.371				0.003
21							0.006		-0.082			
22												
23												
24												
25												
26												
27												
28												
29												
30												
31							-0.160		-0.049	0.013		
32							0.274		0.011	0.053	0.076	
33							0.000					0.062
34				-0.001	0.002	0.002	0.035	0.001	0.001	0.012	0.015	0.570
35			0.001	-0.030	0.021	0.014	-0.178	0.004	-0.006	-0.012	-0.029	0.064
36		0.003		0.027	-0.004	0.026	32.583	0.009	0.036	0.094	0.962	0.219
37			0.023	-0.002	0.001	0.001	-0.023	0.004	0.043	-0.017	-0.020	0.043
38	-0.015											0.001
39		-0.006										0.001
40			-0.031									0.001
41				-0.015	-0.015							0.001
42						-0.039						0.001
43							-0.019					0.001
44			-0.001	-0.001	-0.001	-0.002		-0.020				0.001
45												
46							-0.135		-0.047	0.012		
47							-0.240		-0.023	-0.117		
48	0.733	0.728	0.942	0.779	0.780	0.888	1.482	0.739	0.157	-0.053	-0.035	-0.354

Table 7: Continued.

	X_{xc}	X_{ch}	X_{pr}	X_{li}	X_{su}	X_{aa}	X_{fa}	X_{c4}	X_{pro}	X_{ac}	X_{H2}	X_{I}
1	0.029	0.003	0.001		0.003	0.001		0.001	0.001	0.330	0.001	0.001
2										0.001		
3	-0.099	0.001			0.001				0.001			
4		-0.200			0.001							
5			-0.200			0.001		0.001	0.001	0.001	0.001	
6				-0.200			0.001					
7					0.001							
8												
9	0.001						0.012			0.002	0.002	
10								0.001	0.001			
11									0.002		0.001	
12	0.001									0.007		
13							0.001					
14	0.005			0.001	-0.036		0.001					
15	0.013	0.001			0.001	-0.036			0.001			
16	-0.002						-0.041			-0.006	-0.007	
17	0.005							-0.036		0.000		
18									-0.040	-0.003	-0.007	
19	-0.007	-0.001			-0.001		-0.039	-0.021	-0.038	-0.042	-0.023	
20	0.003						-0.001				-0.036	
21												
22					0.002				0.001			
23												
24												
25												
26												
27												
28												
29												
30												
31										0.002		
32										-0.003		
33												
34	0.613	0.066	0.018	0.001	0.063	0.018	0.001	0.021	0.030	0.022	0.025	0.014
35	0.069	0.900	0.002	0.008	0.861	0.002	0.008	0.060	0.256	0.147	0.209	0.002
36	0.238	0.026	0.978	0.000	0.024	0.971		0.899	0.649	0.337	0.548	0.005
37	0.047	0.005	0.001	0.991	0.048	0.001	0.976	0.004	0.015	0.159	0.199	0.001
38	0.001				0.017							
39	0.001					0.006						
40	0.001						0.035					
41	0.001							0.017				
42	0.001								0.052			
43	0.001									0.010		
44	0.001										0.023	
45												0.108
46										0.001		
47										0.002		
48	0.600	0.951	0.983	0.987	0.227	0.257	0.242	0.253	0.245	0.234	0.246	-0.009

Table 7: Continued.

	pH	S_{va-}	S_{bu-}	S_{pro-}	S_{ac-}	S_{HCO3-}	S_{CO2}	S_{NH3}	S_{NH4+}	$S_{g.H2}$	$S_{g.CH4}$	$S_{g.CO2}$
1	-0.204	-0.009	-0.008	-0.009	-32.016	1.356	8.141	-21.865	0.692	-1.187	1.223	0.347
2	-0.003				-0.077	0.003	0.050	-0.046	0.001	-1.007	-0.961	-0.967
3					0.001							
4												
5					0.003	0.001		0.002	0.001			
6												
7												
8												
9												
10		-0.515	-0.516		0.001			0.001				
11				-0.538	0.001			0.001				
12	0.001				-0.702	0.016	-0.003	0.018	-0.001	-0.001	0.002	-0.003
13		-0.013	-0.013	-0.038	0.000					-0.509		
14					0.001			0.001				
15					0.004	0.001		0.002	0.001			
16						0.001	0.001		0.001	0.001	-0.001	0.001
17		0.504	0.524						0.001			
18	-0.001			7.778	-0.011	-0.007	0.002	-0.008	0.001		-0.001	0.002
19	-0.014	4.255	4.939	4.655	1.540	-0.041	0.032	-0.042	0.004	22.413	-0.022	0.032
20		0.010	0.010	0.031	0.001			0.001		0.371		
21					0.006		-0.004	0.004		0.129		-0.003
22												
23												
24												
25												
26												
27												
28												
29												
30												
31	-0.006				-0.160	0.006	0.110	-0.098	0.003	-0.011	-0.056	0.109
32	0.005				0.275	0.059	-0.025	0.159	0.074	0.003	0.013	-0.025
33												
34		-0.001	0.002	0.002	0.035	0.012	0.007	0.020	0.015	-0.004	-0.002	0.007
35	-0.006	-0.030	0.021	0.013	-0.178	-0.019	0.087	-0.121	-0.026	-0.031	-0.031	0.086
36		0.027	-0.004	0.026	32.583	0.094	0.094	0.962	0.962	-0.062	-0.014	0.091
37		-0.001	0.001	0.001	-0.023	-0.017	-0.021	-0.016	-0.020	-0.021	0.025	-0.022
38												
39												
40												
41		-0.015	-0.015									
42				-0.039								
43					-0.019							
44		-0.001	-0.001	-0.002						-0.020		
45												
46	-0.006				-0.135	0.006	0.105	-0.088	0.003	-0.010	-0.054	0.105
47	-0.011	-0.001		-0.001	-0.240	-0.129	0.052	-0.168	0.005	-0.005	-0.026	0.052
48	-0.007	0.779	0.780	0.888	1.481	-0.061	0.056	-0.147	-0.031	0.574	0.048	0.050

4 CONCLUSION

Although most of the over one hundred parameters have precise and predictable values, several are uncertain, such as the uncertain feedstock quality. On the other hand, input state variables in real-world applications are likewise subject to great uncertainty. As a result,

operating a biogas production unit efficiently requires an in-depth grasp of the system's uncertainties. The sensitivity analysis is crucial in uncertainty analysis with mathematical approaches such as fuzzy set theory. Through a comprehensive local sensitivity analysis and a python implementation of ADM1, the possible effects of varying 48 input parameters and variables on 35 output variables were explored. The sensitivity indices and correlations can be used in further studies on the anaerobic digestion model under uncertainty.

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