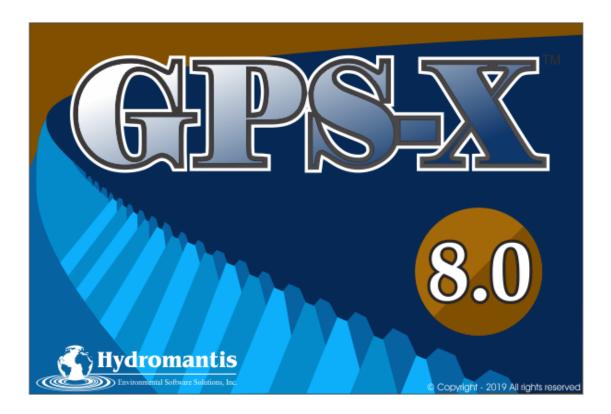
Model Developer GPS-X 8.0

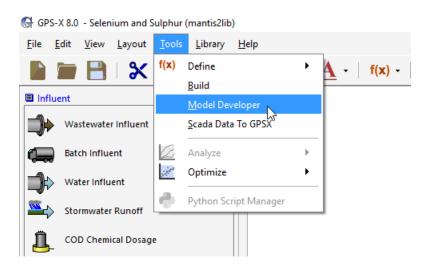


GPS-X Model Developer Tool

1. Background

Model Developer is a utility that allows GPS-X users to create and edit their own models in GPS-X. This model development makes use of the model matrix format for model specification, which is the standard format in the wastewater modelling literature. For more information on model matrix notation, please consult the IWA report on the structure of the ASM1 and ASM2d activated sludge models (Henze, *et al.,* 1987, and Henze *et al.,* 1998, respectively).

This document provides instruction on how to use Model Developer (MD), and assumes the user is familiar with mechanistic dynamic activated sludge models, and the matrix notation format.



Model Developer is accessed from the GPS-X Tools menu.

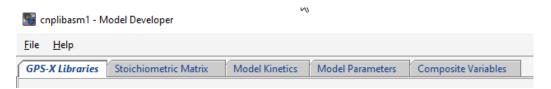
2. MD Components

MD is a application within GPS-X that organizes model content into a series of pages that contain information on model structure, parameters, and GPS-X variables. These pages are used, along with templates found in each GPS-X library, to create a biological model that is written for following GPS-X unit process objects:

Completely Mixed CSTR	Circular Final Settler	Biological Aerated Filter
Anoxic CSTR	Rectangular Final Settler	Simple BAF
Plug Flow	Circular Primary Clarifier	Membrane Bioreactor
Dual-Inlet Plug Flow	Rectangular Primary Clarifier	Membrane Bioreactor Completely Mixed
Sequencing Batch Reactor	Trickling Filter	Membrane Bioreactor Anaerobic
SBR Manual	Submerged Biological Contactor	Downflow Denitrification Filter
SBR Advanced	Rotating Biological contactor	Upflow Denitrification Filter
Continuously Sequencing Reactor	Oxidation Ditch	Hybrid
UASB	Struvite	Digester

In each case, the biological model is implemented with the appropriate physical characteristics and hydraulic configuration appropriate to that object.

There are 5 sections to the Model Developer Tool, accessible through tabs at the top of the MD window: GPS-X Libraries, Stoichiometric Matrix, Model Kinetics, Model Parameters, and Composite Variables.



GPS-X Libraries

The GPS-X Libraries page shows information on the existing set of state variables and composite variable stoichiometry parameters in the GPS-X libraries, as well as the library-specific composite variable calculations. These are not changeable. Models can be made up of a full set or subset of the state variables shown on these pages. Select the appropriate library (from the **Library:** pull down menu) to display the state variable and composite stoichiometry set, and composite variable calculations.

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GPS-X Libraries Stoichiometric Matrix Mo	del Kinetics Model Parameters Composite Variable	15
Library: cnplib		Generate Mo
Library State Variables Library Stoichiometry V	ariables Library Composite Variable Calculations	
Cryptic Name	Description	Units
norganic Suspended Solids		
xii	inert inorganic suspended solids	g/m3
Organic Variables		
si	soluble inert organic material	gCOD/m3
ss	readily biodegradable substrate	gCOD/m3
sf	fermentable readily biodegradable substrate	gCOD/m3
slf	volatile fatty acids	gCOD/m3
xi	particulate inert organic material	gCOD/m3
xs	slowly biodegradable substrate	gCOD/m3
xbh	active heterotrophic biomass	gCOD/m3
xba	active autotrophic biomass	gCOD/m3
xbp	active poly-P accumulating biomass	gCOD/m3
xu	unbiodegradable particulates from cell decay	gCOD/m3
xsto	internal cell storage product	gCOD/m3
xbt	poly-hydroxy-alkanoates (PHA)	gCOD/m3
xgly	stored glycogen	gCOD/m3
Dissolved Oxygen		
50	dissolved oxygen	gO2/m3
hosphorus Compounds		
sp	soluble ortho-phosphate	gP/m3
хрр	stored polyphosphate	gP/m3
xppr	stored polyphosphate (releasable)	gP/m3
Nitrogen Compounds		

Stoichiometric Matrix

The Stoichiometric Matrix tab shows the model matrix for all models available. You can select the appropriate model from the **Model Name:** drop down menu.

GPS-X Libraries	Stoichiometric Matrix	Model Kinetics
Model Name:	asm1 💌	New Res
L	asm1	
Model Stoichio	asm2d	n Matrix
fx	asm3	
	mantis	
	newgenera	Units

The Model Stoichiometry tab shows the model matrix, with state variables in columns and kinetic processes in rows. Textual descriptions of the kinetic processes are shown on the left.

🕤 cr	nplibasm1 - Model Developer										- 🗆	×
<u>F</u> ile	Help											
GPS-	X Libraries Stoichiometric Matrix M	lodel Kinetics	Model Para	meters	Composite Varia	bles						
_	el Name: asm1		store Delet	e							Generate	Model
1100	conservation in the conservation in	INCOM.										
1	fic .											
Ĵ	5x Description	Units	xii	si	\$\$	xi	xs	xbh	xba	xu	50	s
<i>J</i> r1		Units gCOD/m3/d	xii	si	ss -1/yh	xi	XS	xbh	xba	xu	so -(1-yh)/yh	sı - ixbn
	Description		xii	si		xi	xs	xbh 1 1	xba	xu		si - ixbn -ixbn
r1	Description aerobic growth of heterotrophs	gCOD/m3/d	xii	si	-1/yh	xi	xs	xbh 1 1	xba 1	xu		
r1 r2	Description aerobic growth of heterotrophs anoxic growth of heterotrophs	gCOD/m3/d gCOD/m3/d	xii	si	-1/yh	xi	xs	xbh 1 1	xba	xu fu	-(1-yh)/yh	-ixbn
r1 r2 r3	Description aerobic growth of heterotrophs anoxic growth of heterotrophs aerobic growth of autotrophs	gCOD/m3/d gCOD/m3/d gCOD/m3/d	xii	si	-1/yh	xi		1	xba		-(1-yh)/yh	-ixbn
r1 r2 r3 r4	Description aerobic growth of heterotrophs anoxic growth of heterotrophs aerobic growth of autotrophs decay of heterotrophs	gCOD/m3/d gCOD/m3/d gCOD/m3/d gCOD/m3/d	xii	si	-1/yh	xi	1 - fu	1	1	fu	-(1-yh)/yh	-ixbn
r1 r2 r3 r4 r5	Description aerobic growth of heterotrophs anoxic growth of heterotrophs aerobic growth of autotrophs decay of heterotrophs decay of autotrophs	gCOD/m3/d gCOD/m3/d gCOD/m3/d gCOD/m3/d gCOD/m3/d	xii	si	-1/yh	xi	1 - fu	1	1	fu	-(1-yh)/yh	-ixbn

The Conservation Matrix tab shows the elements of the conservation matrix, used to calculate unknown model stoichiometry via mass balance. For more information on using conservation matrices, please see the ASM2d report. The element in the model stoichiometry table that will be calculated from the conservation matrix is filled with the symbol @{var}, where {var} represents the element being conserved, as shown in the left column of the conservation matrix (e.g. @COD).

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Eile <u>H</u> el	lp								
GPS-X Lib	oraries Stoichiometric Matrix Mode	l Kinetics Model Pa	rameters Com	posite Variables					
Model N	ame: asm2d 💌	New Restore De	lete					[Generate N
Model St	oichiometry Matrix Conservation Matri	ix							
_	oichiometry Matrix Conservation Matrix Description		si sf	slf	xi	XS	xbh	xba	50
fx			si sf	slf 1	xi	xs 1	xbh	xba 1	50
fx COD	Description		si sf 1 insf	slf 1	xi 1 inxi	xs 1 inxs	xbh 1 inbm	xba 1 inbm	
_	Description	xii	1	slf 1	1	1	1	1	

Model Kinetics

The Model Kinetics page contains information on the kinetic process rates used in the model (which are represented by rows in the model stoichiometry matrix). The Saturation/Inhibition Functions tab shows all saturation and inhibition functions used in the creation of the kinetic process rates. Each variable is shown with its corresponding equation and units.

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GPS-X Libraries Stoichiometric Mat	rix Model Kinetics Model Parameters	Composite Variables			
Model Name: asm2d	▼ New Restore Delete			Generate	Model
Saturation/Inhibition Functions K	inetic Equations Additional Rates				
fx					
Cryptic Name	Function Definition	Description	Units		
					•
airsat	oxygen saturation function for hydrolysis,	. so/(ko+so)	-		
airinhib	oxygen inhibition function for hydrolysis,	ko/(ko + so)	-		
subsat	slowly biodegradable substrate saturation f	. (xs/(xbh))/(kx+(xs/(xbh)))	-		
snosat	nitrate saturation function for non poly-P	sno/(kno+sno)	-		
snoinhib	nitrate Inhibition function for non poly-P	kno/(sno+kno)	-		
sfsat1	fermentable substrate saturation function f	. sf/(kf+sf)	-		
sfsat2	fermentable substrate saturation function f	. sf/(kfe + sf)	-		
sfinhib	fermentable substrate inhibition function f	kf/(kf+sf)	-		
snhsat	ammonia (as nutrient) saturation function	snh/(knh+snh)	-		
snhinhib	ammonia (as nutrient) inhibition function f	. knh/(snh+knh)	-		- 22
spo4sat	phosphorus (as nutrient) saturation functio	sp/(kpo4 + sp)	-		_

The "Kinetic Equations" tab shows the kinetic equations themselves. The rates and descriptions match those shown on the model stoichiometry tab. The corresponding rate equations and units are shown and edited on this tab. If new rates are added to the stoichiometric matrix, new corresponding rows will show here as well. Any saturation functions that should be applied to the kinetic rates in the biofilm objects (only) can be selected from the drop-down menus in the right-hand column.

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GPS-X L	ibraries Stoichiometric Matrix Model Kinetics	Model Parameters Composite Variables	
Model	Name: asm2d	tore Delete	Generate Model
Saturat	ion/Inhibition Functions Kinetic Equations Additi	onal Rates	
fx			
	Description	Kinetic Equation	Apply Biofilm High-concentration Inhibition
r1	aerobic hydrolysis of slowly biodegradable substrate	kh*airsat*subsat*xbh	None
r2	anoxic hydrolysis of slowly biodegradable substrate	kh*nno3hydrol*airinhib*snosat*subsat*xbh	None
r3	anaerobic hydrolysis of slowly biodegradable substrate	kh*nfe*airinhib*snoinhib*subsat*xbh	None
r4	aerobic growth of heterotrophs on fermentable substrates	muh*airsat*sfsat1*(sf/(sf+slf))*snhsat*spo4sat*salksatHE	Mxbh
r5	aerobic growth of heterotrophs on fermentation products	muh*airsat*slfsatHET*(slf/(sf+slf))*snhsat*spo4sat*salksa	.Mxbh 👻
rб	denitrification with fermentable substrates	muh*nno3HET*airinhib*snosat*sfsat1*(sf/(sf+slf))*snhsa	Mxbh
r7	denitrification with fermentation products	muh*nno3HET*airinhib*snosat*slfsatHET*(slf/(sf+slf))*s	Mxbh
r8	fermentation	qfe*airinhib*snoinhib*sfsat2*salksatHET*xbh	None
r9	lysis of heterotrophs	bh*xbh	None
r10	storage of PHA by poly-P accumulating biomass	qpha*slfsatPAO*salksatHET*xppsat*xbp	None
r11	aerobic storage of poly-P by poly-P accumulating biom	qpp*airsat*spo4satsto*salksatHET*xphasat*(kmax-xpp/(None

Any other additional equations that might be useful to calculate in all reactors can be added in the "Additional Rates" tab.

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<u>F</u> ile <u>H</u> elp			
GPS-X Libraries Stoichiometric Matrix	Model Kinetics Model Parameters C	omposite Variables	
Model Name: asm2d	▼ New Restore Delete		Generate Mode
Saturation/Inhibition Functions Kinetic	Equations Additional Rates		
Cryptic Name	Decription	Value	Units
Actual Oxygen Uptake Rate			
our	actual oxygen uptake rate	-rso	gO2/m3/d
Maximal Oxygen Uptake Rate			
ourmax	maximal oxygen uptake rate (at DO saturati	-(coeffso(4)*muh*sfsat1*(sf/(sf+slf))*snhsa	gO2/m3/d
Actual Nitrogen Utilization Rate (NUR)			
nur	actual nitrogen utilization rate	-(coeffsnh(18)*r18)	gN/m3/d
Maximal Nitrogen Utilization Rate (NUR)			
nurmax	maximal nitrogen utilization rate (at DO sat	-(coeffsnh(18)*muaut*snhsataut*spo4sat*s	gN/m3/d
Denitrification Rate			
dnr	denitrification rate	-(coeffsno(2)*r2+coeffsno(6)*r6+coeffsno(7	gN/m3/d
Phosphorus Uptake Rate			
puraer	phosphorus uptake rate by PAOs under aer	-r11	gP/m3/d
purax	phosphorus uptake rate by PAOs under ano	-r12	gP/m3/d

Model Parameters

The fourth tab of the MD tool (labelled "Model Parameters") contains variables and parameters that are part of the model. Each variable/parameter is listed along with its descriptive name, value and appropriate units. This page includes:

- **State Variables:** the model state variables, and their initial values, and diffusion coefficients for biofilm objects.
- **Stoichiometric parameters:** both model stoichiometric parameters (from the Model Matrix, such as yield, etc.) and organic/nutrient fractions are listed here (e.g. N fraction of biomass).
- **Kinetic parameters:** model kinetic parameters are listed here, including values for 10C and 20C temperatures, or Arrhenius temperature coefficient.

Solution and a main a model Dev	eloper				- 🗆 ×
<u>F</u> ile <u>H</u> elp					
GPS-X Libraries Stoichio	ometric Matrix Model Kinetics	Model Parameters	Composite Variables		
Model Name: asm1	▼ New	Restore Delete			Generate Model
State Variables Stoichio	metric Parameters Kinetic P	arameters			
Cryptic Name	Variable Name	Value at 10°C	Value at 20°C	Arrhenius Coefficient	Units
Active Heterotrophic Biomass					
muh	heterotrophic maximum sp		6.0	1.072	1/d
ksh	readily biodegradable subst		20.00		gCOD/m3
koh	oxygen half saturation coeff		0.2		gO2/m3
kno	nitrate half saturation coeffi		0.500		gN/m3
etag	anoxic growth factor		0.80		-
bh	heterotrophic decay rate		0.62	1.029	1/d
Active Autotrophic Biomass					
mua	autotrophic maximum spec		0.80	1.072	1/d
kna	ammonia half saturation co		1.00		gN/m3
ba	autotrophic decay rate		0.04	1.029	1/d
koa	oxygen half saturation coeff		0.4		gO2/m3
Hydrolysis					
kh	maximum specific hydrolys		3.00	1.072	1/d
kx	slowly biodegradable substr		0.03	1.072	gCOD/gCOD
etah	anoxic hydrolysis factor		0.40		-

Note that if temperatures are entered for both 10C and 20C, the Arrhenius coefficient will be calculated from these values. Alternatively, you can enter just the 20C value, and enter an Arrhenius coefficient directly.

Composite Variables

The final tab on the MD page is the Composite Variable page, where the stoichiometry of the model is assigned to the fixed GPS-X composite variable stoichiometry. For example, GPS-X has a fixed variable name for the nitrogen fraction of particulate inert COD – inxi. These variable names and descriptions are shown in the first two columns, and are not changeable. If your model uses these model conventions, then you can select the appropriate value in the right-hand column. If you have nutrient fractions that are differently named than the fixed GPS-X variable set in the left column, then please select the appropriate variable name from the list. If you do not have an equivalent variable in your model for some of the standard GPS-X variables, you can set the GPS-X variables to zero.

3. Entering Models into Model Developer

The following 5 GPS-X activated sludge models are available in Model Developer by default.

	asm1	-	
	asm1		
br	asm2d		n
-	asm3		
-	mantis		\vdash
	newgeneral		

To create a new model, select File > Save Model As... and save a the model with a new name in the c:/gps-x651/md/models/ folder.

You cannot generate models that have the same name as an existing model in GPS-X – if you wish to regenerate a new, modified version of asm1 (for instance), you will have to give it a new name. This is done to protect the existing library structure.

There are 3 steps involved in preparing a model in MD:

- 1) Entering/editing the model stoichiometric matrix
- Writing the kinetic rate equations (including any internal saturation/inhibition functions) and any other supplemental kinetic rate equations if interest

3) Entering model parameters and default values

Specifying the model in the model stoichiometric matrix

The model matrix is specified in Model Stoichiometry page. New state variables may be added to the model (provided they are part of the GPS-X library) by right-clicking on a column, and selecting a new state variable from the available list. New rates are added by right-clicking on the matrix and adding a new row.

Model stoichiometric relationships can be entered directly into each cell of the matrix by clicking on the appropriate cell, and entering in the equation. Include a decimal place with all real values (including integers), when entering stoichiometric equations. Please note that MD does not support using commas for decimals points.

😼 cr	nplib asm1 - Model Developer					_		\times
<u>F</u> ile	<u>H</u> elp							
GPS-	X Libraries Stoichiometric Matrix M	odel Kinetics	Model Param	eters	Composite Variables			
Mod	lel Name: asm1 💌	New Re	estore Delete]		(Generate I	Nodel
Mod	el Stoichiometry Matrix Conservation M	latrix						
	-							
J	fx 1 - fu							
j	fix 1 - fu Description	Units	xii	si	SS	xi	XS	
j r1		Units gCOD/m3/d	xii	si	ss -1/yh	xi	xs	
-	Description		xii	si		xi	XS	
r1	Description aerobic growth of heterotrophs	gCOD/m3/d	xii	si	-1/yh	xi	XS	
r1 r2	Description aerobic growth of heterotrophs anoxic growth of heterotrophs	gCOD/m3/d gCOD/m3/d	xii	si	-1/yh	xi	xs	
r1 r2 r3	Description aerobic growth of heterotrophs anoxic growth of heterotrophs aerobic growth of autotrophs	gCOD/m3/d gCOD/m3/d gCOD/m3/d	xii	si	-1/yh	хі		
r1 r2 r3 r4	Description aerobic growth of heterotrophs anoxic growth of heterotrophs aerobic growth of autotrophs decay of heterotrophs	gCOD/m3/d gCOD/m3/d gCOD/m3/d gCOD/m3/d	xii	si	-1/yh	xi	1 - fu	
r1 r2 r3 r4 r5	Description aerobic growth of heterotrophs anoxic growth of heterotrophs aerobic growth of autotrophs decay of heterotrophs decay of autotrophs	gCOD/m3/d gCOD/m3/d gCOD/m3/d gCOD/m3/d gCOD/m3/d	xii	si	-1/yh	xi	1 - fu	

The conservation matrix (shown on the conservation matrix tab) may be incorporated by entering values in the matrix that indicate which conservation element is used. For details of using a conservation matrix, please refer to the ASM2d model publication (Henze, *et al.*, 1998).

🛐 cnplib	o asm2d -	Model Developer			_		×
<u>F</u> ile <u>H</u> e	lp						
GPS-X Lil	braries	Stoichiometric Matrix	Model Kinetics	Model Param	eters Com	posite Varia	bles
Model N	lame: a	sm2d 👻	New R	estore Delete	[Generate	Model
Model St	toichiome	etry Matrix Conservatio	n Matrix				
<i>f</i> x i	psf						
		Description	xii	si	sf	slt	F
COD	CO	D		1	1	1	
N	N			insi	insf		
Р	Р			ipsi	ipsf		

The nomenclature to be used in the cell for which the stoichiometry is to be calculated is shown below:

@COD - stoichiometric constant for the current row, based on COD conservation

Each stoichiometric constant that is determined from the conservation matrix must use only one of the conservation elements available (e.g. COD, above). Each conservation element is listed in a separate row in the conservation matrix, and contains the appropriate stoichiometry for each state variable. For a good example of the use of the conservation matrix, please see the ASM2d model in MD.

Model Stoichiometry Matrix Conservation Matrix							
fx @COD							
	Description	Units	xs	xbh	xba	50	snh
r1	aerobic hydrolysis of slowly biodegrada	gCOD/m3/d	-1				@N
r2	anoxic hydrolysis of slowly biodegrada	gCOD/m3/d	-1				@N
r3	anaerobic hydrolysis of slowly biodegra	gCOD/m3/d	-1				@N
r4	aerobic growth of heterotrophs on ferm	gCOD/m3/d		1		@COD	@N
r5	aerobic growth of heterotrophs on ferm	gCOD/m3/d		1		@COD	@N
rб	denitrification with fermentable substra	gCOD/m3/d		1			@N
r7	denitrification with fermentation produ	gCOD/m3/d		1			@N
r8	fermentation	gCOD/m3/d					@N
r9	lysis of heterotrophs	gCOD/m3/d	1-prodfxi	-1			@N

Entering Kinetic Rate equations

On the Model Kinetics page, on the Kinetic Rates tab, the kinetic rate equations for each row of the matrix are shown. The descriptive name of the rate is shown here as well, along with the units.

If the rate equation contains terms that would be useful to have calculated separately (such as inhibition or saturation functions), those can be listed (along with descriptive names) in the "Saturation/Inhibition Functions" tab.

GPS-X	Libraries Stoichiometric Matrix Model Kinetics M	odel Parameters Composite Variables				
Model	Model Name: asm2d New Restore Delete					
Satura	Saturation/Inhibition Functions Kinetic Equations Additional Rates					
fx	qfe*airinhib*snoinhib*sfsat2*salksatHET*xbh					
	Description	Kinetic Equation				
r1	aerobic hydrolysis of slowly biodegradable substrate	kh*airsat*subsat*xbh				
r2	anoxic hydrolysis of slowly biodegradable substrate	kh*nno3hydrol*airinhib*snosat*subsat*xbh				
r3	anaerobic hydrolysis of slowly biodegradable substrate	kh*nfe*airinhib*snoinhib*subsat*xbh				
r4	aerobic growth of heterotrophs on fermentable substrates	muh*airsat*sfsat1*(sf/(sf+slf))*snhsat*spo4sat*salksatHET*xbh				
r5	aerobic growth of heterotrophs on fermentation products	muh*airsat*slfsatHET*(slf/(sf+slf))*snhsat*spo4sat*salksatHET*xbh				
rб	denitrification with fermentable substrates	muh*nno3HET*airinhib*snosat*sfsat1*(sf/(sf+slf))*snhsat*spo4sat*salksatHET*xbh				
r7	denitrification with fermentation products	muh*nno3HET*airinhib*snosat*slfsatHET*(slf/(sf+slf))*snhsat*spo4sat*salksatHET*xbl				
r8	fermentation	qfe*airinhib*snoinhib*sfsat2*salksatHET*xbh				
r9	lysis of heterotrophs	bh*xbh				

The "Apply Biofilm High-Concentration Inhibition" term on the right hand side is a feature that allows a saturation term (which must first be defined on the Saturation/Inhibition Functions tab) to be applied to only the biofilm models in GPS-X (hybrid, denitrification filters, BAF, simple BAF, trickling filter, RBC and SBC). This allows high-concentration inhibition terms to be applied to the appropriate growth equations (in biofilm objects only). Select the appropriate inhibition term from the drop-down menu.

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GPS-X	GPS-X Libraries Stoichiometric Matrix Model Kinetics Model Parameters Composite Variables						
Mode	Model Name: asm2d New Restore Delete Generate Model						
Satura	Saturation/Inhibition Functions Kinetic Equations Additional Rates						
f.x	c						
	Description	Kinetic Equation	Apply Biofilm High-concentration Inhibition				
r1	aerobic hydrolysis of slowly biodegradable substrate	kh*airsat*subsat*xbh	None				
r2	anoxic hydrolysis of slowly biodegradable substrate	kh*nno3hydrol*airinhib*snosat*subsat*xbh	None				
r3	anaerobic hydrolysis of slowly biodegradable substrate	kh*nfe*airinhib*snoinhib*subsat*xbh	None				
r4	aerobic growth of heterotrophs on fermentable substrates	muh*airsat*sfsat1*(sf/(sf+slf))*snhsat*spo4sat*salksatHET*xbh	Mxbh				
r5	aerobic growth of heterotrophs on fermentation products	muh*airsat*slfsatHET*(slf/(sf+slf))*snhsat*spo4sat*salksatHE	slfsatPAO				
rб	denitrification with fermentable substrates	muh*nno3HET*airinhib*snosat*sfsat1*(sf/(sf+slf))*snhsat*sp	xppsat				
r7	itrification with fermentation products muh*nno3HET*airinhib*snosat*slfsatHET*(slf/(sf+slf))*snhsat.		xphasat				
r8	fermentation	qfe*airinhib*snoinhib*sfsat2*salksatHET*xbh	airsataut				
r9	lysis of heterotrophs	bh*xbh	snhsataut				
r10	storage of PHA by poly-P accumulating biomass	qpha*slfsatPAO*salksatHET*xppsat*xbp	salksatHETprec				
r11	aerobic storage of poly-P by poly-P accumulating biomass	qpp*airsat*spo4satsto*salksatHET*xphasat*(kmax-xpp/(xbp))	Mxbh				
r12	anoxic storage of poly-P by poly-P accumulating biomass	qpp*spo4satsto*salksatHET*xphasat*nno3PAO*(kmax-xpp/(Mxba 👻				

Entering model variables and parameters

On the "Model Parameters" page, enter all of the model stoichiometry in the "Stoichiometric Parameters" tab. Right-click on a row to add new parameters, if required.

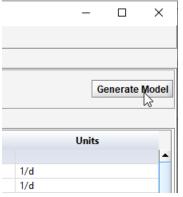
Next, click over to the "Kinetic Parameters" tab, and enter the parameters of the model and their values and units. If the parameter is temperature sensitive, you can list values for 10C and 20C, or Arrhenius coefficient. Right-click on a row to add new rows if required.

S cnplib asm2d - Model Developer					-		Х
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GPS-X Libraries Stoichio	metric Matrix Model Kinetics Mo	odel Parameters Composit	e Variables				
Model Name: asm2d Vew Restore Delete Generate Model							
State Variables Stoichion Cryptic Name	Metric Parameters Kinetic Parameters Variable Name	Value at 10°C	Value at 20°C	Arrhenius Coefficient	Units		
Active Heterotrophic Biomass							-
muh	heterotrophic maximum specif		6.00	1.072	1/d		
bh	lysis and decay rate constant		0.40	1.072	1/d		
nno3HET	denitrification reduction factor		0.80		-		
kf	fermentable substrate half satu		4.00		gCOD/m3		
kIfHET	volatile fatty acids half saturati		4.00		gCOD/m3		
Active Poly-P Accumulating Biomass							
qpha	rate constant for storage of PHA		3.00	1.041	1/d		
qpp	rate constant for storage of pol		1.50	1.041	1/d		
upao	maximum specific growth rate		1.00	1.041	1/d		
bpao	poly-P accumulating biomass I		0.20	1.072	1/d		
bpp	poly-P lysis rate		0.20	1.072	1/d		
bpha	PHA lysis rate		0.20	1.072	1/d		

4. Generating Models

Once the matrix and all other tabs have been filled out, the model can be generated. Note that the model will be generated for the library showing in the Library: pull-down menu on the GPS-X Libraries page.

The model is generated by pressing the "Generate Model" button, as shown below.



You will be prompted to enter the full path to the GPS-X library where the new model will be written (and where the template files are – which are the same by default), as shown below:

📓 Generate Model - cnplib asm1		×				
Generate model to:						
C:\GPS-X80\cnplib		Browse				
Generate Objects:						
Completely Mixed CSTR	Circular Final Settler	Biological Aerated Filter				
Anoxic CSTR	Rectangular Final Settler	Simple BAF				
Plug Flow	Circular Primary Clarifier	Membrane Bioreactor				
Dual-Inlet Plug Flow	Rectangular Primary Clarifier	Membrane Bioreactor Completely Mixed				
Sequencing Batch Reactor	Trickling Filter	Membrane Bioreactor Anaerobic				
SBR Manual	Submerged Biological Contactor	Downflow Denitrification Filter				
SBR Advanced	Rotating Biological contactor	Upflow Denitrification Filter				
Continuously Sequencing Reactor	Oxidation Ditch	Hybrid				
UASB UASB	Struvite	Digester				
	Select All	Generate Model Cancel				

Once you've entered the appropriate paths, you can select which unit processes should be generated (plug flow, MBR, etc.). Use the "Select All" button to generate models for all objects. MD will write out the files containing all the models. This may take up to a minute, depending on the speed of the computer.

Once the models have been written, close MD, and restart GPS-X. Select the library where the new models were written from the pull-down library menu at the top of the GPS-X screen.

When you select one of the objects listed section two (CSTR, plug flow tank, etc.), you will see the new model available under the Models menu.

5. A Note about Using Your New Models

Because your new model is not part of the original GPS-X structure, you will not be able to select it from the "Biological Models" menu in the influent object menu, and the Influent Advisor tool will not be available for your model. We recommend using the STATES influent model to simplify influent characterization when using custom biological models.

6. Technical Support/Troubleshooting

If you have any difficulties using Model Developer, or properly incorporating the models into GPS-X, please contact us at support@hydromantis.com.

7. References

Henze M, Grady C P L, Gujer W, Marais G v R and Matsuo T (1987). Activated sludge model no. 1. IAWPRC Scientific and Technical Report No. 1, IAWPRC, London.

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