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Division of Industrial Electrical Engineering and Automation (IEA)
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Matlab®/Simulink® implementation of ADM1 with physico-chemical modelling within BSM2

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Note that this short document does not by any means provide a complete description of how to use the ADM1 with physico-chemical modelling within the BSM2 system, however it may give some useful hints on the topic and avoid some unnecessary frustration. The document assumes that you are familiar with Matlab®/Simulink® and wastewater treatment process modelling and simulation. The provided models have been implemented in Matlab R2013b release and will also work with later versions. Please, also read the provided *AGREEMENT_ADM1 PCM in BSM2.pdf* document.

UNPACKING THE FILES
The files have been archived using *zip*. Just unzip the files with the software you normally use for this purpose.

FILE DESCRIPTIONS
When the files are unpacked, you will find in the main directory 2 folders and an Excel file. The Excel file contains the correct simulation results for test cases that you can use for comparison. The folder *Documents* contain three files: (1) *2015_Solon et al.pdf*, (2) *AGREEMENT_ADM1 PCM in BSM2.pdf*, and (3) *README_ ADM1 PCM in BSM2.pdf.* While the folder *Matlab files_ADM1 PCM in BSM2* contains most of the files that are associated with BSM2.

Simulink models
1. *bsm2_ol.mdl* - simulate the plant without active control, i.e. in open loop, using dynamic input data
2. *bsm2_ol_influent.slx* - simulate the plant without active control, i.e. in open loop, using dynamic input data, with additional cationic load into the anaerobic digester
3. *bsm2_ss.slx* - simulate the plant without active control, i.e. in open loop, using constant input data
4. *bsm2_ss_influent.slx* - simulate the plant without active control, i.e. in open loop, using constant input data, with additional cationic load into the anaerobic digester

C-files
1. *adm1_DAE2_bsm2.c* - C-file containing the ADM1 implementation.
2. *adm2asm_v3_bsm2.c* and *asm2adm_v3_bsm2.c* - the interface models which enable the connection of the ADM1 to the rest of BSM2 (based on ASM1 variables). More information in the special technical report on the ADM1 and ASM1 interfacing for BSM2.

3. *asm1_bsm2.c* - C-file containing the AS Model no. 1.
4. *combiner_bsm2.c*, *combiner3_bsm2.c*, *combiner4_bsm2.c* - adds two, three or four separate streams into one based on loads.
5. *DAE2_combiner_bsm2.c* - special combiners used for the DAE2 ADM1 implementation.
6. *flowsplitter_bsm2.c* - divides one stream into two.
7. *carboncombiner_bsm2.c* - adds the external carbon flow to the rest of the wastewater.
8. *dewatering_bsm2.c* - the 'ideal' dewatering process model.
9. *hyddelayv3_bsm2.c* - a special delay function (a fast first-order exponential filter) to avoid algebraic loops.
10. *pHdelay_bsm2.c* - small delay model for pH used for all ADM implementations when the current pH .value of the ADM1 is returned to the ADM2AS interface at each integration step.
11. *primclar_bsm2.c* - the Otterpohl-Freund primary clarifier model.
12. *settler1d_bsm2.c* - C-file for a 10-layer one-dimensional settler model.
13. *Sh2solv_bsm2.c* - calculates the Sh2 concentration at each integration step using a Newton-Raphson algorithm. Used by *adm1_DAE2_bsm2.c.*
14. *storage_bsm2.c, storagebypass_bsm2.c, storagedelay_bsm2.c* – three models files that together make up the overall model for the BSM2 reject water storage tank including automatic bypass when full or stop of pumping when becoming empty.
15. *thickener_bsm2.c* – the 'ideal' thickener process model.
16. *UQ_speciation_DAE.c* – calculates the SH+ concentration as well as speciation of the ADM1 variables at each integration step using a Newton-Raphson algorithm. Used by *adm1_DAE2_bsm2.c.*

These 25 files must be compiled on your local machine using the Matlab `mex` command before you can use the models (use the `mexall_bsm2.m` script).

Initialisation files
The initialisation m-files have names associated with the model they influence:
1. *adm1init_bsm2.m*
2. *asm1init_bsm2.m*
3. *dewateringinit_bsm2.m*
4. *hyddelayinit_bsm2.m*
5. *primclarinit_bsm2.m*
6. *reginit_bsm2.m*
7. *settler1dinit_bsm2.m*
8. *speciationinit_bsm2*
9. *storageinit_bsm2.m*
10. *thickenerinit_bsm2.m*

All of these initialization files can be run using the `init_bsm2.m` script.

Input data
In the subdirectory *Influent_data* the various influent data files are provided in .mat format and in ascii format (in case you have to regenerate them).
1. *constinfluent_bsm2.mat* - the constant value influent file, which actually represents the average vales for one full year of dynamic data (also available as .txt file).

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SE-221 00	Ole Römers väg 1,			
Lund, Sweden	Lund, Sweden			

2. *dyninfluent_bsm2.mat* - full dynamic influent data file for 609 days (15 min samples, also available as .txt file).

You can also find in the main directory:

3. *constinfluent_ADM1.mat* – constant value influent file for the anaerobic digester which can be used if you want to simulate additional loads only in the digester.

RUNNING THE BSM2 WITH ADM1 PCM

When the archive has been unzipped, you are ready to run the ADM1 within BSM2 with physico-chemical modelling. A few simple instructions are given below to help you through the first time and to test the system on your computer.

1. Start Matlab and move to the directory containing the model you want to use (folder *Matlab files_ADM1 PCM in BSM2*).
2. Command `mexall_bsm2` (if you have problems with the C-compiler you must solve this). If you change the C-files (which should normally not be done), you need to re-mex all the C-files that you have modified in order for Simulink to use the modified file.
3. Run the initialization file `init_bsm2` (initiates all variables and parameters, loads the data files, etc.).
4. Command `bsm2_ss` (the Simulink model will appear in a new window). If you want to simulate a scenario with an additional cationic load into the anaerobic digester, use `bsm2_ss_influent` instead. Run whichever of the two models you need. The system will simulate 200 days forward using the constant influent data, the open loop configuration and solver ode15s.
5. Command `stateset_bsm2`. The final values of the previous simulation have now been used to initialise all BSM2 models so that you can start your next simulation at the exact same position as where the last one ended. The same data are also automatically stored in a file *states_bsm2.mat*, which you can rename and then use at any time in the future to initialise the BSM2 system. If you want to save all the generated data from a simulation you should simply use the Matlab `save` command.
6. Command `bsm2_ol` (the Simulink model will appear in a new window). If you want to simulate a scenario with an additional cationic load into the anaerobic digester, use `bsm2_ol_influent` instead. Run whichever of the two models you need. The system will simulate 609 days forward using the dynamic influent data, the open loop configuration and solver ode45.
7. After simulation all data are stored in the Matlab workspace and not to files. Use the `who` command to see what variables you have available.
8. When the simulation is finished: command `perf_plant_bsm2`. The script will calculate and print to the screen the complete set of evaluation criteria for the overall plant performance for the simulation from day 245 to 609.

When you have reached this point you can be sure that the BSM2 with ADM1 PCM on your computer works properly. The full dynamic simulations require some time to finish.

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FINAL COMMENTS
Read the documentation about benchmarking from the web site carefully plus other available reports on BSM. Try to understand the structure of the different m-files and c-files to grasp how they relate to each other. You should compare your results with the results provided in the Excel document. If your results are different, then you are doing something incorrectly.

When you feel confident that you understand this implementation you may start to create your own influent files for subsequent simulation studies. Remember that this implementation is simply a starting point and a fully verified simulation platform tor you to start working on your own and testing different scenarios that you're interested in.

Enjoy!