List of keywords in the settings files

The keywords are all read and input in the module named Configure.m.

# Geometry Block

Starts with

*#-------------------------------------------------*

*# GEOMETRY*

*#-------------------------------------------------*

## LENGTH

Length of the core + unit

Example: *LENGTH 15 cm*

## DIAMETER

Diameter of the core + unit

Example: *DIAMETER 7.5 cm*

# Rock Block

Starts with:

*#-------------------------------------------------*

*# ROCK*

*#-------------------------------------------------*

## POROSITY

Porosity of the core in fraction

Example: *POROSITY 0.297*

## PERMEABILITY

Permeability of the core + unit

Example: *PERMEABILITY 260 mD*

## INITIALWATER

Initial water saturation in fraction

Example: *INITIALWATER 1*

# FLUID Block

Starts with

*#-------------------------------------------------*

*# FLUID*

*#-------------------------------------------------*

## DENSITYW

Wetting phase density + unit

Example*: DENSITYW 1000 kg/m^3*

## DENSITYNW

None-wetting phase density + unit

Example: *DENSITYNW 800 kg/m^3*

## VISCOSITYW

Wetting phase viscosity + unit

Example: *VISCOSITYW 1 cP*

## VISCOSITYNW

None-wetting phase viscosity + unit

Example: *VISCOSITYNW 5 cP*

# Process Block

Starts with:

*#-------------------------------------------------*

*# PROCESS*

*#-------------------------------------------------*

Type of the experiment + process

Types: SS, USS, CENT

Processes: Drainage, Imbibition

Example: *SS Imbibition*

# Block Simulation

Starts with:

*#-------------------------------------------------*

*# SIMULATION*

*#-------------------------------------------------*

Defines is one is doing a forward or a history match simulation

Example: *TYPE Forward*

Example: *TYPE HistoryMatch*

The number of cells for the core

Example*: NCELLS 80*

The number of boundary cells at each end of the core and the initial water saturation at these boundary cells

*# number first\_cell\_Sw last\_cell\_Sw*

*BCELLS 1 0 0*

Maximum time step allowed for the simulation + unit

*MAXTIMESTEP 2 hour*

Number of geometric breaks down of the time steps at the beginning of each schedule row

*RAMPUPSTEPS 10*

If used, the maximum saturation change for the solver is set to 5%, which increases the accuracy but reduces simulation speed, useful for e.g. USS experiments with pc=0

*HIGH\_PERCISION\_MODE*

# Schedule Block

Starts with:

*#-------------------------------------------------*

*# SCHEDULE*

*#-------------------------------------------------*

Directory of the schedule file to input

*# fileName*

*FILENAME .\examples\Data\SS\Imbibition\sched\_case1.txt*

Initial pressure of the whole core

*PINI 1 bar*

Initial pressure at the right side of the core (x=core length)

*POUT 1 bar*

Start up time in case of a centrifuge experiment: time + unit + rpm + unit

*STARTUP 100 second 2325 rpm*

Distance between the centre of the centrifuge rotation axis and the centre of the core

*CENTRAD 14.89 cm*

# Observation Block

Starts with

*#-------------------------------------------------*

*# OBSERVATION*

*#-------------------------------------------------*

Input the experimental observations to compare with forward simulation results and history match

Possible keywords: PRESSURE, PRODUCTION, SWAVG, SATPROFILE + file directory

*# fileName*

*PRESSURE .\examples\Data\SS\Imbibition\pressure\_obs\_case1.txt*

*SWAVG .\examples\Data\SS\Imbibition\swavg\_obs\_case1.txt*

*SATPROFILE .\examples\Data\SS\Imbibition\SatProfile\_obs\_case1.xlsx*

# Saturation function Block

Starts with

*#-------------------------------------------------*

*# SATURATION FUNCTIONS*

*#-------------------------------------------------*

KR keyword to input relative permeability saturation function + model name (e.g. MODIFIED-COREY/TABLE + parameters in order and tab separated/ directory to the table for the list and order of the parameters have a look at the “. \ad-scal\models\SaturationFunctions\Forward\Kr\read\_kr\_parameters\_from\_settings.m”

*#KR MODIFIED-COREY Swc Sor krw@Sor kro@Swc nW nNW*

*KR MODIFIED-COREY 0.2 0.2 0.5 0.5 3 3*

Similar to the previous, use PC keyword for capillary pressure. For the list and order of the parameters have a look at “. \ad-scal\models\SaturationFunctions\Forward\Pc\read\_pc\_parameters\_from\_settings.m”

*PC TABLE .\examples\Data\SS\Imbibition\pc\_smooth.txt*

# Plot Options block

Starts with:

*#-------------------------------------------------*

*# PLOT OPTIONS*

*#-------------------------------------------------*

Style can be docked or normal

*STYLE docked*

Colormap can be jet, parula, hsv

*COLORMAP jet*

For possible units have a look at the available units list

*DISPLAYTIME hour*

*DISPLAYLENGTH cm*

*DISPLAYVOLUME cm^3*

*DISPLAYPRESS bar*

*DISPLAYRATE cm^3/hour*

# Output options block

Starts with

*#-------------------------------------------------*

*# OUTPUT OPTIONS*

*#-------------------------------------------------*

Define the desired output options and the directory to output them

*SATPROFILE .\Results\satProfile.xlsx*

Saves a settings file which can be re-used for setting up the simulation

*SAVECONFIG .\Results\config.txt*

*QUANTITIES .\Results\output.txt*

If you use each of the key words here this is means the output is generated for the corresponding property - !make sure to activate this option before activating the parameters below.

*TIME*

Average water saturation

*SWAVG*

Injection and production rates

*INJ*

*PROD*

*DELTAP*

# Objective function configurations block

Starts with

*#-------------------------------------------------*

*# OBJECTIVE FUNCTION CONFIGURATIONS*

*#-------------------------------------------------*

Settings the configurations for history match simulations

The excel directory to input initial point, and boundaries for KR/PC parameters to iterate upon

*EXCEL\_FILE\_NAME kr\_modified\_corey.xlsx*

*EXCEL\_FILE\_PATH .\App\Input\_templates\_for\_SCAL\_history\_match*

If activated, the history matching is started from n random points within the boundary (defined in the random number keyword below) points, to increase the chance of finding the global minimum

*MULTIPOINT*

*MULTIPOINT\_RANDOM\_NUMBERS 10*

If activated, the relative permeability is history matched

*KR*

Define the model of the relative permeability for history match, it has to match the parameters in the excel template, you can also use POINT-BY-POINT

*KR\_MODEL MODIFIED-COREY*

If activated, the capillary pressure is history matched

*PC*

Define the model of the capillary pressure for history match, it has to match the parameters in the excel template, you can also use POINT-BY-POINT

*PC\_MODEL POINT-BY-POINT*

Define the weights of each measurement in the objective function calculations

*PDIFF\_WEIGHT 1*

*SWAVG\_WEIGHT 1*

*PROD\_WEIGHT 1*

*SAT\_PROFILE\_WEIGHT 1*

Define the error of measurements, for normal history matching leave them as 0, for MCMC simulations use the relative error in percentages

*PDIF\_ERROR 0*

*SWAVG\_ERROR 0*

*PROD\_ERROR 0*

*SAT\_PROFILE\_ERROR 0*

# History match configurations block

Starts with:

*#-------------------------------------------------*

*# HISTORY MATCH CONFIGURATIONS*

*#-------------------------------------------------*

If activated uses parallel CPU computation

*USE\_PARALLEL*

Parameters related to the fmincon function of MATLAB

*OPTIMALITY\_TOLERANCE 1e-6*

*STEP\_TOLERANCE 1e-3*

*MAX\_FUNCTION\_EVALUATIONS 6000*

*SCALE\_PROBLEM*

Can use normal here for single history of 1 experiment and Simultaneous to history match 2 experiments at the same time e.g. SS + CENT

*OBJECTIVE\_FUNCTION\_TYPE normal*

Directory of the second experiment setting file to history match

*CENT\_FILE\_NAME ABC.txt*

*CENT\_FILE\_PATH C:\Users\Omidreza\Documents\GitHub\SCAL*

History match algorithm for fmincon (e.g. active-set, interior-point) or can use ga-multi-obj for multi objective optimization with genetic algorithm

*HISTORYMATCH\_ALGORITHM active-set*

# MCMC configurations block

Starts with

*#-------------------------------------------------*

*# MCMC SPECIFIC CONFIGURATIONS*

*#-------------------------------------------------*

Here we set the settings for monte carlo (MCMC) simulations with paramonte package

*RANDOM\_SEED 3751*

*SAMPLE\_REFINEMENT\_COUNT 1*

*CHAINSIZE 5000*

*#MPI\_ENABLED*