BW

This is a file is written using a pre-release version of the meta-flopy-scripting package

Using flopy version 3.2.10

In [ ]:
```
import flopy
import numpy as np
from numpy import rec
```

flopy.modflow

In [ ]:
```
# Name of model.  this string will be used to name the modflow input that are created with
#   write_model. (the default is 'modflowtest')
modelname = 'BW'
# Extension for the namefile (the default is 'nam')
namefile_ext = 'nam'
# Version of modflow to use (the default is 'mf2005').
version = 'mf2005'
# The name of the executable to use (the default is 'mf2005').
exe_name = 'mf2005.exe'
structured = True
# Unit number for the list file (the default is 2).
listunit = 2
# Model workspace.  directory name to create model data sets. (default is the present working
#   directory).
model_ws = '.'
# Location for external files (default is none).
external_path = None
# Print additional information to the screen (default is false).
verbose = False

modflow = flopy.modflow.mf.Modflow(modelname=modelname, namefile_ext=namefile_ext, version=version,
                                   exe_name=exe_name, structured=structured, listunit=listunit,
                                   model_ws=model_ws, external_path=external_path, verbose=verbose)
```

DIS

In [ ]:

```
# The model object (of type :class:`flopy.modflow.modflow`) to which this package will be added.
model = modflow
# Number of model layers (the default is 1).
nlay = 1
# Number of model rows (the default is 2).
nrow = 60
# Number of model columns (the default is 2).
ncol = 100
# Number of model stress periods (the default is 1).
nper = 288
# An array of spacings along a row (the default is 1.0).
delr = np.array([0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01
       ,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,
0.0025,0.0025,0.0025,0.0025,0.0025,0.01
       ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01
       ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01
       ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01
       ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01
       ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,1. ])
# An array of spacings along a column (the default is 0.0).
delc = np.array([0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.0025,0.002
5,0.0025,0.01
       ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01
       ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01
       ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,0.01 ,1. ])
# An array of flags indicating whether or not a layer has a quasi-3d confining bed below it. 0
#   indicates no confining bed, and not zero indicates a confining bed. laycbd for the bottom layer
#   must be 0. (the default is 0)
laycbd = 0
# An array of the top elevation of layer 1. for the common situation in which the top layer
#   represents a water-table aquifer, it may be reasonable to set top equal to land-surface
#   elevation (the default is 1.0)
top = 1.0
# An array of the bottom elevation for each model cell (the default is 0.)
botm = 0.0
# An array of the stress period lengths.
perlen = 0.0034719998948276043
# Number of time steps in each stress period (default is 1).
nstp = 2
# Time step multiplier (default is 1.0).
tsmult = 1.0
# True or false indicating whether or not stress period is steady state (default is true).
steady = True
# Time units, default is days (4)
itmuni = 4
# Length units, default is meters (2)
lenuni = 2

dis = flopy.modflow.mfdis.ModflowDis(model=model, nlay=nlay, nrow=nrow, ncol=ncol, nper=nper,
                                     delr=delr, delc=delc, laycbd=laycbd, top=top, botm=botm,
                                     perlen=perlen, nstp=nstp, tsmult=tsmult, steady=steady,
                                     itmuni=itmuni, lenuni=lenuni)
```

BAS6

In [ ]:

```
# The model object (of type :class:`flopy.modflow.mf.modflow`) to which this package will be added.
model = modflow
# The ibound array (the default is 1).
ibound = np.broadcast_to([[[ 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
         1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
         1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
         1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,-1]]], (1, 60, 100))
# An array of starting heads (the default is 1.0).
strt = 10.0
# Indicates whether or not packages will be written as free format.
ifrefm = True
# Indication of whether model is cross sectional or not (the default is false).
ixsec = False
# Flag indicating that flows between constant head cells should be calculated (the default is
#   false).
ichflg = False
# Percent discrepancy that is compared to the budget percent discrepancy continue when the solver
#   convergence criteria are not met.  execution will unless the budget percent discrepancy is
#   greater than stoper (default is none). modflow-2005 only
stoper = None
# Head value assigned to inactive cells (default is -999.99).
hnoflo = 1e+30

bas6 = flopy.modflow.mfbas.ModflowBas(model=model, ibound=ibound, strt=strt, ifrefm=ifrefm,
                                      ixsec=ixsec, ichflg=ichflg, stoper=stoper, hnoflo=hnoflo)
```

LPF

In [ ]:

```
# The model object (of type :class:`flopy.modflow.mf.modflow`) to which this package will be added.
model = modflow
# Layer type, contains a flag for each layer that specifies the layer type. 0 confined >0
#   convertible <0 convertible unless the thickstrt option is in effect. (default is 0).
laytyp = 0
# Layer average  0 is harmonic mean 1 is logarithmic mean 2 is arithmetic mean of saturated
#   thickness and logarithmic mean of of hydraulic conductivity (default is 0).
layavg = 0
# Contains a value for each layer that is a flag or the horizontal anisotropy. if chani is less
#   than or equal to 0, then variable hani defines horizontal anisotropy. if chani is greater than
#   0, then chani is the horizontal anisotropy for the entire layer, and hani is not read. if any
#   hani parameters are used, chani for all layers must be less than or equal to 0. use as many
#   records as needed to enter a value of chani for each layer. the horizontal anisotropy is the
#   ratio of the hydraulic conductivity along columns (the y direction) to the hydraulic
#   conductivity along rows (the x direction). (default is 1).
chani = 1.0
# A flag for each layer that indicates whether variable vka is vertical hydraulic conductivity or
#   the ratio of horizontal to vertical hydraulic conductivity. 0: vka is vertical hydraulic
#   conductivity not 0: vka is the ratio of horizontal to vertical hydraulic conductivity (default
#   is 0).
layvka = 0
# Contains a flag for each layer that indicates if wetting is active. 0 wetting is inactive not 0
#   wetting is active (default is 0).
laywet = 0
# A flag that is used to determine if cell-by-cell budget data should be saved. if ipakcb is
#   non-zero cell-by-cell budget data will be saved. (default is 53)
ipakcb = 53
# Is the head that is assigned to cells that are converted to dry during a simulation. although
#   this value plays no role in the model calculations, it is useful as an indicator when looking
#   at the resulting heads that are output from the model. hdry is thus similar to hnoflo in the
#   basic package, which is the value assigned to cells that are no-flow cells at the start of a
#   model simulation.  (default is -1.e30).
hdry = 1e+20
iwdflg = 0
# Is a factor that is included in the calculation of the head that is initially established at a
#   cell when it is converted from dry to wet. (default is 0.1).
wetfct = None
# Is the iteration interval for attempting to wet cells. wetting is attempted every iwetit
#   iteration. if using the pcg solver (hill, 1990), this applies to outer iterations, not inner
#   iterations. if iwetit  less than or equal to 0, it is changed to 1. (default is 1).
iwetit = None
# Is a flag that determines which equation is used to define the initial head at cells that become
#   wet.  (default is 0)
ihdwet = None
# Is the hydraulic conductivity along rows. hk is multiplied by horizontal anisotropy (see chani
#   and hani) to obtain hydraulic conductivity along columns.  (default is 1.0).
hk = np.array([[[50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. , 0.0001, 0.0001,
      0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001,
      0.0001, 0.0001, 0.0001, 0.0001,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ], [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. , 0.0001, 0.0001,
      0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001,
      0.0001, 0.0001,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ],
      [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. , 0.0001, 0.0001, 0.0001,
      0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001,
      0.0001,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ], [50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. , 0.0001, 0.0001, 0.0001, 0.0001,
      0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. , 0.0001, 0.0001, 0.0001, 0.0001, 0.0001,
      0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. , 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001,
      0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
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      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. , 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001,
      0.0001, 0.0001,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ], [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,
      0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
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,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
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,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
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,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.], [50. ,50.
,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
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     ,50. ]]])
# Is the ratio of hydraulic conductivity along columns to hydraulic conductivity along rows, where
#   hk of item 10 specifies the hydraulic conductivity along rows. thus, the hydraulic conductivity
#   along columns is the product of the values in hk and hani. (default is 1.0).
hani = 0.0
# Is either vertical hydraulic conductivity or the ratio of horizontal to vertical hydraulic
#   conductivity depending on the value of layvka. (default is 1.0).
vka = np.array([[[50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. , 0.0001, 0.0001,
      0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001,
      0.0001, 0.0001, 0.0001, 0.0001,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
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      ,50. ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
      , 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001,
      0.0001, 0.0001, 0.0001, 0.0001,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
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      0.0001, 0.0001, 0.0001, 0.0001, 0.0001,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
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      0.0001, 0.0001, 0.0001, 0.0001, 0.0001,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
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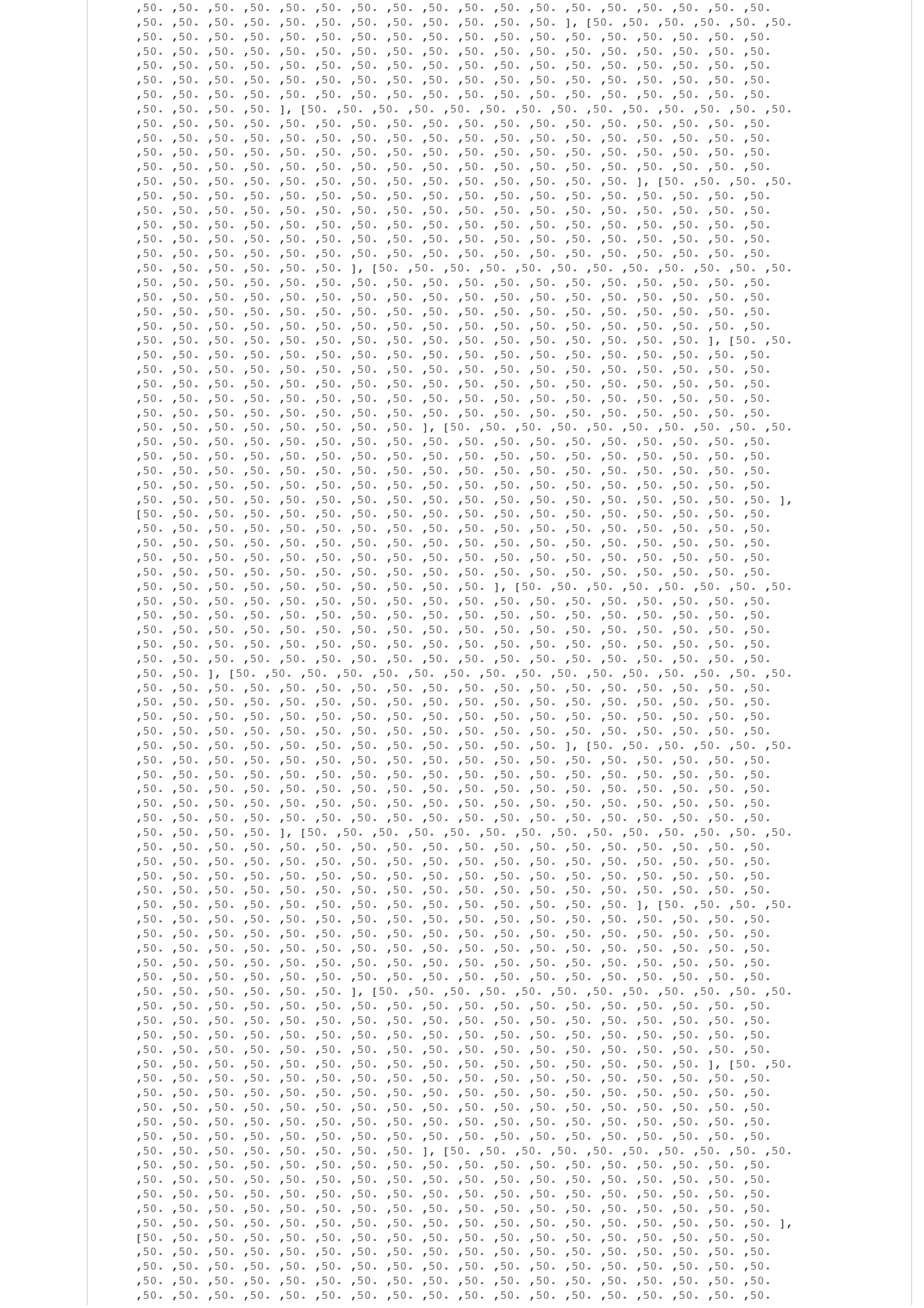

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        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ], [50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ],
        [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ], [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ], [50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50.
        ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ,50. ]]])
# Is specific storage unless the storagecoefficient option is used. when storagecoefficient is
#   used, ss is confined storage coefficient. (default is 1.e-5).
ss = 0.0
# Is specific yield.  (default is 0.15).
sy = 0.0
# Is the vertical hydraulic conductivity of a quasi-three-dimensional confining bed below a layer.
```

```
#   (default is 0.0).  note that if an array is passed for vkcb it must be of size (nlay, nrow,
#   ncol) even though the information for the bottom layer is not needed.
vkcb = 0.0
# Is a combination of the wetting threshold and a flag to indicate which neighboring cells can
#   cause a cell to become wet. (default is -0.01).
wetdry = 0.0
# Indicates that variable ss and ss parameters are read as storage coefficient rather than specific
#   storage.  (default is false).
storagecoefficient = False
#  indicates that vertical conductance for an unconfined cell is  computed from the cell thickness
#   rather than the saturated thickness.  the constantcv option automatically invokes the
#   nocvcorrection  option. (default is false).
constantcv = False
# Indicates that layers having a negative laytyp are confined, and their cell thickness for
#   conductance calculations will be computed as strt-bot rather than top-bot. (default is false).
thickstrt = False
# Indicates that vertical conductance is not corrected when the vertical flow correction is
#   applied. (default is false).
nocvcorrection = False
#  turns off the vertical flow correction under dewatered conditions.  this option turns off the
#   vertical flow calculation described on p.  5-8 of usgs techniques and methods report 6-a16 and
#   the vertical  conductance correction described on p. 5-18 of that report.  (default is false).
novfc = False

lpf = flopy.modflow.mflpf.ModflowLpf(model=model, laytyp=laytyp, layavg=layavg, chani=chani,
                                     layvka=layvka, laywet=laywet, ipakcb=ipakcb, hdry=hdry,
                                     iwdflg=iwdflg, wetfct=wetfct, iwetit=iwetit, ihdwet=ihdwet,
                                     hk=hk, hani=hani, vka=vka, ss=ss, sy=sy, vkcb=vkcb,
                                     wetdry=wetdry, storagecoefficient=storagecoefficient,
                                     constantcv=constantcv, thickstrt=thickstrt,
                                     nocvcorrection=nocvcorrection, novfc=novfc)
```

WEL

In [ ]:

```
# The model object (of type :class:`flopy.modflow.mf.modflow`) to which this package will be added.
model = modflow
# A flag that is used to determine if cell-by-cell budget data should be saved. if ipakcb is
#   non-zero cell-by-cell budget data will be saved. (default is 0).
ipakcb = 53
# Dictionary of boundaries each well is defined through definition of layer (int), row (int),
#   column (int), flux (float). the simplest form is a dictionary with a lists of boundaries for
#   each stress period, where each list of boundaries itself is a list of boundaries. indices of
#   the dictionary are the numbers of the stress period. this gives the form of:
stress_period_data = {0: rec.array([(0,  0, 0,  0.0875), (0,  1, 0,  0.0875), (0,  2, 0,  0.0875),\
                     (0,  3, 0,  0.0875), (0,  4, 0,  0.0875), (0,  5, 0,  0.0875), (0,  6, 0,\
                     0.0875), (0,  7, 0,  0.0875), (0,  8, 0,  0.0875), (0,  9, 0,  0.0875), (0,\
                     10, 0,  0.0875), (0, 11, 0,  0.0875), (0, 12, 0,  0.0875), (0, 13, 0,\
                     0.0875), (0, 14, 0,  0.0875), (0, 15, 0,  0.35  ), (0, 16, 0,  0.35  ), (0,\
                     17, 0,  0.35  ), (0, 18, 0,  0.35  ), (0, 19, 0,  0.35  ), (0, 20, 0,  0.35\
                     ), (0, 21, 0,  0.35  ), (0, 22, 0,  0.35  ), (0, 23, 0,  0.35  ), (0, 24, 0,\
                     0.35  ), (0, 25, 0,  0.35  ), (0, 26, 0,  0.35  ), (0, 27, 0,  0.35  ), (0,\
                     28, 0,  0.35  ), (0, 29, 0,  0.35  ), (0, 30, 0,  0.35  ), (0, 31, 0,  0.35\
                     ), (0, 32, 0,  0.35  ), (0, 33, 0,  0.35  ), (0, 34, 0,  0.35  ), (0, 35, 0,\
                     0.35  ), (0, 36, 0,  0.35  ), (0, 37, 0,  0.35  ), (0, 38, 0,  0.35  ), (0,\
                     39, 0,  0.35  ), (0, 40, 0,  0.35  ), (0, 41, 0,  0.35  ), (0, 42, 0,  0.35\
                     ), (0, 43, 0,  0.35  ), (0, 44, 0,  0.35  ), (0, 45, 0,  0.35  ), (0, 46, 0,\
                     0.35  ), (0, 47, 0,  0.35  ), (0, 48, 0,  0.35  ), (0, 49, 0,  0.35  ), (0,\
                     50, 0,  0.35  ), (0, 51, 0,  0.35  ), (0, 52, 0,  0.35  ), (0, 53, 0,  0.35\
                     ), (0, 54, 0,  0.35  ), (0, 55, 0,  0.35  ), (0, 56, 0,  0.35  ), (0, 57, 0,\
                     0.35  ), (0, 58, 0,  0.35  ), (0, 59, 0, 35.    )],           dtype=[('k',\
                     '<i8'), ('i', '<i8'), ('j', '<i8'), ('flux', '<f4')])}
# If none the default well datatype will be applied (default is none).
dtype = np.dtype([('k', '<i8'), ('i', '<i8'), ('j', '<i8'), ('flux', '<f4')])
# Package options (default is none).
options = []
binary = False

wel = flopy.modflow.mfwel.ModflowWel(model=model, ipakcb=ipakcb,
                                     stress_period_data=stress_period_data, dtype=dtype,
                                     options=options, binary=binary)
```

PCG

In [ ]:
```
# The model object (of type :class:`flopy.modflow.mf.modflow`) to which this package will be added.
model = modflow
# Maximum number of outer iterations. (default is 50)
mxiter = 30
# Maximum number of inner iterations. (default is 30)
iter1 = 30
# Flag used to select the matrix conditioning method. (default is 1). specify npcond = 1 for
#   modified incomplete cholesky. specify npcond = 2 for polynomial.
npcond = 1
# Is the head change criterion for convergence. (default is 1e-5).
hclose = 0.0001
# Is the residual criterion for convergence. (default is 1e-5)
rclose = 0.0001
# Is the relaxation parameter used with npcond = 1. (default is 1.0)
relax = 1.0
# Is only used when npcond = 2 to indicate whether the estimate of the upper bound on the maximum
#   eigenvalue is 2.0, or whether the estimate will be calculated. nbpol = 2 is used to specify the
#   value is 2.0; for any other value of nbpol, the estimate is calculated. convergence is
#   generally insensitive to this parameter. (default is 0).
nbpol = 0
# Solver print out interval. (default is 0).
iprpcg = 0
# If mutpcg = 0, tables of maximum head change and residual will be printed each iteration. if
#   mutpcg = 1, only the total number of iterations will be printed. if mutpcg = 2, no information
#   will be printed. if mutpcg = 3, information will only be printed if convergence fails. (default
#   is 3).
mutpcg = 1
# Is the steady-state damping factor. (default is 1.)
damp = 1.0
# Is the transient damping factor. (default is 1.)
dampt = 0.0
# Is a flag that determines what happens to an active cell that is surrounded by dry cells.
#   (default is 0). if ihcofadd=0, cell converts to dry regardless of hcof value. this is the
#   default, which is the way pcg2 worked prior to the addition of this option. if ihcofadd<>0,
#   cell converts to dry only if hcof has no head-dependent stresses or storage terms.
ihcofadd = 0

pcg = flopy.modflow.mfpcg.ModflowPcg(model=model, mxiter=mxiter, iter1=iter1, npcond=npcond,
                                     hclose=hclose, rclose=rclose, relax=relax, nbpol=nbpol,
                                     iprpcg=iprpcg, mutpcg=mutpcg, damp=damp, dampt=dampt,
                                     ihcofadd=ihcofadd)
```

OC

In [ ]:
```
# The model object (of type :class:`flopy.modflow.mf.modflow`) to which this package will be added.
model = modflow
# Is a code for the format in which heads will be printed. (default is 0).
ihedfm = 0
# Is a code for the format in which drawdown will be printed. (default is 0).
iddnfm = 0
# Is a character value that specifies the format for saving heads. the format must contain 20
#   characters or less and must be a valid fortran format that is enclosed in parentheses. the
#   format must be enclosed in apostrophes if it contains one or more blanks or commas. the
#   optional word label after the format is used to indicate that each layer of output should be
#   preceded with a line that defines the output (simulation time, the layer being output, and so
#   forth). if there is no record specifying chedfm, then heads are written to a binary
#   (unformatted) file. binary files are usually more compact than text files, but they are not
#   generally transportable among different computer operating systems or different fortran
#   compilers. (default is none)
chedfm = None
# Is a character value that specifies the format for saving drawdown. the format must contain 20
#   characters or less and must be a valid fortran format that is enclosed in parentheses. the
#   format must be enclosed in apostrophes if it contains one or more blanks or commas. the
#   optional word label after the format is used to indicate that each layer of output should be
#   preceded with a line that defines the output (simulation time, the layer being output, and so
#   forth). if there is no record specifying cddnfm, then drawdowns are written to a binary
#   (unformatted) file. binary files are usually more compact than text files, but they are not
#   generally transportable among different computer operating systems or different fortran
#   compilers. (default is none)
cddnfm = None
# Is a character value that specifies the format for saving ibound. the format must contain 20
#   characters or less and must be a valid fortran format that is enclosed in parentheses. the
#   format must be enclosed in apostrophes if it contains one or more blanks or commas. the
#   optional word label after the format is used to indicate that each layer of output should be
#   preceded with a line that defines the output (simulation time, the layer being output, and so
#   forth). if there is no record specifying cboufm, then ibounds are written to a binary
#   (unformatted) file. binary files are usually more compact than text files, but they are not
#   generally transportable among different computer operating systems or different fortran
#   compilers. (default is none)
cboufm = None
# Save results in compact budget form. (default is true).
compact = True
# Dictionary key is a tuple with the zero-based period and step  (iperoc, itsoc) for each
#   print/save option list. if stress_period_data is none, then heads are saved for the last time
#   step of each stress period. (default is none)  the list can have any valid modflow oc
#   print/save option:     print head     print drawdown     print budget     save head     save
#   drawdown     save budget     save ibound          the lists can also include (1) ddreference in
#   the list to reset      drawdown reference to the period and step and (2) a list of layers
#   for print head, save head, print drawdown, save drawdown, and     save ibound.
stress_period_data = {(0, 0): ['save head', 'save budget']}
label = 'LABEL'

oc = flopy.modflow.mfoc.ModflowOc(model=model, ihedfm=ihedfm, iddnfm=iddnfm, chedfm=chedfm,
                                  cddnfm=cddnfm, cboufm=cboufm, compact=compact,
                                  stress_period_data=stress_period_data, label=label)
```

flopy.mt3d

In [ ]:
```
# Name of model.  this string will be used to name the modflow input that are created with
#   write_model. (the default is 'mt3dtest')
modelname = 'BW'
# Extension for the namefile (the default is 'nam')
namefile_ext = 'nam'
# This is a flopy modflow model object upon which this mt3dms model is based. (the default is none)
modflowmodel = modflow
ftlfilename = 'mt3d_link.ftl'
# Version of mt3dms to use (the default is 'mt3dms').
version = 'mt3dms'
# The name of the executable to use (the default is 'mt3dms.exe').
exe_name = 'mt3dms.exe'
structured = True
# Unit number for the list file (the default is 2).
listunit = None
# Model workspace.  directory name to create model data sets. (default is the present working
#   directory).
model_ws = '.'
# Location for external files (default is none).
external_path = None
# Print additional information to the screen (default is false).
verbose = False
#  (default is true).
load = True
# (default is 0)
silent = 0

mt3d = flopy.mt3d.mt.Mt3dms(modelname=modelname, namefile_ext=namefile_ext,
                            modflowmodel=modflowmodel, ftlfilename=ftlfilename, version=version,
                            exe_name=exe_name, structured=structured, listunit=listunit,
                            model_ws=model_ws, external_path=external_path, verbose=verbose,
                            load=load, silent=silent)
```

BTN

In [ ]:

```
# The model object (of type :class:`flopy.mt3dms.mt.mt3dms`) to which this package will be added.
model = mt3d
# The total number of chemical species in the simulation. (default is none, will be changed to 1 if
#   sconc is single value)
ncomp = 2
# The total number of 'mobile' species (default is 1). mcomp must be equal or less than ncomp.
mcomp = 2
# The name of unit for time (default is 'd', for 'days'). used for identification purposes only.
tunit = 'D   '
# The name of unit for length (default is 'm', for 'meters'). used for identification purposes
#   only.
lunit = 'M   '
# The name of unit for mass (default is 'kg', for 'kilograms'). used for identification purposes
#   only.
munit = 'KG  '
# The effective porosity of the porous medium in a single porosity system, or the mobile porosity
#   in a dual-porosity medium (the immobile porosity is defined through the chemical reaction
#   package. (default is 0.25).
prsity = 0.3499999940395355
# The icbund array specifies the boundary condition type for solute species (shared by all
#   species). if icbund = 0, the cell is an inactive concentration cell; if icbund < 0, the cell is
#   a constant-concentration cell; if icbund > 0, the cell is an active concentration cell where
#   the concentration value will be calculated. (default is 1).
icbund = 1
# Sconc is the starting concentration for the first species.  to specify starting concentrations
#   for other species in a multi-species simulation, include additional keywords, such as sconc2,
#   sconc3, and so forth.
sconc = 0.0
# The value for indicating an inactive concentration cell. (default is 1e30).
cinact = -1000.0
# The minimum saturated thickness in a cell, expressed as the decimal fraction of its thickness,
#   below which the cell is considered inactive. (default is 0.01).
thkmin = 0.01
# A flag/format code indicating how the calculated concentration should be printed to the standard
#   output text file. format codes for printing are listed in table 3 of the mt3dms manual. if
#   ifmtcn > 0 printing is in wrap form; ifmtcn < 0 printing is in strip form; if ifmtcn = 0
#   concentrations are not printed. (default is 0).
ifmtcn = 0
# A flag/format code indicating how the number of particles should be printed to the standard
#   output text file. the convention is the same as for ifmtcn. (default is 0).
ifmtnp = 0
# A flag/format code indicating how the calculated retardation factor should be printed to the
#   standard output text file. the convention is the same as for ifmtcn. (default is 0).
ifmtrf = 0
# A flag/format code indicating how the distance-weighted dispersion coefficient should be printed
#   to the standard output text file. the convention is the same as for ifmtcn. (default is 0).
ifmtdp = 0
# A logical flag indicating whether the concentration solution should be saved in an unformatted
#   file. (default is true).
savucn = True
# A flag indicating (i) the frequency of the output and (ii) whether the output frequency is
#   specified in terms of total elapsed simulation time or the transport step number. if nprs > 0
#   results will be saved at the times as specified in timprs; if nprs = 0, results will not be
#   saved except at the end of simulation; if nprs < 0, simulation results will be saved whenever
#   the number of transport steps is an even multiple of nprs. (default is 0).
nprs = -999999999
# The total elapsed time at which the simulation results are saved. the number of entries in timprs
#   must equal nprs. (default is none).
timprs = None
obs = None
nprobs = 0
chkmas = True
nprmas = 1
ssflag = 288 * [' ']
dt0 = 0.0
mxstrn = 50000
ttsmult = 1.0
ttsmax = 0.0
species_names = []
# Sconc is the starting concentration for the first species.  to specify starting concentrations
#   for other species in a multi-species simulation, include additional keywords, such as sconc2,
#   sconc3, and so forth.
sconc2 = 12.0

btn = flopy.mt3d.mtbtn.Mt3dBtn(model=model, ncomp=ncomp, mcomp=mcomp, tunit=tunit, lunit=lunit,
                               munit=munit, prsity=prsity, icbund=icbund, sconc=sconc,
                               cinact=cinact, thkmin=thkmin, ifmtcn=ifmtcn, ifmtnp=ifmtnp,
                               ifmtrf=ifmtrf, ifmtdp=ifmtdp, savucn=savucn, nprs=nprs,
                               timprs=timprs, obs=obs, nprobs=nprobs, chkmas=chkmas, nprmas=nprmas,
                               ssflag=ssflag, dt0=dt0, mxstrn=mxstrn, ttsmult=ttsmult,
                               ttsmax=ttsmax, species_names=species_names, sconc2=sconc2)
```

ADV

In [ ]:

```
# The model object (of type :class:`flopy.mt3d.mt.mt3dms`) to which this package will be added.
model = mt3d
# Mixelm is an integer flag for the advection solution option. mixelm = 0, the standard
#   finite-difference method with upstream or central-in-space weighting, depending on the value of
#   nadvfd; = 1, the forward-tracking method of characteristics (moc); = 2, the backward-tracking
#   modified method of characteristics (mmoc); = 3, the hybrid method of characteristics (hmoc)
#   with moc or mmoc automatically and dynamically selected; = -1, the third-order tvd scheme
#   (ultimate).
mixelm = -1
# Percel is the courant number (i.e., the number of cells, or a fraction of a cell) advection will
#   be allowed in any direction in one transport step. for implicit finite-difference or
#   particle-tracking-based schemes, there is no limit on percel, but for accuracy reasons, it is
#   generally not set much greater than one. note, however, that the percel limit is checked over
#   the entire model grid. thus, even if percel > 1, advection may not be more than one cell's
#   length at most model locations. for the explicit finite-difference or the third-order tvd
#   scheme, percel is also a stability constraint which must not exceed one and will be
#   automatically reset to one if a value greater than one is specified.
percel = 1.0
# Mxpart is the maximum total number of moving particles allowed and is used only when mixelm = 1
#   or 3.
mxpart = 0
# Nadvfd is an integer flag indicating which weighting scheme should be used; it is needed only
#   when the advection term is solved using the implicit finite- difference method. nadvfd = 0 or
#   1, upstream weighting (default); = 2,central-in-space weighting.
nadvfd = 0
# Itrack is a flag indicating which particle-tracking algorithm is selected for the
#   eulerian-lagrangian methods. itrack = 1, the first-order euler algorithm is used. = 2, the
#   fourth-order runge-kutta algorithm is used; this option is computationally demanding and may be
#   needed only when percel is set greater than one. = 3, the hybrid first- and fourth-order
#   algorithm is used; the runge-kutta algorithm is used in sink/source cells and the cells next to
#   sinks/sources while the euler algorithm is used elsewhere.
itrack = None
# Is a concentration weighting factor between 0.5 and 1. it is used for operator splitting in the
#   particle- tracking-based methods. the value of 0.5 is generally adequate. the value of wd may
#   be adjusted to achieve better mass balance. generally, it can be increased toward 1.0 as
#   advection becomes more dominant.
wd = None
# Is a small relative cell concentration gradient below which advective transport is considered
dceps = None
# Nplane is a flag indicating whether the random or fixed pattern is selected for initial placement
#   of moving particles. if nplane = 0, the random pattern is selected for initial placement.
#   particles are distributed randomly in both the horizontal and vertical directions by calling a
#   random number generator (figure 18b). this option is usually preferred and leads to smaller
#   mass balance discrepancy in nonuniform or diverging/converging flow fields. if nplane > 0, the
#   fixed pattern is selected for initial placement. the value of nplane serves as the number of
#   vertical 'planes' on which initial particles are placed within each cell block (figure 18a).
#   the fixed pattern may work better than the random pattern only in relatively uniform flow
#   fields. for two-dimensional simulations in plan view, set nplane = 1. for cross sectional or
#   three-dimensional simulations, nplane = 2 is normally adequate. increase nplane if more
#   resolution in the vertical direction is desired.
nplane = None
# Npl is the number of initial particles per cell to be placed at cells where the relative cell
#   concentration gradient is less than or equal to dceps. generally, npl can be set to zero since
#   advection is considered insignificant when the relative cell concentration gradient is less
#   than or equal to dceps. setting npl equal to nph causes a uniform number of particles to be
#   placed in every cell over the entire grid (i.e., the uniform approach).
npl = None
# Nph is the number of initial particles per cell to be placed at cells where the relative cell
#   concentration gradient is greater than dceps. the selection of nph depends on the nature of the
#   flow field and also the computer memory limitation. generally, a smaller number should be used
#   in relatively uniform flow fields and a larger number should be used in relatively nonuniform
#   flow fields. however, values exceeding 16 in two-dimensional simulation or 32 in three-
#   dimensional simulation are rarely necessary. if the random pattern is chosen, nph particles are
#   randomly distributed within the cell block. if the fixed pattern is chosen, nph is divided by
#   nplane to yield the number of particles to be placed per vertical plane, which is rounded to
#   one of the values shown in figure 30.
nph = None
# Is the minimum number of particles allowed per cell. if the number of particles in a cell at the
#   end of a transport step is fewer than npmin, new particles are inserted into that cell to
#   maintain a sufficient number of particles. npmin can be set to zero in relatively uniform flow
#   fields and to a number greater than zero in diverging/converging flow fields. generally, a
#   value between zero and four is adequate.
npmin = None
# Npmax is the maximum number of particles allowed per cell. if the number of particles in a cell
#   exceeds npmax, all particles are removed from that cell and replaced by a new set of particles
#   equal to nph to maintain mass balance. generally, npmax can be set to approximately two times
#   of nph.
npmax = None
# S a flag indicating whether the random or fixed pattern is selected for initial placement of
#   particles to approximate sink cells in the mmoc scheme. the convention is the same as that for
#   nplane. it is generally adequate to set nlsink equivalent to nplane.
nlsink = None
# Is the number of particles used to approximate sink cells in the mmoc scheme. the convention is
#   the same as that for nph. it is generally adequate to set npsink equivalent to nph.
npsink = None
# Dchmoc is the critical relative concentration gradient for controlling the selective use of
#   either moc or mmoc in the hmoc solution scheme. the moc solution is selected at cells where the
#   relative concentration gradient is greater than dchmoc. the mmoc solution is selected at cells
#   where the relative concentration gradient is less than or equal to dchmoc.
```

```
dchmoc = None

adv = flopy.mt3d.mtadv.Mt3dAdv(model=model, mixelm=mixelm, percel=percel, mxpart=mxpart,
                               nadvfd=nadvfd, itrack=itrack, wd=wd, dceps=dceps, nplane=nplane,
                               npl=npl, nph=nph, npmin=npmin, npmax=npmax, nlsink=nlsink,
                               npsink=npsink, dchmoc=dchmoc)
```

DSP

In [ ]:

```
# The model object (of type :class:`flopy.mt3d.mt.mt3dms`) to which this package will be added.
model = mt3d
# Al is the longitudinal dispersivity, for every cell of the model grid (unit, l). (default is
#   0.01)
al = 0.0
# S a 1d real array defining the ratio of the horizontal transverse dispersivity to the
#   longitudinal dispersivity. each value in the array corresponds to one model layer. some recent
#   field studies suggest that trpt is generally not greater than 0.1. (default is 0.1)
trpt = 0.10000000149011612
# Is the ratio of the vertical transverse dispersivity to the longitudinal dispersivity. each value
#   in the array corresponds to one model layer. some recent field studies suggest that trpt is
#   generally not greater than 0.01.  set trpv equal to trpt to use the standard isotropic
#   dispersion model (equation 10 in chapter 2). otherwise, the modified isotropic dispersion model
#   is used (equation 11 in chapter 2). (default is 0.01)
trpv = 0.009999999776482582
# Multidiff option is used. dmcoef is the effective molecular diffusion coefficient (unit, l2t-1).
#   set dmcoef = 0 if the effect of molecular diffusion is considered unimportant. each value in
#   the array corresponds to one model layer. the value for dmcoef applies only to species 1.  see
#   kwargs for entering dmcoef for other species. (default is 1.e-9).
dmcoef = 0.0
# To activate the component-dependent diffusion option, a keyword input record must be inserted to
#   the beginning of the dispersion (dsp) input file. the symbol $ in the first column of an input
#   line signifies a keyword input record containing one or more predefined keywords. above the
#   keyword input record, comment lines marked by the symbol # in the first column are allowed.
#   comment lines are processed but have no effect on the simulation. furthermore, blank lines are
#   also acceptable above the keyword input record. below the keyword input record, the format of
#   the dsp input file must remain unchanged from the previous versions except for the diffusion
#   coefficient as explained below. if no keyword input record is specified, the input file remains
#   backward compatible with all previous versions of mt3dms. the predefined keyword for the
#   component-dependent diffusion option is multidiffusion. the keyword is case insensitive so
#   ''multidiffusion'' is equivalent to either ''multidiffusion'' or ''multidiffusion''. if this
#   keyword is specified in the keyword input record that has been inserted into the beginning of
#   the dsp input file, the component-dependent diffusion option has been activated and the user
#   needs to specify one diffusion coefficient for each mobile solute component and at each model
#   cell. this is done by specifying one mobile component at a time, from the first component to
#   the last component (mcomp). for each mobile component, the real array reader utility (rarray)
#   is used to input the 3-d diffusion coefficient array, one model layer at a time. (default is
#   false)
multiDiff = True
# Multidiff option is used. dmcoef is the effective molecular diffusion coefficient (unit, l2t-1).
#   set dmcoef = 0 if the effect of molecular diffusion is considered unimportant. each value in
#   the array corresponds to one model layer. the value for dmcoef applies only to species 1.  see
#   kwargs for entering dmcoef for other species. (default is 1.e-9).
dmcoef2 = np.array([[[0.1218029 ,0.1218029 ,0.1218029 ,0.1218029 ,0.1218029 ,0.1218029 ,0.1218029
          ,0.1218029 ,0.1218029 ,0.1218029 ,0.1218029 ,0.1218029 ,0.0040039
          ,0.01222244,0.01222244,0.01222244,0.01222244,0.01222244,0.01222244,0.01222244,0.01222244,0.01222244,0.0
1222244,0.01222244,0.01222244,0.01222244,0.01222244,0.01222244,0.0040039
          ,0.1218029 ,0.1218029 ,0.1218029 ,0.1218029 ,0.1218029 ,0.1218029 ,0.1218029 ,0.1218029 ,0.1218029
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        ,0.1218029 ,0.1218029 ,0.1218029 ,0.1218029 ]]])

dsp = flopy.mt3d.mtdsp.Mt3dDsp(model=model, al=al, trpt=trpt, trpv=trpv, dmcoef=dmcoef,
                              multiDiff=multiDiff, dmcoef2=dmcoef2)
```

SSM

In [ ]:

```
# The model object (of type :class:`flopy.mt3d.mt.mt3dms`) to which this package will be added.
model = mt3d
# Crch is the concentration of recharge for species 1. if the recharge flux is positive, it acts as
#   a source whose concentration can be specified as desired. if the recharge flux is negative, it
#   acts as a sink (discharge) whose concentration is always set equal to the concentration of
#   groundwater at the cell where discharge occurs. note that the location and flow rate of
#   recharge/discharge are obtained from the flow model directly through the unformatted
#   flow-transport link file.  crch can be specified as an array, if the array is constant for the
#   entire simulation.  if crch changes by stress period, then the user must provide a dictionary,
#   where the key is the stress period number (zero based) and the value is the recharge array.
#   the recharge concentration can be specified for additional species by passing additional
#   arguments to the mt3dssm constructor.  for example, to specify the recharge concentration for
#   species two one could use crch2={0: 0., 1: 10*np.ones((nrow, ncol), dtype=np.float)} as and
#   additional keyword argument that is passed to mt3dssm when making the ssm object.
crch = None
# Is the concentration of evapotranspiration flux for species 1. evapotranspiration is the only
#   type of sink whose concentration may be specified externally. note that the concentration of a
#   sink cannot be greater than that of the aquifer at the sink cell. thus, if the sink
#   concentration is specified greater than that of the aquifer, it is automatically set equal to
#   the concentration of the aquifer. also note that the location and flow rate of
#   evapotranspiration are obtained from the flow model directly through the unformatted
#   flow-transport link file.  for multi-species simulations, see crch for a description of how to
#   specify additional concentrations arrays for each species.
cevt = None
mxss = 121
# Keys in the dictionary are stress zero-based stress period numbers; values in the dictionary are
#   recarrays of ssm boundaries.  the dtype for the recarray can be obtained using ssm.dtype (after
#   the ssm package has been created).  the default dtype for the recarray is np.dtype([('k',
#   np.int), ("i", np.int), ("j", np.int), ("css", np.float32), ("itype", np.int), ((cssms(n),
#   np.float), n=1, ncomp)]) if there are more than one component species, then additional entries
#   will be added to the dtype as indicated by cssm(n). note that if the number of dictionary
#   entries is less than the number of stress periods, then the last recarray of boundaries will
#   apply until the end of the simulation. full details of all options to specify
#   stress_period_data can be found in the flopy3_multi-component_ssm ipython notebook in the
#   notebook subdirectory of the examples directory. css is the specified source concentration or
#   mass-loading rate, depending on the value of itype, in a single-species simulation, (for a
#   multispecies simulation, css is not used, but a dummy value still needs to be entered here.)
#   note that for most types of sources, css is interpreted as the source concentration with the
#   unit of mass per unit volume (ml-3), which, when multiplied by its corresponding flow rate
#   (l3t-1) from the flow model, yields the mass-loading rate (mt-1) of the source. for a special
#   type of sources (itype = 15), css is taken directly as the mass-loading rate (mt-1) of the
#   source so that no flow rate is required from the flow model. furthermore, if the source is
#   specified as a constant-concentration cell (itype = -1), the specified value of css is assigned
#   directly as the concentration of the designated cell. if the designated cell is also associated
#   with a sink/source term in the flow model, the flow rate is not used. itype is an integer
#   indicating the type of the point source.  an itype dictionary can be retrieved from the ssm
#   object as itype = mt3d.mt3dssm.itype_dict() (cssms(n), n=1, ncomp) defines the concentrations
#   of a point source for multispecies simulation with ncomp>1. in a multispecies simulation, it is
#   necessary to define the concentrations of all species associated with a point source. as an
#   example, if a chemical of a certain species is injected into a multispecies system, the
#   concentration of that species is assigned a value greater than zero while the concentrations of
#   all other species are assigned zero. cssms(n) can be entered in free format, separated by a
#   comma or space between values. several important notes on assigning concentration for the
#   constant-concentration condition (itype = -1) are listed below: the constant-concentration
#   condition defined in this input file takes precedence to that defined in the basic transport
#   package input file. in a multiple stress period simulation, a constant-concentration cell, once
#   defined, will remain a constant- concentration cell in the duration of the simulation, but its
#   concentration value can be specified to vary in different stress periods. in a multispecies
#   simulation, if it is only necessary to define different constant-concentration conditions for
#   selected species at the same cell location, specify the desired concentrations for those
#   species, and assign a negative value for all other species. the negative value is a flag used
#   by mt3dms to skip assigning the constant-concentration condition for the designated species.
stress_period_data = {0: rec.array([(0,  0,  0, 0.,  2, 0., 12.      ), (0,  1,  0, 0.,  2, 0.,\
                     12.      ), (0,  2,  0, 0.,  2, 0., 12.      ), (0,  3,  0, 0.,  2, 0., 12.\
                     ), (0,  4,  0, 0.,  2, 0., 12.      ), (0,  5,  0, 0.,  2, 0., 12.      ),\
                     (0,  6,  0, 0.,  2, 0., 12.      ), (0,  7,  0, 0.,  2, 0., 12.      ), (0,\
                     8,  0, 0.,  2, 0., 12.      ), (0,  9,  0, 0.,  2, 0., 12.      ), (0, 10,\
                     0, 0.,  2, 0., 12.      ), (0, 11,  0, 0.,  2, 0., 12.      ), (0, 12,  0,\
                     0.,  2, 0., 12.      ), (0, 13,  0, 0.,  2, 0., 12.      ), (0, 14,  0, 0.,\
                     2, 0., 12.      ), (0, 15,  0, 0.,  2, 0., 12.      ), (0, 16,  0, 0.,  2,\
                     0., 12.      ), (0, 17,  0, 0.,  2, 0., 12.      ), (0, 18,  0, 0.,  2, 0.,\
                     12.      ), (0, 19,  0, 0.,  2, 0., 12.      ), (0, 20,  0, 0.,  2, 0., 12.\
                     ), (0, 21,  0, 0.,  2, 0., 12.      ), (0, 22,  0, 0.,  2, 0., 12.      ),\
                     (0, 23,  0, 0.,  2, 0., 12.      ), (0, 24,  0, 0.,  2, 0., 12.      ), (0,\
                     25,  0, 0.,  2, 0., 12.      ), (0, 26,  0, 0.,  2, 0., 12.      ), (0, 27,\
                     0, 0.,  2, 0., 12.      ), (0, 28,  0, 0.,  2, 0., 12.      ), (0, 29,  0,\
                     0.,  2, 0., 12.      ), (0, 30,  0, 0.,  2, 0., 12.      ), (0, 31,  0, 0.,\
                     2, 0., 12.      ), (0, 32,  0, 0.,  2, 0., 12.      ), (0, 33,  0, 0.,  2,\
                     0., 12.      ), (0, 34,  0, 0.,  2, 0., 12.      ), (0, 35,  0, 0.,  2, 0.,\
                     12.      ), (0, 36,  0, 0.,  2, 0., 12.      ), (0, 37,  0, 0.,  2, 0., 12.\
                     ), (0, 38,  0, 0.,  2, 0., 12.      ), (0, 39,  0, 0.,  2, 0., 12.      ),\
                     (0, 40,  0, 0.,  2, 0., 12.      ), (0, 41,  0, 0.,  2, 0., 12.      ), (0,\
                     42,  0, 0.,  2, 0., 12.      ), (0, 43,  0, 0.,  2, 0., 12.      ), (0, 44,\
                     0, 0.,  2, 0., 12.      ), (0, 45,  0, 0.,  2, 0., 12.      ), (0, 46,  0,\
                     0.,  2, 0., 12.      ), (0, 47,  0, 0.,  2, 0., 12.      ), (0, 48,  0, 0.,\
                     2, 0., 12.      ), (0, 49,  0, 0.,  2, 0., 12.      ), (0, 50,  0, 0.,  2,\
                     0., 12.      ), (0, 51,  0, 0.,  2, 0., 12.      ), (0, 52,  0, 0.,  2, 0.,\
                     12.      ), (0, 53,  0, 0.,  2, 0., 12.      ), (0, 54,  0, 0.,  2, 0., 12.\
                     ), (0, 55,  0, 0.,  2, 0., 12.      ), (0, 56,  0, 0.,  2, 0., 12.      ),\
```

```
                    (0, 57,  0, 0.,  2, 0., 12.      ), (0, 58,  0, 0.,  2, 0., 12.      ), (0,\
                    59,  0, 0.,  2, 0., 12.      ), (0,  7, 20, 0., 15, 0.,  0.316098)],\
                    dtype=[('k', '<i8'), ('i', '<i8'), ('j', '<i8'), ('css', '<f4'), ('itype',\
                    '<i8'), ('cssm(01)', '<f4'), ('cssm(02)', '<f4')]), 144: rec.array([(0,  0,\
                    0, 0.,  2, 0., 12.), (0,  1,  0, 0.,  2, 0., 12.), (0,  2,  0, 0.,  2, 0.,\
                    12.), (0,  3,  0, 0.,  2, 0., 12.), (0,  4,  0, 0.,  2, 0., 12.), (0,  5,  0,\
                    0.,  2, 0., 12.), (0,  6,  0, 0.,  2, 0., 12.), (0,  7,  0, 0.,  2, 0., 12.),\
                    (0,  8,  0, 0.,  2, 0., 12.), (0,  9,  0, 0.,  2, 0., 12.), (0, 10,  0, 0.,\
                    2, 0., 12.), (0, 11,  0, 0.,  2, 0., 12.), (0, 12,  0, 0.,  2, 0., 12.), (0,\
                    13,  0, 0.,  2, 0., 12.), (0, 14,  0, 0.,  2, 0., 12.), (0, 15,  0, 0.,  2,\
                    0., 12.), (0, 16,  0, 0.,  2, 0., 12.), (0, 17,  0, 0.,  2, 0., 12.), (0, 18,\
                    0, 0.,  2, 0., 12.), (0, 19,  0, 0.,  2, 0., 12.), (0, 20,  0, 0.,  2, 0.,\
                    12.), (0, 21,  0, 0.,  2, 0., 12.), (0, 22,  0, 0.,  2, 0., 12.), (0, 23,  0,\
                    0.,  2, 0., 12.), (0, 24,  0, 0.,  2, 0., 12.), (0, 25,  0, 0.,  2, 0., 12.),\
                    (0, 26,  0, 0.,  2, 0., 12.), (0, 27,  0, 0.,  2, 0., 12.), (0, 28,  0, 0.,\
                    2, 0., 12.), (0, 29,  0, 0.,  2, 0., 12.), (0, 30,  0, 0.,  2, 0., 12.), (0,\
                    31,  0, 0.,  2, 0., 12.), (0, 32,  0, 0.,  2, 0., 12.), (0, 33,  0, 0.,  2,\
                    0., 12.), (0, 34,  0, 0.,  2, 0., 12.), (0, 35,  0, 0.,  2, 0., 12.), (0, 36,\
                    0, 0.,  2, 0., 12.), (0, 37,  0, 0.,  2, 0., 12.), (0, 38,  0, 0.,  2, 0.,\
                    12.), (0, 39,  0, 0.,  2, 0., 12.), (0, 40,  0, 0.,  2, 0., 12.), (0, 41,  0,\
                    0.,  2, 0., 12.), (0, 42,  0, 0.,  2, 0., 12.), (0, 43,  0, 0.,  2, 0., 12.),\
                    (0, 44,  0, 0.,  2, 0., 12.), (0, 45,  0, 0.,  2, 0., 12.), (0, 46,  0, 0.,\
                    2, 0., 12.), (0, 47,  0, 0.,  2, 0., 12.), (0, 48,  0, 0.,  2, 0., 12.), (0,\
                    49,  0, 0.,  2, 0., 12.), (0, 50,  0, 0.,  2, 0., 12.), (0, 51,  0, 0.,  2,\
                    0., 12.), (0, 52,  0, 0.,  2, 0., 12.), (0, 53,  0, 0.,  2, 0., 12.), (0, 54,\
                    0, 0.,  2, 0., 12.), (0, 55,  0, 0.,  2, 0., 12.), (0, 56,  0, 0.,  2, 0.,\
                    12.), (0, 57,  0, 0.,  2, 0., 12.), (0, 58,  0, 0.,  2, 0., 12.), (0, 59,  0,\
                    0.,  2, 0., 12.), (0,  7, 20, 0., 15, 0.,  0.)],           dtype=[('k',\
                    '<i8'), ('i', '<i8'), ('j', '<i8'), ('css', '<f4'), ('itype', '<i8'),\
                    ('cssm(01)', '<f4'), ('cssm(02)', '<f4')])}
# Dtype to use for the recarray of boundaries.  if left as none (the default) then the dtype will
#   be automatically constructed.
dtype = np.dtype([('k', '<i8'), ('i', '<i8'), ('j', '<i8'), ('css', '<f4'), ('itype', '<i8'),
        ('cssm(01)', '<f4'), ('cssm(02)', '<f4')])

ssm = flopy.mt3d.mtssm.Mt3dSsm(model=model, crch=crch, cevt=cevt, mxss=mxss,
                               stress_period_data=stress_period_data, dtype=dtype)
```

GCG

In [ ]:

```
# The model object (of type :class:`flopy.mt3d.mt.mt3dms`) to which this package will be added.
model = mt3d
# Is the maximum number of outer iterations; it should be set to an integer greater than one only
#   when a nonlinear sorption isotherm is included in simulation. (default is 1)
mxiter = 1
# Is the maximum number of inner iterations; a value of 30-50 should be adequate for most problems.
#   (default is 50)
iter1 = 100
# Is the type of preconditioners to be used with the lanczos/orthomin acceleration scheme: = 1,
#   jacobi = 2, ssor = 3, modified incomplete cholesky (mic) (mic usually converges faster, but it
#   needs significantly more memory) (default is 3)
isolve = 3
# Is an integer flag for treatment of dispersion tensor cross terms: = 0, lump all dispersion cross
#   terms to the right-hand-side (approximate but highly efficient). = 1, include full dispersion
#   tensor (memory intensive). (default is 0)
ncrs = 1
# Is the relaxation factor for the ssor option; a value of 1.0 is generally adequate. (default is
#   1)
accl = 1.0
# Is the convergence criterion in terms of relative concentration; a real value between 10-4 and
#   10-6 is generally adequate. (default is 1.e-5)
cclose = 1e-05
# Iprgcg is the interval for printing the maximum concentration changes of each iteration. set
#   iprgcg to zero as default for printing at the end of each stress period. (default is 0)
iprgcg = 0

gcg = flopy.mt3d.mtgcg.Mt3dGcg(model=model, mxiter=mxiter, iter1=iter1, isolve=isolve, ncrs=ncrs,
                               accl=accl, cclose=cclose, iprgcg=iprgcg)
```

RCT

In [ ]:

```
# The model object (of type :class:`flopy.mt3dms.mt.mt3dms`) to which this package will be added.
model = mt3d
# Isothm is a flag indicating which type of sorption (or dual-domain mass transfer) is simulated:
#   isothm = 0, no sorption is simulated; isothm = 1, linear isotherm (equilibrium-controlled);
#   isothm = 2, freundlich isotherm (equilibrium-controlled); isothm = 3, langmuir isotherm
#   (equilibrium-controlled); isothm = 4, first-order kinetic sorption (nonequilibrium); isothm =
#   5, dual-domain mass transfer (without sorption); isothm = 6, dual-domain mass transfer (with
#   sorption). (default is 0).
isothm = 1
# Ireact is a flag indicating which type of kinetic rate reaction is simulated: ireact = 0, no
#   kinetic rate reaction is simulated; ireact = 1, first-order irreversible reaction, ireact =
#   100, zero-order reactions (decay or production). note that this reaction package is not
#   intended for modeling chemical reactions between species. an add-on reaction package developed
#   specifically for that purpose may be used. (default is 0).
ireact = 0
# Igetsc is an integer flag indicating whether the initial concentration for the nonequilibrium
#   sorbed or immobile phase of all species should be read when nonequilibrium sorption (isothm =
#   4) or dual-domain mass transfer (isothm = 5 or 6) is simulated: igetsc = 0, the initial
#   concentration for the sorbed or immobile phase is not read. by default, the sorbed phase is
#   assumed to be in equilibrium with the dissolved phase (isothm = 4), and the immobile domain is
#   assumed to have zero concentration (isothm = 5 or 6). igetsc > 0, the initial concentration for
#   the sorbed phase or immobile liquid phase of all species will be read. (default is 1).
igetsc = 0
# Rhob is the bulk density of the aquifer medium (unit, ml-3). rhob is used if isothm = 1, 2, 3, 4,
#   or 6. if rhob is not user-specified and isothm is not 5 then rhob is set to 1.8e3. (default is
#   none)
rhob = np.array([[[1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,
       0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0.
       ,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,
1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1
722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,17
22.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,172
2.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5],
       [1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,
       0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0. , 0.
       ,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,
1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1722.5,1
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2.5,1722.5,1722.5,1722.5,1722.5]]])
# Prsity2 is the porosity of the immobile domain (the ratio of pore spaces filled with immobile
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#   fluids over the bulk volume of the aquifer medium) when the simulation is intended to represent
#   a dual-domain system. prsity2 is used if isothm = 5 or 6. if prsity2 is not user- specified and
#   isothm = 5 or 6 then prsity2 is set to 0.1. (default is none)
prsity2 = 0.10000000149011612
# Srconc is the user-specified initial concentration for the sorbed phase of the first species if
#   isothm = 4 (unit, mm-1). note that for equilibrium-controlled sorption, the initial
#   concentration for the sorbed phase cannot be specified. srconc is the user-specified initial
#   concentration of the first species for the immobile liquid phase if isothm = 5 or 6 (unit,
#   ml-3). if srconc is not user-specified and isothm = 4, 5, or 6 then srconc is set to 0.
#   (default is none).
srconc = 0.0
# Sp1 is the first sorption parameter for the first species. the use of sp1 depends on the type of
#   sorption selected (the value of isothm). for linear sorption (isothm = 1) and nonequilibrium
#   sorption (isothm = 4), sp1 is the distribution coefficient (kd) (unit, l3m-1). for freundlich
#   sorption (isothm = 2), sp1 is the freundlich equilibrium constant (kf) (the unit depends on the
#   freundlich exponent a). for langmuir sorption (isothm = 3), sp1 is the langmuir equilibrium
#   constant (kl) (unit, l3m-1 ). for dual-domain mass transfer without sorption (isothm = 5), sp1
#   is not used, but still must be entered. for dual-domain mass transfer with sorption (isothm =
#   6), sp1 is also the distribution coefficient (kd) (unit, l3m-1). if sp1 is not specified and
#   isothm > 0 then sp1 is set to 0. (default is none).
sp1 = 0.0
# Sp2 is the second sorption or dual-domain model parameter for the first species. the use of sp2
#   depends on the type of sorption or dual-domain model selected. for linear sorption (isothm =
#   1), sp2 is read but not used. for freundlich sorption (isothm = 2), sp2 is the freundlich
#   exponent a. for langmuir sorption (isothm = 3), sp2 is the total concentration of the sorption
#   sites available ( s ) (unit, mm-1). for nonequilibrium sorption (isothm = 4), sp2 is the
#   first-order mass transfer rate between the dissolved and sorbed phases (unit, t-1). for
#   dual-domain mass transfer (isothm = 5 or 6), sp2 is the first-order mass transfer rate between
#   the two domains (unit, t-1). if sp2 is not specified and isothm > 0 then sp2 is set to 0.
#   (default is none).
sp2 = 0.0
# Rc1 is the first-order reaction rate for the dissolved (liquid) phase for the first species
#   (unit, t-1). rc1 is not used ireact = 0. if a dual-domain system is simulated, the reaction
#   rates for the liquid phase in the mobile and immobile domains are assumed to be equal. if rc1
#   is not specified and ireact > 0 then rc1 is set to 0. (default is none).
rc1 = 0.0
# Rc2 is the first-order reaction rate for the sorbed phase for the first species (unit, t-1). rc2
#   is not used ireact = 0. if a dual-domain system is simulated, the reaction rates for the sorbed
#   phase in the mobile and immobile domains are assumed to be equal. generally, if the reaction is
#   radioactive decay, rc2 should be set equal to rc1, while for biodegradation, rc2 may be
#   different from rc1. note that rc2 is read but not used, if no sorption is included in the
#   simulation. if rc2 is not specified and ireact > 0 then rc2 is set to 0. (default is none).
rc2 = 0.0
# Sp1 is the first sorption parameter for the first species. the use of sp1 depends on the type of
#   sorption selected (the value of isothm). for linear sorption (isothm = 1) and nonequilibrium
#   sorption (isothm = 4), sp1 is the distribution coefficient (kd) (unit, l3m-1). for freundlich
#   sorption (isothm = 2), sp1 is the freundlich equilibrium constant (kf) (the unit depends on the
#   freundlich exponent a). for langmuir sorption (isothm = 3), sp1 is the langmuir equilibrium
#   constant (kl) (unit, l3m-1 ). for dual-domain mass transfer without sorption (isothm = 5), sp1
#   is not used, but still must be entered. for dual-domain mass transfer with sorption (isothm =
#   6), sp1 is also the distribution coefficient (kd) (unit, l3m-1). if sp1 is not specified and
#   isothm > 0 then sp1 is set to 0. (default is none).
sp12 = 0.00020732000120915473
# Sp2 is the second sorption or dual-domain model parameter for the first species. the use of sp2
#   depends on the type of sorption or dual-domain model selected. for linear sorption (isothm =
#   1), sp2 is read but not used. for freundlich sorption (isothm = 2), sp2 is the freundlich
#   exponent a. for langmuir sorption (isothm = 3), sp2 is the total concentration of the sorption
#   sites available ( s ) (unit, mm-1). for nonequilibrium sorption (isothm = 4), sp2 is the
#   first-order mass transfer rate between the dissolved and sorbed phases (unit, t-1). for
#   dual-domain mass transfer (isothm = 5 or 6), sp2 is the first-order mass transfer rate between
#   the two domains (unit, t-1). if sp2 is not specified and isothm > 0 then sp2 is set to 0.
#   (default is none).
sp22 = 0.0
# Rc1 is the first-order reaction rate for the dissolved (liquid) phase for the first species
#   (unit, t-1). rc1 is not used ireact = 0. if a dual-domain system is simulated, the reaction
#   rates for the liquid phase in the mobile and immobile domains are assumed to be equal. if rc1
#   is not specified and ireact > 0 then rc1 is set to 0. (default is none).
rc12 = 0.0
# Rc2 is the first-order reaction rate for the sorbed phase for the first species (unit, t-1). rc2
#   is not used ireact = 0. if a dual-domain system is simulated, the reaction rates for the sorbed
#   phase in the mobile and immobile domains are assumed to be equal. generally, if the reaction is
#   radioactive decay, rc2 should be set equal to rc1, while for biodegradation, rc2 may be
#   different from rc1. note that rc2 is read but not used, if no sorption is included in the
#   simulation. if rc2 is not specified and ireact > 0 then rc2 is set to 0. (default is none).
rc22 = 0.0
# Srconc is the user-specified initial concentration for the sorbed phase of the first species if
#   isothm = 4 (unit, mm-1). note that for equilibrium-controlled sorption, the initial
#   concentration for the sorbed phase cannot be specified. srconc is the user-specified initial
#   concentration of the first species for the immobile liquid phase if isothm = 5 or 6 (unit,
#   ml-3). if srconc is not user-specified and isothm = 4, 5, or 6 then srconc is set to 0.
#   (default is none).
srconc2 = 0.0

rct = flopy.mt3d.mtrct.Mt3dRct(model=model, isothm=isothm, ireact=ireact, igetsc=igetsc, rhob=rhob,
                               prsity2=prsity2, srconc=srconc, sp1=sp1, sp2=sp2, rc1=rc1, rc2=rc2,
                               sp12=sp12, sp22=sp22, rc12=rc12, rc22=rc22, srconc2=srconc2)
```

flopy.seawat

In [ ]:
```
# Name of model.  this string will be used to name the seawat input that are created with
#   write_model. (the default is 'swttest')
modelname = 'BW'
# Extension for the namefile (the default is 'nam')
namefile_ext = 'nam'
modflowmodel = modflow
mt3dmodel = mt3d
# Version of seawat to use (the default is 'seawat').
version = 'seawat'
# The name of the executable to use (the default is 'swt_v4.exe').
exe_name = 'swt_v4'
structured = True
# Unit number for the list file (the default is 2).
listunit = 2
# Model workspace.  directory name to create model data sets. (default is the present working
#   directory).
model_ws = '.'
# Location for external files (default is none).
external_path = None
# Print additional information to the screen (default is false).
verbose = False
#  (default is true).
load = True
# (default is 0)
silent = 0

seawat = flopy.seawat.swt.Seawat(modelname=modelname, namefile_ext=namefile_ext,
                                 modflowmodel=modflowmodel, mt3dmodel=mt3dmodel, version=version,
                                 exe_name=exe_name, structured=structured, listunit=listunit,
                                 model_ws=model_ws, external_path=external_path, verbose=verbose,
                                 load=load, silent=silent)
```

VSC

In [ ]:
```
# The model object (of type :class:`flopy.seawat.swt.seawat`) to which this package will be added.
model = seawat
mt3dmuflg = -1
# Is the minimum fluid viscosity. if the resulting viscosity value calculated with the equation is
#   less than viscmin, the viscosity value is set to viscmin. if viscmin = 0, the computed fluid
#   viscosity is not limited by viscmin (this is the option to use for most simulations). if
#   viscmin > 0, a computed fluid viscosity less than viscmin is automatically reset to viscmin.
viscmin = 0.0
# Is the maximum fluid viscosity. if the resulting viscosity value calculated with the equation is
#   greater than viscmax, the viscosity value is set to viscmax. if viscmax = 0, the computed fluid
#   viscosity is not limited by viscmax (this is the option to use for most simulations). if
#   viscmax > 0, a computed fluid viscosity larger than viscmax is automatically reset to viscmax.
viscmax = 0.0
# Is the fluid viscosity at the reference concentration and reference temperature. for most
#   simulations, viscref is specified as the viscosity of freshwater.
viscref = 0.001266
nsmueos = 1
# Is a flag that specifies the option for including the effect of temperature on fluid viscosity.
#   if mutempopt = 0, the effect of temperature on fluid viscosity is not included or is a simple
#   linear relation that is specified in item 3c. if mutempopt = 1, fluid viscosity is calculated
#   using equation 18. the size of the amucoeff array in item 3e is 4 (muncoeff = 4). if mutempopt
#   = 2, fluid viscosity is calculated using equation 19. the size of the amucoeff array in item 3e
#   is 5 (muncoeff = 5). if mutempopt = 3, fluid viscosity is calculated using equation 20. the
#   size of the amucoeff array in item 3e is 2 (muncoeff = 2). if nsmueos and mutempopt are both
#   set to zero, all fluid viscosities are set to viscref.
mutempopt = 2
# Is the mt3dms species number corresponding to the adjacent dmudc and cmuref.
mtmuspec = 1
# Is the slope of the linear equation that relates fluid viscosity to solute concentration.
dmudc = 1.923e-06
# Is the reference concentration.
cmuref = 0.0
mtmutempspec = 2
# Is the coefficient array of size muncoeff. amucoeff is a in equations 18, 19, and 20.
amucoeff = [0.001, 1.0, 0.015512, -20.0, -1.572]
# Is a flag. invisc is read only if mt3dmuflg is equal to zero. if invisc < 0, values for the visc
#   array will be reused from the previous stress period. if it is the first stress period, values
#   for the visc array will be set to viscref. if invisc = 0, values for the visc array will be set
#   to viscref. if invisc >= 1, values for the visc array will be read from item 5. if invisc = 2,
#   values read for the visc array are assumed to represent solute concentration, and will be
#   converted to viscosity values.
invisc = None
# Is the fluid viscosity array read for each layer using the modflow-2000 u2drel array reader. the
#   visc array is read only if mt3dmuflg is equal to zero. the visc array may also be entered in
#   terms of solute concentration (or any other units) if invisc is set to 2, and the simple linear
#   expression in item 3 can be used to represent the relation to viscosity.
visc = None

vsc = flopy.seawat.swtvsc.SeawatVsc(model=model, mt3dmuflg=mt3dmuflg, viscmin=viscmin,
                                    viscmax=viscmax, viscref=viscref, nsmueos=nsmueos,
                                    mutempopt=mutempopt, mtmuspec=mtmuspec, dmudc=dmudc,
                                    cmuref=cmuref, mtmutempspec=mtmutempspec, amucoeff=amucoeff,
                                    invisc=invisc, visc=visc)
```

Run this thing!

In [ ]:
```
seawat.write_input()
# seawat.run_model()
```