Tutorial

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defining common parameters

```
library(SoilR)
```

```
## Loading required package: deSolve
```

```
##
## Attaching package: 'SoilR'
```

```
## The following object is masked from 'package:deSolve':
##
##     euler
```

```
#inputs
Iy_value=1.1
Io_value=0.5
#init and timesteps
iv<-c(Cy=1, Co=10)
duration=20
time_step=0.1
```

Testing the ICBM model for mass balance

Running the predefined ICBM model

```
#### ICBM
times<-seq(0,duration,by=time_step)
ICBM_run=ICBMModel(t=times, h=0.250, r=1.10, c0=iv, In=Iy_value+Io_value) #Manure
Ct0<-getC(ICBM_run)
Rt0<-getReleaseFlux(ICBM_run)
```

Check the mass balance of the ICBM simulation

```
### mass balance

#SOC difference
SOC_diff<-rowSums(Ct0)[length(times)]-rowSums(Ct0)[1]

#Respiration (cumulated)
RESP_tot<-sum(rowSums(Rt0*time_step)[-1])

#Inputs total
Input_tot<-sum(rep(1.1, duration)+ rep(0.5, duration))
# check mass balance
Input_tot==(SOC_diff+RESP_tot)
```

```
## [1] FALSE
```

```
Input_tot
```

```
## [1] 32
```

```
(SOC_diff+RESP_tot)
```

```
## [1] 32.02862
```

The mass balance is pretty much respected, just minor errors due probably to the solver.

Testing the tutorial model (nonlinearity in inputs) for mass balance

Defining the model

```
TwopoolNonlinearInput<-function(ky=0.8, ko=0.00605, h=0.13, Iy=Iy_value, Io=Io_value){
  time_symbol='t'

  ifs=SoilR:::InFluxList_by_PoolName(
    c(
      SoilR:::InFlux_by_PoolName(
        destinationName='Cy',
        func=function(t, Co){
          Iy*(Co/(0.5*Co))
        }
      ),
      SoilR:::InFlux_by_PoolName(
        destinationName='Co',
        func=function(t){
          Io
        }
      )
    )
  )
```

```
  ofs=SoilR:::OutFluxList_by_PoolName(
    c(
      SoilR:::OutFlux_by_PoolName(
        sourceName='Cy',
        func=function(Cy){
          ky*Cy
        }
      )
      ,
      SoilR:::OutFlux_by_PoolName(
        sourceName='Co',
        func=function(Co){
          ko*Co
        }
      )
    )
  )
  intfs=SoilR:::InternalFluxList_by_PoolName(
    list(
      SoilR:::InternalFlux_by_PoolName(
        sourceName='Cy',
        destinationName='Co',
        func=function(Cy){
          h*ky*Cy
        }
      )
    )
  )

  smod <- SoilR:::SymbolicModel_by_PoolNames(
    in_fluxes=ifs,
    internal_fluxes=intfs,
    out_fluxes=ofs,
    timeSymbol=time_symbol
  )
  smod
}
```

Running the model

```
modelObject<-TwopoolNonlinearInput()
modrun0<-Model_by_PoolNames(smod=modelObject, times=times, initialValues=iv)
Ct0<-getC(modrun0)
Rt0<-getReleaseFlux(modrun0)

# plot(rowSums(Ct0), type="l")
# plot(rowSums(Rt0), type="l")
```

Checking the mass balance

```
### mass balance

#SOC difference
SOC_diff<-rowSums(Ct0)[length(times)]-rowSums(Ct0)[1]

#Respiration (cumulated)
RESP_tot<-sum(rowSums(Rt0*time_step))

#Inputs total
Input_tot<-sum(rep(1.1, duration)+ rep(0.5, duration))

# check mass balance
Input_tot==(SOC_diff+RESP_tot)
```

```
## [1] FALSE
```

```
Input_tot
```

```
## [1] 32
```

```
(SOC_diff+RESP_tot)
```

```
## [1] 54.13648
```

The mass balance is not respected, something weird is happening with this model.