R-package FME : inverse modelling, sensitivity, monte carlo - applied to a steady-state model

Karline Soetaert
NIOO-CEME
The Netherlands

Abstract

Rpackage **FME** (Soetaert 2009) contains functions for model calibration, sensitivity, identifiability, and monte carlo analysis of nonlinear models.

This vignette, (`vignette("FMEsteady")`), applies **FME** to a partial differential equation, solved with a steady-state solver from package **rootSolve**

A similar vignette (`vignette("FMEdyna")`), applies the functions to a dynamic similation model, solved with integration routines from package **deSolve**

A third vignette (`vignette("FMEother")`), applies the functions to a simple nonlinear model

`vignette("FMEmcmc")` tests the markov chain monte carlo (MCMC) implementation

Keywords: steady-state models, differential equations, fitting, sensitivity, Monte Carlo, identifiability, R.

1. A steady-state model of oxygen in a marine sediment

This is a simple model of oxygen in a marine (submersed) sediment, diffusing along a spatial gradient, with imposed upper boundary concentration oxygen is consumed at maximal fixed rate, and including a monod limitation.

See (Soetaert and Herman 2009) for a description of reaction-transport models.

The constitutive equations are:

$$\frac{\partial O_2}{\partial t} = -\frac{\partial Flux}{\partial x} - cons \cdot \frac{O_2}{O_2 + k_s}$$

$$Flux = -D \cdot \frac{\partial O_2}{\partial x}$$

$$O_2(x = 0) = upO2$$

```
> par(mfrow=c(2,2))
> require(FME)
```

First the model parameters are defined...

```
> pars <- c(upO2=360,  # concentration at upper boundary, mmolO2/m3
+           cons=80,   # consumption rate, mmolO2/m3/day
```

```
+           ks=1,       # O2 half-saturation ct, mmolO2/m3
+           D=1)        # diffusion coefficient, cm2/d
```

Next the sediment is vertically subdivided into 100 grid cells, each 0.05 cm thick.

```
> n  <- 100                        # nr grid points
> dx <- 0.05   #cm
> dX <- c(dx/2,rep(dx,n-1),dx/2)  # dispersion distances; half dx near boundaries
> X  <- seq(dx/2,len=n,by=dx)     # distance from upper interface at middle of box
```

The model function takes as input the parameter values and returns the steady-state condition of oxygen. Function `steady.band` from package **rootSolve** ((Soetaert 2008)) does this in a very efficient way (see (Soetaert and Herman 2009)).

```
> O2fun <- function(pars)
+ {
+   derivs<-function(t,O2,pars)
+   {
+   with (as.list(pars),{
+
+     Flux <- -D* diff(c(upO2,O2,O2[n]))/dX
+     dO2  <- -diff(Flux)/dx-cons*O2/(O2+ks)
+
+     return(list(dO2,UpFlux = Flux[1],LowFlux = Flux[n+1]))
+   })
+  }
+
+  # Solve the steady-state conditions of the model
+  ox <- steady.band(y=runif(n),func=derivs,parms=pars,nspec=1,positive=TRUE)
+  data.frame(X=X,O2=ox$y)
+ }
```

The model is run

```
> ox<-O2fun(pars)
```

and the results plotted...

```
> plot(ox$O2,ox$X,ylim=rev(range(X)),xlab="mmol/m3",
+      main="Oxygen", ylab="depth, cm",type="l",lwd=2)
```

2. Global sensitivity analysis : Sensitivity ranges

The sensitivity of the oxygen profile to parameter `cons`, the consumption rate is estimated. We assume a normally distributed parameter, with mean = 80 (`parMean`), and a variance=100 (`parCovar`). The model is run 100 times (`num`).

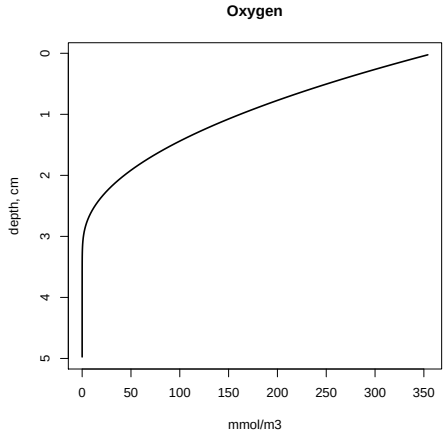

Figure 1: The modeled oxygen profile - see text for R-code

```
> print(system.time(
+ Sens2 <- sensRange(parms=pars,func=O2fun,dist="norm",
+            num=100,parMean=c(cons=80),parCovar=100)
+ ))

   user  system elapsed
   1.05    0.00    1.05
```

The results can be plotted in two ways:

```
> par(mfrow=c(1,2))
> plot(Sens2,xyswap=TRUE,xlab= "O2",
+      ylab="depth, cm",main="Sensitivity runs")
> plot(summary(Sens2),xyswap=TRUE,xlab= "O2",
+      ylab="depth, cm",main="Sensitivity ranges")
> par(mfrow=c(1,1))
```

3. Local sensitivity analysis : Sensitivity functions

Local sensitivity analsysis starts by calculating the sensitivity functions

```
> O2sens <- sensFun(func=O2fun,parms=pars)
```

The summary of these functions gives information about which parameters have the largest effect (univariate sensitivity):

```
> summary(O2sens)
```

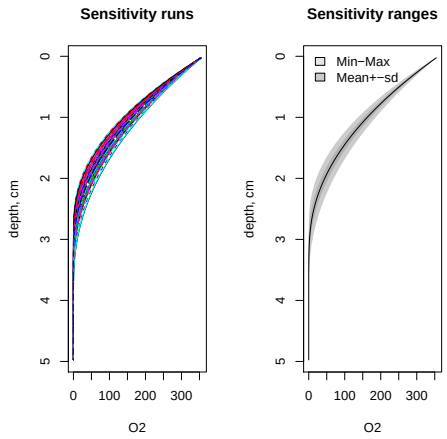

Figure 2: Results of the sensitivity run - left: all model runs, right: summary - see text for R-code

```
     value scale  L1   L2 Mean      Min      Max   N
upO2   360   360 7.0 0.88  7.0  1.0e+00 13.4176 100
cons    80    80 8.1 1.14 -8.1 -2.2e+01 -0.0084 100
ks       1     1 2.2 0.37  2.2  1.2e-04  9.6137 100
D        1     1 7.2 0.99  7.2  8.4e-03 19.3522 100
```

In bivariate sensitivity the pair-wise relationship and the correlation is estimated and/or plotted:

```
> pairs(O2sens)
```

```
> cor(O2sens[,-(1:2)])
```

```
           upO2       cons         ks          D
upO2  1.0000000 -0.9787945  0.8375805  0.9794693
cons -0.9787945  1.0000000 -0.9317286 -0.9989001
ks    0.8375805 -0.9317286  1.0000000  0.9275991
D     0.9794693 -0.9989001  0.9275991  1.0000000
```

Multivariate sensitivity is done by estimating the collinearity between parameter sets (Brun, Reichert, and Kunsch 2001).

```
> Coll <- collin(O2sens)
> Coll
```

```
   upO2 cons ks D N collinearity
1     1    1  0 0 2          7.7
2     1    0  1 0 2          2.9
```

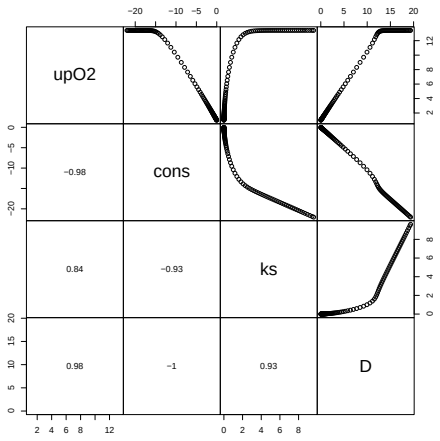

Figure 3: pairs plot - see text for R-code

```
3     1    0  0 1 2          8.3
4     0    1  1 0 2          4.4
5     0    1  0 1 2         39.3
6     0    0  1 1 2          4.2
7     1    1  1 0 3         25.5
8     1    1  0 1 3         41.9
9     1    0  1 1 3         25.0
10    0    1  1 1 3         42.3
11    1    1  1 1 4         42.3
```

```
> plot(Coll,log="y")
```

4. Fitting the model to the data

Assume both the oxygen flux at the upper interface and a vertical profile of oxygen has been measured.

These are the data:

```
> O2dat <- data.frame(x=seq(0.1,3.5,by=0.1),
+     y = c(279,260,256,220,200,203,189,179,165,140,138,127,116,
+           109,92,87,78,72,62,55,49,43,35,32,27,20,15,15,10,8,5,3,2,1,0))
> O2depth <- cbind(name="O2",O2dat)        # oxygen versus depth
> O2flux  <- c(UpFlux=170)                 # measured flux
```

First a function is defined that returns only the required model output.

```
> O2fun2 <- function(pars)
+ {
```

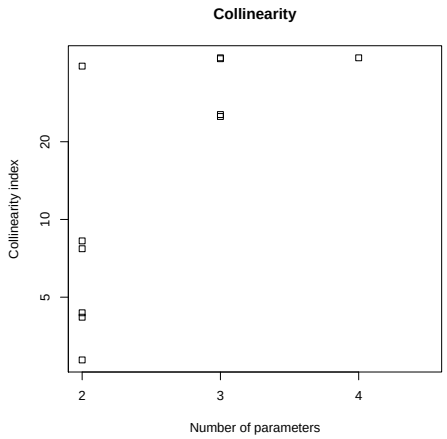

Figure 4: collinearity - see text for R-code

```
+   derivs<-function(t,O2,pars)
+   {
+   with (as.list(pars),{
+
+     Flux <- -D*diff(c(upO2,O2,O2[n]))/dX
+     dO2  <- -diff(Flux)/dx-cons*O2/(O2+ks)
+
+     return(list(dO2,UpFlux = Flux[1],LowFlux = Flux[n+1]))
+     })
+   }
+
+  ox <- steady.band(y=runif(n),func=derivs,parms=pars,nspec=1,
+                    positive=TRUE,rtol=1e-8,atol=1e-10)
+
+  list(data.frame(x=X,O2=ox$y),
+       UpFlux=ox$UpFlux)
+ }
```

The function used in the fitting algorithm returns an instance of type `modCost`. This is created by calling function `modCost` twice. First with the modeled oxygen profile, then with the modeled flux.

```
> Objective <- function (P)
+ {
+  Pars <- pars
+  Pars[names(P)]<-P
+  modO2 <- O2fun2(Pars)
+
+  # Model cost: first the oxygen profile
+  Cost  <- modCost(obs=O2depth,model=modO2[[1]],x="x",y="y")
```

```
+
+  # then the flux
+  modFl <- c(UpFlux=mod02$UpFlux)
+  Cost  <- modCost(obs=O2flux,model=modFl,x=NULL,cost=Cost)
+
+  return(Cost)
+ }
```

We first estimate the identifiability of the parameters, given the data:

```
> print(system.time(
+ sF<-sensFun(Objective,parms=pars)
+ ))

   user  system elapsed
   0.13    0.00    0.13

> summary(sF)

     value scale   L1   L2  Mean      Min  Max  N
upO2   360   360 4.25 0.97  4.25   0.5069 13.3 36
cons    80    80 3.68 0.99 -3.65 -15.3722  0.5 36
ks       1     1 0.40 0.14  0.40  -0.0069  3.1 36
D        1     1 3.68 0.99  3.68   0.0342 15.4 36

> collin(sF)

   upO2 cons ks D N collinearity
1     1    1  0 0 2          8.6
2     1    0  1 0 2          3.1
3     1    0  0 1 2          8.7
4     0    1  1 0 2          4.2
5     0    1  0 1 2         50.6
6     0    0  1 1 2          4.2
7     1    1  1 0 3         14.2
8     1    1  0 1 3         50.8
9     1    0  1 1 3         14.7
10    0    1  1 1 3         50.6
11    1    1  1 1 4         51.0
```

The collinearity of the full set is too high, but as the oxygen diffusion coefficient is well known, it is left out of the fitting. The combination of the three remaining parameters has a low enough collinearity to enable automatic fitting. The parameters are constrained to be >0

```
> collin(sF,parset=c("upO2","cons","ks"))

  upO2 cons ks D N collinearity
1    1    1  1 0 3           14
```

```
> print(system.time(
+ Fit<-modFit(p=c(upO2=360,cons=80,ks=1),
+                   f=Objective,lower=c(0,0,0))
+                   ))

   user  system elapsed
   0.80    0.00    0.79

> (SFit<-summary(Fit))

Parameters:
     Estimate Std. Error t value Pr(>|t|)
upO2  292.937      2.104 139.242   <2e-16 ***
cons   49.686      2.367  20.991   <2e-16 ***
ks      1.297      1.363   0.951    0.348
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.401 on 33 degrees of freedom

Parameter correlation:
       upO2   cons     ks
upO2 1.0000 0.5791 0.2976
cons 0.5791 1.0000 0.9012
ks   0.2976 0.9012 1.0000
```

We next plot the residuals

```
> plot(Objective(Fit$par),xlab="depth",ylab="",main="residual",legpos="top")
```

and show the best-fit model

```
> Pars <- pars
> Pars[names(Fit$par)]<- Fit$par
> modO2 <- O2fun(Pars)

> plot(O2depth$y,O2depth$x,ylim=rev(range(O2depth$x)),pch=18,
+      main="Oxygen-fitted", xlab="mmol/m3",ylab="depth, cm")
> lines(modO2$O2,modO2$X)
```

5. Running a Markov Chain Monte Carlo

We use the parameter covariances of previous fit to update parameters, while the mean squared residual of the fit is use as prior fo the model variance.

```
> Covar   <- SFit$cov.scaled * 2.4^2/3
> s2prior <- SFit$modVariance
```

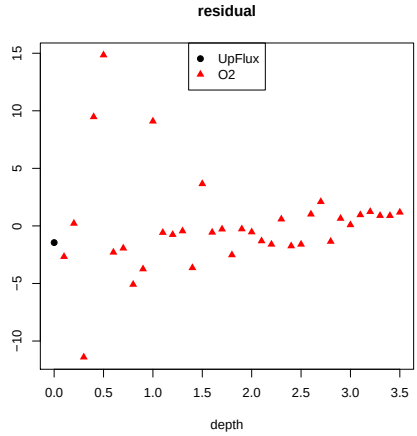

Figure 5: residuals - see text for R-code

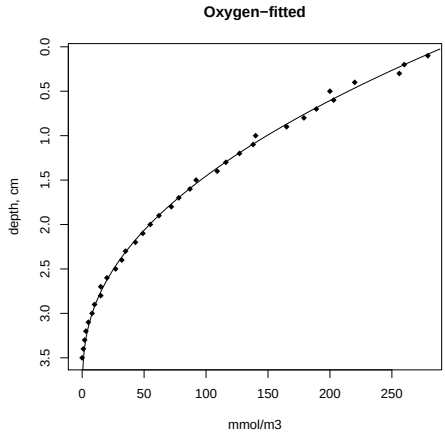

Figure 6: Best fit model - see text for R-code

We run an adaptive metropolis, making sure that ks does not become negative...

```
> print(system.time(
+ MCMC <- modMCMC(f=Objective,p=Fit$par,jump=Covar,niter=1000,ntrydr=2,
+                  var0=s2prior,wvar0=1,updatecov=100,lower=c(NA,NA,0))
+ ))

number of accepted runs: 692 out of 1000 (69.2%)
   user  system elapsed
  30.20    0.00   30.35

> MCMC$count

     dr_steps     Alfasteps  num_accepted num_covupdate
          647          1941           692             9
```

Plotting the results is similar to previous cases.

```
> plot(MCMC,Full=TRUE)
```



```
> hist(MCMC,Full=TRUE)
```



```
> pairs(MCMC,Full=TRUE)
```


or summaries can be created:

```
> summary(MCMC)

           up02      cons           ks          sig
mean 293.954101 52.225347  3.185296500   174.565911
sd     3.434314  3.962297  2.833760823  1066.194652
min  284.024349 43.264511  0.007592786     2.019988
max  311.145216 73.872993 17.221154659 29768.849736
q025 291.847724 49.656103  1.269370688    11.734273
q050 293.586568 51.324609  2.384834973    27.886227
q075 296.040493 53.390916  4.176343626    95.190492

> cor(MCMC$pars)

          up02      cons        ks
up02 1.0000000 0.5022937 0.2107447
cons 0.5022937 1.0000000 0.8989099
ks   0.2107447 0.8989099 1.0000000
```

Note: we pass to sensRange the full parameter vector (`parms`) and the parameters sampled during the MCMC (`parInput`).

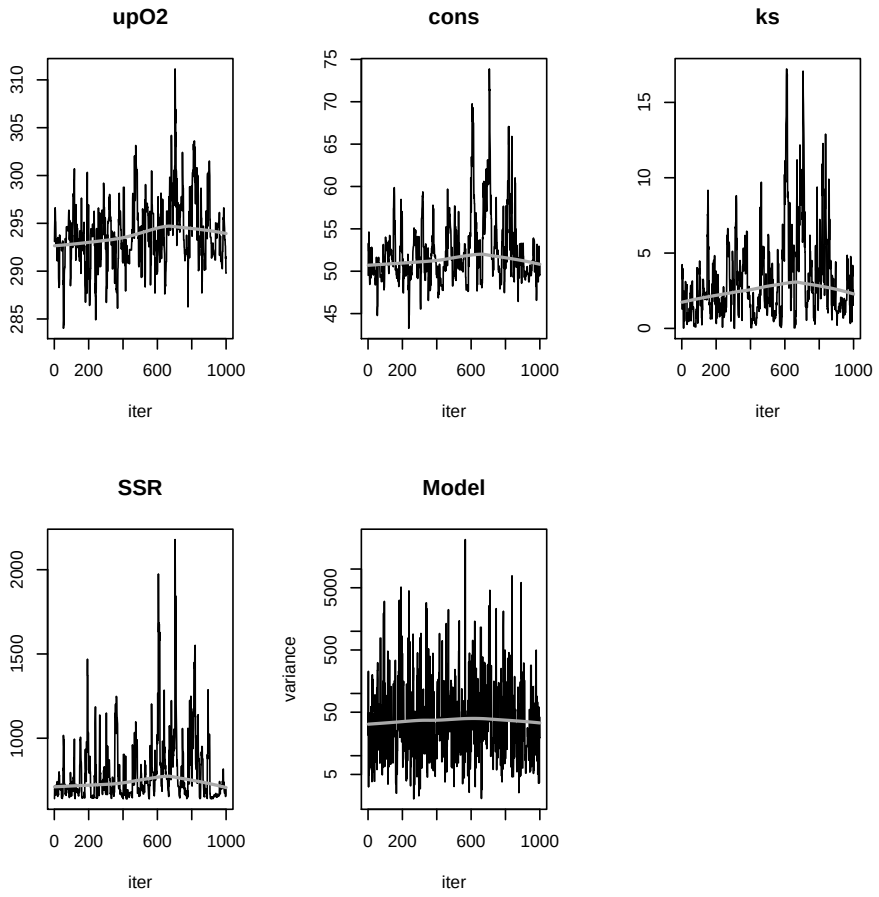

Figure 7: MCMC plot results - see text for R-code

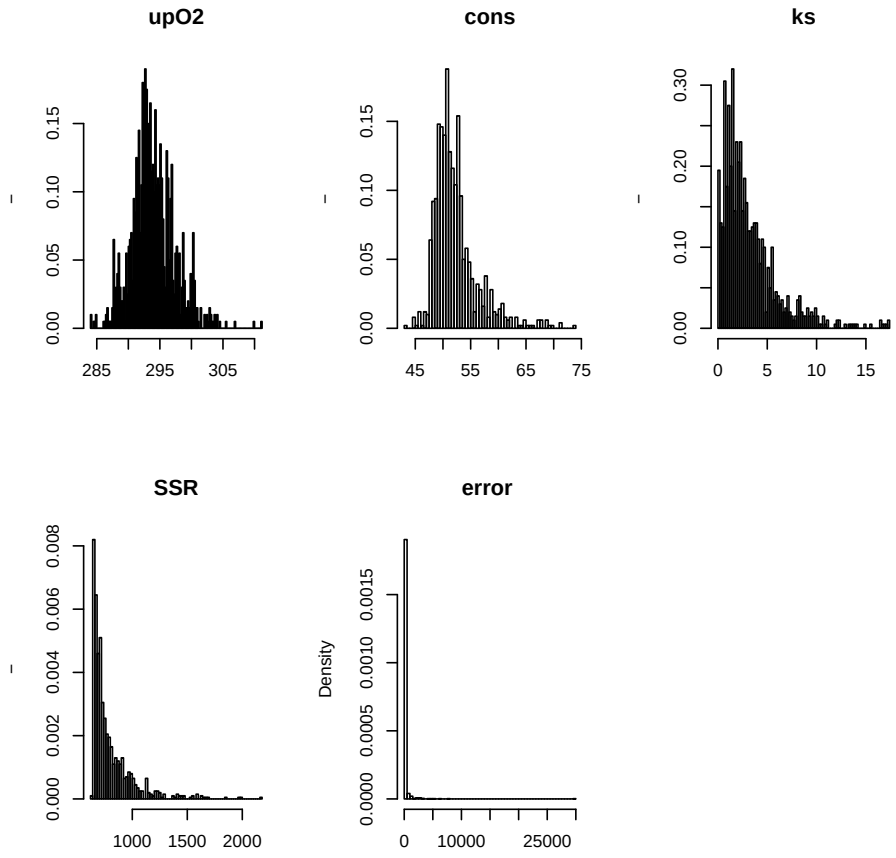

Figure 8: MCMC histogram results - see text for R-code

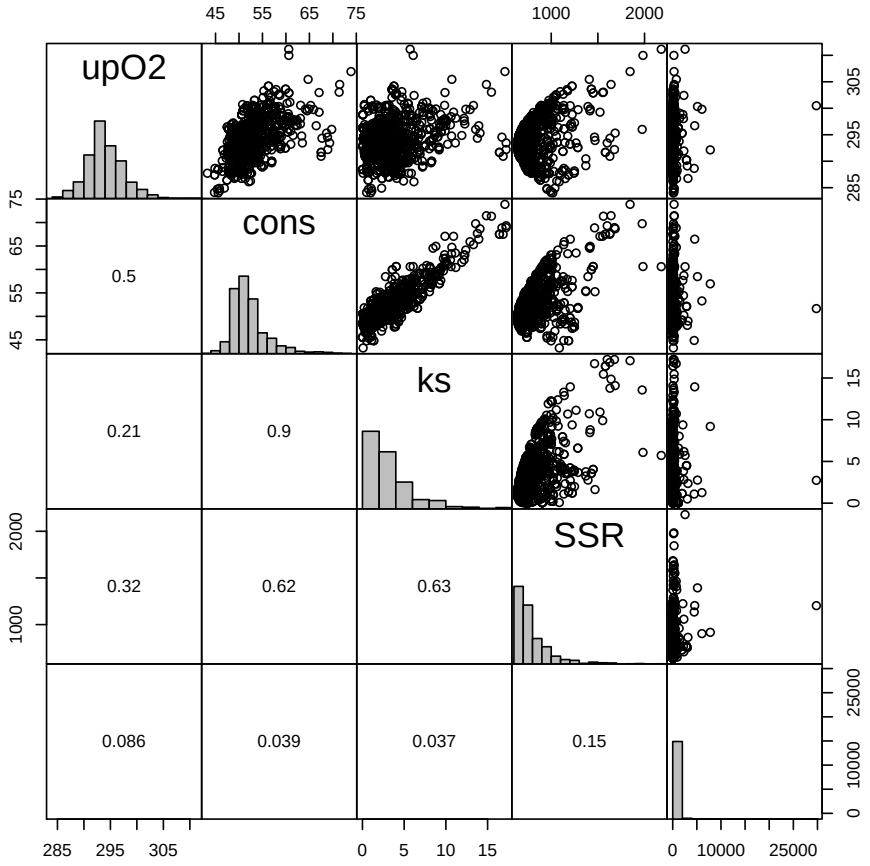

Figure 9: MCMC pairs plot - see text for R-code

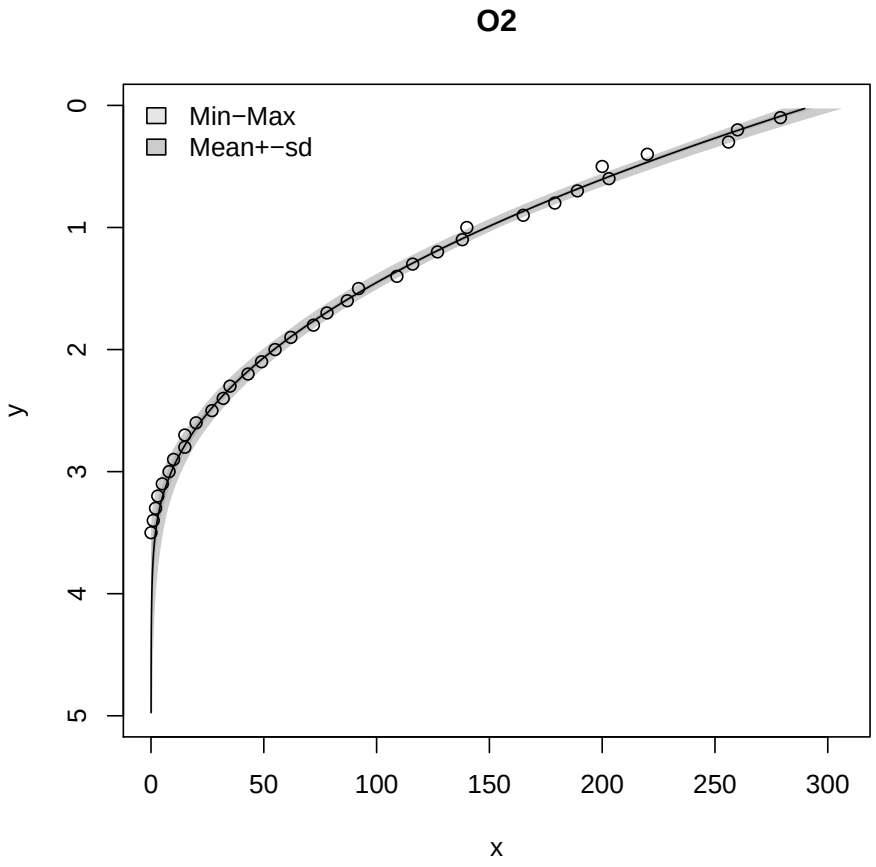

Figure 10: MCMC range plot - see text for R-code

```
> plot(summary(sensRange(parms=pars,parInput=MCMC$par,f=O2fun,num=500)),
+   xyswap=TRUE)
> points(O2depth$y,O2depth$x)
```

6. finally

This vignette is a Sweave (Leisch 2002) translation of part of the **FME** examples.

References

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Affiliation:

Karline Soetaert
Centre for Estuarine and Marine Ecology (CEME)
Netherlands Institute of Ecology (NIOO)
4401 NT Yerseke, Netherlands
E-mail: k.soetaert@nioo.knaw.nl
URL: http://www.nioo.knaw.nl/users/ksoetaert